

A novel hybrid evolutionary mating algorithm for Covid19 confirmed cases prediction based on vaccination

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ABSTRACT

Microorganisms may cause illness when they enter the body, multiply, and spread to other parts. The rapid spread of COVID-19 to neighboring countries is examined in this research. Anticipating a positive COVID-19 occurrence helps in determining risks and creating countermeasures. As a result, developing robust mathematical models with small error margins for predictions is crucial. Based on these findings, a combined method of evaluating confirmed cases of COVID-19 with universal immunization is recommended. First, the best hyperparameter values of the RBF kernel-based LSSVM (least square support vector machine) were determined using the most recent Evolutionary Mating Algorithm (EMA). After that, LSSVM will complete the task of prediction. This hybrid method has been utilized for time series forecasting in Malaysia since the country's immunization program against COVID-19 got underway. We evaluate our results next to those of well-known methodologies in nature-inspired metaheuristics.

KEYWORDS

Metaheuristics; Optimization; Prediction; Machine Learning; Covid-19 case

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