

#### Islamic University of Technology (IUT)

# How Divide and Conquer Algorithm can be used in my Research domain

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#### 0.1 My research area

As a member of a bioinformatics research team focused on agricultural applications, my present research interest is on using object detection techniques to identify diseases in rice leaves. Our goal is to use sophisticated techniques to effectively detect areas of disease within rice crops. The mission entails using image processing techniques to separate rice leaf pictures into smaller parts for research purposes. This approach seeks to minimize the detection process, increase computational efficiency, and improve disease identification accuracy. In addition, we extract features from these segmented regions, focusing on key characteristics such as texture, color, and form, in order to properly describe distressed areas.

#### 0.2 Divide and conquer in my research area

In this section I will discuss how divide and conquer can be used in my research. In the case of rice leaf disease identification, divide and conquer techniques can significantly improve the system's efficiency and accuracy.

#### 0.2.1 Image processing

Image processing is frequently used to detect diseased rice leaves. By fragmenting the image into smaller components or segments, each segment can be examined individually for signs of disease. This split enables parallel processing, resulting in faster and more efficient identification, especially when working with enormous data sets or photographs with high resolutions.

#### 0.2.2 Feature Extraction

Extracting significant data from rice leaf images serves as essential for accurate disease identification. Divide and conquer algorithms can be used to extract properties like texture, color, and shape from separate sections of a picture. These obtained characteristics can then be merged to represent the complete leaf, which improves feature extraction accuracy and speed, especially for challenging or detailed photos.

#### 0.2.3 Machine Learning

Machine learning techniques specifically object detection models, play an important role in automated rice leaf disease diagnosis. Divide and conquer strategies can be used inside these algorithms by splitting down the detection work into smaller sub-problems. Advanced models, such as the Detection Transformer (DETR) algorithm, have been developed to determine rice leaf diseases more rapidly by splitting the image into smaller portions and assessing each region separately for disease symptoms. Similarly, Convolutional Neural Networks (CNNs) may process various portions of an image to identify and classify diseases. This strategy not only improves computing efficiency, but it also improves the model's capacity to detect diseases over a wide range of rice leaf images.

#### 0.2.4 My Proposed Divide and Conquer Strategy

**Divide:** Split the high-resolution images of rice leaves into different scales. Each scale focuses on patterns of spotting and diseases within a particular size range.

**Conquer:** Use modified object detection models for each size individually. These algorithms are taught to recognize disease patterns unique to their given scale.

Combine: Combine the detection data from all scales to get a full diagnostic that includes all existing diseases and their severity.

The proposed method uses a hierarchical network architecture for processing rice leaf images at different resolutions, extracting useful data for each level. Adaptive thresholding techniques are used at each scale to effectively distinguish between healthy and distressed tissue. To ensure reliability, training has been carried out using a large dataset that includes images of rice leaves with various diseases taken under various circumstances. Ensemble learning is then used to combine the data from each scale, increasing overall detection accuracy. This technique employs the divide and conquer principle, breaking down the complicated process of illness detection into smaller, more manageable tasks adapted to the unique characteristics of disease patterns at various scales. If successful, this method of analysis has an opportunity to significantly improve the accuracy of rice leaf disease classification, benefiting farmers and agricultural bioinformatics researchers.

## 0.3 Divide and conquer in other areas of bioinformatics

#### 0.3.1 Sequence Alignment

Divide and conquer can help to enhance sequence alignment algorithms. For example, SEAL (a divide-and-conquer approach for sequence alignment) integrates

this approach with the largest contiguous subarray solution to achieve alignments with greater scores than heuristic methods.

#### 0.3.2 Motif Location Prediction

Divide and conquer can be helpful in motif discovery because it helps reduce the search space. Researchers can focus on possible motifs[1] by breaking each DNA sequence into nucleotide subsequences (A, C, G, T), especially since 'G' is found in almost every transcription factor binding sites.

#### 0.3.3 Genome Assembly

In genome assembly[3], the divide and conquer strategy can be used to combine small sequences of DNA into longer ones. Splitting down the genome into smaller segments allows algorithms to control the assembly process with greater effectiveness, especially when dealing with big genomes.

#### 0.3.4 Phylogenetic Tree Construction

This method is also used for constructing phylogenetic trees, where enormous evolutionary trees are generated by initially solving for smaller subtrees and then integrating them to produce the whole tree. This can considerably reduce the computational complexity of the task.

#### 0.3.5 Big Data Analysis

The process is breaking down a large dataset into smaller ones, examining each set independently, and then integrating the results. This method can be particularly beneficial when dealing with the enormous quantity of data produced in bioinformatics research [2].

#### 0.3.6 Underdetermined Systems

The divide-and-conquer method can also be used to assess underdetermined biochemical models[4] by splitting down the global estimate problem into different subproblems that can be resolved with steady-state omics measurement data.

## **Bibliography**

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