

## List of IC@N Research Projects and Supervisors

<b>Lee Kong Chian School of Medicine</b>	
<b>Name of Supervisor</b>	<b>Research Project Description</b>
<b>Asst. Prof Navin Kumar Verma</b> <a href="mailto:nkverma@ntu.edu.sg">nkverma@ntu.edu.sg</a>	<b>Development of novel antisense ssDNA-based skin lightening agent</b>  Skin colour is determined by a brown pigment, called melanin, which is produced by melanocytes. The process of melanin synthesis or melanogenesis is catalysed by an enzyme tyrosinase. Therefore, currently used skin lightening formulations contain tyrosinase inhibitors (e.g. hydroquinone, kojic acid) to suppress melanogenesis. However, these inhibitors cause several undesirable effects. With better understanding of the melanogenesis pathway, we propose to target a downstream regulator Tyrp1 using antisense ssDNA-based molecules as a safer alternative approach. The aim of this interdisciplinary project is to develop new-generation antisense ssDNA-based molecules specifically targeting Tyrp1 for suppressing melanogenesis in melanocytes that can be used for developing a topical formulation. The student will gain specialized training in cell culture, gene silencing technique, topical drug delivery, microscopy, and variety of molecular and biochemical assays.
	<b>Targeting STAT3 In Drug Resistant Haematolymphoid Malignant Cells</b>  Drug resistance is a major problem with the current therapies for hematologic malignancies. Specific Targeting of STAT3 is an effective approach to cancer treatment with promising outcomes in clinical trials. The aim of the inter-disciplinary project is to target STAT3 using new-generation antisense oligonucleotide-based gene silencers and deter the effect in terms of anti-cancer drug sensitivity in haematolymphoid cells. We will elucidate the molecular mechanism of action of such combinatorial approach in inhibiting tumor cell growth. The student will gain specialised training in cell culture, gene silencing technique, apoptosis, microscopy, and variety of molecular and biochemical assays.
<b>Asst. Prof Wilson Goh (Dr)</b> <a href="mailto:wilsongoh@ntu.edu.sg">wilsongoh@ntu.edu.sg</a>	<b>Development of data science techniques for predicting natural compound medicinal indications</b>  Tropical herbs have been used in TCM and other traditional medical practices in treatment. However, the genomic, proteomic, and metabolic profiles of these plants are not well-characterized. By linking the molecular profiles of local plants against known data repositories of known pharmaceutically active compounds, the goal is to identify the potential medical usage of these novel plants.  Using a combination of computational biology, machine learning, and data science methods, you will construct appropriate knowledge bases

of natural or synthetic compounds and their medical usage. You will devise comparative approaches allowing you to measure compound similarities so that we can transfer appropriate labels and use indicators to novel natural compounds. You will also develop transductive approaches for predicting the appropriate medical usage of novel plants.

Highly motivated candidates with strong computing/ mathematical/ statistical skills, computational biology and/ or analytical chemistry skills are strongly encouraged to apply.

#### **AI for pandemic preparedness**

The covid-19 pandemic has impacted lives economically and socially. The emergence of more contagious and deadly variants has also raised concerns about our overall preparedness and ability to act proactively. We may use data analytics to pre-emptively model possible mutations, relate it to biological outcomes, and also model possible treatment compounds.

You will help in developing a platform for predicting and understanding viral mutations of representative viruses of recombination and reassortment mutations to cross-apply our unique methods of 1) viral mutation method generation experimentally, 2) probabilistic genetic code mutation analysis, and 3) AI and Complex Systems methods such as network analysis, robust statistical model building, time series, stacking models and random signature analysis to be supplemented with 3D structural methods involving normal mode analysis. We aim to deliver predicted mutations and potential novel conserved viral targets within the viral classes for broad spectrum targeting. This marks the platform which increases pandemic preparedness and informs downstream vaccine, therapeutic and diagnostic developments.

Highly motivated candidates with strong computing/ mathematical/ statistical skills, computational biology and/ or analytical chemistry skills are strongly encouraged to apply.