



# Development of *in - silico* classifier to predict drug resistance in Malaria

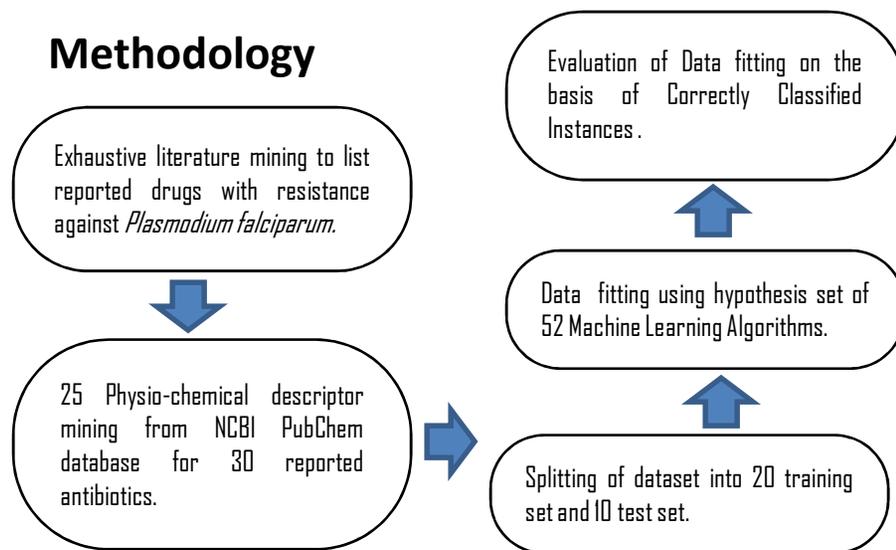
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## Background

Malaria is one of the most menacingly dreadful disease costing lives worldwide. Moreover, the emergence of multiple drug resistance associated has resulted in substantial increase of its severity. Therefore, the generation of mathematical model to classify the resistant drug versus nonresistant drug is a forwarding step to overcome the effect of this disease.

## Methodology



## Results and Discussion

The present work was carried out to utilize resistant drug reports to find pattern that can be indicative of factors responsible for drug resistance against malaria. However, 2 out of 52 classifiers viz. SMD and VFI could classify correctly in 70% of instances. Rest of the classifiers classified correctly in only 60% of instances. We believe the generalization of the models will be bettered by implementing this protocol to a larger database.

## Reference

Carolina Lopez, Carolina Saravia, Andromeda Gomez, Johan Hoebeke, Manuel A. Patarroyo (2010) Mechanisms of genetically-based resistance to malaria, *Gene*, (467) 1-12.

Elizabeth N Allen, Adiel K Mushi, Isolide S Massawe, Lasse S Vestergaard, Martha Lemnge, Sarah G Staedke, Ushma Mehta, Karen I Barnes and Clare IR Chandle (2013). How experiences become data: the process of eliciting adverse event, medical history and concomitant medication reports in antimalarial and antiretroviral interaction trials, *BMC Medical Research Methodology*, 2013, 13:140.