



## Seminars in Biotechnology BTEC 592 & BTEC 692

### **“Bioinformatics for Vaccine Target Discovery”**

**Thursday, May 12, 2022**

**13:30**

**Institute of Biotechnology, Classroom-1**

**Associate Professor Mohammad Asif KHAN**

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Mohammad Asif Khan, PhD, is an Associate Professor at the School of Data Sciences, Perdana University, Malaysia. He is also a recipient of the prestigious “International Fellowship for Outstanding Researchers”, awarded by the Scientific and Technological Research Council of Turkey (TÜBİTAK), and is currently hosted as a Visiting Professor by Bezmialem Vakıf University, Turkey while maintaining his faculty position in Malaysia. He was the Founding Dean of the School of Data Sciences and Founding Director of the Centre for Bioinformatics, both at Perdana University. He completed his PhD at National University of Singapore and before moving to Malaysia was appointed as a faculty at the Department of Pharmacology and Molecular Sciences, Johns Hopkins University School of Medicine (JHUSOM), USA, which he later maintained as an adjunct faculty and a visiting scientist. His research interests are in the area of biological data warehousing and applications of bioinformatics to the study of immune responses, vaccines, inhibitory drugs, venom toxins, and disease biomarkers. He has published more than 75 articles and has developed several novel bioinformatics methodologies, tools, and specialized databases, and currently has three patent applications granted. He is currently the elected President of the Asia-Pacific Bioinformatics Network (APBioNET; <https://www.apbionet.org>), one of the largest and oldest bioinformatics organisations in the region. He is also an elected executive board member of the Global Organisation for Bioinformatics Learning, Education and Training (GOBLET; <https://www.mygoblet.org>) and Vice President of the Association for Medical and Bioinformatics, Singapore (AMBIS; <http://www.ambis.org.sg>). He has done various important roles in the organization of many local and international bioinformatics conferences, meetings, and workshops.

## **Abstract**

Vaccination is one of the most efficacious forms of medical intervention. It has significantly decreased human morbidity and mortality due to infectious diseases in all regions of the world. Currently, more than 50 successful vaccines are widely used on the human population. Over the years, major advances in the life sciences, including immunology and the “Omics” technologies, and information technology have provided insights into the underlying causes for the limitation of conventional approaches. These include the formidable variation in the human immune system, which contributes to the differences in individuals response to vaccines, and the large diversity in disease agents that allow immune escape. By greatly improving our understanding of the immune system and disease agents, these advances provide an unprecedented opportunity to develop rational approaches for new, safe, and effective vaccines. The advances have led to the generation of large amounts of data, which provide tremendous amount of information useful for vaccine research, such as for target identification and better understanding of the interaction between host and disease agents. Bioinformatics approaches are necessary to support collection of large amounts of data from diverse sources, management of these data through storage in databases using data-warehousing principles, and to provide a means for systematic study of the data. The use of bioinformatics approaches in combination with experimental validation enable systematic investigation of the utility of antigen sequences to act as targets for vaccine formulation and allow analyses that may lead to new insights.