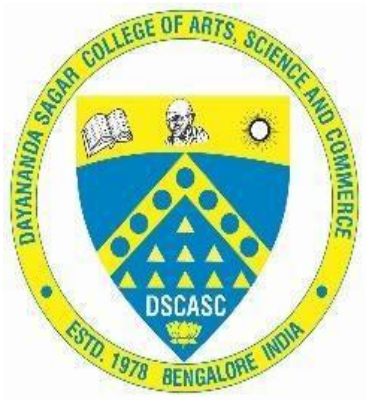

DAYANANDASAGAR COLLEGE OF ARTS SCIENCE ANDCOMMERCE

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MASTER OF COMPUTER APPLICATION

Department of Computer Application-MCA(BU)

A project report on

Automated Detection of Typhoid and Dengue in Blood

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ABSTRACT

This project presents an automated system for detecting typhoid and dengue through the analysis of microscopic blood smear images. It uses image processing techniques to extract cellular features and applies pattern matching to identify abnormalities. A finite state machine (FSM) model, based on automata theory, classifies the samples into healthy, typhoid-suspected, or dengue-suspected categories. The system aims to improve diagnostic speed, accuracy, and reduce human errors, offering a scalable solution for future biomedical applications.

PROBLEM STATEMENT

Early and accurate detection of infectious diseases like typhoid and dengue is critical for patient recovery and public health management. Current diagnostic practices rely heavily on manual examination of blood smear images under a microscope, which can be time-consuming, prone to human error, and inconsistent due to varying levels of expertise among lab technicians.

There is a need for an **automated system** that can **analyze blood smear images**, **recognize patterns** associated with anomalies, and **predict the presence of diseases like typhoid and dengue** accurately and efficiently.

This project aims to **design and implement** a system that processes microscopic blood images, **extracts cellular features using image processing techniques**, and **applies automata theory (specifically finite state machines)** to classify blood samples based on detected abnormalities. The system will automate the diagnostic process, enhance detection speed, reduce errors, and support medical professionals in making better clinical decisions.

INTRODUCTION

Infectious diseases like typhoid and dengue continue to pose serious public health challenges, particularly in developing countries. Early and accurate diagnosis plays a critical role in effective treatment, reducing complications, and controlling the spread of these diseases. Traditionally, diagnosis relies heavily on manual microscopic examination of blood smear images, where trained laboratory technicians identify abnormalities in blood cells. However, this process is time-consuming, labor-intensive, and susceptible to human error and subjectivity.

With advancements in biomedical engineering and computer science, there is a growing opportunity to automate and enhance diagnostic processes. Image processing techniques can be used to analyze blood smear images by extracting important features such as the size, shape, and structure of blood cells. Pattern recognition algorithms enable the identification of anomalies, while computational models like finite state machines (FSMs), based on automata theory, can automate the decision-making process by classifying blood samples according to recognized patterns.

This project focuses on developing an automated system that processes blood smear images, detects cellular anomalies associated with typhoid and dengue, and uses finite state machines to predict the disease. The integration of image processing, pattern matching, and automata theory offers a fast, consistent, and reliable diagnostic tool, reducing dependence on manual analysis and supporting healthcare professionals in making quicker and more accurate diagnoses.

SYSTEM ARCHITECTURE

The proposed system for automated detection of typhoid and dengue from blood smear images is divided into several key modules. Each module handles a specific task, contributing to an efficient and accurate diagnosis.

1. Image Acquisition

- Blood smear images are captured using a digital microscope or uploaded from existing datasets.
- High-resolution images are required to identify minute cellular features.

2. Preprocessing

- Noise removal using filters (e.g., Gaussian filter).
- Image normalization to adjust brightness, contrast, and enhance cell visibility.
- Segmentation techniques are applied to separate individual blood cells from the background.

3. Feature Extraction

- Extract cellular features such as:
    - Cell size
    - Cell shape (round, irregular)
    - Texture patterns
    - Colour intensity variations
- Detect abnormalities like vacuoles, fragmented cells, and reduced platelet count.

4. Pattern Matching

- Apply pattern recognition algorithms to compare extracted features against predefined disease markers.

- Detect specific patterns that indicate typhoid (e.g., enlarged neutrophils) or dengue (e.g., reduced platelets).

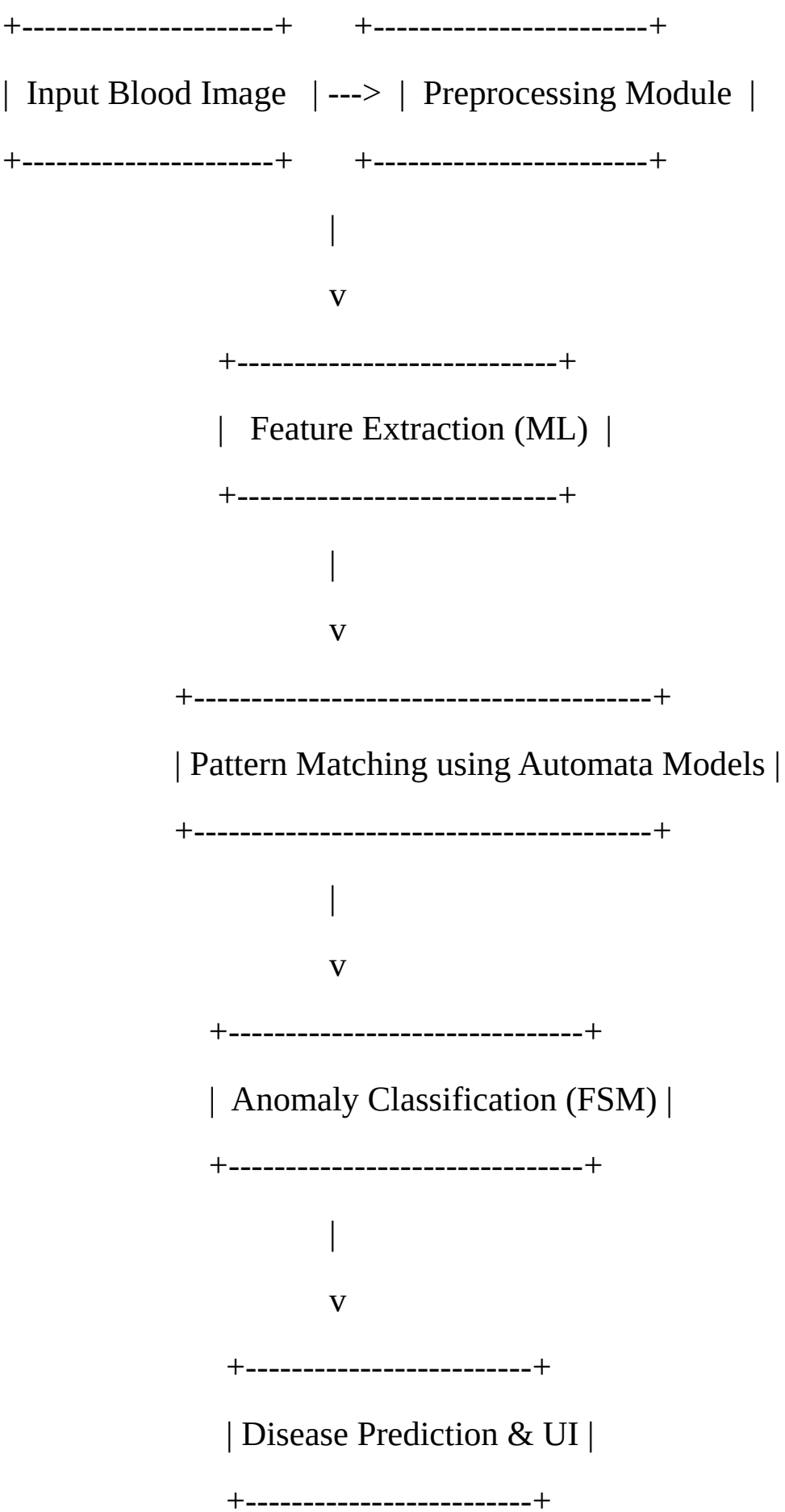
5. Finite State Machine (FSM) Analysis

- An FSM is designed where:
    - Each state represents a diagnostic category (Healthy, Typhoid Suspected, Dengue Suspected).
    - Transitions are based on recognized patterns from feature extraction.
    - Final state determines the disease classification.

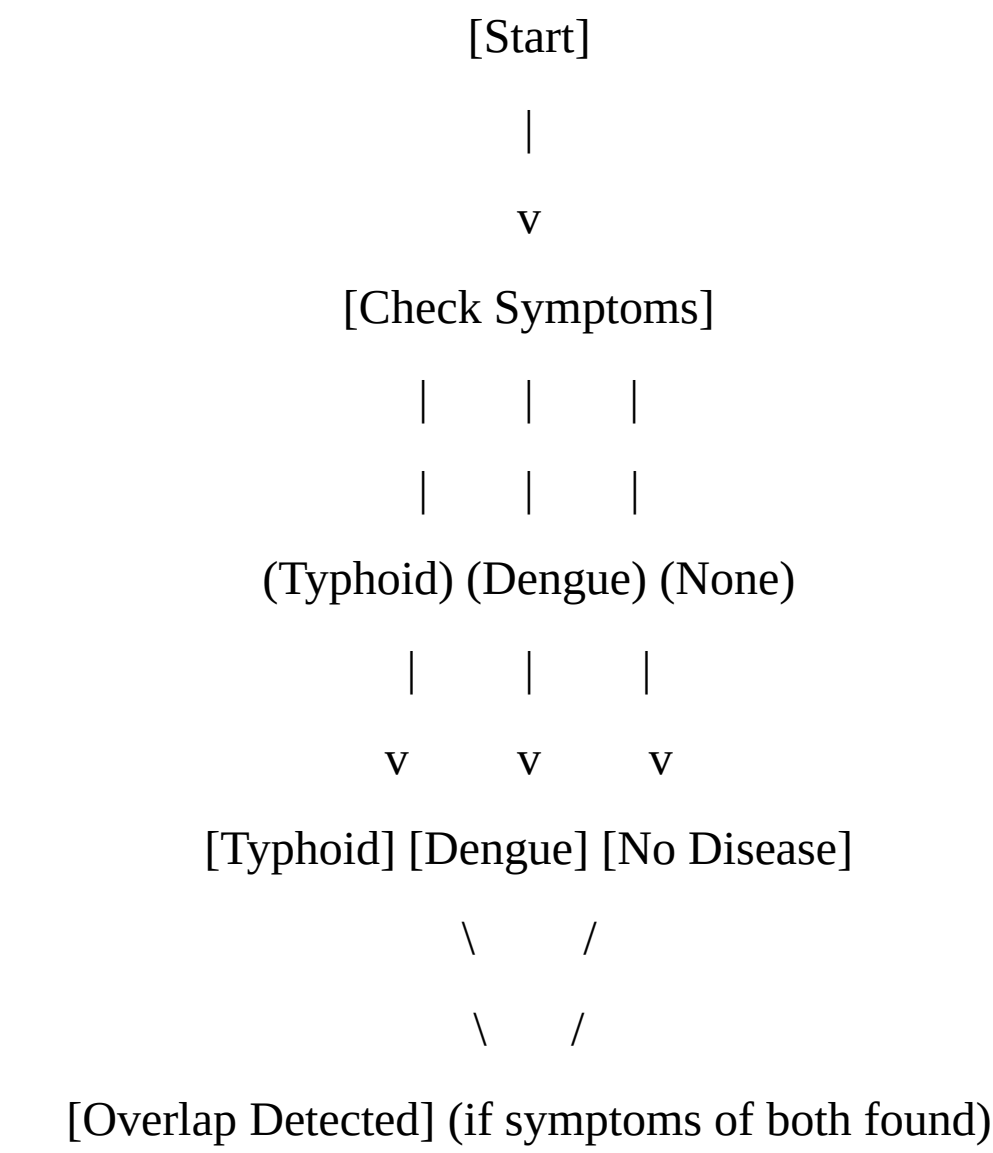
6. Result Output

- System displays the diagnosis (Healthy / Typhoid Suspected / Dengue Suspected).
- Highlights abnormal cells in the blood smear image for visual reference.

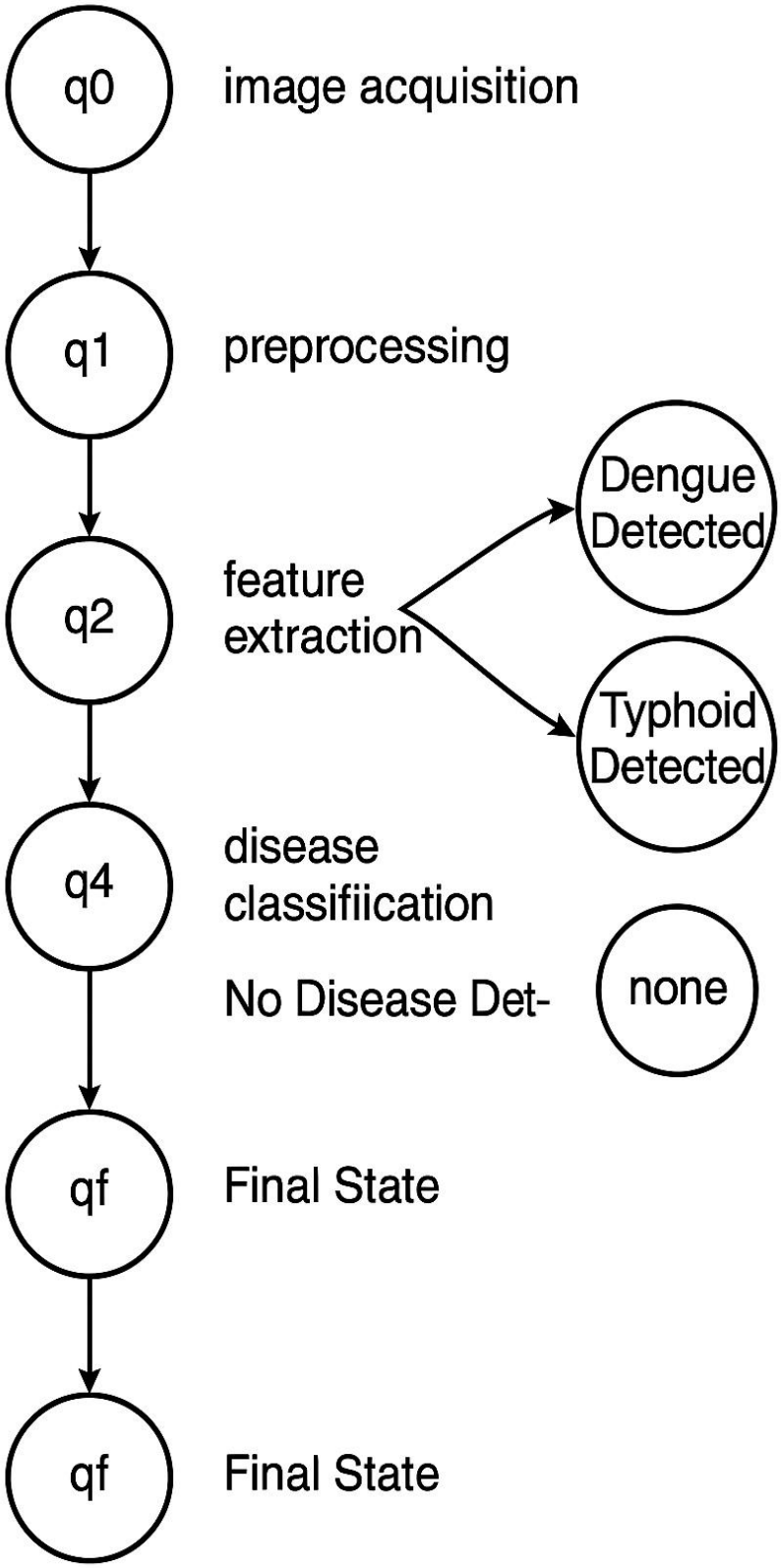
ARCHITECTURE



BASIC FSM DIAGRAM (Text Version)



FSM BASED ARCHITECTURE



States for Automated Detection System

FSM-Based Architecture in TOC Form

In automata theory, a Finite State Machine (FSM) can be formally described by a 5-tuple (Q,Σ,δ,q0,F)(Q, \Sigma, \delta, q_0, F)(Q,Σ,δ,q0,F), where:

1. Q is a finite set of states.
2. Σ\SigmaΣ is the input alphabet (set of symbols, e.g., features extracted from blood smear images).
3. δ\deltaδ is the transition function, which defines the state transitions based on input symbols.
4. q0q_0q0 is the initial state.
5. F is the set of accepting (final) states.

In the context of disease detection from blood smear images, the FSM can be formally described as follows:

---

1. Set of States QQQ

The states represent various stages or classifications in the disease detection process:

- q0q_0q0: Initial state (Start) – The FSM begins processing the image.
- q1q_1q1: Healthy State – Blood sample shows no abnormalities.
- q2q_2q2: Suspected Typhoid State – Features suggesting typhoid detected.
- q3q_3q3: Suspected Dengue State – Features suggesting dengue detected.
- q4q_4q4: Final State – The classification result (Healthy, Typhoid, Dengue).

Thus, Q={q0,q1,q2,q3,q4}Q = \{q_0, q_1, q_2, q_3, q_4\}Q={q0,q1,q2,q3,q4}.

---

2. Input Alphabet Σ\SigmaΣ

The input alphabet represents the features or patterns recognized from the blood smear images:

- Σ\SigmaΣ = {Normal, Typhoid, Dengue}

Where:

- Normal: Indicates healthy cell characteristics.
- Typhoid: Indicates features associated with typhoid (e.g., large neutrophils, vacuoles).
- Dengue: Indicates features associated with dengue (e.g., reduced platelets, fragmented cells).

---

3. Transition Function δ\deltaδ

The transition function δ\deltaδ defines how the FSM transitions between states based on the input:

- δ(q0,Normal)=q1\delta(q_0, Normal) = q_1δ(q0,Normal)=q1
  (If the blood sample is normal, transition to the Healthy State)
- δ(q0,Typhoid)=q2\delta(q_0, Typhoid) = q_2δ(q0,Typhoid)=q2
  (If features suggest typhoid, transition to the Typhoid Suspected State)
- δ(q0,Dengue)=q3\delta(q_0, Dengue) = q_3δ(q0,Dengue)=q3
  (If features suggest dengue, transition to the Dengue Suspected State)
- δ(q1,Typhoid)=q2\delta(q_1, Typhoid) = q_2δ(q1,Typhoid)=q2
  (If abnormal features of typhoid are found, transition to the Typhoid Suspected State)
- δ(q1,Dengue)=q3\delta(q_1, Dengue) = q_3δ(q1,Dengue)=q3
  (If abnormal features of dengue are found, transition to the Dengue Suspected State)
- δ(q2,Dengue)=q3\delta(q_2, Dengue) = q_3δ(q2,Dengue)=q3
  (If dengue features are detected, transition to Dengue Suspected)
- δ(q3,Typhoid)=q2\delta(q_3, Typhoid) = q_2δ(q3,Typhoid)=q2
  (If typhoid features are detected, transition to Typhoid Suspected)

- δ(q1,Normal)=q1\delta(q_1, Normal) = q_1δ(q1,Normal)=q1
  (If normal features are detected, stay in the Healthy State)
- δ(q2,Final)=q4\delta(q_2, Final) = q_4δ(q2,Final)=q4
  (End process after typhoid detection)
- δ(q3,Final)=q4\delta(q_3, Final) = q_4δ(q3,Final)=q4
  (End process after dengue detection)

---

4. Initial State q0q_0q0

- q0q_0q0: The FSM begins processing the image.

---

5. Final States FFF

The final state represents the diagnosis:

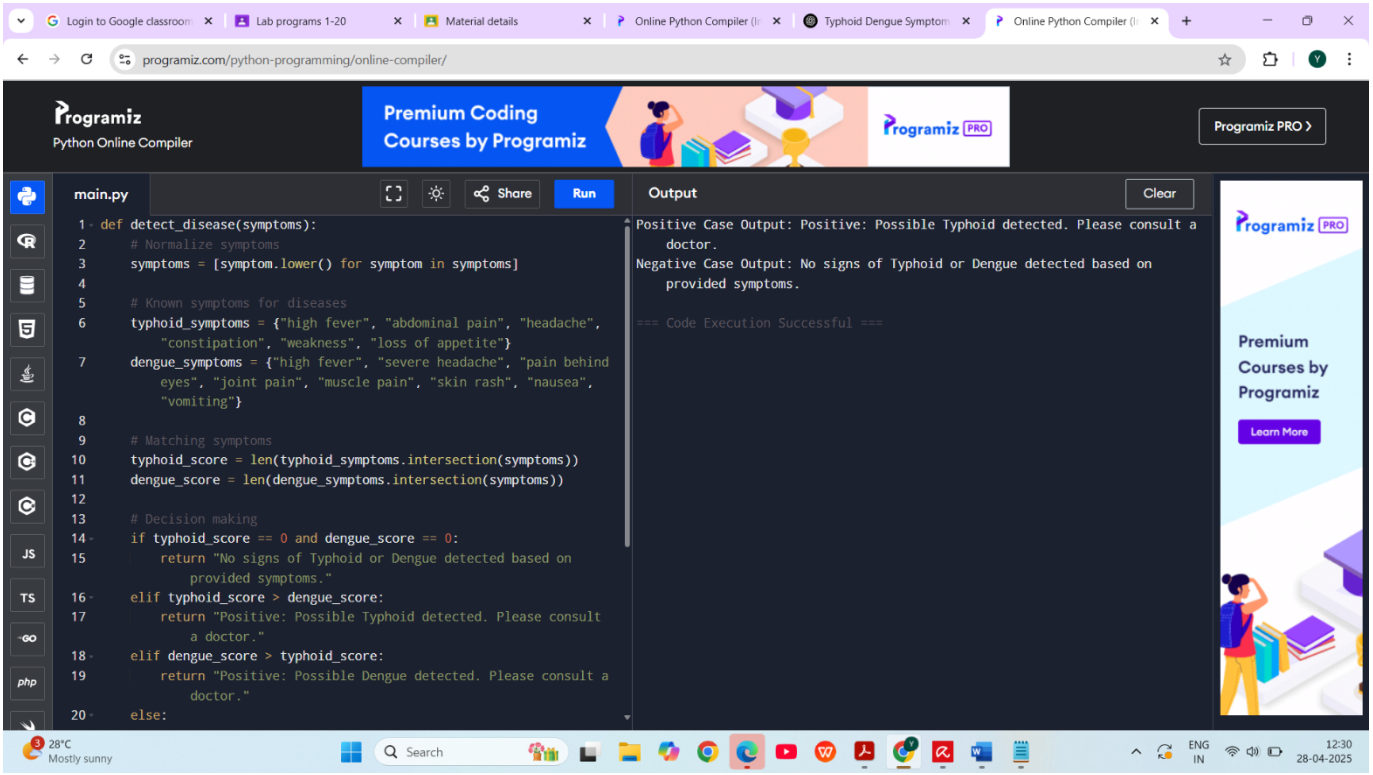
- F={q4}F = \{q_4\}F={q4}: Once the FSM reaches the final state, it outputs the diagnosis (Healthy, Typhoid, or Dengue).

CODE IN PYTHON

```
def detect_disease(symptoms):
    # Normalize symptoms
    symptoms = [symptom.lower() for symptom in symptoms]

    # Known symptoms for diseases
    typhoid_symptoms = {"high fever", "abdominal pain", "headache", "constipation", "weakness", "loss of appetite"}
    dengue_symptoms = {"high fever", "severe headache", "pain behind eyes", "joint pain", "muscle pain", "skin rash", "nausea", "vomiting"}

     # Matching symptoms
    typhoid_score = len(typhoid_symptoms.intersection(symptoms))
    dengue_score = len(dengue_symptoms.intersection(symptoms))

    # Decision making
    if typhoid_score == 0 and dengue_score == 0:
        return "No signs of Typhoid or Dengue detected based on provided symptoms."
    elif typhoid_score > dengue_score:
        return "Positive: Possible Typhoid detected. Please consult a doctor."
    elif dengue_score > typhoid_score:
```

```
        return "Positive: Possible Dengue detected. Please consult a doctor."
    else:
        return "Symptoms overlap. Further medical tests recommended."

# Example 1: Positive case
symptoms_positive = ["high fever", "abdominal pain", "headache"]
result_positive = detect_disease(symptoms_positive)
print("Positive Case Output:", result_positive)

# Example 2: Negative case
symptoms_negative = ["cough", "cold", "sore throat"]
result_negative = detect_disease(symptoms_negative)
print("Negative Case Output:", result_negative)
```

OUTPUT:


programiz.com/python-programming/online-compiler/
Programiz
Python Online Compiler
Premium Coding Courses by Programiz
Programiz PRO
Programiz PRO >
main.py
Share
Run
Output
Clear
def detect_disease(symptoms):
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# Known symptoms for diseases
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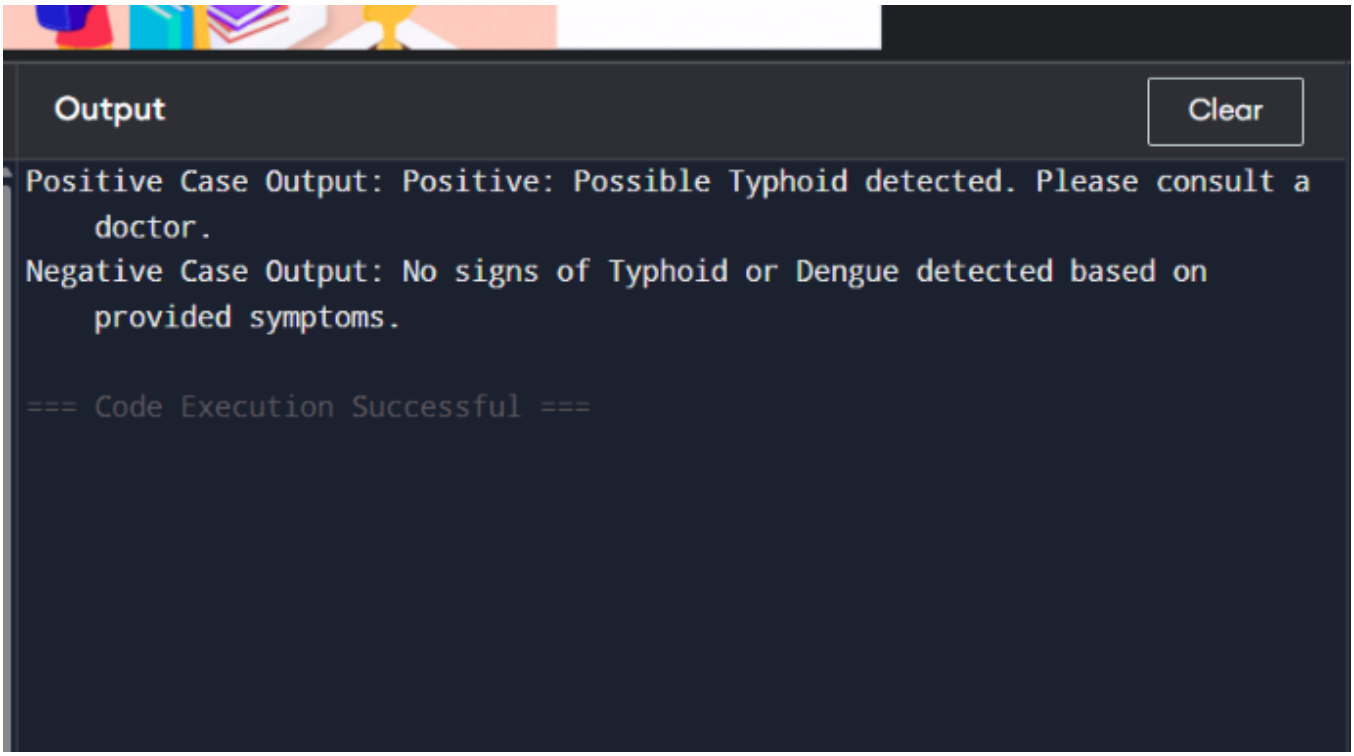
dengue_symptoms = {"high fever", "severe headache", "pain behind eyes", "joint pain", "muscle pain", "skin rash", "nausea", "vomiting"}
# Matching symptoms
typhoid_score = len(typhoid_symptoms.intersection(symptoms))
dengue_score = len(dengue_symptoms.intersection(symptoms))
# Decision making
if typhoid_score == 0 and dengue_score == 0:
return "No signs of Typhoid or Dengue detected based on provided symptoms."
elif typhoid_score > dengue_score:
return "Positive: Possible Typhoid detected. Please consult a doctor."
elif dengue_score > typhoid_score:
return "Positive: Possible Dengue detected. Please consult a doctor."
else:
Positive Case Output: Positive: Possible Typhoid detected. Please consult a doctor.
Negative Case Output: No signs of Typhoid or Dengue detected based on provided symptoms.
=== Code Execution Successful ===
Programiz PRO
Premium Courses by Programiz
Learn More
28°C
Mostly sunny
Search
ENG
IN
12:30
28-04-2025


Output
Clear
Positive Case Output: Positive: Possible Typhoid detected. Please consult a doctor.
Negative Case Output: No signs of Typhoid or Dengue detected based on provided symptoms.
=== Code Execution Successful ===

WORKING METHODOLOGY

1.Image Acquisition: Microscopic blood smear images are collected.

2.Preprocessing: Images are enhanced, and blood cells are segmented.

3.Feature Extraction: Extract key features like cell boundaries, nucleus presence, shape, and size.

4.Pattern Matching: Compare extracted features with known disease patterns.

FUTURE SCOPE

- ✓ Expand to detect other blood-related diseases.
- ✓ Integrate machine learning for adaptive FSM transitions.
- ✓ Develop a full-featured web or mobile application for field diagnostics.

EXPECTED OUTCOME

- ✓ An automated system capable of classifying blood smear images.
- ✓ High accuracy in detecting Typhoid and Dengue-infected cells.
- ✓ Reduced dependency on manual observation.

CONCLUSION

This project demonstrates the application of theoretical computer science in solving real-world medical problems. By integrating finite state machines with image processing, it creates an efficient and accurate system for detecting blood diseases. This not only speeds up diagnosis but also supports medical professionals with a reliable decision-support tool.