Using a Hidden Markov Model for Crop Disease Detection
Capstone Project by Juliana Crystal Holder

Describe the Observations:
 In the crop disease detection system, the **observations** are measurable image features extracted from leaf images over time (e.g., color histograms, texture patterns, lesion size, shape descriptors). If images are captured periodically (e.g., daily), each image provides an observation in the form of a feature vector representing the crop's current visual condition.

Type of HMM Problem:
 This is a **partially observable, unsupervised learning problem**. While we can observe visual symptoms (spots, discoloration, etc.), the **underlying disease state** (e.g., healthy, early infection, advanced infection) is not directly known and must be inferred. Therefore, this is a **learning problem** where hidden states are unknown and must be estimated from the observed image data.

Training Algorithm:
 a. **Known at the Start:**

- Observation sequences (time-series of leaf image features)

- The assumed number of hidden states (e.g., 3: healthy, infected, severely infected)

- Initial estimates for transition and emission probabilities (can be initialized uniformly)

b. **Unknown and Needs to be Learned:**

- Actual disease progression states (hidden states)

- State transition probabilities (likelihood of disease progressing from one stage to another)

- Emission probabilities (likelihood of an observation given a hidden state)

- Initial state probabilities

Training is done using the **Baum-Welch algorithm**, an Expectation-Maximization method that iteratively refines model parameters to maximize the likelihood of the observed data.

Parameter Updates:
 The HMM training process will update the following parameters:

- **Transition matrix (A):** Probabilities of transitioning from one disease state to another over time.

- **Emission matrix (B):** Probabilities of observing specific image features from each disease state.

- **Initial state distribution (π):** The probability of each disease state at the start of observation.

By modeling crop disease progression as a temporal process with HMMs, the system can more accurately predict the stage of disease and intervene at the right time.