

Title of Article : Computational Discovery of Drugs Resistance Mechanism(s) of the Malaria Parasite to Tetracyclines and Chloroquines

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Outlet: *Journal of Computer Science and its Applications*, (An international Journal of Nigeria Computer Society), Nigeria. Vol 17. No 2 Dec, 2009.

Abstract: At the genomics level, we use the microarray technology to produce gene expression data for various organisms under many conditions. A desirable advancement is the need to extract from this gene expression data, information that will be useful toward given answers to the questions targeted at the design of the microarray experiment. Analysis of gene expression data of P.f when induced with two anti-malaria drugs (such as chloroquine) has shown that the P.f resistance mechanisms may not be elucidate-able at the genomics level. But on a proteomic level, biochemical research has elucidated an increasingly complete image of the metabolic architecture of organisms that included that of P.f. In this work, we sought to use the biochemical network of P.f to deduce its drugs resistance mechanism(s) using the two gene expression data obtained when P.f is treated with chloroquine and tetracycline. We do this by mapping these gene expression data onto the enzymatic reaction nodes of the metabolic network. A consecutive ones clustering method is used to derived important clusters. Further, a wavelet and feature extraction methods is applied to study these clusters. These clusters give us important insight into the mechanisms that P.f deplores for resisting these anti-malaria drugs.