1. Introduction

The emergence of pathogens with various potentials has many opportunities to spread to countries that were previously unaffected due to several factors such as environmental factors, climate change, global trade, economics, and the mobility of individuals, which is continuously increasing every time. This can disrupt a country's public health and hamper various aspects such as economic development and production, recreation, and overall public welfare [1]. It can be said that pathogens can mutate and often undergo a very rapid evolutionary process that can result in the phenomenon of pathogen diversity, where several different strains can coexist [2], one example of which of the many types is Viruses.

Viruses are obligate intracellular submicroscopic DNA or RNA containing organisms protected by a capsid envelope that depend on cellular metabolism and biosynthesis to multiply. By parasitizing host cells in search of vital components like amino acids, lipids, and nucleotides, viruses can sustain themselves and carry out other metabolic operations [3]. With high-speed evolutionary characteristics, which are still in a pandemic situation caused by SARS-CoV- 2 or Coronavirus, can mutate with various other types of strains such as Beta, Delta, Omicron, and other types [4]. However, other early-onset viruses, such as Influenza and Ebola, are said to have significant variability, often characterized by high variability and unpredictable behavior [5]. Several researchers have used several methods to identify virus types in the last decade using the TEM (Transmission Electron Microscopy) technique. TEM is a sensitive diagnostic technique that can directly visualize the virus's structure with nanometer-scale units [6]. However, using this method requires experience and excellent accuracy in identifying every pattern, particle, and characteristic of microbiological types, including viruses which can take more time [7]. Therefore, to cover these deficiencies, it is necessary to utilize technology that can help work that is quite complicated with equally good results.

Machine Learning techniques have been widely applied in various fields, such as research conducted by Ferdinand et al. [8] in Broccoli Leaf Disease Classification using SVM with PSO based on feature selection can produce a Training accuracy of 97.63% and a Testing accuracy of 94.48%. Chalik et al. [9] researched the quality of clove leaves using CNN in combination with HSV color space with the E-5C-64LS-4D architecture and produced an accuracy of 96%. Then study on the classification of ornamental betta fish using CNN method with ResNet-50 model and Grabcut Segmentation was conducted by Hibban et al. [10] capable of producing an accuracy of 80%. Farhanah et al. [11] detecting Hops plant disease using feature selection based on SVM-BPSO yields an accuracy of up to 95%. Also, research related to intra-high class interest variations using the hybrid method was conducted by FR. Siregar et al. [12] produced an accuracy of 88.74% based on the stratified k-fold cross validation test.

Based on the research above, Machine Learning can help work in various sectors. SVM (Support Vector Machine) is an algorithm that is still widely used today because it has the property of converting signals into high-dimensional feature spaces [13], so this algorithm is still popular because it can solve classification problems with strong generalization capacity [14]. However, SVM relies heavily on parameter selection to produce optimal accuracies such as selecting regularization parameter values or C, Gamma, and the type of Kernel used. Often, the value of this parameter is determined by assuming the best value and choosing it at random. Therefore, in this study the authors used one of the metaheuristic algorithms, the Clonal Selection Algorithm. This algorithm belongs to the Artificial Immune System (AIS) class which is claimed to have strong global optimization capabilities, high-speed convergence properties, and better at dealing with noise problems [15–16]. With these characteristics, the Clonal Selection Algorithm is expected to help optimize the SVM algorithm's parameter values in classifying virus types through TEM (Transmission Electron Microscopy) images to produce optimal output.