World Health Organization (WHO) reported that dengue incidence has grown exponentially around the world in recent years. It is estimated that 390 million dengue cases reported per year.  Studies reveals that 3,900 million people living in 128 countries are at risk. The dengue is spread by a mosquito vector. A moderate temperature helps increase the mosquito population rapidly. Rainfall makes idea breeding grounds for mosquitoes.

The dengue mitigation is a major research area among scientist who are working towards an effective management of the dengue epidemic. An effective dengue mitigation requires several other important components. These components include an accurate epidemic modeling, an efficient epidemic prediction, and an efficient resource allocation for controlling of the spread of the dengue disease. Past studies assumed homogeneous response pattern of the dengue epidemic to climate conditions throughout the regions. The dengue epidemic is climate dependent and also it is geographically dependent. A global model is not sufficient to capture the local variations of the epidemic. We propose a novel method of epidemic modeling considering local variation and that uses micro ensemble of regressors for each region. There are three regressor are used in the construction of the ensemble. Those are Support Vector Regression, Ordinary Least Square Regression, and a k-Nearest Neighbor Regression. The best performing regressors get selected into the ensemble. The proposed ensemble determines the risk of dengue epidemic in each region in advance. The risk is then used in risk-based resource allocation. The proposing resource allocation is built based on the Genetic Algorithm. The algorithm exploits the Genetic Algorithm with major modifications to its main components, mutation and crossover. The proposed resource allocation converges faster than the standard Genetic Algorithm and also produces a better allocation compared to the standard algorithm.