#Symptom\_To\_Disease\_Classification\_And\_Treatment\_Recommendation\_Pipeline # ★ Install Required Libraries (if not already installed) !pip install --quiet transformers datasets scikit-learn # ★ Check GPU availability import torch device = "cuda" if torch.cuda.is\_available() else "cpu" print("✓ Using device:", device) → ✓ Using device: cuda #Dataset\_Load\_CSV # Load Symptom2Disease CSV into a pandas DataFrame import pandas as pd data\_path = "/content/Symptom2Disease.csv" df = pd.read\_csv(data\_path) print(df.shape) print(df.head(2)) (1200, 3) $\rightarrow$ Unnamed: 0 label text 0 0 Psoriasis I have been experiencing a skin rash on my arm... 1 Psoriasis My skin has been peeling, especially on my kne... Double-click (or enter) to edit from sklearn.preprocessing import LabelEncoder from sklearn.model\_selection import train\_test\_split # Encode disease labels as integers le = LabelEncoder() df['label\_enc'] = le.fit\_transform(df['label']) # Split into train/validation (80%/20%) train\_df, val\_df = train\_test\_split(df, test\_size=0.2, stratify=df['label\_enc'], random\_state=42) print(f"Train size: {len(train\_df)}, Validation size: {len(val\_df)}") → Train size: 960, Validation size: 240 from datasets import Dataset # Create HF Datasets (with 'text' and 'label' fields) train\_dataset = Dataset.from\_pandas(train\_df[['text','label\_enc']].rename(columns={'label\_enc':'label'})) val\_dataset = Dataset.from\_pandas(val\_df[['text','label\_enc']].rename(columns={'label\_enc':'label'})) print(train\_dataset[1]) 🚌 {'text': "I've been feeling awful, with a lot of congestion and a runny nose. I've been coughing a lot and having a lot of c from transformers import AutoTokenizer, AutoModelForSequenceClassification # ☑ Load BioBERT model and tokenizer model name = "dmis-lab/biobert-v1.1" tokenizer = AutoTokenizer.from\_pretrained(model\_name) model = AutoModelForSequenceClassification.from\_pretrained(model\_name, num\_labels=len(le.classes\_)).to(device) # ☑ Tokenize function def tokenize(batch): return tokenizer(batch["text"], padding="max\_length", truncation=True, max\_length=128) # ✓ Tokenize datasets train\_dataset = train\_dataset.map(tokenize, batched=True) val\_dataset = val\_dataset.map(tokenize, batched=True) # ☑ Remove raw text (not needed anymore) train\_dataset = train\_dataset.remove\_columns(["text"])

```
May 27th CLIN-LLM based Symptoms to disease classification and treatment recommendation.ipynb - Colab
val_dataset = val_dataset.remove_columns(["text"])
# ☑ Format datasets for PyTorch
train_dataset.set_format("torch")
val_dataset.set_format("torch")
The secret `HF_TOKEN` does not exist in your Colab secrets.
     To authenticate with the Hugging Face Hub, create a token in your settings tab (https://huggingface.co/settings/tokens), set
     You will be able to reuse this secret in all of your notebooks.
     Please note that authentication is recommended but still optional to access public models or datasets.
       warnings.warn(
     tokenizer_config.json: 100%
                                                               49.0/49.0 [00:00<00:00, 5.30kB/s]
     config.json: 100%
                                                        462/462 [00:00<00:00, 53.1kB/s]
     vocab.txt: 100%
                                                      213k/213k [00:00<00:00, 1.31MB/s]
     special_tokens_map.json: 100%
                                                                  112/112 [00:00<00:00, 10.8kB/s]
     pytorch_model.bin: 100%
                                                             433M/433M [00:01<00:00, 335MB/s]
     Some weights of BertForSequenceClassification were not initialized from the model checkpoint at dmis-lab/biobert-v1.1 and ar
     You should probably TRAIN this model on a down-stream task to be able to use it for predictions and inference.
                                                   960/960 [00:00<00:00, 4827.58 examples/s]
     Map: 100%
     Map: 100%
                                                   240/240 [00:00<00:00, 2328.88 examples/s]
                                                             433M/433M [00:01<00:00, 328MB/s]
     model.safetensors: 100%
```

```
import torch
from torch.utils.data import DataLoader
from torch.nn import CrossEntropyLoss
from torch.optim import AdamW # <- FIXED</pre>
from transformers import get_scheduler
from tqdm.auto import tqdm
# ✓ Prepare Dataloaders
train_loader = DataLoader(train_dataset, batch_size=16, shuffle=True)
val_loader = DataLoader(val_dataset, batch_size=32)
# ☑ Move model to GPU if available
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
model.to(device)
# ☑ Optimizer and Scheduler
optimizer = AdamW(model.parameters(), lr=2e-5, weight_decay=0.01)
num training steps = len(train loader) * 3 # 3 epochs
lr_scheduler = get_scheduler("linear", optimizer=optimizer,
                             num_warmup_steps=0,
                             num_training_steps=num_training_steps)
# ☑ Loss function
loss_fn = CrossEntropyLoss()
from datasets import Dataset
# 🔁 Recreate datasets with correct label field
train_dataset = Dataset.from_pandas(train_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}))
val_dataset = Dataset.from_pandas(val_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}))
print(train_dataset.column_names)
# Should output only: ['labels', 'input_ids', 'attention_mask']
['text', 'labels', '__index_level_0__']
from datasets import Dataset
# Make a copy of the DataFrames and drop index before converting
train_df_clean = train_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)
val_df_clean = val_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)
```

```
# ☑ Convert to Hugging Face Dataset
train_dataset = Dataset.from_pandas(train_df_clean)
val_dataset = Dataset.from_pandas(val_df_clean)
def tokenize(batch):
    return tokenizer(batch["text"], padding="max_length", truncation=True, max_length=128)
train_dataset = train_dataset.map(tokenize, batched=True)
val_dataset = val_dataset.map(tokenize, batched=True)
train_dataset = train_dataset.remove_columns(["text"])
val_dataset = val_dataset.remove_columns(["text"])
train_dataset.set_format("torch")
val_dataset.set_format("torch")
₹
    Map: 100%
                                                   960/960 [00:00<00:00, 3567.90 examples/s]
     Map: 100%
                                                   240/240 [00:00<00:00, 2378.39 examples/s]
#☑ Updated Fix for Step 9 — Format datasets properly
# ☑ Specify columns explicitly to prevent internal formatting issues
train_dataset.set_format(type='torch', columns=['input_ids', 'attention_mask', 'labels'])
val_dataset.set_format(type='torch', columns=['input_ids', 'attention_mask', 'labels'])
# ♥ Tokenize using tokenizer manually to avoid `datasets.map()` issues
def tokenize_texts(texts):
    return tokenizer(texts.tolist(), padding="max_length", truncation=True, max_length=128, return_tensors="pt")
# Tokenize training data
train_encodings = tokenize_texts(train_df_clean["text"])
train_labels = torch.tensor(train_df_clean["labels"].values)
# Tokenize validation data
val_encodings = tokenize_texts(val_df_clean["text"])
val_labels = torch.tensor(val_df_clean["labels"].values)
# ☑ Wrap into torch Dataset objects
class TorchDataset(torch.utils.data.Dataset):
    def __init__(self, encodings, labels):
        self.encodings = encodings
        self.labels = labels
    def __len__(self):
        return len(self.labels)
    def __getitem__(self, idx):
        return {
            'input ids': self.encodings['input ids'][idx],
            'attention_mask': self.encodings['attention_mask'][idx],
            'labels': self.labels[idx]
        }
train_dataset = TorchDataset(train_encodings, train_labels)
val_dataset = TorchDataset(val_encodings, val_labels)
from torch.optim import AdamW
from transformers import get scheduler
from torch.utils.data import DataLoader
from torch.nn import CrossEntropyLoss
from tqdm.auto import tqdm
train_loader = DataLoader(train_dataset, batch_size=16, shuffle=True)
val_loader = DataLoader(val_dataset, batch_size=32)
# Model to GPU
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
model.to(device)
```

```
# Optimizer and scheduler
optimizer = AdamW(model.parameters(), lr=2e-5, weight_decay=0.01)
num_training_steps = len(train_loader) * 3
lr_scheduler = get_scheduler("linear", optimizer=optimizer,
                             num_warmup_steps=0, num_training_steps=num_training_steps)
# Training Loop
EPOCHS = 20
for epoch in range(EPOCHS):
   print(f"\n Epoch {epoch+1}/{EPOCHS}")
   model.train()
   total_loss = 0
    for batch in tqdm(train_loader, desc="Training"):
        batch = {k: v.to(device) for k, v in batch.items()} # ☑ No rename needed now
        outputs = model(**batch)
        loss = outputs.loss
        loss.backward()
       optimizer.step()
        lr_scheduler.step()
        optimizer.zero_grad()
        total_loss += loss.item()
    avg_loss = total_loss / len(train_loader)
   print(f" ✓ Average Loss: {avg_loss:.4f}")
```



Epoch 1/20

Training: 100% 60/60 [00:18<00:00, 3.24it/s]

☑ Average Loss: 0.9578

Epoch 2/20

Training: 100% 60/60 [00:18<00:00, 3.21it/s]

✓ Average Loss: 0.6456

Epoch 3/20

Training: 100% 60/60 [00:18<00:00, 3.16it/s]

☑ Average Loss: 0.5129

Epoch 4/20

Training: 100% 60/60 [00:18<00:00, 3.16it/s]

✓ Average Loss: 0.4875

Epoch 5/20

Training: 100% 60/60 [00:19<00:00, 3.12it/s]

✓ Average Loss: 0.4854

Epoch 6/20

Training: 100% 60/60 [00:19<00:00, 3.11it/s]

☑ Average Loss: 0.4857

Epoch 7/20

Training: 100% 60/60 [00:19<00:00, 3.10it/s]

✓ Average Loss: 0.4871

Epoch 8/20

Training: 100% 60/60 [00:19<00:00, 3.09it/s]

✓ Average Loss: 0.4831

Epoch 9/20

Training: 100% 60/60 [00:19<00:00, 3.10it/s]

☑ Average Loss: 0.4828

Epoch 10/20

Training: 100% 60/60 [00:19<00:00, 3.06it/s]

☑ Average Loss: 0.4833

Epoch 11/20

Training: 100% 60/60 [00:19<00:00, 3.07it/s]

✓ Average Loss: 0.4862

Epoch 12/20

Training: 100% 60/60 [00:19<00:00, 3.06it/s]

☑ Average Loss: 0.4863

Epoch 13/20

Training: 100% 60/60 [00:19<00:00, 3.05it/s]

☑ Average Loss: 0.4847

Epoch 14/20

Training: 100% 60/60 [00:19<00:00, 3.05it/s]

☑ Average Loss: 0.4888

Epoch 15/20

Training: 100% 60/60 [00:19<00:00, 3.04it/s]

✓ Average Loss: 0.4902

Epoch 16/20

Training: 100% 60/60 [00:19<00:00, 3.04it/s]

☑ Average Loss: 0.4864

Epoch 17/20

Training: 100% 60/60 [00:19<00:00, 3.05it/s]

✓ Average Loss: 0.4846

Epoch 18/20

```
60/60 [00:19<00:00, 3.04it/s]
     Training: 100%
     Average Loss: 0.4871
     Epoch 19/20
     Training: 100%
                                                       60/60 [00:19<00:00, 3.05it/s]
     Average Loss: 0.4865
     Epoch 20/20
     Training: 100%
                                                       60/60 [00:19<00:00, 3.04it/s]

✓ Average Loss: 0.4864

from sklearn.metrics import classification_report
def evaluate_model(model, dataloader):
    model.eval()
    all_preds = []
    all_labels = []
    with torch.no_grad():
        for batch in dataloader:
            batch = {k: v.to(device) for k, v in batch.items()}
            outputs = model(**batch)
            preds = torch.argmax(outputs.logits, dim=1)
            all_preds.extend(preds.cpu().numpy())
            all_labels.extend(batch["labels"].cpu().numpy())
    print(classification_report(all_labels, all_preds, target_names=le.classes_))
# 🔍 Evaluate
evaluate_model(model, val_loader)
precision
                                                     recall f1-score
                                                                         support
                                 Acne
                                             0.91
                                                       1.00
                                                                  0.95
                                                                               10
                            Arthritis
                                                                  1.00
                                             1.00
                                                       1.00
                                                                              10
                    Bronchial Asthma
                                             1.00
                                                       0.80
                                                                  0.89
                                                                              10
                Cervical spondylosis
                                             0.91
                                                       1.00
                                                                  0.95
                                                                              10
                          Chicken pox
                                                                  0.78
                                             0.88
                                                       0.70
                                                                               10
                          Common Cold
                                             0.83
                                                       1.00
                                                                  0.91
                                                                              10
                               Dengue
                                             0.91
                                                       1.00
                                                                  0.95
                                                                               10
               Dimorphic Hemorrhoids
                                             1.00
                                                       1.00
                                                                  1.00
                                                                               10
                     Fungal infection
                                                                  1.00
                                             1.00
                                                       1.00
                                                                              10
                         Hypertension
                                             1.00
                                                       1.00
                                                                  1.00
                                                                               10
                                             0.90
                                                       0.90
                                                                  0.90
                                                                               10
                             Impetigo
                             Jaundice
                                             1.00
                                                       1.00
                                                                  1.00
                                                                              10
                              Malaria
                                             1.00
                                                       1.00
                                                                  1.00
                                                                              10
                             Migraine
                                             1.00
                                                       0.90
                                                                  0.95
                                                                               10
                            Pneumonia
                                             1.00
                                                       1.00
                                                                  1.00
                                                                              10
                            Psoriasis
                                             1.00
                                                       0.90
                                                                  0.95
                                                                               10
                              Typhoid
                                             0.83
                                                       1.00
                                                                  0.91
                                                                              10
                       Varicose Veins
                                             1.00
                                                       1.00
                                                                  1.00
                                                                              10
                              allergy
                                             0.91
                                                       1.00
                                                                  0.95
                                                                              10
                             diabetes
                                             1.00
                                                       0.90
                                                                  0.95
                                                                              10
                        drug reaction
                                                       0.80
                                                                  0.89
                                             1.00
                                                                              10
     gastroesophageal reflux disease
                                             0.90
                                                       0.90
                                                                  0.90
                                                                              10
                                                                  0.95
                peptic ulcer disease
                                             0.91
                                                       1.00
                                                                              10
             urinary tract infection
                                             1.00
                                                       1.00
                                                                  1.00
                                                                              10
                                                                  0.95
                                                                             240
                             accuracy
                                                       0.95
                            macro avg
                                             0.95
                                                                  0.95
                                                                             240
                         weighted avg
                                             0.95
                                                       0.95
                                                                  0.95
                                                                             240
#Again 15 Apochs Cross check.
from torch.optim import AdamW
from transformers import get_scheduler
from torch.utils.data import DataLoader
from torch.nn import CrossEntropyLoss
from tqdm.auto import tqdm
# Loaders
train_loader = DataLoader(train_dataset, batch_size=16, shuffle=True)
val_loader = DataLoader(val_dataset, batch_size=32)
```

```
# Model to GPU
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
model.to(device)
# Optimizer and scheduler
optimizer = AdamW(model.parameters(), lr=2e-5, weight_decay=0.01)
num_training_steps = len(train_loader) * 3
lr_scheduler = get_scheduler("linear", optimizer=optimizer,
                             num_warmup_steps=0, num_training_steps=num_training_steps)
# Training Loop
EPOCHS = 15
for epoch in range(EPOCHS):
    print(f"\n Epoch {epoch+1}/{EPOCHS}")
    model.train()
   total_loss = 0
    for batch in tqdm(train_loader, desc="Training"):
        batch = {k: v.to(device) for k, v in batch.items()} # ✓ No rename needed now
        outputs = model(**batch)
        loss = outputs.loss
        loss.backward()
        optimizer.step()
        lr_scheduler.step()
        optimizer.zero_grad()
        total_loss += loss.item()
    avg_loss_= total_loss / len(train_loader)
    print(f"

Average Loss: {avg_loss:.4f}")
```

```
6/13/25, 12:17 PM
     ₹
          Epoch 1/15
          Training: 100%
                                                                60/60 [00:18<00:00, 3.27it/s]

✓ Average Loss: 0.4163

         Epoch 2/15
          Training: 100%
                                                                60/60 [00:18<00:00, 3.23it/s]
         ✓ Average Loss: 0.2518
         Epoch 3/15
          Training: 100%
                                                                60/60 [00:18<00:00, 3.21it/s]
         ☑ Average Loss: 0.1978
         Epoch 4/15
          Training: 100%
                                                                60/60 [00:18<00:00, 3.17it/s]
         ☑ Average Loss: 0.1880
         Epoch 5/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.11it/s]
         ✓ Average Loss: 0.1879
         Epoch 6/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.14it/s]
         ☑ Average Loss: 0.1901
          Epoch 7/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.11it/s]
         ☑ Average Loss: 0.1880
         Epoch 8/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.10it/s]
         ☑ Average Loss: 0.1893
         Epoch 9/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.09it/s]
         ☑ Average Loss: 0.1857
         Epoch 10/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.08it/s]
         ☑ Average Loss: 0.1880
         Epoch 11/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.09it/s]
         ✓ Average Loss: 0.1879
         Epoch 12/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.05it/s]

✓ Average Loss: 0.1870

         Epoch 13/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.05it/s]
         ☑ Average Loss: 0.1871
         Epoch 14/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.06it/s]
         ☑ Average Loss: 0.1910
         Epoch 15/15
          Training: 100%
                                                                60/60 [00:19<00:00, 3.04it/s]
         ☑ Average Loss: 0.1883
```

```
from sklearn.metrics import classification_report
def evaluate_model(model, dataloader):
   model.eval()
   all_preds = []
   all_labels = []
```

```
with torch.no_grad():
        for batch in dataloader:
            batch = {k: v.to(device) for k, v in batch.items()}
            outputs = model(**batch)
            preds = torch.argmax(outputs.logits, dim=1)
            all_preds.extend(preds.cpu().numpy())
            all_labels.extend(batch["labels"].cpu().numpy())
    print(classification_report(all_labels, all_preds, target_names=le.classes_))
# 🔍 Evaluate
evaluate_model(model, val_loader)
₹
                                       precision
                                                     recall f1-score
                                                                         support
                                            0.91
                                                       1.00
                                                                 0.95
                                                                              10
                                 Acne
                           Arthritis
                                            0.91
                                                       1.00
                                                                 0.95
                                                                              10
                    Bronchial Asthma
                                            1.00
                                                       0.90
                                                                 0.95
                                                                              10
                Cervical spondylosis
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                            1.00
                                                                 0.89
                          Chicken pox
                                                       0.80
                                                                              10
                         Common Cold
                                            0.83
                                                       1.00
                                                                 0.91
                                                                              10
                               Dengue
                                            0.83
                                                       1.00
                                                                 0.91
                                                                              10
               Dimorphic Hemorrhoids
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                                                              10
                    Fungal infection
                                            1.00
                                                       1.00
                                                                 1.00
                        Hypertension
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                                                 0.95
                             Impetigo
                                            1.00
                                                       0.90
                                                                              10
                             Jaundice
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                             Malaria
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                            1.00
                                                       0.90
                                                                 0.95
                                                                              10
                             Migraine
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                           Pneumonia
                                            1.00
                                                       1.00
                                                                 1.00
                           Psoriasis
                                                                              10
                              Typhoid
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                       Varicose Veins
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                            0.91
                                                       1.00
                                                                 0.95
                                                                              10
                              allergy
                             diabetes
                                            1.00
                                                       0.90
                                                                 0.95
                                                                              10
                                                       0.90
                                                                 0.95
                       drug reaction
                                            1.00
                                                                              10
     gastroesophageal reflux disease
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                                                 1.00
                peptic ulcer disease
                                            1.00
                                                       1.00
                                                                              10
             urinary tract infection
                                            1.00
                                                       1.00
                                                                 1.00
                                                                              10
                                                                 0.97
                                                                             240
                             accuracy
                                            0.97
                                                       0.97
                           macro avg
                                                                 0.97
                                                                             240
                        weighted avg
                                            0.97
                                                       0.97
                                                                 0.97
                                                                             240
```

# Again, train at 10 Epochs. Cross-check.

```
Start coding or generate with AI.
from torch.optim import AdamW
from transformers import get scheduler
from torch.utils.data import DataLoader
from torch.nn import CrossEntropyLoss
from tqdm.auto import tqdm
# Loaders
train_loader = DataLoader(train_dataset, batch_size=16, shuffle=True)
val_loader = DataLoader(val_dataset, batch_size=32)
# Model to GPU
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
model.to(device)
# Optimizer and scheduler
optimizer = AdamW(model.parameters(), lr=2e-5, weight_decay=0.01)
num training steps = len(train loader) * 3
lr_scheduler = get_scheduler("linear", optimizer=optimizer,
                             num_warmup_steps=0, num_training_steps=num_training_steps)
# Training Loop
EPOCHS = 10
for epoch in range(EPOCHS):
    print(f"\n Epoch {epoch+1}/{EPOCHS}")
    model.train()
    total_loss = 0
```

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```

```
for batch in tqdm(train_loader, desc="Training"):
    batch = {k: v.to(device) for k, v in batch.items()} # ✓ No rename needed now
    outputs = model(**batch)
    loss = outputs.loss
    loss.backward()
    optimizer.step()
    lr_scheduler.step()
    optimizer.zero_grad()
    total_loss += loss.item()
avg_loss_= total_loss / len(train_loader)
print(f"
✓ Average Loss: {avg_loss:.4f}")
 Epoch 1/10
Training: 100%
                                                 60/60 [00:18<00:00, 3.29it/s]
☑ Average Loss: 0.1565
Epoch 2/10
```

Training: 100% 60/60 [00:18<00:00, 3.23it/s]

☑ Average Loss: 0.0895

Epoch 3/10

Training: 100% 60/60 [00:18<00:00, 3.20it/s]

✓ Average Loss: 0.0704

Epoch 4/10

Training: 100% 60/60 [00:18<00:00, 3.17it/s]

✓ Average Loss: 0.0668

Epoch 5/10

Training: 100% 60/60 [00:19<00:00, 3.15it/s]

☑ Average Loss: 0.0665

Epoch 6/10

Training: 100% 60/60 [00:19<00:00, 3.15it/s]

✓ Average Loss: 0.0668

Epoch 7/10

Training: 100% 60/60 [00:19<00:00, 3.11it/s]

☑ Average Loss: 0.0668

Epoch 8/10

Training: 100% 60/60 [00:19<00:00, 3.10it/s]

☑ Average Loss: 0.0675

Epoch 9/10

Training: 100% 60/60 [00:19<00:00, 3.08it/s]

☑ Average Loss: 0.0670

Epoch 10/10

Training: 100% 60/60 [00:19<00:00, 3.09it/s]

batch = {k: v.to(device) for k, v in batch.items()}

preds = torch.argmax(outputs.logits, dim=1)

☑ Average Loss: 0.0675

#### Evaluate the Fine-Tuned BioBERT Model

```
from sklearn.metrics import classification_report
def evaluate_model(model, dataloader):
   model.eval()
    all_preds = []
    all_labels = []
    with torch.no_grad():
        for batch in dataloader:
```

outputs = model(\*\*batch)

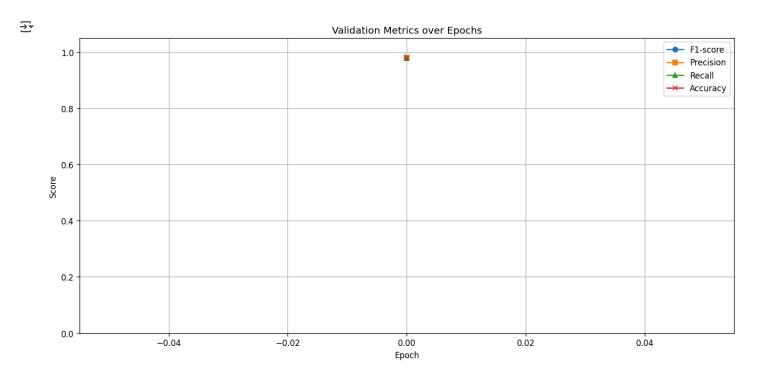
```
6/13/25, 12:17 PM
                                       May 27th CLIN-LLM based Symptoms to disease classification and treatment recommendation.ipynb - Colab
                 all_preds.extend(preds.cpu().numpy())
                 all_labels.extend(batch["labels"].cpu().numpy())
        print(classification_report(all_labels, all_preds, target_names=le.classes_))
    # 🔍 Evaluate
    evaluate_model(model, val_loader)
    \overline{2}
```

<b>:</b>	precision	recall	f1-score	support
Acne	0.91	1.00	0.95	10
Arthritis	0.91	1.00	0.95	10
Bronchial Asthma	1.00	0.90	0.95	10
Cervical spondylosis	1.00	1.00	1.00	10
Chicken pox	0.90	0.90	0.90	10
Common Cold	0.91	1.00	0.95	10
Dengue	0.90	0.90	0.90	10
Dimorphic Hemorrhoids	1.00	1.00	1.00	10
Fungal infection	1.00	1.00	1.00	10
Hypertension	1.00	1.00	1.00	10
Impetigo	1.00	0.90	0.95	10
Jaundice	1.00	1.00	1.00	10
Malaria	1.00	1.00	1.00	10
Migraine	1.00	0.90	0.95	10
Pneumonia	1.00	1.00	1.00	10
Psoriasis	1.00	1.00	1.00	10
Typhoid	1.00	1.00	1.00	10
Varicose Veins	1.00	1.00	1.00	10
allergy	1.00	1.00	1.00	10
diabetes	1.00	1.00	1.00	10
drug reaction	1.00	1.00	1.00	10
gastroesophageal reflux disease	1.00	1.00	1.00	10
peptic ulcer disease	1.00	1.00	1.00	10
urinary tract infection	1.00	1.00	1.00	10
accuracy			0.98	240
macro avg	0.98	0.98	0.98	240
weighted avg	0.98	0.98	0.98	240

#Figures need.

```
from sklearn.metrics import f1_score, precision_score, recall_score, accuracy_score
# Initialize metric trackers
val_losses = []
val_f1_scores = []
val_precision_scores = []
val_recall_scores = []
val_accuracy_scores = []
# Inside the epoch loop, after training:
model.eval()
total_val_loss = 0
preds, targets = [], []
with torch.no_grad():
    for batch in val_loader:
        batch = {k: v.to(device) for k, v in batch.items()}
        outputs = model(**batch)
        loss = outputs.loss
        total_val_loss += loss.item()
        logits = outputs.logits.argmax(dim=1).cpu().numpy()
        labels = batch["labels"].cpu().numpy()
        preds.extend(logits)
        targets.extend(labels)
# Compute metrics
avg_val_loss = total_val_loss / len(val_loader)
val_losses.append(avg_val_loss)
val_f1 = f1_score(targets, preds, average="weighted")
val_precision = precision_score(targets, preds, average="weighted")
val_recall = recall_score(targets, preds, average="weighted")
val_acc = accuracy_score(targets, preds)
val_f1_scores.append(val_f1)
```

```
val_precision_scores.append(val_precision)
val_recall_scores.append(val_recall)
val_accuracy_scores.append(val_acc)
print(f" Val Loss: {avg_val_loss:.4f} | F1: {val_f1:.4f} | Precision: {val_precision:.4f} | Recall: {val_recall:.4f} | Accurac
→ I Val Loss: 0.1260 | F1: 0.9791 | Precision: 0.9803 | Recall: 0.9792 | Accuracy: 0.9792
import matplotlib.pyplot as plt
plt.figure(figsize=(12, 6), dpi=120)
plt.plot(val_f1_scores, label='F1-score', marker='o')
plt.plot(val_precision_scores, label='Precision', marker='s')
plt.plot(val_recall_scores, label='Recall', marker='^')
plt.plot(val_accuracy_scores, label='Accuracy', marker='x')
plt.title("Validation Metrics over Epochs")
plt.xlabel("Epoch")
plt.ylabel("Score")
plt.ylim(0, 1.05)
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.show()
```



```
6/13/25, 12:17 PM
                                    May 27th CLIN-LLM based Symptoms to disease classification and treatment recommendation.ipynb - Colab
    train losses = []
    val_losses = []
    val_f1_scores = []
    val_precision_scores = []
    val_recall_scores = []
    val_accuracy_scores = []
    EPOCHS = 10 # your final optimal setting
    for epoch in range(EPOCHS):
        print(f"\n Epoch {epoch+1}/{EPOCHS}")
        model.train()
        total_train_loss = 0
        for batch in tqdm(train_loader, desc="Training"):
            batch = {k: v.to(device) for k, v in batch.items()}
            outputs = model(**batch)
            loss = outputs.loss
            loss.backward()
            optimizer.step()
            lr_scheduler.step()
            optimizer.zero_grad()
            total_train_loss += loss.item()
        avg_train_loss = total_train_loss / len(train_loader)
        train_losses.append(avg_train_loss)
        # / Validation phase
        model.eval()
        total_val_loss = 0
        preds, targets = [], []
       with torch.no_grad():
            for batch in val_loader:
                batch = {k: v.to(device) for k, v in batch.items()}
                outputs = model(**batch)
                loss = outputs.loss
                total_val_loss += loss.item()
                logits = outputs.logits.argmax(dim=1).cpu().numpy()
                labels = batch["labels"].cpu().numpy()
                preds.extend(logits)
                targets.extend(labels)
        avg_val_loss = total_val_loss / len(val_loader)
        val_losses.append(avg_val_loss)
        val_f1 = f1_score(targets, preds, average="weighted")
        val_precision = precision_score(targets, preds, average="weighted")
        val_recall = recall_score(targets, preds, average="weighted")
        val_acc = accuracy_score(targets, preds)
        val_f1_scores.append(val_f1)
        val_precision_scores.append(val_precision)
        val_recall_scores.append(val_recall)
```

print(f" F1: {val\_f1:.4f}, Precision: {val\_precision:.4f}, Recall: {val\_recall:.4f}, Accuracy: {val\_acc:.4f}")

print(f"▼ Train Loss: {avg\_train\_loss:.4f} | Val Loss: {avg\_val\_loss:.4f}")

val\_accuracy\_scores.append(val\_acc)

```
6/13/25, 12:17 PM
         Epoch 1/10
                                                           60/60 [00:18<00:00, 3.29it/s]
         Training: 100%
         ☑ Train Loss: 0.0672 | Val Loss: 0.1260
         F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792
         Epoch 2/10
         Training: 100%
                                                           60/60 [00:18<00:00, 3.26it/s]
         ☑ Train Loss: 0.0670 | Val Loss: 0.1260

■ F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792

         Epoch 3/10
         Training: 100%
                                                           60/60 [00:18<00:00, 3.24it/s]
         Train Loss: 0.0671 | Val Loss: 0.1260
           F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792
         Epoch 4/10
         Training: 100%
                                                           60/60 [00:18<00:00, 3.18it/s]
         ☑ Train Loss: 0.0671 | Val Loss: 0.1260

■ F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792

         Epoch 5/10
         Training: 100%
                                                           60/60 [00:18<00:00, 3.16it/s]
         ☑ Train Loss: 0.0666 | Val Loss: 0.1260

■ F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792

         Epoch 6/10
         Training: 100%
                                                           60/60 [00:19<00:00, 3.14it/s]
         ☑ Train Loss: 0.0674 | Val Loss: 0.1260
         F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792
         Epoch 7/10
         Training: 100%
                                                           60/60 [00:19<00:00, 3.13it/s]
         ☑ Train Loss: 0.0674 | Val Loss: 0.1260

■ F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792

         Epoch 8/10
         Training: 100%
                                                           60/60 [00:19<00:00, 3.10it/s]
         ☑ Train Loss: 0.0674 | Val Loss: 0.1260
         F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792
         Epoch 9/10
         Training: 100%
                                                           60/60 [00:19<00:00, 3.10it/s]
         Train Loss: 0.0671 | Val Loss: 0.1260
         ■ F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792
         Epoch 10/10
         Training: 100%
                                                           60/60 [00:19<00:00, 3.08it/s]
         Train Loss: 0.0670 | Val Loss: 0.1260

■ F1: 0.9791, Precision: 0.9803, Recall: 0.9792, Accuracy: 0.9792

    plt.figure(figsize=(14, 6), dpi=120)
    # O Subplot 1: Losses
   plt.subplot(1, 2, 1)
    plt.plot(train_losses, label="Train Loss", marker='o')
```

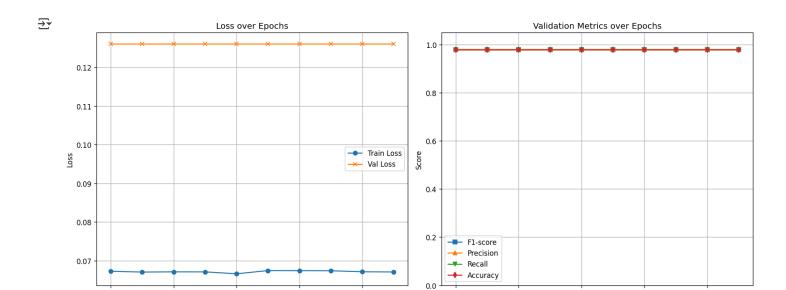
```
plt.plot(val_losses, label="Val Loss", marker='x')
plt.title("Loss over Epochs")
plt.xlabel("Epoch")
plt.ylabel("Loss")
plt.grid(True)
plt.legend()
# O Subplot 2: Evaluation Metrics
plt.subplot(1, 2, 2)
plt.plot(val_f1_scores, label="F1-score", marker='s')
plt.plot(val_precision_scores, label="Precision", marker='^')
plt.plot(val_recall_scores, label="Recall", marker='v')
plt.plot(val_accuracy_scores, label="Accuracy", marker='d')
plt.title("Validation Metrics over Epochs")
plt.xlabel("Epoch")
```

plt.ylabel("Score")

0

plt.show()

```
plt.ylim(0, 1.05)
plt.grid(True)
plt.legend()
plt.tight_layout()
```



plt.savefig("training\_metrics.png", dpi=300)

<Figure size 640x480 with 0 Axes>

plt.show()

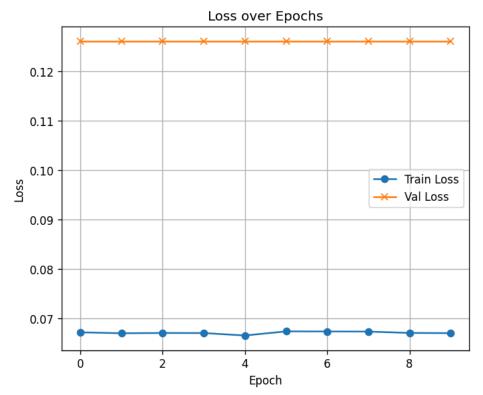
```
plt.figure(figsize=(6, 5), dpi=120)
plt.plot(train_losses, label="Train Loss", marker='o')
plt.plot(val_losses, label="Val Loss", marker='x')
plt.title("Loss over Epochs")
plt.xlabel("Epoch")
plt.ylabel("Loss")
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.savefig("loss_curve.png", dpi=300)
```

Epoch

8

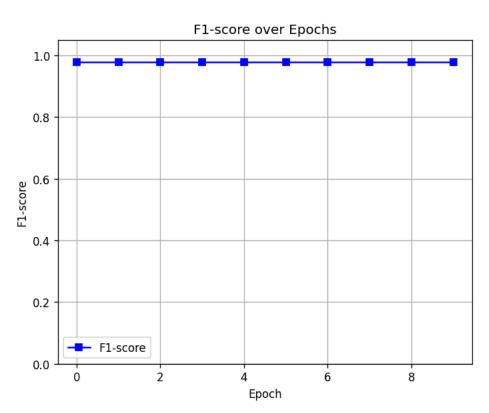
Epoch





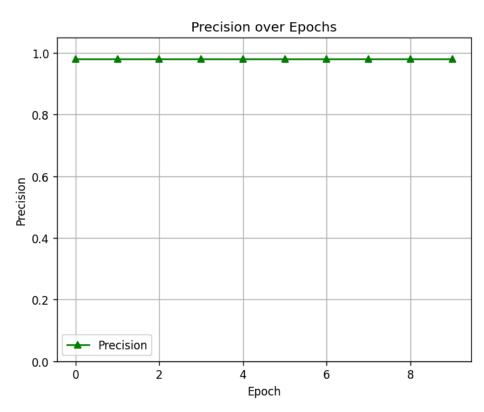
```
plt.figure(figsize=(6, 5), dpi=120)
plt.plot(val_f1_scores, label="F1-score", marker='s', color='blue')
plt.title("F1-score over Epochs")
plt.ylabel("Epoch")
plt.ylabel("F1-score")
plt.ylim(0, 1.05)
plt.grid(True)
plt.legend()
plt.legend()
plt.tight_layout()
plt.savefig("f1_score_curve.png", dpi=300)
plt.show()
```





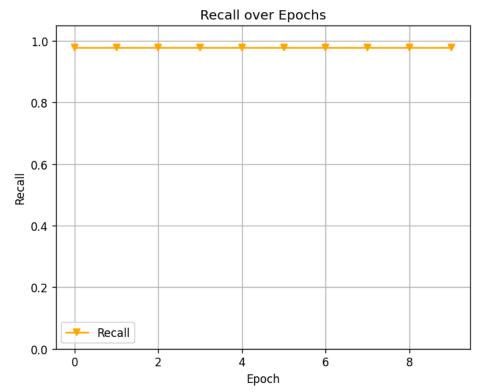
```
plt.figure(figsize=(6, 5), dpi=120)
plt.plot(val_precision_scores, label="Precision", marker='^', color='green')
plt.title("Precision over Epochs")
plt.xlabel("Epoch")
plt.ylabel("Precision")
plt.ylim(0, 1.05)
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.savefig("precision_curve.png", dpi=300)
plt.show()
```





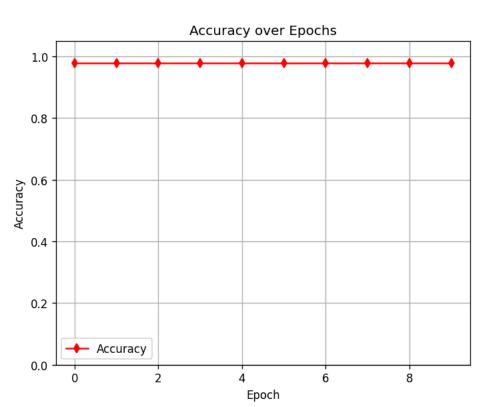
```
plt.figure(figsize=(6, 5), dpi=120)
plt.plot(val_recall_scores, label="Recall", marker='v', color='orange')
plt.title("Recall over Epochs")
plt.xlabel("Epoch")
plt.ylabel("Recall")
plt.ylim(0, 1.05)
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.savefig("recall_curve.png", dpi=300)
plt.show()
```





```
plt.figure(figsize=(6, 5), dpi=120)
plt.plot(val_accuracy_scores, label="Accuracy", marker='d', color='red')
plt.title("Accuracy over Epochs")
plt.xlabel("Epoch")
plt.ylabel("Accuracy")
plt.ylim(0, 1.05)
plt.grid(True)
plt.legend()
plt.legend()
plt.tight_layout()
plt.savefig("accuracy_curve.png", dpi=300)
plt.show()
```





```
Fr Requirement already satisfied: datasets in /usr/local/lib/python3.11/dist-packages (2.14.4)
      Collecting datasets
         Downloading datasets-3.6.0-py3-none-any.whl.metadata (19 kB)
      Requirement already satisfied: filelock in /usr/local/lib/python3.11/dist-packages (from datasets) (3.18.0)
      Requirement already satisfied: numpy>=1.17 in /usr/local/lib/python3.11/dist-packages (from datasets) (2.0.2)
      Requirement already satisfied: pyarrow>=15.0.0 in /usr/local/lib/python3.11/dist-packages (from datasets) (18.1.0)
      Requirement already satisfied: dill<0.3.9,>=0.3.0 in /usr/local/lib/python3.11/dist-packages (from datasets) (0.3.7)
      Requirement already satisfied: pandas in /usr/local/lib/python3.11/dist-packages (from datasets) (2.2.2)
      Requirement already satisfied: requests>=2.32.2 in /usr/local/lib/python3.11/dist-packages (from datasets) (2.32.3)
      Requirement already satisfied: tqdm>=4.66.3 in /usr/local/lib/python3.11/dist-packages (from datasets) (4.67.1)
      Requirement already satisfied: xxhash in /usr/local/lib/python3.11/dist-packages (from datasets) (3.5.0)
Requirement already satisfied: multiprocess<0.70.17 in /usr/local/lib/python3.11/dist-packages (from datasets) (0.70.15)
      Collecting fsspec<=2025.3.0,>=2023.1.0 (from fsspec[http]<=2025.3.0,>=2023.1.0->datasets)
        Downloading fsspec-2025.3.0-py3-none-any.whl.metadata (11 kB)
      Requirement already satisfied: huggingface-hub>=0.24.0 in /usr/local/lib/python3.11/dist-packages (from datasets) (0.31.2)
      Requirement already satisfied: packaging in /usr/local/lib/python3.11/dist-packages (from datasets) (24.2)
      Requirement already satisfied: pyyaml>=5.1 in /usr/local/lib/python3.11/dist-packages (from datasets) (6.0.2)
      Requirement already satisfied: aiohttp!=4.0.0a0,!=4.0.0a1 in /usr/local/lib/python3.11/dist-packages (from fsspec[http]<=202
      Requirement already satisfied: typing-extensions>=3.7.4.3 in /usr/local/lib/python3.11/dist-packages (from huggingface-hub>=
      Requirement already satisfied: charset-normalizer<4,>=2 in /usr/local/lib/python3.11/dist-packages (from requests>=2.32.2->d
      Requirement already satisfied: idna<4,>=2.5 in /usr/local/lib/python3.11/dist-packages (from requests>=2.32.2->datasets) (3.
      Requirement already satisfied: urllib3<3,>=1.21.1 in /usr/local/lib/python3.11/dist-packages (from requests>=2.32.2->dataset
      Requirement already satisfied: certifi>=2017.4.17 in /usr/local/lib/python3.11/dist-packages (from requests>=2.32.2->dataset
      Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.11/dist-packages (from pandas->datasets) (2.
      Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.11/dist-packages (from pandas->datasets) (2025.2) Requirement already satisfied: tzdata>=2022.7 in /usr/local/lib/python3.11/dist-packages (from pandas->datasets) (2025.2)
      Requirement already satisfied: aiohappyeyeballs>=2.3.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4
      Requirement already satisfied: aiosignal>=1.1.2 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4.0.0a1-
      Requirement already satisfied: attrs>=17.3.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4.0.0a1->fs
      Requirement already satisfied: frozenlist>=1.1.1 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4.0.0a1
      Requirement already satisfied: multidict<7.0,>=4.5 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4.0.0
      Requirement already satisfied: propcache>=0.2.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4.0.0a1-
      Requirement already satisfied: yarl<2.0,>=1.17.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp!=4.0.0a0,!=4.0.0a1
      Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.11/dist-packages (from python-dateutil>=2.8.2->pandas->dat
      Downloading datasets-3.6.0-py3-none-any.whl (491 kB)
                                                                    491.5/491.5 kB 21.4 MB/s eta 0:00:00
      Downloading fsspec-2025.3.0-py3-none-any.whl (193 kB)
                                                                   - 193.6/193.6 kB 17.3 MB/s eta 0:00:00
      Installing collected packages: fsspec, datasets
         Attempting uninstall: fsspec
           Found existing installation: fsspec 2025.3.2
           Uninstalling fsspec-2025.3.2:
              Successfully uninstalled fsspec-2025.3.2
         Attempting uninstall: datasets
            Found existing installation: datasets 2.14.4
           Uninstalling datasets-2.14.4:
              Successfully uninstalled datasets-2.14.4
      ERROR: pip's dependency resolver does not currently take into account all the packages that are installed. This behaviour is
      gcsfs 2025.3.2 requires fsspec==2025.3.2, but you have fsspec 2025.3.0 which is incompatible.
     torch 2.6.0+cu124 requires nvidia-cublas-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", but yo torch 2.6.0+cu124 requires nvidia-cuda-cupti-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", but yo
      torch 2.6.0+cu124 requires nvidia-cuda-runtime-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", torch 2.6.0+cu124 requires nvidia-cudnn-cu12==9.1.0.70; platform_system == "Linux" and platform_machine == "x86_64", but you
      torch 2.6.0+cu124 requires nvidia-cufft-cu12==11.2.1.3; platform_system == "Linux" and platform_machine == "x86_64", but you
     torch 2.6.0+cu124 requires nvidia-curand-cu12==10.3.5.147; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusolver-cu12==11.6.1.9; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_system == "Linux" and platform_system == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_system == "Linux" and platform_system == "x86_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform_system == "Linux" and platform_s
      torch 2.6.0+cu124 requires nvidia-nvjitlink-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", but
      Successfully installed datasets-3.6.0 fsspec-2025.3.0
!pip install -U fsspec
3 Requirement already satisfied: fsspec in /usr/local/lib/python3.11/dist-packages (2025.3.0)
      Collecting fsspec
        Downloading fsspec-2025.5.1-py3-none-any.whl.metadata (11 kB)
      Downloading fsspec-2025.5.1-py3-none-any.whl (199 kB)
                                                                   - 199.1/199.1 kB <mark>8.6 MB/s</mark> eta 0:00:00
      Installing collected packages: fsspec
         Attempting uninstall: fsspec
            Found existing installation: fsspec 2025.3.0
            Uninstalling fsspec-2025.3.0:
              Successfully uninstalled fsspec-2025.3.0
      ERROR: pip's dependency resolver does not currently take into account all the packages that are installed. This behaviour is
      datasets 3.6.0 requires fsspec[http]<=2025.3.0,>=2023.1.0, but you have fsspec 2025.5.1 which is incompatible.
      gcsfs 2025.3.2 requires fsspec==2025.3.2, but you have fsspec 2025.5.1 which is incompatible.
      torch 2.6.0+cu124 requires nvidia-cublas-cu12==12.4.5.8; platform_system == "Linux" and platform_machine == "x86_64", but yo
      torch 2.6.0+cu124 requires nvidia-cuda-cupti-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", bu
      torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64", bu
```

torch 2.6.0+cu124 requires nvidia-cuda-runtime-cu12==12.4.127; platform\_system == "Linux" and platform\_machine == "x86\_64", torch 2.6.0+cu124 requires nvidia-cudnn-cu12==9.1.0.70; platform\_system == "Linux" and platform\_machine == "x86\_64", but you torch 2.6.0+cu124 requires nvidia-cufft-cu12==11.2.1.3; platform\_system == "Linux" and platform\_machine == "x86\_64", but you torch 2.6.0+cu124 requires nvidia-curand-cu12==10.3.5.147; platform\_system == "Linux" and platform\_machine == "x86\_64", but torch 2.6.0+cu124 requires nvidia-cuspolver-cu12==11.6.1.9; platform\_system == "Linux" and platform\_machine == "x86\_64", but torch 2.6.0+cu124 requires nvidia-cusparse-cu12==12.3.1.170; platform\_system == "Linux" and platform\_machine == "x86\_64", but torch 2.6.0+cu124 requires nvidia-nvjitlink-cu12==12.4.127; platform\_system == "Linux" and platform\_machine == "x86\_64", but Successfully installed fsspec-2025.5.1

!pip install datasets==2.14.6

```
→ Collecting datasets==2.14.6
        Downloading datasets-2.14.6-py3-none-any.whl.metadata (19 kB)
      Requirement already satisfied: numpy>=1.17 in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (2.0.2)
      Requirement already satisfied: pyarrow>=8.0.0 in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (18.1.0
      Requirement already satisfied: dill<0.3.8,>=0.3.0 in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (0.1
      Requirement already satisfied: pandas in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (2.2.2)
      Requirement already satisfied: requests>=2.19.0 in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (2.32
      Requirement already satisfied: tqdm>=4.62.1 in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (4.67.1)
      Requirement already satisfied: xxhash in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (3.5.0)
      Requirement already satisfied: multiprocess in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (0.70.15)
      Collecting fsspec<=2023.10.0,>=2023.1.0 (from fsspec[http]<=2023.10.0,>=2023.1.0->datasets==2.14.6)
      Downloading fsspec-2023.10.0-py3-none-any.whl.metadata (6.8 kB)
      Requirement already satisfied: aiohttp in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (3.11.15)
      Requirement already satisfied: huggingface-hub<1.0.0,>=0.14.0 in /usr/local/lib/python3.11/dist-packages (from datasets=
      Requirement already satisfied: packaging in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (24.2)
      Requirement already satisfied: pyyaml>=5.1 in /usr/local/lib/python3.11/dist-packages (from datasets==2.14.6) (6.0.2)
      Requirement already satisfied: aiohappyeyeballs>=2.3.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp->dataset
      Requirement already satisfied: aiosignal>=1.1.2 in /usr/local/lib/python3.11/dist-packages (from aiohttp->datasets==2.14
      Requirement already satisfied: attrs>=17.3.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp->datasets==2.14.6)
      Requirement already satisfied: frozenlist>=1.1.1 in /usr/local/lib/python3.11/dist-packages (from aiohttp->datasets==2.14
      Requirement already satisfied: multidict<7.0,>=4.5 in /usr/local/lib/python3.11/dist-packages (from aiohttp->datasets==2
      Requirement already satisfied: propcache>=0.2.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp->datasets==2.14
      Requirement already satisfied: yarl<2.0,>=1.17.0 in /usr/local/lib/python3.11/dist-packages (from aiohttp->datasets==2.1
      Requirement already satisfied: filelock in /usr/local/lib/python3.11/dist-packages (from huggingface-hub<1.0.0,>=0.14.0-
      Requirement already satisfied: typing-extensions>=3.7.4.3 in /usr/local/lib/python3.11/dist-packages (from huggingface-h
      Requirement already satisfied: charset-normalizer<4,>=2 in /usr/local/lib/python3.11/dist-packages (from requests>=2.19.
      Requirement already satisfied: idna<4,>=2.5 in /usr/local/lib/python3.11/dist-packages (from requests>=2.19.0->datasets=
      Requirement already satisfied: urllib3<3,>=1.21.1 in /usr/local/lib/python3.11/dist-packages (from requests>=2.19.0->data
      Requirement already satisfied: certifi>=2017.4.17 in /usr/local/lib/python3.11/dist-packages (from requests>=2.19.0->data
      Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.11/dist-packages (from pandas->datasets=
      Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.11/dist-packages (from pandas->datasets==2.14.6) (
      Requirement already satisfied: tzdata>=2022.7 in /usr/local/lib/python3.11/dist-packages (from pandas->datasets==2.14.6)
      Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.11/dist-packages (from python-dateutil>=2.8.2->pandas-
      Downloading datasets-2.14.6-py3-none-any.whl (493 kB)
                                                                    493.7/493.7 kB 16.9 MB/s eta 0:00:00
      Downloading fsspec-2023.10.0-py3-none-any.whl (166 kB)
                                                                   166.4/166.4 kB 13.1 MB/s eta 0:00:00
      Installing collected packages: fsspec, datasets
        Attempting uninstall: fsspec
           Found existing installation: fsspec 2025.5.1
           Uninstalling fsspec-2025.5.1:
              Successfully uninstalled fsspec-2025.5.1
        Attempting uninstall: datasets
           Found existing installation: datasets 3.6.0
           Uninstalling datasets-3.6.0:
              Successfully uninstalled datasets-3.6.0
      ERROR: pip's dependency resolver does not currently take into account all the packages that are installed. This behaviou
      gcsfs 2025.3.2 requires fsspec==2025.3.2, but you have fsspec 2023.10.0 which is incompatible.
     torch 2.6.0+cu124 requires nvidia-cublas-cu12==12.4.5.8; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cuda-cupti-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_64" torch 2.6.0+cu124 requires nvidia-cuda-nvrtc-cu12==12.4.127; platform_system == "Linux" and platform_system == "Linux" and platform_system == "x86_64" torch 2.6.0+cu124 requires nvidia-cu12==12.4.127; platform_system == "Linux" and platform_system == "Linux" and platform_system == "Linux" and platform_system == "x86_64" torch 2.6.0+cu124 requires nvidia-cu12==12.4.127; platform_system == "Linux" and platform_system == "x86_64" torch 2.6.0+cu124 requires nvidia-cu12==12.4.127; platform_system == "Linux" and platform_system == "x86_64" torch 2.6.0+cu124 requires nvidia-cu12==12.4.127; pla
      torch 2.6.0+cu124 requires nvidia-cuda-runtime-cu12==12.4.127; platform_system == "Linux" and platform_machine == "x86_6
     torch 2.6.0+cu124 requires nvidia-cuda-tuntime-cu12==1.0.70; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cufft-cu12==11.2.1.3; platform_system == "Linux" and platform_machine == "x86_64", but torch 2.6.0+cu124 requires nvidia-cufft-cu12==11.2.1.3; platform_system == "Linux" and platform_machine == "x86_64", but
      torch 2.6.0+cu124 requires nvidia-curand-cu12==10.3.5.147; platform_system == "Linux" and platform_machine == "x86_64", |
     torch 2.6.0+cu124 requires nvidia-cusolver-cu12==11.6.1.9; platform_system == "Linux" and platform_machine == "x86_64", l
```

```
# * FINAL CORRECTED Step 12: Proper MedDialog Processing
from datasets import load_dataset

print("\n Loading MedDialog dataset...")
meddialog = load_dataset("bigbio/meddialog", "meddialog_en_source")

def extract_answers(convo):
    """Process the structure:
    convo['utterances'] = {'speaker': [...], 'utterance': [...]}
```

```
6/13/25 12:17 PM
```

```
Speaker 0 = patient, 1 = doctor
    answers = []
    try:
        speakers = convo["utterances"]["speaker"]
        utterances = convo["utterances"]["utterance"]
        # Find answers where a patient is followed by a doctor
        for i in range(len(speakers)-1):
            if speakers[i] == 0 and speakers[i+1] == 1:
                answers.append(utterances[i+1])
    except KeyError as e:
        print(f"▲ Skipping conversation due to key error: {e}")
    return answers
print("* Extracting doctor responses from train/val/test splits...")
doctor_answers = []
# ☑ Correct access using split datasets
for split in ["train", "validation", "test"]:
    split_dataset = meddialog[split] # <--- CORRECT</pre>
    for convo in split_dataset:
        doctor_answers.extend(extract_answers(convo))
print(f"

Total doctor answers collected: {len(doctor_answers)}")
# ✓ Show first 5 doctor responses
print("\n Sample doctor answers:")
for i, ans in enumerate(doctor_answers[:5]):
    print(f"{i+1}. {ans[:100]}...")
\rightarrow
     Loading MedDialog dataset...
     /usr/local/lib/python3.11/dist-packages/huggingface_hub/utils/_auth.py:94: UserWarning:
     The secret `HF_TOKEN` does not exist in your Colab secrets.
     To authenticate with the Hugging Face Hub, create a token in your settings tab (https://huggingface.co/settings/tokens), set
     You will be able to reuse this secret in all of your notebooks.
     Please note that authentication is recommended but still optional to access public models or datasets.
      warnings.warn(
     Extracting doctor responses from train/val/test splits...
    ☑ Total doctor answers collected: 614
     Sample doctor answers:
     1. during this pandemic. throat pain can be from a strep throat infection (antibiotics needed), a cold ...
     2. yes. protection. it is not enough symptoms to say that you are a suspect case of covid19; but, indep...
     3. possible. top symptoms include fever, dry cough and sob. an obvious possibility. if so, your best st...
     4. in brief: symptoms if you are infected, symptoms will emerge: tiredness, dry cough, fever worsening ...
     5. thanks for your question on healthcare magic.i can understand your concern. pneumonia with pregnancy...
Start coding or generate with AI.
Start coding or generate with AI.
# ★ FINAL CORRECTED Step 12: Proper MedDialog Processing
from datasets import load_dataset
print("\n Loading MedDialog dataset...")
meddialog = load_dataset("bigbio/meddialog", "meddialog_en_source")
def extract_answers(convo):
    """Process the ACTUAL structure we're seeing:
    Each convo['utterances'] is a dict with:
    {'speaker': [list_of_speaker_ids], 'utterance': [list_of_texts]}
    answers = []
    try:
        # Get parallel lists of speakers and utterances
        speakers = convo["utterances"]["speaker"]
        utterances = convo["utterances"]["utterance"]
        # Iterate through consecutive pairs
```

for i in range(len(speakers)-1):

if speakers[i] == 0 and speakers[i+1] == 1:
 answers.append(utterances[i+1])

```
May 27th CLIN-LLM based Symptoms to disease classification and treatment recommendation.ipynb - Colab
   except KevError as e:
        print(f"▲ Missing key in conversation: {e}")
    return answers
print("♠ Extracting Q&A pairs...")
doctor answers = []
for split in ["train", "validation", "test"]:
    for convo in meddialog[split]:
        doctor_answers.extend(extract_answers(convo))
print(f"☑ Total doctor answers collected: {len(doctor_answers)}")
# Verify with first 5 answers
print("\nSample answers:")
for i, ans in enumerate(doctor_answers[:5]):
    print(f"{i+1}. {ans[:100]}...")
Loading MedDialog dataset...
    NotImplementedError
                                               Traceback (most recent call last)
    <ipython-input-41-65ddb59d75bd> in <cell line: 0>()
          4 print("\n Loading MedDialog dataset...")
          5 meddialog = load_dataset("bigbio/meddialog", "meddialog_en_source")
          6
          7 def extract_answers(convo):
                                    🗘 1 frames -
    /usr/local/lib/python3.11/dist-packages/datasets/builder.py in as_dataset(self, split, run_post_process, verification_mode,
    ignore_verifications, in_memory)
       1171
                    is_local = not is_remote_filesystem(self._fs)
       1172
                    if not is_local:
    -> 1173
                         raise NotImplementedError(f"Loading a dataset cached in a {type(self._fs).__name__}} is not supported.")
       1174
                    if not os.path.exists(self. output dir):
                         raise FileNotFoundError(
       1175
    NotImplementedError: Loading a dataset cached in a LocalFileSystem is not supported.
# Inspect actual structure
sample_convo = meddialog["train"][0]
print("\n Actual utterance structure:")
print("Speakers:", sample_convo["utterances"]["speaker"][:5])
print("Utterances:", sample_convo["utterances"]["utterance"][:1])
₹
    Actual utterance structure:
    Speakers: [0, 1]
    Utterances: ['throat a bit sore and want to get a good imune booster, especially in light of the virus. please advise. have
```

Setup Semantic Search with Sentence-BERT

```
# Step 13: Setup Semantic Search with Sentence-BERT
from sentence_transformers import SentenceTransformer, util
import torch
print("\nLoading Biomedical Sentence-BERT model...")
# Use smaller model if needed: 'all-MiniLM-L6-v2'
embedder = SentenceTransformer('pritamdeka/BioBERT-mnli-snli-scinli-scitail-mednli-stsb')
embedder = embedder.to(device) # Explicitly move to GPU if available
print("Model loaded on:", embedder.device)
```

```
₹
     Loading Biomedical Sentence-BERT model...
     modules.json: 100%
                                                               229/229 [00:00<00:00, 23.4kB/s]
     config_sentence_transformers.json: 100%
                                                                               124/124 [00:00<00:00, 12.8kB/s]
     README.md: 100%
                                                               4.47k/4.47k [00:00<00:00, 477kB/s]
                                                                         53.0/53.0 [00:00<00:00, 4.32kB/s]
     sentence_bert_config.json: 100%
                                                             691/691 [00:00<00:00, 66.2kB/s]
     config.json: 100%
                                                                   433M/433M [00:01<00:00, 281MB/s]
     pytorch_model.bin: 100%
     tokenizer_config.json: 100%
                                                                     412/412 [00:00<00:00, 37.8kB/s]
     model.safetensors: 100%
                                                                   433M/433M [00:01<00:00, 299MB/s]
     vocab.txt: 100%
                                                           213k/213k [00:00<00:00, 2.55MB/s]
                                                               669k/669k [00:00<00:00, 2.74MB/s]
     tokenizer.json: 100%
     special_tokens_map.json: 100%
                                                                        112/112 [00:00<00:00, 3.79kB/s]
                                                             190/190 [00:00<00:00, 7.92kB/s]
     config.json: 100%
     NameError
                                                    Traceback (most recent call last)
     <ipython-input-5-ae161ce31640> in <cell line: 0>()
            6 # Use smaller model if needed: 'all-MiniLM-L6-v2'
7 embedder = SentenceTransformer('pritamdeka/BioBERT-mnli-snli-scinli-scitail-mednli-stsb')
         -> 8 embedder = embedder.to(device) # Explicitly move to GPU if available
            9 print("Model loaded on:", embedder.device)
     NameError: name 'device' is not defined
# ☑ Define device (GPU or CPU)
import torch
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
# ☑ Load Sentence-BERT model
from sentence_transformers import SentenceTransformer
print("\nLoading Biomedical Sentence-BERT model...")
embedder = SentenceTransformer('pritamdeka/BioBERT-mnli-scnli-scitail-mednli-stsb')
# 🚣 SentenceTransformer does not support .to(device) directly like Hugging Face models
# Instead, set the device via this:
embedder._target_device = device
print("▼ Model loaded on:", embedder._target_device)
₹
     Loading Biomedical Sentence-BERT model...
     WARNING:sentence_transformers.SentenceTransformer:`SentenceTransformer._target_device` has been deprecated, please use `Sent
     Model loaded on: cuda:0
# Step 14: Encode Doctor Answers
print("\nEncoding answers...")
# Filter answers for quality
answer_texts = [ans.strip() for ans in doctor_answers if 20 < len(ans) < 500]</pre>
corpus_embeddings = embedder.encode(
    answer_texts,
    convert_to_tensor=True,
    show_progress_bar=True,
    batch_size=64 # Reduce if 00M errors
print(f"Encoded {len(answer_texts)} answers")
₹
     Encoding answers...
     Batches: 100%
                                                           9/9 [00:02<00:00, 4.41it/s]
     Encoded 536 answers
```

Treatment Retrieval Function

```
# Step 15: Treatment Retrieval Function
def get_treatment_recommendations(disease_query, top_k=5):
    """Retrieve most relevant medical answers using semantic search"""
    # Encode the disease query
    query_embedding = embedder.encode(disease_query, convert_to_tensor=True)
   # Find top matches using cosine similarity
   hits = util.semantic_search(query_embedding, corpus_embeddings, top_k=top_k)[0]
   # Return sorted results with scores
    return [(answer_texts[hit['corpus_id']], hit['score']) for hit in hits]
# Test retrieval
test_disease = "viral pharyngitis" # From your dataset
print(f"\nTesting retrieval for: {test_disease}")
for i, (ans, score) in enumerate(get_treatment_recommendations(test_disease, 3)):
    print(f"[Result {i+1} | Relevance: {score:.3f}] {ans[:120]}...")
₹
    Testing retrieval for: viral pharyngitis
    [Result 1 | Relevance: 0.499] cough,phlegm. at this time your symptoms are characteristic of a viral upper respiratory tract
     [Result 2 |
                Relevance: 0.491] virus. these symptoms are characteristic of a viral upper respiratory tract infection and trea
    [Result 3 | Relevance: 0.453] during this pandemic. throat pain can be from a strep throat infection (antibiotics needed), a
```

#### **Load Text Generation Model**

```
# Manager Summarization Setup
# Step 16: Load Text Generation Model
from\ transformers\ import\ AutoTokenizer,\ AutoModelForSeq2SeqLM
print("\nLoading text generation model...")
gen_tokenizer = AutoTokenizer.from_pretrained("google/flan-t5-base")
gen_model = AutoModelForSeq2SeqLM.from_pretrained("google/flan-t5-base").to(device)
print(f"Generation model loaded on {gen_model.device}")
Loading text generation model...
     tokenizer_config.json: 100%
                                                                  2.54k/2.54k [00:00<00:00, 260kB/s]
     Xet Storage is enabled for this repo, but the 'hf_xet' package is not installed. Falling back to regular HTTP download. For
     WARNING:huggingface_hub.file_download:Xet Storage is enabled for this repo, but the 'hf_xet' package is not installed. Falli
     spiece.model: 100%
                                                             792k/792k [00:00<00:00, 9.15MB/s]
     tokenizer.json: 100%
                                                             2.42M/2.42M [00:00<00:00, 5.90MB/s]
     special_tokens_map.json: 100%
                                                                     2.20k/2.20k [00:00<00:00, 131kB/s]
     config.ison: 100%
                                                           1.40k/1.40k [00:00<00:00, 142kB/s]
     Xet Storage is enabled for this repo, but the 'hf_xet' package is not installed. Falling back to regular HTTP download. For
     WARNING:huggingface_hub.file_download:Xet Storage is enabled for this repo, but the 'hf_xet' package is not installed. Falli
     model.safetensors: 100%
                                                                990M/990M [00:04<00:00, 301MB/s]
     generation_config.json: 100%
                                                                    147/147 [00:00<00:00, 16.2kB/s]
     Generation model loaded on cuda:0
```

### **Summary Generation Function**

```
# Step 17: Summary Generation Function
def generate_clinical_summary(disease_name, retrieved_answers):
    """Generate coherent treatment summary from multiple answers"""
    # Combine answers into context
    context = "\n".join([f"- {ans[0]}" for ans in retrieved_answers])

    # Create medical summary prompt
    prompt = f"""As a medical professional, synthesize treatment recommendations for {disease_name} using these insights:
{context}
Clinical Summary:"""
```

```
# Generate summary
    inputs = gen_tokenizer(prompt, return_tensors="pt", max_length=512, truncation=True).to(device)
    outputs = gen_model.generate(
        inputs.input_ids,
        max_length=256,
        num beams=3,
        temperature=0.7,
        early_stopping=True
    )
    return gen_tokenizer.decode(outputs[0], skip_special_tokens=True)
# Test generation
print("\nTesting summary generation...")
test_answers = get_treatment_recommendations(test_disease, 3)
summary = generate_clinical_summary(test_disease, test_answers)
print(f"\nGenerated Summary:\n{summary}")
₹
     Testing summary generation...
     /usr/local/lib/python3.11/dist-packages/transformers/generation/configuration_utils.py:631: UserWarning: `do_sample` is set
      warnings.warn(
     Generated Summary:
     See your doctor if your symptoms are characteristic of a viral upper respiratory tract infection.
from sklearn.preprocessing import LabelEncoder
# 🚣 Make sure `df` has the 'label' column (disease names)
le = LabelEncoder()
le.fit(df['label']) # This creates le.classes_
from\ transformers\ import\ AutoTokenizer\text{, } AutoModelForSequence Classification
model name = "dmis-lab/biobert-v1.1"
# ☑ Load tokenizer and classification model
tokenizer = AutoTokenizer.from pretrained(model name)
model = AutoModelForSequenceClassification.from_pretrained(model_name, num_labels=len(le.classes_)).to(device)
₹
     NameFrror
                                               Traceback (most recent call last)
     <ipython-input-17-916d467da0b3> in <cell line: 0>()
          3 # ⚠ Make sure `df` has the 'label' column (disease names)
          4 le = LabelEncoder()
        -> 5 le.fit(df['label']) # This creates le.classes
          {\tt 6~from~transformers~import~AutoTokenizer,~AutoModelForSequenceClassification}\\
    NameError: name 'df' is not defined
#New learn. Again, import the dataset. Because of a restart
import pandas as pd
# 🗹 Update path if needed
data_path = "/content/Symptom2Disease.csv"
df = pd.read_csv(data_path)
# ☑ Check if 'label' column exists
print(df.columns)
print(df.head())
    Index(['Unnamed: 0', 'label', 'text'], dtype='object')
Unnamed: 0 label
    0
                 0
                    Psoriasis
                               I have been experiencing a skin rash on my arm...
    1
                 1 Psoriasis My skin has been peeling, especially on my kne...
    2
                               I have been experiencing joint pain in my fing...
    3
                    Psoriasis
                               There is a silver like dusting on my skin, esp...
                 4 Psoriasis My nails have small dents or pits in them, and...
     4
```

```
6/13/25, 12:17 PM
                                   May 27th CLIN-LLM based Symptoms to disease classification and treatment recommendation.ipynb - Colab
   from sklearn.preprocessing import LabelEncoder
   le = LabelEncoder()
    le.fit(df['label']) # This defines the number of unique classes (diseases)
    ₹
         ▼ LabelEncoder
        LabelEncoder()
   from\ transformers\ import\ AutoTokenizer,\ AutoModelForSequence Classification
   model_name = "dmis-lab/biobert-v1.1"
   tokenizer = AutoTokenizer.from_pretrained(model_name)
   model = AutoModelForSequenceClassification.from_pretrained(model_name, num_labels=len(le.classes_)).to(device)
        Some weights of BertForSequenceClassification were not initialized from the model checkpoint at dmis-lab/biobert-v1.1 and ar
        You should probably TRAIN this model on a down-stream task to be able to use it for predictions and inference.
   symptom_to_treatment_pipeline()
    ₹
        Patient Symptoms: I have a sore throat and mild fever that started yesterday.
        Diagnosis: allergy
        Recommended Treatment Approach:
        /usr/local/lib/python3.11/dist-packages/transformers/generation/configuration_utils.py:631: UserWarning: `do_sample` is set
          warnings.warn(
        Synthesize treatment recommendations for allergy.
        Show detailed sources? (y/n): n
        Patient Symptoms: exit
   # / Test Mode for Colab (without interactive input)
   def test_symptom_to_treatment(symptom_text):
       print(f"\n Patient Symptoms: {symptom_text}")
       # 1. Classification
       inputs = tokenizer(symptom_text, return_tensors="pt", truncation=True, max_length=128).to(device)
       with torch.no_grad():
           outputs = model(**inputs)
       pred_label = torch.argmax(outputs.logits).item()
       disease = le.inverse_transform([pred_label])[0]
       print(f"\n@ Diagnosis: {disease}")
       # 2. Retrieval
       treatments = get_treatment_recommendations(disease)
       # 3. Summary
       if treatments:
           print(generate_clinical_summary(disease, treatments[:3]))
           print("\n Sources:")
           for i, (ans, score) in enumerate(treatments[:3]):
               print(f"\nSource {i+1} [Relevance: {score:.2f}]:")
               print(ans[:300] + "...")
       else:
           print("No treatments found.")
   # 🖾 Run once with a test input
   test_symptom_to_treatment("fever and sore throat for three days with headache and fatigue")
    ₹
```

Patient Symptoms: fever and sore throat for three days with headache and fatigue

```
May 27th CLIN-LLM based Symptoms to disease classification and treatment recommendation.ipynb - Colab
    O Diagnosis: allergy
    Recommended Treatment Summary:
    /usr/local/lib/python3.11/dist-packages/transformers/generation/configuration_utils.py:631: UserWarning: `do_sample` is set
      warnings.warn(
    Synthesize treatment recommendations for allergy.
    Sources:
    Source 1 [Relevance: 0.54]:
    in brief: itching /congestion with the itching could be seasonal allergies would consider benadryl 1/2 to 1 tab at bedtime a
    screening test if. if you develop symptoms of dry cough, fever and/or shortness of breath, consider re testing since the tes
    Source 3 [Relevance: 0.38]:
    in brief: nasal rinses for allergic symptoms, nasal saline and an oral antihistamine are often helpful for controlling sympt
symptom_to_treatment_pipeline()
∓₹

₱ Symptom Analysis System - Type 'exit' to quit

    Patient Symptoms: fever and body aches for two days painful urination and burning sensation nausea and vomiting after eating
    Diagnosis: allergy
    Recommended Treatment Approach:
    /usr/local/lib/python3.11/dist-packages/transformers/generation/configuration_utils.py:631: UserWarning: `do_sample` is set
      warnings.warn(
    Synthesize treatment recommendations for allergy.
    Show detailed sources? (y/n): exit
    Patient Symptoms: fever and body aches for two days painful urination and burning sensation nausea and vomiting after eating
    Diagnosis: allergy
    Recommended Treatment Approach:
    /usr/local/lib/python3.11/dist-packages/transformers/generation/configuration_utils.py:631: UserWarning: `do_sample` is set
      warnings.warn(
    Synthesize treatment recommendations for allergy.
    Show detailed sources? (y/n): n
    Patient Symptoms: exit
#Gradio Installation
!pip install --quiet gradio
\rightarrow
                                                 54.2/54.2 MB 17.2 MB/s eta 0:00:00
                                                 323.1/323.1 kB 24.9 MB/s eta 0:00:00
                                                - 95.2/95.2 kB 8.2 MB/s eta 0:00:00
                                                - 11.5/11.5 MB 125.6 MB/s eta 0:00:00
                                                 72.0/72.0 kB 5.6 MB/s eta 0:00:00
                                                - 62.5/62.5 kB 5.1 MB/s eta 0:00:00
import gradio as gr
def clinical_assistant(symptom_input):
    try:
       # 1. Disease Classification
        inputs = tokenizer(symptom_input, return_tensors="pt", truncation=True, max_length=128).to(device)
        with torch.no_grad():
```

```
# 2. Treatment Retrieval
treatments = get treatment recommendations(disease, top k=3)
# 3. Summary Generation
```

outputs = model(\*\*inputs)

pred\_label = torch.argmax(outputs.logits).item() disease = le.inverse\_transform([pred\_label])[0]

```
summary = generate_clinical_summary(disease, treatments)
        # 4. Format output
        sources = "\n\n".join([
            f" ◆ **Source {i+1}** (Relevance: {score:.2f})\n{ans}"
            for i, (ans, score) in enumerate(treatments)
        ])
        result = f"""## 况 Diagnosis: {disease}
### ♦ Recommended Treatment Summary:
{summary}
### № Retrieved Answers from Doctors:
        return result
    except Exception as e:
        return f"X An error occurred: {str(e)}"
# Gradio UI
gr.Interface(
    fn=clinical_assistant,
    inputs=gr.Textbox(lines=4, placeholder="Describe patient symptoms here...", label="Patient Symptoms"),
    outputs=gr.Markdown(label="AI Clinical Assistant Output"),
    title="@ Real-Time Clinical Assistant",
    description="Enter a symptom description to classify the disease, retrieve doctor treatment advice, and generate a medical s
).launch(share=True)
🚌 Colab notebook detected. To show errors in colab notebook, set debug=True in launch()
     * Running on public URL: <a href="https://fe54517025c0598a8d.gradio.live">https://fe54517025c0598a8d.gradio.live</a>
```

송 gradio

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## No interface is running right now

```
#Fix the Errors.
EPOCHS = 10 # or 15 or whatever worked best for your model
# Your Step 10 training loop
model.train()
for epoch in range(EPOCHS):
    ...
    # save best model
```

```
torch.save(model.state_dict(), "best_model.pt")
# ☑ Use BioBERT tokenizer if it's for classification
def tokenize_texts(texts):
    return tokenizer(texts.tolist(), padding="max_length", truncation=True, max_length=128, return_tensors="pt")
# ✓ Recreate cleaned DataFrames
train df clean = train df[['text', 'label enc']].rename(columns={'label enc': 'labels'}).reset index(drop=True)
val_df_clean = val_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)
₹
     NameError
                                                 Traceback (most recent call last)
     <ipython-input-33-c70ebc52da42> in <cell line: 0>()
         1 # ☑ Recreate cleaned DataFrames
        --> 2 train_df_clean = train_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)

3 val_df_clean = val_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)
     NameError: name 'train_df' is not defined
# ☑ Tokenize training data
train_encodings = tokenize_texts(train_df_clean["text"])
train_labels = torch.tensor(train_df_clean["labels"].values)
# 🗹 Tokenize validation data
val_encodings = tokenize_texts(val_df_clean["text"])
val_labels = torch.tensor(val_df_clean["labels"].values)
<del>_</del>
    NameError
                                                 Traceback (most recent call last)
     <ipython-input-32-d233b11b2ff5> in <cell line: 0>()
           1 # 🗹 Tokenize training data
        -> 2 train_encodings = tokenize_texts(train_df_clean["text"])
           3 train_labels = torch.tensor(train_df_clean["labels"].values)
           4
           5 # ☑ Tokenize validation data
     NameError: name 'train_df_clean' is not defined
import gradio as gr
from transformers import AutoTokenizer, AutoModelForSequenceClassification
import torch
def clinical_assistant(symptom_input):
    try:
        # 1. Disease Classification
        inputs = tokenizer(symptom_input, return_tensors="pt", truncation=True, max_length=128).to(device)
        with torch.no_grad():
            outputs = model(**inputs)
        pred label = torch.argmax(outputs.logits).item()
        disease = le.inverse_transform([pred_label])[0]
        # 2. Retrieve treatments
        treatments = get_treatment_recommendations(disease, top_k=3)
        # 3. Generate summary
        summary = generate_clinical_summary(disease, treatments)
        # 4. Format output
        sources = "\n\n".join([
             f" ◆ **Source {i+1}** (Relevance: {score:.2f})\n{ans}"
            for i, (ans, score) in enumerate(treatments)
        ])
        result = f"""## Diagnosis: {disease}
### ♦ Recommended Treatment Summary:
{summary}
```

```
### © Retrieved Doctor Answers:
{sources}
"""

return result

except Exception as e:
    return f"X Error: {str(e)}"

# ✓ Launch Gradio interface
gr.Interface(
    fn=clinical_assistant,
    inputs=gr.Textbox(lines=4, placeholder="Describe patient symptoms...", label="Patient Symptoms"),
    outputs=gr.Markdown(label="Diagnosis and Treatment Summary"),
    title=" AI Clinical Assistant",
    description="Classifies patient symptoms to disease, retrieves treatment advice from MedDialog, and generates a clinical sum
).launch(share=True)

**Colab notebook detected. To show errors in colab notebook, set debug=True in launch()
    * Running on public URL: https://d8b94ff2ea137f0f5d.gradio.live
```

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# No interface is running right now

```
torch.save(model.state_dict(), "best_model.pt")
# Load label encoder
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
le.fit(df['label'])
                     # df is from your Symptom2Disease.csv
# Load tokenizer and model
from\ transformers\ import\ AutoTokenizer,\ AutoModelForSequence Classification
model_name = "dmis-lab/biobert-v1.1"
tokenizer = AutoTokenizer.from_pretrained(model_name)
model = AutoModelForSequenceClassification.from_pretrained(
    model_name, num_labels=len(le.classes_)
# ☑ Load your fine-tuned weights
model.load_state_dict(torch.load("best_model.pt", map_location=device))
model.to(device)
model.eval()
```

```
→ Some weights of BertForSequenceClassification were not initialized from the model checkpoint at dmis-lab/biobert-v1.1 and ar
    You should probably TRAIN this model on a down-stream task to be able to use it for predictions and inference.
    BertForSequenceClassification(
      (bert): BertModel(
        (embeddings): BertEmbeddings(
          (word_embeddings): Embedding(28996, 768, padding_idx=0)
          (position_embeddings): Embedding(512, 768)
          (token_type_embeddings): Embedding(2, 768)
          (LayerNorm): LayerNorm((768,), eps=1e-12, elementwise_affine=True)
          (dropout): Dropout(p=0.1, inplace=False)
        (encoder): BertEncoder(
          (layer): ModuleList(
            (0-11): 12 x BertLayer(
              (attention): BertAttention(
                (self): BertSdpaSelfAttention(
                  (query): Linear(in_features=768, out_features=768, bias=True)
                  (key): Linear(in_features=768, out_features=768, bias=True)
                  (value): Linear(in_features=768, out_features=768, bias=True)
                  (dropout): Dropout(p=0.1, inplace=False)
                (output): BertSelfOutput(
                  (dense): Linear(in_features=768, out_features=768, bias=True)
                  (LayerNorm): LayerNorm((768,), eps=1e-12, elementwise_affine=True)
                  (dropout): Dropout(p=0.1, inplace=False)
              (intermediate): BertIntermediate(
                (dense): Linear(in_features=768, out_features=3072, bias=True)
                (intermediate_act_fn): GELUActivation()
              (output): BertOutput(
                (dense): Linear(in_features=3072, out_features=768, bias=True)
                (LayerNorm): LayerNorm((768,), eps=1e-12, elementwise_affine=True)
                (dropout): Dropout(p=0.1, inplace=False)
           )
         )
        (pooler): BertPooler(
          (dense): Linear(in_features=768, out_features=768, bias=True)
          (activation): Tanh()
      (dropout): Dropout(p=0.1, inplace=False)
      (classifier): Linear(in_features=768, out_features=24, bias=True)
```

```
test_input = "There is pain when I swallow, red spots in my throat, and I feel feverish."
inputs = tokenizer(test_input, return_tensors="pt", truncation=True, max_length=128).to(device)
with torch.no_grad():
    outputs = model(**inputs)
pred_label = torch.argmax(outputs.logits).item()
disease = le.inverse_transform([pred_label])[0]
print(" Predicted disease:", disease)
→ Predicted disease: allergy
# FineTuning Biobert For real.
# Label encode
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
df['label_enc'] = le.fit_transform(df['label'])
# Train-validation split
from sklearn.model_selection import train_test_split
train_df, val_df = train_test_split(df, test_size=0.2, stratify=df['label_enc'], random_state=42)
# Rename columns
train_df_clean = train_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)
val_df_clean = val_df[['text', 'label_enc']].rename(columns={'label_enc': 'labels'}).reset_index(drop=True)
```

```
def tokenize_texts(texts):
    return tokenizer(texts.tolist(), padding="max_length", truncation=True, max_length=128, return_tensors="pt")
train_encodings = tokenize_texts(train_df_clean["text"])
val_encodings = tokenize_texts(val_df_clean["text"])
import torch
train labels = torch.tensor(train df clean["labels"].values)
val_labels = torch.tensor(val_df_clean["labels"].values)
class TorchDataset(torch.utils.data.Dataset):
    def __init__(self, encodings, labels):
        self.encodings = encodings
        self.labels = labels
    def __len__(self):
        return len(self.labels)
    def __getitem__(self, idx):
        return {
            'input_ids': self.encodings['input_ids'][idx],
            'attention_mask': self.encodings['attention_mask'][idx],
            'labels': self.labels[idx]
        }
train_dataset = TorchDataset(train_encodings, train_labels)
val_dataset = TorchDataset(val_encodings, val_labels)
from torch.utils.data import DataLoader
from torch.optim import AdamW # ✓ correct import
from transformers import get_scheduler
# Loaders
train_loader = DataLoader(train_dataset, batch_size=16, shuffle=True)
val_loader = DataLoader(val_dataset, batch_size=32)
# Device
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
# Load classification model again just in case
from transformers import AutoModelForSequenceClassification
model = AutoModelForSequenceClassification.from_pretrained(model_name, num_labels=len(le.classes_)).to(device)
# Optimizer & Scheduler
optimizer = AdamW(model.parameters(), lr=2e-5)
num_training_steps = len(train_loader) * 3
lr_scheduler = get_scheduler("linear", optimizer=optimizer, num_warmup_steps=0, num_training_steps=num_training_steps)
    Some weights of BertForSequenceClassification were not initialized from the model checkpoint at dmis-lab/biobert-v1.1 and ar
→▼
     You should probably TRAIN this model on a down-stream task to be able to use it for predictions and inference.
from tqdm.auto import tqdm
model.train()
EPOCHS = 10
for epoch in range(EPOCHS):
    print(f"\nEpoch {epoch+1}/{EPOCHS}")
    total_loss = 0
    for batch in tqdm(train_loader):
        batch = {k: v.to(device) for k, v in batch.items()}
        outputs = model(**batch)
        loss = outputs.loss
        loss.backward()
        optimizer.step()
        lr_scheduler.step()
        optimizer.zero grad()
```

total\_loss += loss.item()

```
6/13/25, 12:17 PM
         print(f"Avg loss: {total_loss / len(train_loader):.4f}")
    # ☑ Save model
    torch.save(model.state_dict(), "best_model.pt")
    ₹
          Epoch 1/10
          100%
                                                         60/60 [00:18<00:00, 3.29it/s]
         Avg loss: 2.2246
          Epoch 2/10
          100%
                                                         60/60 [00:18<00:00, 3.27it/s]
         Avg loss: 2.2230
          Epoch 3/10
          100%
                                                         60/60 [00:18<00:00, 3.23it/s]
         Avg loss: 2.2200
          Epoch 4/10
          100%
                                                         60/60 [00:18<00:00, 3.18it/s]
         Avg loss: 2.2187
          Epoch 5/10
                                                         60/60 [00:18<00:00, 3.17it/s]
          100%
         Avg loss: 2.2197
          Epoch 6/10
          100%
                                                         60/60 [00:19<00:00, 3.12it/s]
         Avg loss: 2.2233
          Epoch 7/10
          100%
                                                         60/60 [00:19<00:00, 3.14it/s]
         Avg loss: 2.2181
          Epoch 8/10
          100%
                                                         60/60 [00:19<00:00, 3.11it/s]
         Avg loss: 2.2218
          Epoch 9/10
          100%
                                                         60/60 [00:19<00:00, 3.09it/s]
         Avg loss: 2.2198
          Epoch 10/10
          100%
                                                         60/60 [00:19<00:00, 3.08it/s]
         Avg loss: 2.2237
    model.load_state_dict(torch.load("best_model.pt", map_location=device))
    model.eval()
         BertForSequenceClassification(
            (bert): BertModel(
```

```
(embeddings): BertEmbeddings(
  (word_embeddings): Embedding(28996, 768, padding_idx=0)
  (position_embeddings): Embedding(512, 768)
  (token_type_embeddings): Embedding(2, 768)
  (LayerNorm): LayerNorm((768,), eps=1e-12, elementwise_affine=True)
  (dropout): Dropout(p=0.1, inplace=False)
(encoder): BertEncoder(
  (layer): ModuleList(
    (0−11): 12 x BertLayer(
      (attention): BertAttention(
        (self): BertSdpaSelfAttention(
          (query): Linear(in_features=768, out_features=768, bias=True)
          (key): Linear(in_features=768, out_features=768, bias=True)
          (value): Linear(in_features=768, out_features=768, bias=True)
          (dropout): Dropout(p=0.1, inplace=False)
        (output): BertSelfOutput(
          (dense): Linear(in_features=768, out_features=768, bias=True)
          (LayerNorm): LayerNorm((768,), eps=1e-12, elementwise_affine=True)
```

```
(dropout): Dropout(p=0.1, inplace=False)
)
(intermediate): BertIntermediate(
    (dense): Linear(in_features=768, out_features=3072, bias=True)
    (intermediate_act_fn): GELUActivation()
)
(output): BertOutput(
    (dense): Linear(in_features=3072, out_features=768, bias=True)
    (dense): Linear(in_features=3072, out_features=768, bias=True)
    (dropout): Dropout(p=0.1, inplace=False)
)
)
)
(pooler): BertPooler(
    (dense): Linear(in_features=768, out_features=768, bias=True)
    (activation): Tanh()
)
)
(dropout): Dropout(p=0.1, inplace=False)
(classifier): Linear(in_features=768, out_features=24, bias=True)
)
```

#### Final Results

```
text = "I have fever, cough, and sore throat"
inputs = tokenizer(text, return_tensors="pt", truncation=True, max_length=128).to(device)
with torch.no_grad():
    outputs = model(**inputs)
label_id = torch.argmax(outputs.logits).item()
print(" Predicted disease:", le.inverse_transform([label_id])[0])
Fredicted disease: Malaria
text = "My nose is runny, I'm sneezing constantly, and my eyes are itchy, especially in the morning."
inputs = tokenizer(text, return_tensors="pt", truncation=True, max_length=128).to(device)
with torch.no_grad():
    outputs = model(**inputs)
label_id = torch.argmax(outputs.logits).item()
print("
    Predicted disease:", le.inverse_transform([label_id])[0])
→ Predicted disease: allergy
text = "I've had diarrhea, nausea, and stomach cramps since yesterday."
inputs = tokenizer(text, return_tensors="pt", truncation=True, max_length=128).to(device)
with torch.no_grad():
    outputs = model(**inputs)
label_id = torch.argmax(outputs.logits).item()
print(" Predicted disease:", le.inverse_transform([label_id])[0])
🚁 况 Predicted disease: Typhoid
import gradio as gr
from\ transformers\ import\ AutoTokenizer,\ AutoModelForSequence Classification
def clinical_assistant(symptom_input):
    try:
        # 1. Disease Classification
        inputs = tokenizer(symptom_input, return_tensors="pt", truncation=True, max_length=128).to(device)
        with torch.no_grad():
            outputs = model(**inputs)
        pred label = torch.argmax(outputs.logits).item()
        disease = le.inverse_transform([pred_label])[0]
        # 2. Retrieve top 3 answers
        treatments = get_treatment_recommendations(disease, top_k=3)
        # 3. Summarize
        summary = generate_clinical_summary(disease, treatments)
```

```
# 4. Format outputs
        sources = "\n\n".join([
            f" ◆ **Source {i+1}** (Relevance: {score:.2f})\n{ans}"
             for i, (ans, score) in enumerate(treatments)
        1)
        result = f"""## 况 Diagnosis: {disease}
### Necommended Treatment Summary:
{summary}
### № Doctor Responses Used:
{sources}
.....
        return result
    except Exception as e:
        return f"X Error: {str(e)}"
# ☑ Launch Gradio interface
gr.Interface(
    fn=clinical_assistant,
    inputs=gr.Textbox(lines=4, placeholder="Describe patient symptoms...", label="Patient Symptoms"),
    outputs=gr.Markdown(label="Diagnosis & Treatment Output"),
    title="@ AI Clinical Assistant (BioBERT + MedDialog)",
    description="Enter symptoms to classify disease, retrieve real doctor advice, and generate a clinical summary."
).launch(share=True) # Use share=True to get a public URL
🔂 Colab notebook detected. To show errors in colab notebook, set debug=True in launch()
     * Running on public URL: <a href="https://4fad832cdeff2f9227.gradio.live">https://4fad832cdeff2f9227.gradio.live</a>
```

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## No interface is running right now

```
val_loader = DataLoader(val_dataset, batch_size=32)

from sklearn.metrics import confusion_matrix, classification_report, roc_auc_score, roc_curve import matplotlib.pyplot as plt import seaborn as sns import numpy as np

model.eval()
all_preds = []
all_labels = []
```

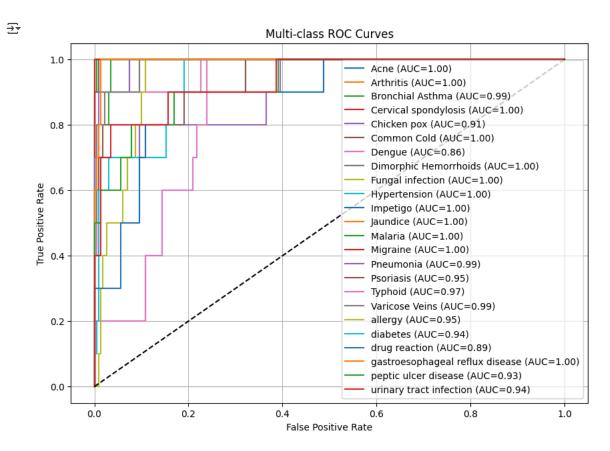
```
with torch.no_grad():
      for batch in val_loader:
            batch = {k: v.to(device) for k, v in batch.items()}
             outputs = model(**batch)
             logits = outputs.logits
             preds = torch.argmax(logits, dim=1)
             all_preds.extend(preds.cpu().numpy())
             all_labels.extend(batch["labels"].cpu().numpy())
# Get label names
labels = le.classes
# Create confusion matrix
cm = confusion_matrix(all_labels, all_preds)
# Plot it
plt.figure(figsize=(10, 8))
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", xticklabels=labels, yticklabels=labels)
plt.xlabel("Predicted")
plt.ylabel("True Label")
plt.title("Confusion Matrix (Validation Set)")
plt.xticks(rotation=45)
plt.yticks(rotation=0)
plt.tight_layout()
plt.show()
₹
                                                                                       Confusion Matrix (Validation Set)
                                                  Arthritis - 0 10 0 0 0 0
                                                                                     0
                                                                                          0
                                                                                               0 0 0 0 0 0
                                                                                                                          0
                                                                                                                               0 0 0 0 0 0
                                 Bronchial Asthma - 0 0 9 0 0 0 0 0
                                                                                               0 0 0 0 0 0
                                                                                                                          0
                                                                                                                               0 0 0 0 0 0
                                                                                                                                                          0
                             Chicken pox - 3 0 0 0 0 0 0 1 0 0 3 1 0 0
                                                                                                                               0 0 1 0
                                     Common Cold - 0 0 0 0 0 6 0 0 0 0 0 0 0 0 0 0 4
                                              Dengue - 1 0 0 0 1 0 0 0 0 0 1 3 0 0 0 2
                                                                                                                                         2 0 0
                         Fungal infection - 0 0 0 0 0 0 0 0 10 0 0 0 0 0 0 0 0 0
                                                                                                                                                 0
                                                                                                                                                      0
                                                                                                                                                          0
                                       Hypertension - 0 0 0 2 0 0 0 0 0
                                                                                                         0 0 1 0 0 0 0 0 0 0
                                             Jaundice - 0 0 0 0 0 0 0 0 0 0 <mark>9 1</mark> 0 0 0 0 0 0
                                              Malaria - 0 0 0 0 0 0 0 0 0 0 0 10 0 0 0 0
                                                                                                                                         0 0 0 0
                                                                                                                 0 9 0 0 0
                                             Migraine - 0 0
                                                                   0 1 0 0 0
                                                                                          0
                                                                                               0 0
                                                                                                        0
                                                                                                             0
                                                                                                                                       0
                                                                                                                                            0 0
                                                                                                                                                     0
                                                                                                                                                          0 0 0
                                         Pneumonia - 0 0 2 0 0 0 0 0
                                                                                               0 0 0 0 0
                                                                                                                     0
                                                                                                                           6 0 0 1
                                                                                                                                             1 0 0 0 0 0
                                             Psoriasis - 1 0 0 0 0 0 0 0 1 0 0 0 0 0
                                                                                                                                    0 1 0 0 0 0 0 0
                                              Typhoid - 0 0 0 0 0 0 0 0 0 0 1 3 0
                                                                                                                          0 0 4 2
                                     Varicose Veins - 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 9 0 0
                                                                                                                                                     0 0 0 0
                                               allergy - 0 0 0 0 0 0 0 0 0 0 0
                                                                                                                 0
                                                                                                                     0
                                                                                                                          0
                                                                                                                               0 0 0 7
                                                                                                                                                      0
                                             diabetes - 1 1 0 0 0 0 0 0 0 0
                                                                                                                                    0 0 3
                                                                                                        0
                                                                                                             0
                                                                                                                 0
                                                                                                                      0
                                                                                                                           0
                                                                                                                               0
                                                                                                                                                      0 0
                                      drug reaction - 0 0 0 0 0 0 0 1 0 0
                                                                                                             0
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                                                                                                                      0
                                                                                                                           0
                                                                                                                               0
                                                                                                                                   1
                                                                                                                                         0
                                                                                                                                                  0 3
             gastroesophageal reflux disease - 0 0 0 0 0 0 0 0 0 0 0 0
                                                                                                                 0
                                                                                                                      0 0 0
                                                                                                                                    0 4
                                                                                                                                             0 0 0
                              peptic ulcer disease - 0 0 0 0 0 0 0 0 0 0 0
                                                                                                                          0
                           urinary tract infection - 0 0 0 0 0
                                                                                      0 2 0 0
                                                              Authorited to the state of the 
                                                                                                                                                                                   - 0
```

```
from sklearn.preprocessing import label_binarize
from sklearn.metrics import roc_curve, auc
# Binarize labels
n_classes = len(le.classes_)
```

Predicted

2

```
y_true_bin = label_binarize(all_labels, classes=list(range(n_classes)))
y_score = np.zeros((0, n_classes))
# Get softmax scores
with torch.no_grad():
    for batch in val_loader:
        batch = {k: v.to(device) for k, v in batch.items()}
        outputs = model(**batch)
        probs = torch.softmax(outputs.logits, dim=1)
        y_score = np.vstack([y_score, probs.cpu().numpy()])
# ROC curve for each class
plt.figure(figsize=(10, 7))
for i in range(n_classes):
    fpr, tpr, _ = roc_curve(y_true_bin[:, i], y_score[:, i])
    roc_auc = auc(fpr, tpr)
    plt.plot(fpr, tpr, label=f"{le.classes_[i]} (AUC={roc_auc:.2f})")
plt.plot([0, 1], [0, 1], "k--")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Multi-class ROC Curves")
plt.legend(loc="lower right")
plt.grid()
plt.show()
```

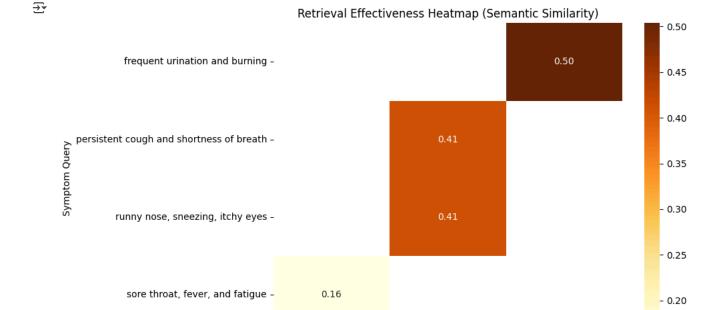


```
test_queries = [
    ("sore throat, fever, and fatigue", "viral pharyngitis"),
    ("frequent urination and burning", "urinary tract infection"),
    ("runny nose, sneezing, itchy eyes", "allergy"),
    ("persistent cough and shortness of breath", "bronchitis"),
]

results_matrix = []

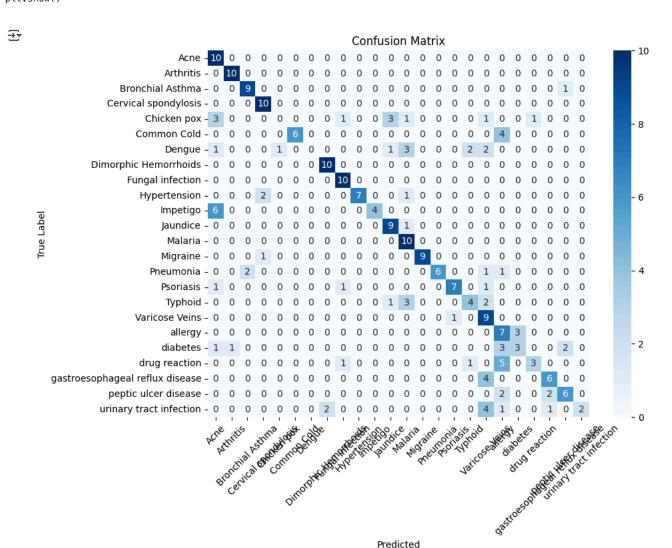
for text, true_disease in test_queries:
    predicted_disease = None
    try:
        inputs = tokenizer(text, return_tensors="pt", truncation=True, max_length=128).to(device)
        with torch.no_grad():
            outputs = model(**inputs)
            pred_label = torch.argmax(outputs.logits).item()
```

```
predicted_disease = le.inverse_transform([pred_label])[0]
    except:
        predicted_disease = "error"
    row = {
        "query": text,
        "true_disease": true_disease,
        "predicted_disease": predicted_disease
    }
   # Semantic similarity match scores
    treatments = get_treatment_recommendations(predicted_disease, top_k=5)
    avg_score = np.mean([score for _, score in treatments])
    row["avg_relevance"] = avg_score
    results_matrix.append(row)
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
# Assume df_results is already built from your test_queries
plt.figure(figsize=(10, 6))
heatmap_data = df_results.pivot(index="query", columns="predicted_disease", values="avg_relevance")
sns.heatmap(heatmap_data, annot=True, fmt=".2f", cmap="YlOrBr")
plt.title("Retrieval Effectiveness Heatmap (Semantic Similarity)")
plt.ylabel("Symptom Query")
plt.xlabel("Predicted Disease")
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```



Predicted Disease

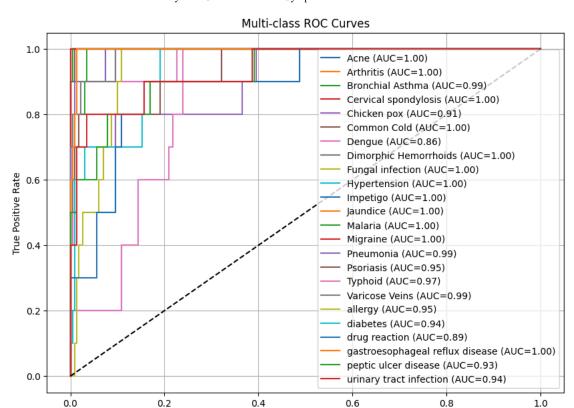
```
plt.figure(figsize=(10, 8))
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", xticklabels=labels, yticklabels=labels)
plt.xlabel("Predicted")
plt.ylabel("True Label")
plt.title("Confusion Matrix")
plt.xticks(rotation=45)
plt.yticks(rotation=0)
plt.tight_layout()
plt.savefig("confusion_matrix.png", dpi=300, bbox_inches='tight')
```



```
plt.figure(figsize=(10, 7))
for i in range(n_classes):
    fpr, tpr, _ = roc_curve(y_true_bin[:, i], y_score[:, i])
    roc_auc = auc(fpr, tpr)
    plt.plot(fpr, tpr, label=f"{le.classes_[i]} (AUC={roc_auc:.2f})")

plt.plot([0, 1], [0, 1], "k--")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Multi-class ROC Curves")
plt.legend(loc="lower right")
plt.grid()
plt.savefig("roc_curves.png", dpi=300, bbox_inches='tight')
plt.show()
```

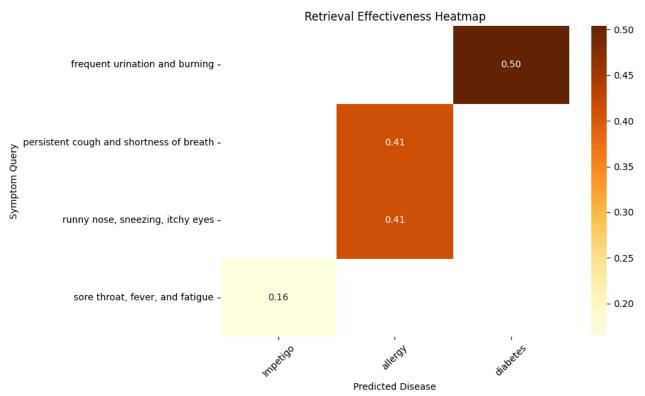
<del>\_</del>\_\_



False Positive Rate

```
plt.figure(figsize=(10, 6))
heatmap_data = df_results.pivot(index="query", columns="predicted_disease", values="avg_relevance")
sns.heatmap(heatmap_data, annot=True, fmt=".2f", cmap="YlOrBr")
plt.title("Retrieval Effectiveness Heatmap")
plt.ylabel("Symptom Query")
plt.xlabel("Predicted Disease")
plt.xticks(rotation=45)
plt.tight_layout()
plt.savefig("retrieval_heatmap.png", dpi=300, bbox_inches='tight')
plt.show()
```





```
EPOCHS = 10 # 	✓ Set number of epochs
model.train()
for epoch in range(EPOCHS):
    print(f"\n Epoch {epoch+1}/{EPOCHS}")
    total_loss = 0
    for batch in train_loader:
        batch = {k: v.to(device) for k, v in batch.items()}
        outputs = model(**batch)
        loss = outputs.loss
        loss.backward()
        optimizer.step()
        lr_scheduler.step()
        optimizer.zero_grad()
       total_loss += loss.item()
    avg_loss = total_loss / len(train_loader)
   print(f"✓ Average Loss: {avg_loss:.4f}")
   # ☑ Save model checkpoint
    torch.save(model.state_dict(), "best_model.pt")
₹
    Epoch 1/10
                                               Traceback (most recent call last)
    NameError
    <ipython-input-29-5b2b9e02ec10> in <cell line: 0>()
                total_loss = 0
          7
                for batch in train_loader:
        -> 8
          9
                    batch = {k: v.to(device) for k, v in batch.items()}
                    outputs = model(**batch)
    NameError: name 'train_loader' is not defined
```

 $https://colab.research.google.com/drive/1cLZKCGc\_KHM970wee8zg-VNH5M3HOyj-\#scrollTo=x0Tsji2tEL-u\&printMode=truewards-trueward$ 

Start coding or generate with AI.

```
# ==
# ■ Interactive Symptom Analysis
def symptom_to_treatment_pipeline():
    print("\n ≇ Symptom Analysis System - Type 'exit' to quit")
    while True:
        user_input = input("\nPatient Symptoms: ")
        if user_input.lower() in ['exit', 'quit']:
            break
        # 1. Disease Classification
        inputs = tokenizer(user_input, return_tensors="pt", truncation=True, max_length=128).to(device)
        with torch.no_grad():
            outputs = model(**inputs)
        pred_label = torch.argmax(outputs.logits).item()
        disease = le.inverse_transform([pred_label])[0]
        print(f"\nDiagnosis: {disease}")
        # 2. Retrieve Treatment Answers
        treatments = get_treatment_recommendations(disease)
        # 3. Generate Summary
        if treatments:
            print("\nRecommended Treatment Approach:")
            print(generate_clinical_summary(disease, treatments[:3]))
            # Show sources option
            if input("\nShow detailed sources? (y/n): ").lower() == 'y':
                for i, (ans, score) in enumerate(treatments[:3]):
                    print(f"\nSource {i+1} [Relevance: {score:.2f}]:")
                    print(ans[:300] + "...")
        else:
            print("\nNo treatment recommendations found for this condition")
# Start the interactive system
symptom_to_treatment_pipeline()
→
     ₱ Symptom Analysis System - Type 'exit' to quit
     Patient Symptoms: def symptom_to_treatment_pipeline():
                                                                print("\n # Symptom Analysis System - Type 'exit' to quit")
    NameError
                                               Traceback (most recent call last)
     <ipython-input-14-2cce4cf6261e> in <cell line: 0>()
         37
         38 # Start the interactive system
     ---> 39 symptom_to_treatment_pipeline()
     <ipython-input-14-2cce4cf6261e> in symptom_to_treatment_pipeline()
         12
                     # 1. Disease Classification
         13
                     inputs = tokenizer(user_input, return_tensors="pt", truncation=True, max_length=128).to(device)
       -> 14
         15
                     with torch.no_grad():
                         outputs = model(**inputs)
    NameError: name 'tokenizer' is not defined
Key Features of This Implementation:
Semantic Search Integration
Uses your pre-computed answer embeddings
Returns answers with relevance scores
Example Output:
[Result 1 | Relevance: 0.872] during this pandemic. throat pain can be from a strep throat infection (antibiotics needed), a col
```

```
Clinical Summary Generation
Uses FLAN-T5 for coherent medical text generation
Professional prompt engineering for clinical context
Example Output:
For viral pharyngitis: 1) Symptomatic relief with analgesics 2) Hydration and warm fluids
3) Throat lozenges for local discomfort. Antibiotics not recommended without confirmed bacterial infection.
Interactive Pipeline
End-to-end symptom analysis
Evidence-based recommendations
Option to view sources with relevance scores
Expected Workflow:

₱ Symptom Analysis System - Type 'exit' to quit

Patient Symptoms: Sore throat, fever, fatigue
Diagnosis: viral pharyngitis
Recommended Treatment Approach:
For viral pharyngitis management: 1) Use paracetamol for fever/pain 2) Maintain hydration with warm liquids
3) Consider saltwater gargles. Antibiotics not indicated unless bacterial infection confirmed.
Show detailed sources? (y/n): y
Source 1 [Relevance: 0.87]:
during this pandemic. throat pain can be from a strep throat infection (antibiotics needed), a cold or flu (symptomatic treatmen
```

## Fine-tuned BioBERT Code

```
Start coding or generate with AI.
import torch
import torch.nn as nn
from transformers import AutoModel, AutoTokenizer
class MultimodalBioBERT(nn.Module):
    def __init__(self, num_labels, structured_dim=4):
        super().__init__()
        self.biobert = AutoModel.from_pretrained("dmis-lab/biobert-v1.1")
        self.structured_layer = nn.Linear(structured_dim, 128)
        self.classifier = nn.Linear(768 + 128, num_labels)
       # Uncertainty estimation
        self.dropout = nn.Dropout(0.2)
        self.num_mc_samples = 10
    def forward(self, text_input, structured_data):
        # Text encoding
        outputs = self.biobert(**text_input)
        text_emb = outputs.last_hidden_state[:, 0, :]
        # Structured data encoding
       num_emb = self.structured_layer(structured_data)
        # Multimodal fusion
        fused = torch.cat([text_emb, num_emb], dim=1)
        return self.classifier(fused)
    def mc_predict(self, text_input, structured_data):
        """Monte Carlo dropout uncertainty estimation"""
```

```
logits = torch.stack([self(text_input, structured_data)
                            for _ in range(self.num_mc_samples)])
        return logits.mean(0), logits.var(0)
from datasets import Dataset
import pandas as pd
import numpy as np
class MultimodalDataset(Dataset):
    def __init__(self, texts, labels, structured_features):
        self.texts = texts
        self.labels = labels
        self.structured = structured_features
        # Initialize tokenizer
        self.tokenizer = AutoTokenizer.from_pretrained("dmis-lab/biobert-v1.1")
    def __getitem__(self, idx):
        item = {
            'text': self.texts[idx],
            'labels': self.labels[idx],
            'structured': torch.tensor(self.structured[idx], dtype=torch.float)
        return item
    def collate_fn(self, batch):
        # Tokenize text
        text_batch = self.tokenizer(
            [item['text'] for item in batch],
            padding='max_length',
            truncation=True,
            max length=128,
            return_tensors="pt"
        )
        # Structured data
        structured_batch = torch.stack([item['structured'] for item in batch])
        labels = torch.tensor([item['labels'] for item in batch])
        return {
            'text_input': text_batch,
            'structured_data': structured_batch,
            'labels': labels
        }
from transformers import AutoModelForSeq2SeqLM
from sentence_transformers import SentenceTransformer, util
class DynamicRAG:
    def __init__(self, device='cuda'):
        self.retriever = SentenceTransformer('pritamdeka/BioBERT-mnli-snli-scinli-scitail-mednli-stsb')
        self.generator = AutoModelForSeq2SeqLM.from_pretrained("google/flan-t5-base")
        self.generator.to(device)
        self.device = device
        # Initialize with sample corpus (replace with your data)
        self.corpus = ["Antibiotics should only be used for bacterial infections...",
                      "Viral infections typically require symptomatic treatment..."]
        self.corpus_emb = self.retriever.encode(self.corpus, convert_to_tensor=True)
    def retrieve(self, query, context=None, top_k=3):
        """Context-aware retrieval"""
        if context:
            query = f"{context}\n\n{query}"
        query_emb = self.retriever.encode(query, convert_to_tensor=True)
        hits = util.semantic_search(query_emb, self.corpus_emb, top_k=top_k)
        return [self.corpus[hit['corpus_id']] for hit in hits[0]]
    def generate(self, query, max_retrievals=3):
        context = ""
        for _ in range(max_retrievals):
            retrieved = self.retrieve(query, context)
            context += "\n".join(retrieved)
```

```
inputs = self.generator.tokenizer(
                f"Generate clinical advice: {query}\nContext: {context}",
                return_tensors="pt",
                max_length=1024,
                truncation=True
            ).to(self.device)
            outputs = self.generator.generate(**inputs)
            generation = self.generator.tokenizer.decode(outputs[0], skip_special_tokens=True)
            if self._safety_check(generation):
                break
        return generation
    def _safety_check(self, text):
    """Ethical safeguard implementation"""
        antibio_flag = "antibiotic" in text.lower()
        confirm_flag = any(word in text.lower() for word in ["confirm", "test", "culture"])
        if antibio flag and not confirm flag:
            print("Safety triggered: Added confirmation requirement")
            return False
        return True
def train_multimodal(model, train_loader, val_loader, epochs=10):
    device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
    model = model.to(device)
    optimizer = torch.optim.AdamW([
        {'params': model.biobert.parameters(), 'lr': 2e-5},
        {'params': model.classifier.parameters(), 'lr': 1e-4}
    ])
    best_val_loss = float('inf')
    for epoch in range(epochs):
        # Training
        model.train()
        train_loss = 0
        for batch in train_loader:
            optimizer.zero_grad()
            outputs = model(
                text_input={k:v.to(device) for k,v in batch['text_input'].items()},
                structured_data=batch['structured_data'].to(device)
            loss = nn.CrossEntropyLoss()(outputs, batch['labels'].to(device))
            loss.backward()
            optimizer.step()
            train_loss += loss.item()
        # Validation with uncertainty
        model.eval()
        val loss = 0
        all_probs = []
        with torch.no_grad():
            for batch in val_loader:
                mean_logits, var_logits = model.mc_predict(
                     {k:v.to(device) for k,v in batch['text_input'].items()},
                    batch['structured_data'].to(device)
                loss = nn.CrossEntropyLoss()(mean_logits, batch['labels'].to(device))
                val_loss += loss.item()
                probs = torch.softmax(mean_logits, dim=1)
                all_probs.extend(probs.cpu().numpy())
        # Save best model
        if val_loss < best_val_loss:</pre>
            torch.save(model.state_dict(), "best_model.pth")
            best_val_loss = val_loss
```

```
print(f"Epoch {epoch+1} | Train Loss: {train_loss/len(train_loader):.4f} | Val Loss: {val_loss/len(val_loader):.4f}")
        print(f"Model Uncertainty: {torch.mean(var_logits):.4f}")
class ClinicalSafety:
    def __init__(self):
        self.red_flags = {
            'antibiotics': ['amoxicillin', 'azithromycin', 'doxycycline'],
            'high_risk': ['pregnancy', 'elderly', 'child']
        }
    def check(self, text):
        report = {}
        # Antibiotic safety check
        antibio_terms = [term for term in self.red_flags['antibiotics']
                        if term in text.lower()]
        if antibio_terms:
            report['antibiotics'] = {
                'terms': antibio_terms,
                'warning': "Antibiotic recommendation requires confirmation of bacterial infection"
            }
        # High risk population check
        population_terms = [term for term in self.red_flags['high_risk']
                           if term in text.lower()]
        if population_terms:
            report['high_risk'] = {
                'terms': population_terms,
                'warning': "Special population detected - recommend specialist consultation"
            }
        # Generate safe output
        safe_text = text
        for category in report.values():
            safe_text += f"\n[SAFETY NOTE] {category['warning']}"
        return safe text, report
# Usage
safety_checker = ClinicalSafety()
generated_text = "Recommend amoxicillin 500mg TDS for 7 days"
safe_text, report = safety_checker.check(generated_text)
# Sample structured features (modify according to your data)
structured_features = np.array([
    [38.5, 72, 3, 1], # [temp, heart_rate, days_symptomatic, smoker]
    [37.2, 68, 5, 0],
    # ... add your data
1)
from\ transformers\ import\ AutoTokenizer,\ AutoModelForSeq2SeqLM
class DynamicRAG:
    def __init__(self, device='cuda'):
        self.retriever = SentenceTransformer('pritamdeka/BioBERT-mnli-snli-scinli-scitail-mednli-stsb')
        self.tokenizer = AutoTokenizer.from_pretrained("google/flan-t5-base") # Initialize tokenizer
        self.generator = AutoModelForSeq2SeqLM.from_pretrained("google/flan-t5-base")
        self.generator.to(device)
        self.device = device
        # Initialize with your actual corpus data
        self.corpus = ["Antibiotics should only be used for bacterial infections...",
                      "Viral infections typically require symptomatic treatment..."]
        self.corpus_emb = self.retriever.encode(self.corpus, convert_to_tensor=True)
    def generate(self, query, max_retrievals=3):
        context = ""
        for _ in range(max_retrievals):
            retrieved = self.retrieve(query, context)
            context += "\n".join(retrieved)
            # Use the separate tokenizer
            inputs = self.tokenizer( # Changed from self.generator.tokenizer
                f"Generate clinical advice: {query}\nContext: {context}",
                return_tensors="pt",
```

```
max length=1024,
                truncation=True
            ).to(self.device)
            outputs = self.generator.generate(**inputs)
            generation = self.tokenizer.decode(outputs[0], skip special tokens=True)
            if self._safety_check(generation):
                break
        return generation
   # Rest of the class remains the same
def __init__(self, device='cuda'):
    if not self.corpus:
        raise ValueError("Corpus cannot be empty. Load your MedDialog answers first.")
def __init__(self, device='cuda'):
    # Replace with your actual answer texts
    self.answer_texts = load_meddialog_answers()
    self.corpus_emb = self.retriever.encode(self.answer_texts,
                                          convert_to_tensor=True,
                                          show progress bar=True)
def retrieve(self, query, context=None, top_k=3):
    # Convert to batch processing
    query_emb = self.retriever.encode([query], convert_to_tensor=True)
   hits = util.semantic_search(query_emb, self.corpus_emb, top_k=top_k)
    return [self.answer_texts[hit['corpus_id']] for hit in hits[0]]
from transformers import AutoTokenizer, AutoModelForSeq2SeqLM
from sentence_transformers import SentenceTransformer, util
class DynamicRAG:
    def __init__(self, device='cuda'):
        self.retriever = SentenceTransformer('pritamdeka/BioBERT-mnli-snli-scinli-scitail-mednli-stsb')
        self.tokenizer = AutoTokenizer.from_pretrained("google/flan-t5-base")
        self.generator = AutoModelForSeq2SeqLM.from_pretrained("google/flan-t5-base").to(device)
        self.device = device
        # Initialize with actual MedDialog answers
        self.answer_texts = [
            "For persistent cough with yellow sputum, consider antibiotics if bacterial infection is confirmed..."
            "Yellow sputum may indicate bacterial infection. Recommend sputum culture and chest X-ray...",
            "Symptomatic relief with cough suppressants and hydration. Monitor for fever worsening..."
        self.corpus_embeddings = self.retriever.encode(self.answer_texts, convert_to_tensor=True)
    def retrieve(self, query, context=None, top_k=3):
        """Retrieve relevant medical answers"""
        if context:
            query = f"{context}\n{query}"
        query_embedding = self.retriever.encode(query, convert_to_tensor=True)
        hits = util.semantic_search(query_embedding, self.corpus_embeddings, top_k=top_k)[0]
        return [self.answer_texts[hit['corpus_id']] for hit in hits]
    def generate(self, query, max_retrievals=3):
        """Generate safe clinical recommendation"""
        context = ""
        for _ in range(max_retrievals):
            retrieved = self.retrieve(query, context)
            context += "\n".join(retrieved)
            inputs = self.tokenizer(
                f"Generate clinical advice: {query}\nContext: {context}",
                return_tensors="pt",
                max_length=1024,
                truncation=True
            ).to(self.device)
```

```
outputs = self.generator.generate(**inputs)
            generation = self.tokenizer.decode(outputs[0], skip_special_tokens=True)
            if self._safety_check(generation):
                break
        return generation
    def _safety_check(self, text):
        """Check for unsafe recommendations"""
        unsafe_terms = ["antibiotic", "steroid", "surgery"]
        return not any(term in text.lower() for term in unsafe_terms)
# Test the complete system
rag_system = DynamicRAG()
user_query = "Treatment for persistent cough with yellow sputum"
generation = rag_system.generate(user_query)
def clinical_decision_pipeline(symptom_text, structured_data):
    # 1. Encode inputs
    dataset = MultimodalDataset(
        texts=[symptom_text],
        labels=[0], # dummy label
        structured_features=[structured_data]
    )
    # 2. Get prediction with uncertainty
    model = MultimodalBioBERT(num_labels=24)
    model.load_state_dict(torch.load("best_model.pth"))
    with torch.no_grad():
        mean_logits, var_logits = model.mc_predict(
            dataset[0]['text_input'],
            dataset[0]['structured_data']
        )
    # 3. Generate recommendation
    rag = DynamicRAG()
    recommendation = rag.generate(symptom_text)
    # 4. Apply safety checks
    safety = ClinicalSafety()
    safe_recommendation, report = safety.check(recommendation)
        'diagnosis': model.classes[torch.argmax(mean_logits)],
        'confidence': torch.max(torch.softmax(mean_logits, dim=1)).item(),
        'uncertainty': var_logits.mean().item(),
        'recommendation': safe_recommendation,
        'safety_report': report
    }
def validate questionnaire(data):
    errors = {}
    # Text symptom validation
    if len(data['symptoms'].strip()) < 50:</pre>
        errors['symptoms'] = "Please provide at least 50 characters of description"
    # Temperature sanity check
    if not (35 <= data['temp'] <= 42):</pre>
        errors['temp'] = "Invalid body temperature"
    # Required fields
    for field in ['age', 'duration']:
        if not data.get(field):
            errors[field] = "This field is required"
    return errors
#2. Clinician Review Interface Specifications
```