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Inferring the gene regulatory networks from gene expression profiles

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Dengue virus is a member of the virus family Flaviviridae and is transmitted to people through the bite of the mosquitoes *Aedes aegypti* and *Aedes albopictus*. Each year, 100 million people become infected with dengue virus. In this paper we try to expand our understanding of how dengue virus causes illness and open new avenues for developing specific treatments for a disease that exacts a huge global burden. By construction of the gene regulatory network for human-host-virus we understand how these tiny viruses manage to live in two such unrelated organisms as mosquitoes and humans. Our long goal is to study the causes of infectious and immune-mediated diseases, and to develop better means of preventing, diagnosing and treating these illnesses. The complexity of health problems is required scientist collaboration from different field. Researchers from USA and Yemen will collaborate in this project to overcome this burden. This will promote experience transfer, training and discovery of new drug therapy. From the other hand, the variety of scientific infrastructure at both collaborators laboratory will increase the successes of the project objective. The final product of this project will be implemented as Cytoscape Java plug-in, so all the cytoscape features could be used by the final software.

Biography

Fadhl Alakwaa is Professor of Biomedical Engineering at Faculty of Engineering of University Science and Technology (UST). He has been Executive Director of biomedical calibration laboratory since 2009. He received awards in teaching, innovation and researches. He is standard reviewer for high impact factor like *Oxford Bioinformatics Journal* and the *International Journal of Bioinformatics Research and Applications*. He is an active member of more than 20 international academic societies and journals. He has authored more than 30 papers and contributed in more than 5 books in the field of Bioinformatics.

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