

**Research Theme: Computational Biology; Functional Genomics**

**MSc Research Project Title: Characterizing the regulatory landscape of cancer drivers and vulnerabilities**

**Principal Investigator/Supervisor: Asst/Prof Li Yinghui**

**Co-supervisor/ Collaborator(s) (if any):**

### **Project Description**

#### **a) Background:**

Cancer is a heterogeneous disease that comprises of diverse subtypes harboring different genetic dependencies. Different cancers rely on distinct sets of genes that can interact with or function together to drive the aberrant activity of various signaling pathways essential for their survival and proliferation. Recent advances in whole-genome sequencing have led to the identification of multiple genetic abnormalities associated with distinct cancer types. These mutations frequently occur in non-coding, regulatory DNA including gene promoters, enhancers, silencers and insulators, which regulate the expression of cancer driver genes via transcriptional or epigenetic mechanisms. This project aims to identify the essential gene regulatory networks in specific cancer types and characterize the molecular events involved in the activation of these candidate cancer drivers.

#### **b) Proposed work:**

This project involves a combination of molecular biology (wet lab) and computational biology (in silico) work. Using a variety of CRISPR-Cas tools, you will generate a panel of isogenic cancer cell lines carrying targeted disruption of aberrant pathways and analyze their gene expression and proteomic profiles. You will also perform various functional genomics experiments such as ChIP-seq and ATAC-seq on these cancer cells to investigate the epigenetic changes that occur following targeted disruption and/or drug treatment. You will learn existing bioinformatics tools to analyze these data and develop computational methods with these data to uncover potential cancer drivers and vulnerabilities in specific cancer types or treatment regimens with anti-cancer drugs.

#### **c) Preferred skills:**

Highly motivated candidates with strong molecular biology skills are strongly encouraged to apply. For those with a keen interest in the computational aspects of the project, it will be desirable to possess solid statistical foundations as well as experience with Python or R programming.

#### **Supervisor contact:**

**If you have questions regarding this project, please email the Principal Investigator:**  
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Please apply at the following:

**Application portal:**

<https://venus.wis.ntu.edu.sg/GOAL/OnlineApplicationModule/frmOnlineApplication.ASPX>