

**Title of Article :** Clustering Plasmodium falciparum Genes to their Functional Roles Using k-means.

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**Outlet:** *IACSIT International Journal of Engineering and Technology*

**Abstract:** We developed recently a new and novel Metric Matrices k-means (MMk-means) clustering algorithm to cluster genes to their functional roles with a view of obtaining further knowledge on many P. falciparum genes. To further pursue this aim, in this study, we compare three different k-means algorithms (including MMk-means) results from an in-vitro microarray data (Le Roch et al., Science, 2003) with the classification from an in-vivo microarray data (Daily et al., Nature, 2007) in order to perform a comparative functional classification of P. falciparum genes and further validate the effectiveness of our MMk-means algorithm. Results from this study indicate that the resulting distribution of the comparison of the three algorithms' in-vitro clusters against the in-vivo clusters are similar thereby authenticating our MMk-means method and its effectiveness. However, Daily et al. claim that the physiological state (the environmental stress response) of P. falciparum in selected malaria-infected patients observed in one of their clusters can not be found in any in-vitro clusters is not true as our analysis reveal many in-vitro clusters representation in this cluster.