

List of Research Projects Available for Prospective PhD Students at LKCMedicine

The list of research projects is grouped by the following 9 Research Areas.

1. Neuroscience & Mental Health
2. Nutrition, Metabolism & Health
3. Population & Global Health
4. Respiratory & Infectious Diseases
5. Skin Disease & Wound Repair
6. Data Science & Artificial Intelligence
7. Cancer Discovery & Regenerative Medicine
8. Microbiome Medicine
9. Medical Education
10. Others

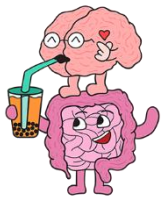
Notes:

Prospective candidates are strongly encouraged to contact the respective project main supervisor directly to discuss project scope.

Some research projects may offer scholarship opportunities. Where applicable, **remarks** will be indicated under the ***Project Title***.

No	Project Title with Brief Description	Principal Investigator
1. Neuroscience & Mental Health		
1.1	Brain mechanisms for executive function and their vulnerability to ageing, stress, and psychosis The project aims to elucidate the brain-wide mechanisms underpinning executive functions and their deterioration due to ageing, stress, and psychosis using behaving mice as a model system. The student will address this problem utilizing cutting-edge neuroscience technologies, including in-vivo calcium imaging, optogenetics, and the development of behavioral paradigms. Additionally, the student will receive extensive training in coding and data analysis. References:	Asst Prof Tsukasa Kamigaki tsukasar@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp01272

1.2	Chong HR., Ranjbar-Slamloo Y., Ho MZH., Ouyang X., and Kamigaki T.(2023) Functional alterations of the prefrontal circuit underlying cognitive aging in mice. <i>Nature Communications</i>,14, 7254. Kamigaki T., and Dan Y. (2017). Delay Activity of Specific Prefrontal Interneuron Subtypes Modulates Memory-Guided Behavior. <i>Nature Neuroscience</i>, 20, 854-863. Understanding Mechanisms of Cellular Cholesterol Distribution: Implications for Brain Health Neurodegeneration and age-associated decline in cognitive function are often associated with altered compositions of lipids (or “fats”) in the brain. Lipids play very important roles in regulating brain function, and abnormal distribution of lipids in neurons results in numerous neurological disorders. Among various lipids, cholesterol serves as a major building block for cellular membranes and maintains healthy neurons. In this project, we will use various cutting-edge techniques, including advanced microscopy, stem cells, and animal models, including <i>C. elegans</i>, to identify key molecular machineries that are responsible for the distribution of cellular cholesterol. As cholesterol metabolism plays an important role in brain health and animal physiology, our research has the potential to reveal new therapeutic targets for guiding major drug discovery efforts toward treating devastating neurodegenerative disorders, such as Alzheimer’s disease. Selected References: (1) Naito T, Ercan B, Krshnan L, Triebl A, Koh DHZ, Wei FY, Tomizawa K, Torta FT, Wenk MR, and Saheki Y (2019). Movement of accessible plasma membrane cholesterol by the GRAMD1 lipid transfer protein complex. eLife. 8: e51401. (2) Ercan B*, Naito T*, Koh DHZ, Dharmawan D,	Assoc Prof Yasunori Saheki yasunori.saheki@ntu.edu.sg Lab Webpage: www.thesahekilab.com
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1.3	and Saheki Y (2021). Molecular basis of accessible plasma membrane cholesterol recognition by the GRAM domain of GRAMD1b. EMBO J. 40: e106524. *Co-first authors. (3) Naito T and Saheki Y (2021). GRAMD1-mediated accessible cholesterol sensing and transport. BBA - Molecular and Cell Biology of Lipids. 1866: 158957. (4) Naito T, Yang H, Koh DHZ, Mahajan D, Lu L, and Saheki Y (2023). Regulation of cellular cholesterol distribution via non-vesicular lipid transport at ER-Golgi contact sites. Nature Communications. 14: 5867. (5) Koh DHZ, Naito T, Na M, Yeap YJ, Rozario P, Zhong FL, Lim KL, and Saheki Y (2023). Visualization of accessible cholesterol using a GRAM domain-based biosensor. Nature Communications. 14: 6773. Gut-brain neurobiology: microbiome control of neural circuits and behaviour The trillions of bacteria living in our body encode over 46 million genes – suggesting tremendous functional capacity (by contrast, the human genome has less than a thousandth of that). Moreover, emerging evidence suggests that the gut microbiota profoundly influences host physiology and behaviour. In this project, we will investigate the fundamental biological basis of “gut-feelings”, how microorganisms and chemicals in the gut signal to brain to modulate neural substrates that control physiology and behaviour. We employ a range of experimental techniques in mice to study the mammalian gut-brain axis including sequencing, metabolomics, in vivo neural imaging/recording, and genetically-guided functional interrogation.	Asst Prof Hwei-Ee TAN hweiee.tan@ntu.edu.sg 
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1.4	Structural and Functional Study of Extracellular Vesicles in Aging-related Neurodegeneration Aging-related neurodegeneration, including Alzheimer's Disease and Parkinson's Disease, is a growing global health challenge, especially in aging societies like Singapore. Extracellular vesicles (EVs) are emerging as key players in neurodegeneration, potentially mediating disease propagation through altered lipid composition and transport of toxic proteins. This project aims to investigate how different ApoE isoforms, particularly the risk-associated ApoE4 and protective ApoE2, influence lipid regulation in EVs across aging. We will apply mass spectrometry-based lipidomics and cryo-electron microscopy to characterize EV lipid profiles and protein structures. The findings may uncover novel biomarkers for early dementia diagnosis and guide lipid-targeted therapeutic strategies to improve brain health in aging populations.	Dr Chuchu Wang choicewang0820@hotmail.com Website https://scholar.google.com/citations?user=1SQy-gQAAAAJ&hl=en&oi=ao
1.5	Bat-inspired targets to fight human diseases and aging The objective is to learn from bats with exceptional disease resistance and healthy longevity, aiming to translate these lessons into new targets to fight human diseases and extend healthspan. The pioneering work in bat inflammation (<i>Nat Micro</i> 2019, <i>PNAS</i> 2020, <i>Nature</i> 2021, <i>Cell</i> 2023 and ongoing development of a new class of anti-inflammatory drugs) has helped establish bats as a great model to uncover new strategies to fight human diseases and has just scratched the surface of what we can learn from bats to benefit humans. The three different and synergistic approaches include 1) 'unbiased' multi-omics aging atlas of bats 2) 'disease centric' disease-free bat models including metabolic and neurological diseases and 3) 'more targeted' study of enhanced proliferation/regeneration and increased apoptosis as potential anti-aging/cancer mechanisms.	Asst Prof Ahn Matae matae.ahn@ntu.edu.sg https://dr.ntu.edu.sg/entities/person/Matae-Ahn

1.6	Unravelling the brain-wide encoding of emotion states <i>Remarks: Project may be supported by scholarship funding</i> How are emotions represented in the brain? The Nair lab at LKCMedicine investigates how neural circuits in the brain and AI models control and represent emotion states, including aggression and fear. This project will utilize new advances in high-density brain recordings in mice to understand the brain-wide encoding of complex emotion states. The student will work closely with AI experts in the group to model high-dimensional neural data as dynamical systems using interpretable AI techniques, building on prior work in the lab (Nair et al., Cell 2023, Vinograd*, Nair* et al., Nature 2024 and Nair et al., Science 2025). The ideal candidate will have a strong prior background in systems neuroscience techniques and experience in rodent neuroscience, including stereotaxic surgery.	Asst Prof Aditya Nair aditya.nair@ntu.edu.sg Lab Webpage: https://www.nairlab.science
1.7	Building a brain foundation model to predict and decode neural signals of emotion in mental health disorders <i>Remarks: Project may be supported by scholarship funding</i> Can we predict a person's neural state from just their behavior? The Nair lab at LKCMedicine works at the intersection of neuroscience and AI and has been at the forefront of decoding neural signals of aggression and fear in the brain (see Nair et al., 2023 Cell and Nair et al., 2025 Science). In this project, the student will work with the lab to create a foundation model that is capable of predicting and decoding the neural signals underlying states of anger or fear from just behavioral measurements across species. This project has the potential to advance the development of "digital twins" of the brain, which could eventually enable personalized therapies based on individualized brain models capable of accurately predicting activity under disease and disorder states. The ideal candidate will possess a strong programming background and prior experience in handling neural	Asst Prof Aditya Nair aditya.nair@ntu.edu.sg Lab Webpage: https://www.nairlab.science

1.8	datasets and deep learning frameworks such as PyTorch. Understanding the neural computation of emotion in foundation AI models and brain circuits <i>Remarks: Project may be supported by scholarship funding</i> How are emotions represented in the brain and in deep neural networks? The Nair lab at LKCMedicine investigates how neural circuits in the brain and AI models control and represent emotion states, including aggression and fear. This project will utilize new advances in explainable and interpretable AI to reveal hidden neural computations in high-dimensional brain data and in foundation AI models including vision transformers Building on previous efforts from the lab (Nair et al., Cell 2023, Vinograd*, Nair* et al., Nature 2024 and Nair et al., Science 2025), the student will work at the intersection of neuroscience and machine learning to unravel the degree of similarity in how deep networks and brain circuits process emotion. The ideal candidate will possess a strong programming background and prior experience in handling neural datasets and deep learning frameworks such as PyTorch.	Asst Prof Aditya Nair aditya.nair@ntu.edu.sg Lab Webpage: https://www.nairlab.science
1.9	Building a deep learning system for high-throughput behavioral analysis of emotion states in models of neurodevelopmental disorders <i>Remarks: Project may be supported by scholarship funding</i> How can we know if a person or animal is in a state of emotion? Building on recent advancements in computer vision from the Nair lab at LKCMedicine, this project will utilize new vision transformer models to predict behavioral states of emotion across species, from mice to humans. The student will work with the lab to train new multimodal large language models which can segment and create interpretable	Asst Prof Aditya Nair aditya.nair@ntu.edu.sg Lab Webpage: https://www.nairlab.science

1.10	representations of diverse emotion states, including aggression. The student will also explore how behavioral representations of emotions are altered in animal models of neurodevelopmental disorders. This research has the potential to advance high throughput screening of drug targets and create a platform for behavioral phenotyping towards translational applications. The ideal candidate will possess a strong programming background and prior experience in handling neural datasets and deep learning frameworks such as PyTorch. Direct cell reprogramming for biomedical applications <i>Remarks: Project may be supported by scholarship funding</i> The manufacture of advanced stem cell-based products and therapies through directed differentiation faces significant challenges in achieving efficient, reliable, and scalable production of specialized cell types especially in a cGMP setting. Cell differentiation approaches involve stepwise culture of (pluripotent) stem cells to direct their development into target cell types. However, current manufacturing methods are generally not fit for purpose - being often hampered by complex, lengthy and costly protocols, low cell yield, purity and/or quality, and inconsistent outcomes - limiting industrial applications. Direct (or forward) cell programming offers a promising alternative by enabling the direct conversion of one cell type into another by activating gene regulatory networks that determine cell identity. This approach has the potential greatly to streamline the manufacturing process, reduce the time and resources required, and improve the consistency and functionality of cellular products. As the advanced therapy field develops, establishing robust, scalable manufacturing technology platforms (such as by direct cell programming) will become key to the success of the regenerative medicine and cell therapy industry. Programming of cells using lineage control networks	Associate Prof Yen CHOO yen.choo@ntu.edu.sg
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1.11	has the potential to transform how we make cell therapies and immunotherapies, develop regenerative medicines, and create cellular models for research. However, identifying specific combinations of master regulatory genes known as transcription factors (TFs) that lead to highly efficient conversion of a scalable starting cell (e.g. iPSC, fibroblast) into desired cell types for biomedical applications (e.g. T cell, b cell) remains a significant challenge and a longstanding, critical bottleneck in the field. In this programme we will use an innovative combinatorial screening technology to rapidly assess the effectiveness of thousands of combinations of TFs in programming various human cell types into specific lineages that enable high value biomedical applications. Cell types we may derive in this project have diverse applications, including in: 1) developing advanced cellular/tissue models for biomedical R&D, 2) cGMP manufacturing of cell and gene therapies, including allogeneic immunotherapies, and 3) in vivo reprogramming for regenerative medicine and autologous immunotherapies. Viral-Induced Brain Developmental Disorders and Calcification <i>Remarks: Project may be supported by scholarship funding</i> Singapore's declining birth rate has placed increasing importance on safeguarding the long-term health and developmental outcomes of every child. Early-life infection with neurotropic viruses such as Zika virus (ZIKV), which remain a regional concern in Southeast Asia, has been associated with brain calcifications and long-term neurological deficits. However, the molecular mechanisms driving these outcomes remain poorly understood. Emerging evidence suggests that viral components can persist after infection and disrupt normal cellular processes in the developing brain. In this study, we investigate how	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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1.12	viral exposure alters molecular pathways that regulate brain homeostasis and tissue remodeling. The student will gain training in advanced virology, neuroimmunology, and multi-omics approaches, and will have opportunities to engage with Singapore's vibrant biomedical research ecosystem and clinical collaborators. Overall, this study aims to define how viral infection and persistence shape brain development and calcification, providing a foundation for therapeutic strategies and biomarkers to protect child health in Singapore and the broader region. Selected References: 1. Fraczek M, Breckenridge H, Melano I, Squillacioti E, Nielsen-Saines K, Recinos V, Chen W (2025) Intracranial calcifications in congenital viral infections: mechanisms and cellular roles. Curr Opin Virol 73: 101479 2. Chen W, et al (2021) Zika virus NS3 protease induces bone morphogenetic protein-dependent brain calcification in human fetuses. Nat Microbiol 6: 455–466 3. Azamor T, Familiar-Macedo D, Salem GM, et al (2024) Transplacental SARS-CoV-2 protein ORF8 binds to complement C1q to trigger fetal inflammation. EMBO J 43: 5494–5529 4. Foo SS, et al (2024) Sustained chronic inflammation and altered childhood vaccine responses in children exposed to Zika virus. EBioMedicine 106: 105249 5. Zarb Y, et al (2021) Microglia control small vessel calcification via TREM2. Sci Adv 7: eabc4898 Viral-Induced Chronic Musculoskeletal Disease in Aging <i>Remarks: Project may be supported by scholarship funding</i> Singapore's rapidly aging population has led to a growing burden of chronic musculoskeletal disorders, a leading cause of disability and reduced quality of life. Viral infections are increasingly recognized as triggers of persistent joint pain, inflammation, and tissue degeneration, particularly in the context of emerging arboviruses in a changing climate. However, the mechanisms linking viral infection to chronic	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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1.13	musculoskeletal disease and aging remain poorly understood. Joint-resident cells such as chondrocytes play critical roles in maintaining cartilage integrity and regulating bone remodeling, yet how viral infection disrupts these processes is unclear. In this study, we investigate how viral infection alters cellular function and tissue homeostasis in the joint. The student will employ integrated approaches including virology, multi-omics profiling, and advanced 2D and 3D human joint models with biomechanical stimulation. Overall, this study aims to define how viral infection drives chronic musculoskeletal disease and interacts with aging, providing a foundation for therapeutic strategies targeting infection-associated arthritis and age-related joint degeneration. Selected References: 1. Bartholomeeusen K, et al (2023) Chikungunya fever. <i>Nat Rev Dis Primers</i> 9: 17 2. Baxter VK, Heise MT (2020) Immunopathogenesis of alphaviruses. <i>Adv Virus Res</i> 107: 315–382 3. Chen W, et al (2014) Arthritogenic alphaviral infection perturbs osteoblast function and triggers pathologic bone loss. <i>Proc Natl Acad Sci USA</i> 111: 6040–6045 4. Chen W, et al (2015) Arthritogenic alphaviruses: new insights into arthritis and bone pathology. <i>Trends Microbiol</i> 23: 35–43 5. Chen W, et al (2017) Specific inhibition of NLRP3 in chikungunya disease reveals a role for inflammasomes in alphavirus-induced inflammation. <i>Nat Microbiol</i> 2: 1435–1445 Neuroprotection for Parkinson’s disease – Lesson from a long-lived animal Parkinson’s disease (PD) is a prevalent progressive and debilitating neurodegenerative disorder that affects millions of predominantly elderly individuals worldwide. Despite intensive research over several decades, the disease remains incurable. Clearly, more effective treatment options for PD need to be developed. To gain insights into novel neuroprotective strategies, we have turned to learning lessons from nature, specifically from the naked mole rat (NMR), an extraordinarily long-lived rodent that is relatively free from diseases including neurodegeneration. NMR	Prof Lim Kah Leong kahleong.lim@ntu.edu.sg Webpage: https://dr.ntu.edu.sg/entities/person/Lim-Kah-Leong
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1.14	defies Gompertzian laws by showing no age-associated exponential increase in mortality nor neurodegeneration. We hypothesize that NMRs must have evolved to carry a suite of neuroprotective mechanisms to maintain neuronal integrity during aging, and hence are better protected against the development of neurodegenerative diseases. This project aims to unlock the mysteries of how these animals could defy normal brain aging, which holds promise to shed important insights on how we could devise strategies to protect dopaminergic (DA) neurons in PD from degenerating. Autophagy and autophagy-linked signalling in neurodegeneration and cancer <i>Remarks: Project may be supported by scholarship funding</i> Cells maintain their integrity through autophagy - literally “self-eating” - a fundamental quality control pathway that identifies and sequesters damaged cellular components within double-membrane structures called autophagosomes, delivering them to lysosomes for degradation and recycling. A specialized form of this process, mitophagy, selectively removes damaged mitochondria, the cell’s energy-producing organelles, through diverse and flexible initiation mechanisms (Nguyen et al, <i>Mol Cell</i>, 2023; Adriaenssens et al., <i>Nat Struct & Mol Biol</i>, 2024; Küng et al, <i>Curr Opin Cell Biol</i>, 2025). These pathways are essential for cellular homeostasis, and their dysregulation is increasingly linked to aging, neurodegeneration, and cancer. ◇ Project 1: Regulators of mitophagy in neuronal systems and disease Mitophagy is central to mitochondrial quality control and cellular homeostasis, yet how it is initiated and regulated in different cellular contexts remains incompletely understood. This project aims to identify novel regulators of mitophagy and define their roles in neuronal function and disease. Building on our recent work uncovering distinct mechanisms of mitophagy initiation (Nguyen et al, <i>Molecular Cell</i>, 2023), the study will integrate biochemical, molecular, and cell	Asst Prof Thanh (Ricky) Nguyen Thanhngoc.nguyen@ntu.edu.sg Webpage: Asst Prof Ricky (Thanh) Nguyen Academic Profile DR-NTU Research NTU Singapore Thanh (Ricky) Nguyen LinkedIn
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	biological approaches, including CRISPR-based screening, proteomics, and advanced imaging, to identify factors required to maintain mitophagy in 2D and 3D neuronal systems. There will be opportunities to extend these findings into in vivo models to understand how mitophagy dysregulation contributes to aging, neurodegeneration, and cancer. ◇ Project 2: ATG8ylation – A novel protein modification in autophagy and cellular stress Autophagy and cellular stress responses are controlled by complex and incompletely understood regulatory mechanisms. This project focuses on ATG8ylation, a novel protein modification that we identified (Nguyen et al, <i>Molecular Cell</i>, 2021), and its role in controlling protein function and pathway dynamics. The work will integrate biochemical, molecular, and cell biological approaches including proteomics and advanced imaging such as confocal and electron microscopy to identify targets and define regulatory networks. There will be opportunities to extend findings into in vivo models to explore how ATG8ylation contributes to cellular homeostasis and how its dysregulation leads to disease. <i>Additional project directions are available within the lab and can be tailored to the candidate's interests and strengths.</i>	
2. Nutrition, Metabolism & Health		
2.1	Investigating the role of gut microbiome in cardiometabolic diseases In recent years, it has become evident that the gut bacteria living in our intestine significantly impact health and disease. This influence extends beyond intestinal disorders like inflammatory bowel disease to encompass a wide range of conditions including obesity, diabetes, and neurodegenerative diseases. Our laboratory has previously reported that certain gut bacteria contributes to the progression of	Asst Prof Kazuyuki Kasahara kazuyuki.kasahara@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp02039 https://kasaharalab.com

2.2	cardiovascular disease (PMID: 30397344, 37279756). This PhD project focuses on gut microbiota and lipid metabolism, employing state-of-the-art technologies such as anaerobic culture systems, mouse models, and next-generation sequencing to advance research in this field. Investigating the role of Midkine in Porcine Myocardial Infarction Model Ischemic heart disease lacks curative treatments. Stem cell-derived cardiovascular progenitors (CVPs) offer regenerative potential, but poor vascularization and immune rejection limit their survival. Spatial transcriptomics revealed that Midkine (MDK) is involved in early vascular and inflammatory responses. We hypothesize that MDK-driven angiogenesis and early modulation are critical for CVP longevity post-MI. This project will investigate the effects of MDK therapy in a porcine MI model using multi-modal vascular assessment and spatial multi-omics (spatial transcriptomics, spatial proteomics, single-cell RNA sequencing). This research aims to improve the success of regenerative cardiology by boosting blood vessel formation and reducing fibrosis, potentially leading to safer and more effective treatments for ischemic heart disease. Yap L*; Chong L.Y.; Tan C.; Adusumalli S.; Seow M.; Guo J.; Cai Z.; Loo S.J.; Lim E.; Lath N.; Ye L.; Petretto E.; Tryggvason K.* (*Co-Corresponding) Pluripotent Stem Cell-derived cardiovascular progenitors differentiated on laminin221 regenerate and improve the function of infarcted swine hearts. <i>Npj Regenerative Medicine</i>, 8(1), 26. (2023) Yap, L., Wang, J.W., Moreno-Moral, A., Sun, Y., Chong, L.Y., Harmston, N., Wang, X.Y., Chong, S.Y., Ohman, M., Wei, H., <i>et al.</i> (2019). Reproducible defined human laminin-driven stem cell differentiation to cardiomyocyte progenitors generating functional cardiac muscle in post-infarct heart <i>Cell Rep</i> 26, 3231-3245 e3239	Asst Prof Lynn Yap lynn.yap@ntu.edu.sg Website https://dr.ntu.edu.sg/entities/person/Lynn-Yap
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2.3	Systematically Investigating Molecular Mechanisms Underlying Aging-Related Human Diseases through Multi-Omics Profiling Aging is a complex biological process characterized by a gradual decline in physiological functions, which increases susceptibility to diseases and death. This process is influenced by a myriad of genetic, environmental, and lifestyle factors. To better understand aging and study the relationship between aging and aging-related diseases, our research group is focused on building predictive models using machine learning techniques. The model is to integrate multi-omics datasets, focusing specifically on gut microbiome and metabolomics data. The comprehensive analysis of these multi-omic datasets aims to unveil crucial molecular indicators, intricate biological pathways, and influential regulatory circuits that play a role in the aging process and the pathogenesis of age-associated disorders. Such an understanding is likely to be helpful in the development of innovative therapeutic interventions to promote healthy aging and to address the onset and progression of neurodegenerative conditions such as Alzheimer's and Parkinson's diseases.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
2.4	Modulation of digestive enzyme activity as a safe approach to improve metabolism and health This project aims to design new therapeutic targets, with structure-function lead optimisation of compounds that inhibit luminal carbohydrate enzymes. Guided by naturally occurring plant-based compounds, this project involves side-chain modifications to improve enzyme inhibition selectivity and specificity. From chemistry to biology, this project will continue with the characterization of luminal carbohydrate digestion modulation on the recipient host. Investigations will include an assessment of intestinal health, alterations in gut microbiome, impact on immunology and finally carbohydrate metabolism and homeostasis.	Assoc Prof Yusuf Ali Yusuf.ali@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00609 Assoc Prof Zaher Judeh (Co-sup)

2.5	Nutritional intervention and the impact on muscle health in elderly health This project aims to molecularly dissect pathways that are altered under (i) intermittent fasting conditions and (ii) plant-based nutritional intake. These dietary interventions are increasingly being suggested as disease-modifiers, but the molecular mechanisms that support these claims are still not well-defined. With a focus on insulin sensitivity, immunology and metabolic organ homeostasis and health, the candidate will undertake a series of in vitro and in vivo experiments to understand the role of intracellular lipid regulation response to both dietary interventions. In collaboration with exercise physiologists from the National Institute of Education, candidate will also undertake a human study to validate translation and clinical relevance.	Assoc Prof Yusuf Ali Yusuf.ali@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00609 Assoc Prof Steven Burns (Co-sup)
2.6	In-vivo functional genetic screen to identify novel modulators of Non-Alcoholic Fatty Liver Disease (NAFLD) <i>Remarks: Project may be supported by scholarship funding</i> The project focuses on employing in-vivo mouse models that resemble and recapitulate human disease to study NAFLD disease progression. Our preliminary results have identified several shRNAs that confer a negative or positive effect on the regenerative capacity of the hepatocytes. Further approach will be focused on validation of these shRNAs, such as their cell migration and cell proliferation characteristics using various in-vitro assays, followed by selection of the top performing shRNAs for in-vivo validation. In addition, combined transcriptomic and proteomic approaches will be undertaken to unravel new insights with the aim of identifying targets for therapeutic intervention and treatment of the disease.	Assoc Prof Torsten Wuestefeld Torsten.Wuestefeld@ntu.edu.sg

2.7	Identification of novel senolytic targets for improving liver regeneration <i>Remarks: Project may be supported by scholarship funding</i> The project focuses on conducting in vivo & in vitro functional genetic screens to identify targets to eliminate senescent cells. Senescent cells are known to drive inflammaging attenuating the regenerative capacity of the liver. Through a negative selection screen in senescent cells we can identify vulnerabilities of these cells. The goal is to identify novel senolytic targets for therapeutic purposes.	Assoc Prof Torsten Wuestefeld Torsten.Wuestefeld@ntu.edu.sg
2.8	Identifying novel biomarkers in liquid biopsy derived exosomes <i>Remarks: Project may be supported by scholarship funding</i> The project focuses on identifying novel blood-based biomarkers for liver disease. Mouse models of chronic liver disease will be used, exosomes will be isolated from the blood and the content will be analyzed by transcriptomic and proteomic approaches. The same approach will be applied for liver patient derived blood samples. The goal is to identify novel conserved biomarkers for liver disease.	Assoc Prof Torsten Wuestefeld Torsten.Wuestefeld@ntu.edu.sg
2.9	Ageing of bone microenvironments Our skeletons play a crucial role in regulating key physiological processes, including mineral homeostasis, energy metabolism, and blood cell production. The presence of multiple blood vessel (BV) subtypes and the distinct microenvironments they support contribute to the skeleton's multifaceted functions. Vascular aging is a key factor in the age-related functional and physical changes observed in the skeleton. Understanding vascular niches and their age-related alterations could help target specific functional niches for managing age-related bone and blood diseases. In this study, we aim to identify and characterize bone vascular microenvironments and their functions.	Assoc Prof Saravana Kumar Ramasamy saravana.kr@ntu.edu.sg

2.10	Leveraging cutting-edge techniques developed in our laboratory—including high-resolution 3D imaging, single-cell and spatial transcriptomics, metabolic analysis, and advanced mouse genetics—the candidate will have the opportunity to: • Characterize different types of microenvironments in bone. • Understand how blood vessels support these niches. • Identify strategies to replace or target aging blood vessel subtypes specifically. Metabolic control of bone marrow microenvironments The mammalian skeletal system undergoes continuous remodelling throughout life, intricately interacting with whole-body physiology. Metabolic changes significantly influence bone health by altering the cellular composition and functional dynamics of bone tissue. However, the cellular and molecular mechanisms underlying these dynamic changes remain poorly understood. In this study, we investigate the impact of metabolism on the mesenchymal composition of bone microenvironments. Specifically, the student will 1. Map and characterize the distribution patterns of mesenchymal cell subtypes in bone. 2. Explore how metabolic conditions such as diabetes, modulate mesenchymal cell composition 3. Identify metabolic targets to modulate mesenchymal cell differentiation and composition. The student will employ advanced techniques, including confocal and intravital imaging, single-cell and spatial transcriptomics, metabolic profiling, and state-of-the-art mouse transgenics. Overall, this study aims to uncover the mechanisms driving bone pathology in metabolic diseases like diabetes,	Assoc Prof Saravana Kumar Ramasamy saravana.kr@ntu.edu.sg
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2.11	providing a foundation for targeted therapeutic strategies. Deciphering the Role of Atypical LPS and MAMPs in Gut Barrier Dysfunction and MASLD The gut barrier is a critical defense system, preventing harmful microbes and toxins from entering circulation while supporting a balanced relationship with gut bacteria. When this barrier is compromised, it contributes to a cascade of chronic diseases. One of the most pressing concerns is Metabolic-Associated Steatotic Liver Disease (MASLD), a leading cause of chronic liver disease worldwide, which is increasingly linked to gut microbial imbalances. This PhD project will explore how microbe-associated molecular patterns (MAMPs), specifically classical and atypical lipopolysaccharides (LPS), influence gut barrier integrity via Angiopoietin-like protein 4 (Angptl4), a key regulator of lipid metabolism and inflammation. However, the precise molecular mechanisms by which these LPSs regulate Angptl4 remain unknown. Using cutting-edge microbiome analysis, biochemical characterization, and in vivo models, you will uncover how microbial signals shape gut-liver communication. The candidate will analyze bacterial LPS, assess receptor activation and gut permeability, and utilize germ-free mouse models. Why Join This Project? You'll gain expertise in host-microbe interactions, molecular biology, and immunology, with opportunities for clinical collaborations. Who Should Apply? We welcome applications from motivated candidates with a background in microbiology, molecular biology, immunology, bioinformatics, or a related field. A passion for host-microbe interactions and translational medicine is essential. Join us in uncovering how the gut microbiome influences metabolic disease and paving the way for microbiome-based therapeutics!	Assoc Prof Andrew Tan Nguan Soon nstan@ntu.edu.sg https://dr.ntu.edu.sg/cris/rp/rp00393
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	References: Low, ZS, Chua, D., Cheng, H.S. et. al (2024). The LIDPAD Mouse Model Captures the Multisystem Interactions and Extrahepatic Complications in MASLD. Adv. Sci. 11(35): e2404326.	
2.12	Discovery of Gut Microbiome-Metabolized Bioactive Compounds from Traditional Chinese Medicine We propose to culture human gut microbiomes with Traditional Chinese Medicine (TCM) extracts and apply a novel computational algorithm to identify new bioactive compounds metabolized by the microbiota. This integrative platform enables systematic discovery of microbiome-derived metabolites from natural products, uncovering mechanisms underlying TCM efficacy and revealing potential therapeutic agents. Beyond discovery, we aim to construct a comprehensive atlas of gut microbiome-metabolized TCM and natural products. This resource will serve as a foundation for drug development and precision therapeutics based on host-microbe-metabolite interactions.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
2.13	Metabolic feature-based functional module analysis based on the large language model We propose to develop featureFMA, a novel large language model (LLM)-guided computational framework for metabolic feature-based functional module analysis in LC-MS untargeted metabolomics. Traditional pathway analysis lacks specificity and coverage for metabolomics data. featureFMA will integrate metabolite annotation, metabolic network modeling, and LLM-based functional interpretation to identify dysregulated modules linked to biological functions and diseases. This project includes software development (R package, Shiny app, and cloud platform), multi-species validation, and diverse case studies (e.g., enzyme mutation and gut microbiome). featureFMA will provide a scalable, intelligent solution for interpreting complex metabolomics data and accelerating functional discovery in systems biology.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)

2.14	Bat-inspired targets to fight human diseases and aging The objective is to learn from bats with exceptional disease resistance and healthy longevity, aiming to translate these lessons into new targets to fight human diseases and extend healthspan. The pioneering work in bat inflammation (<i>Nat Micro</i> 2019, <i>PNAS</i> 2020, <i>Nature</i> 2021, <i>Cell</i> 2023 and ongoing development of a new class of anti-inflammatory drugs) has helped establish bats as a great model to uncover new strategies to fight human diseases and has just scratched the surface of what we can learn from bats to benefit humans. The three different and synergistic approaches include 1) ‘unbiased’ multi-omics aging atlas of bats 2) ‘disease centric’ disease-free bat models including metabolic and neurological diseases and 3) ‘more targeted’ study of enhanced proliferation/regeneration and increased apoptosis as potential anti-aging/cancer mechanisms.	Asst Prof Ahn Matae matae.ahn@ntu.edu.sg https://dr.ntu.edu.sg/entities/person/Matae-Ahn
2.15	The role of eating behaviour in cardiometabolic health in Asian Population Suboptimal dietary habit and underlying eating behaviour are risk factors for excess adiposity. We hypothesise that adverse eating behaviour and dietary habit contribute to excess visceral adiposity and cardiometabolic disease burden in the Asian population. In this project, we aim to i) comprehensively quantify eating behaviour using validated questionnaires in multi-ethnic Asians using Theoretical Domain Framework¹, ii) identify eating behavioural risk factors that promote excess adiposity in the multiethnic Asian population through epidemiological investigations using high-throughput approach such as Phenome-wide Association Studies (PheWAS)² and identify biological signatures using multi-omic data available through linkage with the Health for Life in Singapore (HELIOS) Study. We will leverage on the ongoing AETSCAPE Study that has collected from the HELIOS Study participants and the approved data linkage with the comprehensive lifestyle, health, and multi-omic data.	Asst Prof Theresia Mina Theresia.hm@ntu.edu.sg https://www.researchgate.net/profile/Theresia-Mina

2.16	Reference: 1. Atkins L, et al. Implementation Science 2017; 12. DOI:10.1186/s13012-017-0605-9. 2. Mina, et al. Brief Communications: Phenome-wide Association Study of Cognitive Function in Multiethnic Asian population. MedRxiv https://doi.org/10.1101/2025.06.18.25329738 Direct cell reprogramming for biomedical applications <i>Remarks: Project may be supported by scholarship funding</i> The manufacture of advanced stem cell-based products and therapies through directed differentiation faces significant challenges in achieving efficient, reliable, and scalable production of specialized cell types especially in a cGMP setting. Cell differentiation approaches involve stepwise culture of (pluripotent) stem cells to direct their development into target cell types. However, current manufacturing methods are generally not fit for purpose - being often hampered by complex, lengthy and costly protocols, low cell yield, purity and/or quality, and inconsistent outcomes - limiting industrial applications. Direct (or forward) cell programming offers a promising alternative by enabling the direct conversion of one cell type into another by activating gene regulatory networks that determine cell identity. This approach has the potential greatly to streamline the manufacturing process, reduce the time and resources required, and improve the consistency and functionality of cellular products. As the advanced therapy field develops, establishing robust, scalable manufacturing technology platforms (such as by direct cell programming) will become key to the success of the regenerative medicine and cell therapy industry. Programming of cells using lineage control networks has the potential to transform how we make cell therapies and immunotherapies, develop regenerative medicines, and create cellular models for research. However, identifying specific combinations of master	Associate Prof Yen CHOO yen.choo@ntu.edu.sg
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2.17	regulatory genes known as transcription factors (TFs) that lead to highly efficient conversion of a scalable starting cell (e.g. iPSC, fibroblast) into desired cell types for biomedical applications (e.g. T cell, b cell) remains a significant challenge and a longstanding, critical bottleneck in the field. In this programme we will use an innovative combinatorial screening technology to rapidly assess the effectiveness of thousands of combinations of TFs in programming various human cell types into specific lineages that enable high value biomedical applications. Cell types we may derive in this project have diverse applications, including in: 1) developing advanced cellular/tissue models for biomedical R&D, 2) cGMP manufacturing of cell and gene therapies, including allogeneic immunotherapies, and 3) in vivo reprogramming for regenerative medicine and autologous immunotherapies. Viral-Induced Brain Developmental Disorders and Calcification <i>Remarks: Project may be supported by scholarship funding</i> Singapore's declining birth rate has placed increasing importance on safeguarding the long-term health and developmental outcomes of every child. Early-life infection with neurotropic viruses such as Zika virus (ZIKV), which remain a regional concern in Southeast Asia, has been associated with brain calcifications and long-term neurological deficits. However, the molecular mechanisms driving these outcomes remain poorly understood. Emerging evidence suggests that viral components can persist after infection and disrupt normal cellular processes in the developing brain. In this study, we investigate how viral exposure alters molecular pathways that regulate brain homeostasis and tissue remodeling. The student will gain training in advanced virology, neuroimmunology, and multi-omics approaches, and will have opportunities to engage with Singapore's	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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2.18	vibrant biomedical research ecosystem and clinical collaborators. Overall, this study aims to define how viral infection and persistence shape brain development and calcification, providing a foundation for therapeutic strategies and biomarkers to protect child health in Singapore and the broader region. Selected References: 1. Fraczek M, Breckenridge H, Melano I, Squillaciotti E, Nielsen-Saines K, Recinos V, Chen W (2025) Intracranial calcifications in congenital viral infections: mechanisms and cellular roles. Curr Opin Virol 73: 101479 2. Chen W, et al (2021) Zika virus NS3 protease induces bone morphogenetic protein-dependent brain calcification in human fetuses. Nat Microbiol 6: 455–466 3. Azamor T, Familiar-Macedo D, Salem GM, et al (2024) Transplacental SARS-CoV-2 protein ORF8 binds to complement C1q to trigger fetal inflammation. EMBO J 43: 5494–5529 4. Foo SS, et al (2024) Sustained chronic inflammation and altered childhood vaccine responses in children exposed to Zika virus. EBioMedicine 106: 105249 5. Zarb Y, et al (2021) Microglia control small vessel calcification via TREM2. Sci Adv 7: eabc4898 Viral-Induced Chronic Musculoskeletal Disease in Aging <i>Remarks: Project may be supported by scholarship funding</i> Singapore's rapidly aging population has led to a growing burden of chronic musculoskeletal disorders, a leading cause of disability and reduced quality of life. Viral infections are increasingly recognized as triggers of persistent joint pain, inflammation, and tissue degeneration, particularly in the context of emerging arboviruses in a changing climate. However, the mechanisms linking viral infection to chronic musculoskeletal disease and aging remain poorly understood. Joint-resident cells such as chondrocytes play critical roles in maintaining cartilage integrity and regulating bone remodeling, yet how viral infection disrupts these processes is unclear. In this study, we	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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2.19	investigate how viral infection alters cellular function and tissue homeostasis in the joint. The student will employ integrated approaches including virology, multi-omics profiling, and advanced 2D and 3D human joint models with biomechanical stimulation. Overall, this study aims to define how viral infection drives chronic musculoskeletal disease and interacts with aging, providing a foundation for therapeutic strategies targeting infection-associated arthritis and age-related joint degeneration. Selected References: 1. Bartholomeeusen K, et al (2023) Chikungunya fever. <i>Nat Rev Dis Primers</i> 9: 17 2. Baxter VK, Heise MT (2020) Immunopathogenesis of alphaviruses. <i>Adv Virus Res</i> 107: 315–382 3. Chen W, et al (2014) Arthritogenic alphaviral infection perturbs osteoblast function and triggers pathologic bone loss. <i>Proc Natl Acad Sci USA</i> 111: 6040–6045 4. Chen W, et al (2015) Arthritogenic alphaviruses: new insights into arthritis and bone pathology. <i>Trends Microbiol</i> 23: 35–43 5. Chen W, et al (2017) Specific inhibition of NLRP3 in chikungunya disease reveals a role for inflammasomes in alphavirus-induced inflammation. <i>Nat Microbiol</i> 2: 1435–1445 The role of urine metabolomics in lifestyle and cardiometabolic health in multiethnic Asian population Urine metabolomics reflect individual dietary habit, exposure to environmental toxins and cardiometabolic health status. Dietary habit and environmental exposome vary globally, and there is a lack of urine metabolomics study in multiethnic Asian settings. The project proposes a urine metabolomics pilot study in Singapore, to provide preliminary insights on the relationship of urine metabolites and dietary intake and blood metabolites in multiethnic Asian population, using Liquid Chromatography- Mass Spectrometry (LC-MS) platforms. We will leverage on the existing urine sample repository in a large population health cohort study in Singapore, the Health for Life in Singapore (HELIOS) Study. We will compare service providers and assay fasted spot urine samples from participants with proportionate demographic distribution. We will then link the urine metabolomics	Asst Prof Theresia Mina Theresia.hm@ntu.edu.sg https://www.researchgate.net/profile/Theresia-Mina
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	data with participant's dietary recall data to evaluate correlations with key foods and beverages with established urine metabolites. This exercise will be invaluable in shaping the strategies for larger scale urine metabolomics for community resources, accelerating biomarker discovery for disease detection, subclassification and prognostication ranging from diabetes to cancers to chronic kidney diseases. Reference: 1. Beckmann, M. et al. Dietary exposure biomarker-lead discovery based on metabolomics analysis of urine samples. in Proceedings of the Nutrition Society vol. 72 352–361 (2013). 2. Hoher, B. & Adamski, J. Metabolomics for clinical use and research in chronic kidney disease. Nature Reviews Nephrology vol. 13 269–284 Preprint at https://doi.org/10.1038/nrneph.2017.30 (2017). 3. Zhu, Y. et al. Psychological distress and metabolomic markers: A systematic review of posttraumatic stress disorder, anxiety, and subclinical distress. Neuroscience and Biobehavioral Reviews vol. 143 Preprint at https://doi.org/10.1016/j.neubiorev.2022.104954 (2022). 4. Goerdten, J. et al. Reproducibility of the Blood and Urine Exposome: A Systematic Literature Review and Meta-Analysis. Cancer Epidemiology Biomarkers and Prevention vol. 31 1683–1692 Preprint at https://doi.org/10.1158/1055-9965.EPI-22-0090 (2022).	
3. Population & Global Health		
3.1	Comprehensive Multi-omics Analysis of Human Aging Using the Large Language Module based Functional Module Annotation Multi-omic methods provide great opportunities to systematically reveal the critical molecular alterations of aging from a multidimensional perspective, while matching and investigating the biological information and functions from multi could be a heavy subjective work. Large Language Models (LLMs) has shown high efficiency and accuracy in repetitive search and collection work, which will help us to extensively and quickly investigate potential research objects and validate them with published works to prove their roles and molecular mechanism. So in this project, we aim to build up a tool utilizing LLM, such as GPT4, to	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)

	accelerate and improve the biological investigation in multi-omics data for aging research. 3.2 Climate and health – mapping the impacts towards positive action This PhD is located within a wider multidisciplinary project NTU “Climate Transformation Program” that seeks to map and model impacts of climate change. World Health Organization (WHO) emphatically noted that the risks of the climate crisis to human health extend way beyond physical impact(s) to mental health and called for intervention(s), mitigation and adaptation. The evidence however on mental health impacts in Singapore and Southeast Asia is limited. The PHD project will integrate evidence synthesis and observational mixed methods approached to identify mental health risks and at risk populations. 3.3 Mapping and Optimising Public involvement in Biobanks Biobanks play an important and emerging role in supporting basic and translational research. The PHD project will be nested in a population cohort study (HELIOS; https://www.healthforlife.sg), established and led by Lee Kong Chian School of Medicine that aims to identify environmental, lifestyle and genetic factors that cause heart disease, diabetes, cancer and other chronic diseases in Singapore. The work will seek (a) to sunthesise evidence on Patient Public Involvement in context of biobanks; (b) to develop implement and evaluate Patient Public Involvement initiatives and (c) to conduct mixed methods study related to return of results procedures. The work will involve scoping literature reviews, preparatory work for evaluation studies including public and community involvement and engagement activities, collection analysing qualitative and quantitative data, building relationships with relevant stakeholders.	Assoc Prof Konstadina Griva Konstadina.griva@ntu.edu.sg https://earthobservatory.sg/research/climate-transformation-programme Co-supervisor: Assoc Prof Steve Yim Assoc Prof Konstadina Griva Konstadina.griva@ntu.edu.sg Co-supervisor: Prof John Chambers
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3.4	Ageing of bone microenvironments Our skeletons play a crucial role in regulating key physiological processes, including mineral homeostasis, energy metabolism, and blood cell production. The presence of multiple blood vessel (BV) subtypes and the distinct microenvironments they support contribute to the skeleton's multifaceted functions. Vascular aging is a key factor in the age-related functional and physical changes observed in the skeleton. Understanding vascular niches and their age-related alterations could help target specific functional niches for managing age-related bone and blood diseases. In this study, we aim to identify and characterize bone vascular microenvironments and their functions. Leveraging cutting-edge techniques developed in our laboratory—including high-resolution 3D imaging, single-cell and spatial transcriptomics, metabolic analysis, and advanced mouse genetics—the candidate will have the opportunity to: • Characterize different types of microenvironments in bone. • Understand how blood vessels support these niches. • Identify strategies to replace or target aging blood vessel subtypes specifically.	Assoc Prof Saravana Kumar Ramasamy saravana.kr@ntu.edu.sg
3.5	Metabolic control of bone marrow microenvironments The mammalian skeletal system undergoes continuous remodelling throughout life, intricately interacting with whole-body physiology. Metabolic changes significantly influence bone health by altering the cellular composition and functional dynamics of bone tissue. However, the cellular and molecular mechanisms underlying these dynamic changes remain poorly understood. In this study, we investigate the impact of metabolism on the mesenchymal	Assoc Prof Saravana Kumar Ramasamy saravana.kr@ntu.edu.sg

3.6	composition of bone microenvironments. Specifically, the student will 1. Map and characterize the distribution patterns of mesenchymal cell subtypes in bone. 2. Explore how metabolic conditions such as diabetes, modulate mesenchymal cell composition 3. Identify metabolic targets to modulate mesenchymal cell differentiation and composition. The student will employ advanced techniques, including confocal and intravital imaging, single-cell and spatial transcriptomics, metabolic profiling, and state-of-the-art mouse transgenics. Overall, this study aims to uncover the mechanisms driving bone pathology in metabolic diseases like diabetes, providing a foundation for targeted therapeutic strategies. Understanding the tumor microenvironment: High-resolution 3D and multiplex imaging approach for deciphering cancer progression Endothelial cells are pivotal architects of blood and lymphatic vessel integrity, forming the inner lining that regulates inflammation, immune cell trafficking, and organ-specific vascular functions. Perivascular and mesenchymal stromal cells dynamically shape vascular microenvironments, playing essential roles in tissue homeostasis and disease. In cancer, the tumor microenvironment (TME) drives disease progression by orchestrating a complex interplay among cancer cells, vascular networks, and stromal components. This dynamic milieu enhances metastatic potential and contributes to therapeutic resistance. Central to this process is epithelial-mesenchymal transition (EMT), which equips cancer cells with invasive properties. Critically, stromal and vascular cells are key enablers of EMT and therapy resistance, making them highly attractive targets for innovative therapeutic strategies. Despite their significance, the complexity, heterogeneity, and spatial interactions of tumor stroma	Assoc Prof Anjali Parmanand Kusumbe anjali.pkusumbe@ntu.edu.sg https://dr.ntu.edu.sg/cris/rp/rp02539
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	and vasculature remain poorly understood across different stages of cancer progression. This knowledge gap limits the development of precision therapies. To address this challenge, we propose leveraging cutting-edge high-resolution light-sheet microscopy and multiplex imaging to define, at an unprecedented level, the spatial interactions between vascular, stromal, and cancer cells throughout disease progression. Our approach focuses on three malignancies with distinct clinical and biological challenges: head and neck cancers, glioblastoma, and breast tumors. This study aims to illuminate the spatial interactions within the TME, providing a foundation not only for the development of targeted interventions to disrupt the stromal-vascular axis in cancer progression but also for precise diagnostic and prognostic strategies throughout the course of the disease.	
3.7	Discovery of Gut Microbiome-Metabolized Bioactive Compounds from Traditional Chinese Medicine We propose to culture human gut microbiomes with Traditional Chinese Medicine (TCM) extracts and apply a novel computational algorithm to identify new bioactive compounds metabolized by the microbiota. This integrative platform enables systematic discovery of microbiome-derived metabolites from natural products, uncovering mechanisms underlying TCM efficacy and revealing potential therapeutic agents. Beyond discovery, we aim to construct a comprehensive atlas of gut microbiome-metabolized TCM and natural products. This resource will serve as a foundation for drug development and precision therapeutics based on host-microbe-metabolite interactions.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
3.8	Optimising cancer screening in primary care Cancer is the leading cause of death in Singapore, with three in 10 people expected to die of the condition. When cancer is diagnosed earlier, treatment is more effective and costs less, while survival rates increase and carer quality of life is improved. Cancer screening aims to detect early stage cancer to realise these benefits, however screening uptake is currently suboptimal in Singapore. This PhD	Assoc Prof Jo-Anne Elizabeth Manski-Nankervis joanne.mn@ntu.edu.sg Website

3.9	will explore development and implementation of a multicancer risk tool to communicate risk of cancer and facilitate appropriate screening. Can polygenic risk scores be used to facilitate cancer screening in primary care? Polygenic risk scores have been proposed as a solution to stratify cancer risk, resulting in tailoring of screening recommendations in order to increase the detection of cancers in those at younger age, reduce risks associated with false positives and reduce harms associated with unnecessary biopsies and invasive treatments. This PhD will explore acceptability and feasibility of polygenic risk scores for risk stratification of cancer screening in primary care. This will inform future implementation with the aim of combining the reach of primary health care with Singapore's goal of achieving precision medicine to overcome the challenge of late cancer diagnosis related to suboptimal breast cancer and colorectal cancer screening.	https://www.ntu.edu.sg/pcfm Assoc Prof Jo-Anne Elizabeth Manski-Nankervis joanne.mn@ntu.edu.sg Website https://www.ntu.edu.sg/pcfm
3.10	Implementation of a family history tool in primary care to identify people that may benefit from predictive genetic testing in primary care Primary care roles in health assessment, screening, early detection and prevention have been strengthened by HealthierSG strategy. With genetic testing expected to transform the practice of medicine in the next 10 years, there is a need to explore effective implementation of clinical workflows in primary care. The estimated prevalence of familial hypercholesterolaemia (FH) in Singapore is 1 in 140 people; Approximately 1 in 150 Singaporeans carry a pathogenic variant of hereditary breast and ovarian cancer syndrome (HBOC), and 1 in 530 have a pathogenic variant of Lynch syndrome. However, the majority of carriers in the population are not identified until they actually develop one of the conditions associated with the genetic variant. Recording of family history in primary care needs to be optimised to identify people that may benefit from predictive genetic	Assoc Prof Jo-Anne Elizabeth Manski-Nankervis joanne.mn@ntu.edu.sg Website https://www.ntu.edu.sg/pcfm

	testing. This PhD will involve the development of clinical workflows, incorporating a digital family history self-completion tool for patients, exploring key determinants of behavioural intention towards genetic testing through a survey; and development and evaluation of customized genetic risk communication strategies in shaping outcomes in primary care settings.	
3.11	HealthierSG in private general practice: opportunities and challenges HealthierSG aims to encourage and facilitate healthier living amongst Singaporeans. This includes promoting regular exercise, a balanced diet, mental well-being, and regular health screenings. Private general practices, where 80% of family doctors work, will play a key role in ensuring the success of HealthierSG. This PhD will explore the experiences of GPs and patients attending private general practice in relation to HealthierSG and explore models of care that facilitate chronic disease and preventive health outcomes.	Assoc Prof Jo-Anne Elizabeth Manski-Nankervis joanne.mn@ntu.edu.sg Website https://www.ntu.edu.sg/pcfm
3.12	Metabolic feature-based functional module analysis based on the large language model We propose to develop featureFMA, a novel large language model (LLM)-guided computational framework for metabolic feature-based functional module analysis in LC-MS untargeted metabolomics. Traditional pathway analysis lacks specificity and coverage for metabolomics data. featureFMA will integrate metabolite annotation, metabolic network modeling, and LLM-based functional interpretation to identify dysregulated modules linked to biological functions and diseases. This project includes software development (R package, Shiny app, and cloud platform), multi-species validation, and diverse case studies (e.g., enzyme mutation and gut microbiome). featureFMA will provide a scalable, intelligent solution for interpreting complex metabolomics data and accelerating functional discovery in systems biology.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)

3.13	Sustainable Precision Healthcare: Predictive Modelling and Global Strategies for Environmentally Linked Diseases Precision healthcare promises to transform disease prevention, diagnosis, treatment and prognosis by tailoring interventions to individual risk profiles. However, its adoption faces challenges of cost, feasibility, and contextual relevance. This research addresses these gaps by: (1) developing and evaluating predictive modelling frameworks for environmentally dependent diseases including respiratory illnesses; (2) quantifying the incremental predictive and clinical value of biomarkers, molecular signatures, phenotypes, endotypes, and external determinants including environmental exposures and socio-economic risks; and (3) assessing implementation feasibility and implications across high-income and low- and middle-income countries. The findings will provide evidence to guide equitable and sustainable precision healthcare strategies globally.	Dr Michele Nguyen michele.nguyen@ntu.edu.sg Website www.drmichelenguyen.com Co-Supervisor: Assoc Prof Sanjay Chotirmall Asst Prof Liang Yao
3.14	The "Burden of Evidence" in Respiratory and Infectious Medicine: Quantifying the Impact of Low-Quality Research on Health Equity and AI Integrity <i>Remarks: Project may be supported by scholarship funding</i> The annual output of MEDLINE-indexed articles now exceeds one million, creating a paradox where more information often leads to less clarity. Medical knowledge increasingly reaches clinicians through fragmented feeds designed for engagement rather than accuracy. This phenomenon has created a "burden of evidence." Analogous to the "burden of disease," this concept measures the systemic prevalence of low-quality, biased, and redundant research. This burden is not merely a waste of resources; it is an active pollutant in the healthcare ecosystem that distorts clinical guidelines, threatens health equity, and poisons the datasets used to train the next generation of medical Artificial Intelligence (AI).	Dr Liang Yao Liang.yao@ntu.edu.sg Website https://www.liamyao.com/ Co-Supervisor: Asst Prof Michele Nguyen Assoc Prof Sanjay Chotirmall

3.15	To address this, we must shift from celebrating research volume to interrogating its integrity. This PhD project aims to quantify and characterize the burden of evidence specifically within Respiratory and Infectious Diseases—a field critically impacted by rapid, high-volume publication cycles. The research will proceed in two objectives: (1) Primary Research Assessment: Systematically evaluate the prevalence of "high risk of bias" in pivotal randomized controlled trials and observational studies within the field. (2) Synthesis quality assessment: Determine the proportion of evidence summaries (systematic reviews and meta-analyses) that are proved as low-certainty evidence to form conclusions. (3) Impact and uptake analysis: Trace the downstream penetration of this low-quality evidence by quantifying how frequently these flawed studies are cited in major clinical guidelines and policy documents. By mapping the extent of this "evidence burden" this project will provide a framework to decontaminate clinical decision-making and ensure that future health policies and AI tools are built upon a foundation of trustworthy data. Viral-Induced Brain Developmental Disorders and Calcification <i>Remarks: Project may be supported by scholarship funding</i> Singapore's declining birth rate has placed increasing importance on safeguarding the long-term health and developmental outcomes of every child. Early-life infection with neurotropic viruses such as Zika virus (ZIKV), which remain a regional concern in Southeast Asia, has been associated with brain calcifications and long-term neurological deficits. However, the molecular mechanisms driving these outcomes remain poorly understood. Emerging evidence suggests that viral components can persist after infection and disrupt normal cellular processes in the developing brain. In this study, we investigate how viral exposure alters molecular pathways that regulate brain homeostasis and tissue remodeling. The student will gain training in advanced virology, neuroimmunology, and multi-omics approaches, and will have opportunities to engage with Singapore's	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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3.16	vibrant biomedical research ecosystem and clinical collaborators. Overall, this study aims to define how viral infection and persistence shape brain development and calcification, providing a foundation for therapeutic strategies and biomarkers to protect child health in Singapore and the broader region. Selected References: 1. Fraczek M, Breckenridge H, Melano I, Squillaciotti E, Nielsen-Saines K, Recinos V, Chen W (2025) Intracranial calcifications in congenital viral infections: mechanisms and cellular roles. Curr Opin Virol 73: 101479 2. Chen W, et al (2021) Zika virus NS3 protease induces bone morphogenetic protein-dependent brain calcification in human fetuses. Nat Microbiol 6: 455–466 3. Azamor T, Familiar-Macedo D, Salem GM, et al (2024) Transplacental SARS-CoV-2 protein ORF8 binds to complement C1q to trigger fetal inflammation. EMBO J 43: 5494–5529 4. Foo SS, et al (2024) Sustained chronic inflammation and altered childhood vaccine responses in children exposed to Zika virus. EBioMedicine 106: 105249 5. Zarb Y, et al (2021) Microglia control small vessel calcification via TREM2. Sci Adv 7: eabc4898 Viral-Induced Chronic Musculoskeletal Disease in Aging <i>Remarks: Project may be supported by scholarship funding</i> Singapore's rapidly aging population has led to a growing burden of chronic musculoskeletal disorders, a leading cause of disability and reduced quality of life. Viral infections are increasingly recognized as triggers of persistent joint pain, inflammation, and tissue degeneration, particularly in the context of emerging arboviruses in a changing climate. However, the mechanisms linking viral infection to chronic musculoskeletal disease and aging remain poorly understood. Joint-resident cells such as chondrocytes play critical roles in maintaining cartilage integrity and regulating bone remodeling, yet how viral infection disrupts these processes is unclear. In this study, we	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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	investigate how viral infection alters cellular function and tissue homeostasis in the joint. The student will employ integrated approaches including virology, multi-omics profiling, and advanced 2D and 3D human joint models with biomechanical stimulation. Overall, this study aims to define how viral infection drives chronic musculoskeletal disease and interacts with aging, providing a foundation for therapeutic strategies targeting infection-associated arthritis and age-related joint degeneration. Selected References: 1. Bartholomeeusen K, et al (2023) Chikungunya fever. Nat Rev Dis Primers 9: 17 2. Baxter VK, Heise MT (2020) Immunopathogenesis of alphaviruses. Adv Virus Res 107: 315–382 3. Chen W, et al (2014) Arthritogenic alphaviral infection perturbs osteoblast function and triggers pathologic bone loss. Proc Natl Acad Sci USA 111: 6040–6045 4. Chen W, et al (2015) Arthritogenic alphaviruses: new insights into arthritis and bone pathology. Trends Microbiol 23: 35–43 Chen W, et al (2017) Specific inhibition of NLRP3 in chikungunya disease reveals a role for inflammasomes in alphavirus-induced inflammation. Nat Microbiol 2: 1435–1445	Asst Prof Huang Tao tao.huang@ntu.edu.sg Webpage: https://dr.ntu.edu.sg/entities/person/Huang-Tao
3.17	Physio-Climate Heat Warning for Population Health and Heat Resilience <i>Remarks: Project may be supported by scholarship funding</i> This PhD project offers an exciting opportunity to develop a new physio-climate heat warning framework for climate adaptation and public health. The student will work across climate science, heat physiology, epidemiology, and urban health, using a biophysical model and physio-climate indices to understand how much heat different groups of people can safely tolerate. By combining data from France, Hong Kong, and Singapore, the project will build more precise, population-sensitive heat warning systems for humid and warming cities. This programme is well suited for students interested in climate and health, heat resilience, environmental epidemiology, physiological modelling, and data-driven adaptation policy.	

3.18	Heat, Chronic Illness, and Climate Adaptation in Singapore <i>Remarks: Project may be supported by scholarship funding</i> This PhD project will investigate how rising heat exposure affects people living with chronic illnesses in Singapore and identify effective strategies for heat-health adaptation. The student will work at the intersection of climate science, epidemiology, chronic disease, and public health, using local health and environmental data to quantify heat-related risks across cardiovascular, respiratory, renal, and metabolic conditions. The project will examine multiple dimensions of heat exposure, including air temperature, humidity, radiation, and wind, assess variation by age and gender, and evaluate how future warming may alter risks. It will also explore awareness, healthcare use, productivity impacts, and trusted interventions to protect vulnerable populations.	Asst Prof Huang Tao tao.huang@ntu.edu.sg Webpage: https://dr.ntu.edu.sg/entities/person/Huang-Tao
3.19	Climate and Health Communication This PhD is embedded within the NTU Climate Transformation Programme, which seeks to map and respond to the impacts of climate change. The World Health Organization highlights that climate change poses wide-ranging risks to human health, yet how these risks are communicated and understood by the public in Singapore and Southeast Asia remains unclear. This project will examine how climate–health risks are communicated and interpreted across different population groups, and how message framing influences understanding, risk perception, and behavioural responses. Using mixed methods—including evidence synthesis, surveys, and qualitative research—the study will identify effective communication strategies tailored to diverse socio-cultural segments.	Assoc Prof Konstadina Griva Konstadina.griva@ntu.edu.sg

3.20	Menopause at Work: Impact and Wellbeing Menopause is a critical life-course transition that often coincides with peak career and caregiving responsibilities. Symptoms such as fatigue, sleep disturbance, mood changes, and cognitive complaints (“brain fog”) can affect daily functioning and workplace performance, yet their impact in occupational settings remains poorly understood in Singapore. This PhD will map menopause-related symptoms and their functional impact among working women, examining how they influence productivity, engagement, and wellbeing across different job types and socio-cultural contexts. Using mixed methods—including surveys, and qualitative interviews—the study will capture symptom patterns, coping strategies, and workplace challenges.	Assoc Prof Konstadina Griva Konstadina.griva@ntu.edu.sg
3.21	Strengthening Menopause Care in Primary Care: Perspectives and Support Needs Menopause care is often under-recognised in primary care, where women first seek help. Symptoms may be overlooked, misattributed, or insufficiently managed due to limited awareness, training, and structured care pathways. This PhD will explore how primary care healthcare professionals understand and manage menopause, and identify gaps in knowledge, confidence, and system-level support. Using surveys and qualitative interviews with clinicians, alongside insights from datasets such as HELIOS Study, the study will examine current practices, barriers, and opportunities to improve care.	Assoc Prof Konstadina Griva Konstadina.griva@ntu.edu.sg
3.22	From Guidance to Practice: Implementing Patient and Public Involvement in Singapore Health Research This PhD will examine the implementation of a newly developed national Patient and Public Involvement (PPI) guidance document for health research in Singapore. Using an implementation science lens, the	Assoc Prof Jo-Anne Elizabeth Manski-Nankervis joanne.mn@ntu.edu.sg Website

	project will explore how researchers, institutions, and patient partners interpret, adopt, and operationalise the guidance in real-world research settings. This will include case studies of research projects, interviews with researchers and patient partners, and assessment of barriers, facilitators, and contextual influences on uptake, including training needs. Findings will inform refinement of the guidance and the development of practical implementation strategies to support sustained, meaningful PPI in research. Reference: Sim-Devadas AL, Soon SBS, Lakshmanan EM, Jain R, Chotirmall SH, Manski-Nankervis JA. OPENing the door for patient and public involvement in medical research in Singapore. Res Involv Engagem. 2025 Oct 27;11(1):125. doi: 10.1186/s40900-025-00789-x. PMID: 41146246; PMCID: PMC12560399	https://www.ntu.edu.sg/pcfmr Co-Sup: Assoc Prof Konstadina Griva
4. Respiratory & Infectious Diseases		
4.1	Exploring RNA Viral Vectors for mRNA Therapy Applications This project aims to investigate the molecular mechanisms of RNA viral vectors and their implications in developing next-generation mRNA therapies for infectious diseases, cancer, and other chronic conditions. Leveraging the unique properties of RNA viral vectors, such as high transfection efficiency and low immunogenicity, we propose to systematically characterize the vector-host interactions at the molecular level. This will involve the use of cutting-edge biotechnological tools, including CRISPR-Cas9 genome editing and next-generation sequencing, to optimize vector design and functionality. By elucidating the molecular basis of RNA viral vector-mediated mRNA delivery, this research intends to pave the way for highly effective and targeted therapies. The outcomes are expected to	Assoc Prof Luo Dahai luodahai@ntu.edu.sg Website https://www.ntu.edu.sg/research/faculty-directory/detail/rp00464

	have profound impacts on the treatment strategies for a wide range of diseases, enhancing the therapeutic efficacy while minimizing adverse effects.	
4.2	Molecular Basis of the Flavivirus Replication Process Dengue is a critical public health issue with severe forms affecting hundreds of thousands annually. Without a vaccine offering lasting protection against all DENV serotypes, treatment relies on symptomatic care and antivirals. The replication of the virus involves a complex known as the replication complex (RC), which is central to viral replication and a prime target for drug development. Despite advances in understanding individual components of the RC, its full architecture and interactions remain elusive. his project aims to uncover key protein-protein and protein-RNA interactions within the DENV RC using methods from biochemistry, biophysics, structural biology, cell biology, and virology. Approaches include reconstituting the RC with selected proteins and isolating it from infected cells to study its composition and functionality.	Assoc Prof Luo Dahai luodahai@ntu.edu.sg Website https://www.ntu.edu.sg/research/faculty-directory/detail/rp00464
4.3	Protein Lipidation (S-acylation) in Membrane Damage during Infection and Immunity <i>Remarks: Project may be supported by scholarship funding</i> Cell membranes are highly vulnerable to oxidative stress that damages organelles and threatens cell viability. Such membrane damage is a hallmark of infection, neurodegeneration, and inflammatory disease. We discovered that cells counteract lipid damage through a transcriptional and epigenetic program that promotes detoxification and innate immunity (accepted Nat. Commun. 2025). A key component of this response is the reversible switch of protein fatty acid acylation, which regulates central aspects of cell biology, contributes to innate immune defense, and directly influences SARS-CoV-2 infection.	Asst Prof Francisco Sarmiento Mesquita https://www.mesquitallab.com

4.4	This project will investigate the links between membrane lipid damage, protein lipidation, and innate immunity. Using genetic screens, transcriptomics, molecular and chemical biology, and advanced imaging, we will identify cellular sensors of lipid damage, define their protective roles in infection, and evaluate protein lipidation as a host-directed therapeutic target. <i>Relevant Publications (Mesquita et al):</i> https://www.biorxiv.org/content/10.1101/2025.02.25.640160v2 https://www.nature.com/articles/s41467-023-43027-2 https://infoscience.epfl.ch/entities/patent/de39ac78-a6d5-418d-a6fa-5bdb09775e5a <i>How Viruses Remodel Host Membranes</i> <i>Remarks: Project may be supported by scholarship funding</i> Enveloped RNA viruses such as SARS-CoV-2 remodel host membranes to assemble infectious virions and to build replication organelles. Viral structural proteins undergo extensive S-acylation, a lipid modification that we showed is critical for SARS-CoV-2, as it regulates Spike protein function, virion lipid composition, and infectivity. These findings raise fundamental questions about how protein lipidation and membrane remodeling shape host–virus interactions. This project will investigate how viruses select and reorganize host lipids to support envelope biogenesis and replication. We will combine mutagenesis of viral proteins, viral expression systems, lipidomics and proteomics, structural studies, and high-resolution imaging of infection to uncover conserved principles of viral membrane remodeling and identify host factors that may be targeted for antiviral intervention. <i>Relevant Publications (Mesquita et al):</i> DOI: 10.1016/j.devcel.2021.09.016 https://www.nature.com/articles/s41467-023-35921-6	Asst Prof Francisco Sarmiento Mesquita https://www.mesquitlab.com
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4.5	Sustainable Precision Healthcare: Predictive Modelling and Global Strategies for Environmentally Linked Diseases Precision healthcare promises to transform disease prevention, diagnosis, treatment and prognosis by tailoring interventions to individual risk profiles. However, its adoption faces challenges of cost, feasibility, and contextual relevance. This research addresses these gaps by: (1) developing and evaluating predictive modelling frameworks for environmentally dependent diseases including respiratory illnesses; (2) quantifying the incremental predictive and clinical value of biomarkers, molecular signatures, phenotypes, endotypes, and external determinants including environmental exposures and socio-economic risks; and (3) assessing implementation feasibility and implications across high-income and low- and middle-income countries. The findings will provide evidence to guide equitable and sustainable precision healthcare strategies globally.	Dr Michele Nguyen michele.nguyen@ntu.edu.sg Website www.drnichelenguyen.com Co-Supervisor: Assoc Prof Sanjay Chotirmall Asst Prof Liang Yao
4.6	The "Burden of Evidence" in Respiratory and Infectious Medicine: Quantifying the Impact of Low-Quality Research on Health Equity and AI Integrity <i>Remarks: Project may be supported by scholarship funding</i> The annual output of MEDLINE-indexed articles now exceeds one million, creating a paradox where more information often leads to less clarity. Medical knowledge increasingly reaches clinicians through fragmented feeds designed for engagement rather than accuracy. This phenomenon has created a "burden of evidence." Analogous to the "burden of disease," this concept measures the systemic prevalence of low-quality, biased, and redundant research. This burden is not merely a waste of resources; it is an active pollutant in the healthcare ecosystem that distorts clinical guidelines, threatens health equity, and poisons the datasets used to train the next generation of medical Artificial Intelligence (AI).	Dr Liang Yao Liang.yao@ntu.edu.sg Website https://www.liamyao.com/ Co-Supervisor: Asst Prof Michele Nguyen Assoc Prof Sanjay Chotirmall

4.7	To address this, we must shift from celebrating research volume to interrogating its integrity. This PhD project aims to quantify and characterize the burden of evidence specifically within Respiratory and Infectious Diseases—a field critically impacted by rapid, high-volume publication cycles. The research will proceed in two objectives: (1) Primary Research Assessment: Systematically evaluate the prevalence of "high risk of bias" in pivotal randomized controlled trials and observational studies within the field. (2) Synthesis quality assessment: Determine the proportion of evidence summaries (systematic reviews and meta-analyses) that are proved as low-certainty evidence to form conclusions. (3) Impact and uptake analysis: Trace the downstream penetration of this low-quality evidence by quantifying how frequently these flawed studies are cited in major clinical guidelines and policy documents. By mapping the extent of this "evidence burden" this project will provide a framework to decontaminate clinical decision-making and ensure that future health policies and AI tools are built upon a foundation of trustworthy data. Direct cell reprogramming for biomedical applications <i>Remarks: Project may be supported by scholarship funding</i> The manufacture of advanced stem cell-based products and therapies through directed differentiation faces significant challenges in achieving efficient, reliable, and scalable production of specialized cell types especially in a cGMP setting. Cell differentiation approaches involve stepwise culture of (pluripotent) stem cells to direct their development into target cell types. However, current manufacturing methods are generally not fit for purpose - being often hampered by complex, lengthy and costly protocols, low cell yield, purity and/or quality, and inconsistent outcomes - limiting industrial applications. Direct (or forward) cell programming offers a promising alternative by enabling the direct conversion of one cell type into another by activating gene regulatory networks that determine cell identity. This approach has the potential greatly to streamline the manufacturing process, reduce the time and resources required, and improve the consistency and	Associate Prof Yen CHOO yen.choo@ntu.edu.sg
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4.8	functionality of cellular products. As the advanced therapy field develops, establishing robust, scalable manufacturing technology platforms (such as by direct cell programming) will become key to the success of the regenerative medicine and cell therapy industry. Programming of cells using lineage control networks has the potential to transform how we make cell therapies and immunotherapies, develop regenerative medicines, and create cellular models for research. However, identifying specific combinations of master regulatory genes known as transcription factors (TFs) that lead to highly efficient conversion of a scalable starting cell (e.g. iPSC, fibroblast) into desired cell types for biomedical applications (e.g. T cell, b cell) remains a significant challenge and a longstanding, critical bottleneck in the field. In this programme we will use an innovative combinatorial screening technology to rapidly assess the effectiveness of thousands of combinations of TFs in programming various human cell types into specific lineages that enable high value biomedical applications. Cell types we may derive in this project have diverse applications, including in: 1) developing advanced cellular/tissue models for biomedical R&D, 2) cGMP manufacturing of cell and gene therapies, including allogeneic immunotherapies, and 3) in vivo reprogramming for regenerative medicine and autologous immunotherapies. Viral-Induced Brain Developmental Disorders and Calcification <i>Remarks: Project may be supported by scholarship funding</i> Singapore's declining birth rate has placed increasing importance on safeguarding the long-term health and developmental outcomes of every child. Early-life infection with neurotropic viruses such as Zika virus (ZIKV), which remain a regional concern in Southeast Asia, has been associated with brain calcifications and long-term neurological deficits. However, the molecular mechanisms driving these outcomes remain poorly understood. Emerging evidence suggests that viral components can persist after infection and disrupt normal cellular processes in the	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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4.9	developing brain. In this study, we investigate how viral exposure alters molecular pathways that regulate brain homeostasis and tissue remodeling. The student will gain training in advanced virology, neuroimmunology, and multi-omics approaches, and will have opportunities to engage with Singapore's vibrant biomedical research ecosystem and clinical collaborators. Overall, this study aims to define how viral infection and persistence shape brain development and calcification, providing a foundation for therapeutic strategies and biomarkers to protect child health in Singapore and the broader region. Selected References: 1. Fraczek M, Breckenridge H, Melano I, Squillacioti E, Nielsen-Saines K, Recinos V, Chen W (2025) Intracranial calcifications in congenital viral infections: mechanisms and cellular roles. Curr Opin Virol 73: 101479 2. Chen W, et al (2021) Zika virus NS3 protease induces bone morphogenetic protein-dependent brain calcification in human fetuses. Nat Microbiol 6: 455–466 3. Azamor T, Familiar-Macedo D, Salem GM, et al (2024) Transplacental SARS-CoV-2 protein ORF8 binds to complement C1q to trigger fetal inflammation. EMBO J 43: 5494–5529 4. Foo SS, et al (2024) Sustained chronic inflammation and altered childhood vaccine responses in children exposed to Zika virus. EBioMedicine 106: 105249 5. Zarb Y, et al (2021) Microglia control small vessel calcification via TREM2. Sci Adv 7: eabc4898 Viral-Induced Chronic Musculoskeletal Disease in Aging <i>Remarks: Project may be supported by scholarship funding</i> Singapore's rapidly aging population has led to a growing burden of chronic musculoskeletal disorders, a leading cause of disability and reduced quality of life. Viral infections are increasingly recognized as triggers of persistent joint pain, inflammation, and tissue degeneration, particularly in the context of emerging arboviruses in a changing climate. However, the	Asst Prof Weiqiang (Javier) Chen weiqiang.chen@ntu.edu.sg Lab Webpage: https://weiqchen.wixsite.com/jchenlab https://dr.ntu.edu.sg/entities/person/Weiqiang-Chen
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	mechanisms linking viral infection to chronic musculoskeletal disease and aging remain poorly understood. Joint-resident cells such as chondrocytes play critical roles in maintaining cartilage integrity and regulating bone remodeling, yet how viral infection disrupts these processes is unclear. In this study, we investigate how viral infection alters cellular function and tissue homeostasis in the joint. The student will employ integrated approaches including virology, multi-omics profiling, and advanced 2D and 3D human joint models with biomechanical stimulation. Overall, this study aims to define how viral infection drives chronic musculoskeletal disease and interacts with aging, providing a foundation for therapeutic strategies targeting infection-associated arthritis and age-related joint degeneration. Selected References: 1. Bartholomeeusen K, et al (2023) Chikungunya fever. Nat Rev Dis Primers 9: 17 2. Baxter VK, Heise MT (2020) Immunopathogenesis of alphaviruses. Adv Virus Res 107: 315–382 3. Chen W, et al (2014) Arthritogenic alphaviral infection perturbs osteoblast function and triggers pathologic bone loss. Proc Natl Acad Sci USA 111: 6040–6045 4. Chen W, et al (2015) Arthritogenic alphaviruses: new insights into arthritis and bone pathology. Trends Microbiol 23: 35–43 Chen W, et al (2017) Specific inhibition of NLRP3 in chikungunya disease reveals a role for inflammasomes in alphavirus-induced inflammation. Nat Microbiol 2: 1435–1445	
4.10	Quantifying Zoonotic Spillover Risk from Wildlife through Integrated Exposure and Transmission Modelling Zoonotic diseases pose a growing global threat as environmental change, land-use intensification, and biodiversity loss increase human-wildlife contact and spillover risk. Preventing future outbreaks requires quantitative approaches that move beyond retrospective analyses. This project estimates zoonotic infection potential from mammalian wildlife	Asst Prof Michele Nguyen michele.nguyen@ntu.edu.sg Lab Webpage: www.drnichelenguyen.com Assoc Prof Janelle Thompson

	using an integrated modelling framework. It will model human-wildlife interactions based on shedding events, pathogen concentrations, wildlife distributions, and human exposure pathways; infer dose-response relationships for novel pathogens from epidemiological data and similarities with known pathogens; and assess the role of reverse zoonosis in sustaining wildlife reservoirs. The research will advance zoonotic risk science, inform evidence-based policy, and support One Health surveillance and pandemic preparedness. Interested candidates are encouraged to apply for the Interdisciplinary Graduate Programme (IGP) at NTU as well.	
5. Skin Disease & Wound Repair		
5.1	The role of microtrauma in human hair regrowth and regeneration Androgenetic alopecia (or male pattern baldness) affects more than half of men by the time they reach middle age, whereby hair follicles miniaturise over time. We currently do not understand the mechanism of the human hair cycle, or how to reverse miniaturization. The popularity of treatments like microneedling suggest that subclinical wounding (ie. Microtrauma) has a role in allowing hair follicle stem cells and their microenvironment to regenerate. Our team is focused on understanding the basic mechanisms of microtrauma on human skin and hair follicles, and translating these findings into exciting new treatments for hair loss.	Co-Supervisor: Asst Prof Etienne Wang etienne@nsc.com.sg

5.2	Post-Translational Modifications of the Integrin LFA-1 in the Regulation of T-Cell Motility Leukocyte function-associated antigen-1 (LFA-1) is an integrin expressed on T-cells and plays a crucial role in T-cell signaling, adhesion, and motility. Protein post-translational modifications are known to influence integrin functions. However, LFA-1 post-translational modifications and their functional roles are not clearly understood. This project aims to determine the impact of glycosylation and sulfation on LFA-1 activation, clustering, and signaling, investigate how these post-translation modifications affect T-cell motility. The outcomes of this research will provide deep insights into the molecular mechanisms that underpin T-cell immunology, which could lead to developing novel and safe strategies to fine tune T-cell function.	Assoc Prof Navin Kumar Verma nkverma@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00490
5.3	Understanding the Role of DDX3 in Lymphoma Drug Resistance Despite the use of multi-agent chemotherapy for non-Hodgkin lymphoma, treatment outcomes remain poor due to the development of chemoresistance and high relapse rates. We have recently reported that loss-of-function mutations in the X-linked RNA helicase DDX3X are associated with chemoresistance and poor prognosis in non-Hodgkin lymphoma subtypes. This project aims to further investigate DDX3X involvement in Epstein-Barr virus (EBV)-associated Natural killer/T-cell lymphoma (NKTCL), which is an Asian-prevalent aggressive subtype. The outcomes will advance our understanding of non-Hodgkin lymphoma disease mechanism and drug resistance that would have profound impact on treatment strategies.	Assoc Prof Navin Kumar Verma nkverma@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00490
5.4	Design of microneedle for skin tissue health and disease profiling The skin, being the largest organ of the body that interfaces with the external environment, offers an excellent site for drug administration (injection) and retrieval of human biological materials (blood draw). Microneedles are medical devices that comprises of	Asst Prof Liang Kun kun.liang@ntu.edu.sg Website www.klianglab.com

5.5	an array of micron-sized needles, designed to overcome the physical barrier imposed by the outer most layer of skin (stratum corneum). Owing to their minimally-invasiveness, relatively pain-free application and ease of use, they have emerged as attractive options for both cutaneous delivery and the collection of biological samples for health monitoring. Herein, we aim to leverage on the speed and versatility of additive manufacturing to fabricate microneedles with features that are tailored for the extraction of biospecimens, such as microbiome, interstitial fluid and nucleic acids from the host human skin tissue, which will offer a simple and patient-friendly method for the prediction and diagnosis of skin health and disease. Therapeutic marine collagen hydrogels for skin repair and rejuvenation The skin, being the tissue that forms the main interface with the external environment, is prone to various insults and injuries including wounds, natural aging, and ultraviolet-induced damage. Hence there is increasing interest in developing strategies for skin repair and rejuvenation. Collagen, which is the main component of our dermal extracellular matrix, has been traditionally used for such purposes. Nevertheless, commercially available mammalian collagen has limitations such as zoonotic disease transmission and religious restrictions. To address these challenges, we have developed a scalable process to extract purified collagen from fish skin and demonstrated the ability to support skin regeneration <i>in vitro</i>. Herein we aim to investigate the supplementation of the collagen hydrogels with therapeutic moieties that deliver photo and/or electrical stimulation to enhance skin repair <i>in vivo</i>. We hypothesize that the anti-inflammatory and antioxidative properties conferred by these hydrogels can decrease proinflammatory cytokines and reduce oxidative damage, leading to accelerated skin repair and rejuvenation of ageing skin.	Asst Prof Liang Kun kun.liang@ntu.edu.sg Website www.klianglab.com
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5.6	Direct cell reprogramming for biomedical applications <i>Remarks: Project may be supported by scholarship funding</i> The manufacture of advanced stem cell-based products and therapies through directed differentiation faces significant challenges in achieving efficient, reliable, and scalable production of specialized cell types especially in a cGMP setting. Cell differentiation approaches involve stepwise culture of (pluripotent) stem cells to direct their development into target cell types. However, current manufacturing methods are generally not fit for purpose - being often hampered by complex, lengthy and costly protocols, low cell yield, purity and/or quality, and inconsistent outcomes - limiting industrial applications. Direct (or forward) cell programming offers a promising alternative by enabling the direct conversion of one cell type into another by activating gene regulatory networks that determine cell identity. This approach has the potential greatly to streamline the manufacturing process, reduce the time and resources required, and improve the consistency and functionality of cellular products. As the advanced therapy field develops, establishing robust, scalable manufacturing technology platforms (such as by direct cell programming) will become key to the success of the regenerative medicine and cell therapy industry. Programming of cells using lineage control networks has the potential to transform how we make cell therapies and immunotherapies, develop regenerative medicines, and create cellular models for research. However, identifying specific combinations of master regulatory genes known as transcription factors (TFs) that lead to highly efficient conversion of a scalable starting cell (e.g. iPSC, fibroblast) into desired cell types for biomedical applications (e.g. T cell, b cell) remains a significant challenge and a longstanding, critical bottleneck in the field. In this programme we will use an innovative combinatorial screening technology to rapidly assess the effectiveness of thousands of combinations of TFs in programming various human cell types into specific	Associate Prof Yen CHOO yen.choo@ntu.edu.sg
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	lineages that enable high value biomedical applications. Cell types we may derive in this project have diverse applications, including in: 1) developing advanced cellular/tissue models for biomedical R&D, 2) cGMP manufacturing of cell and gene therapies, including allogeneic immunotherapies, and 3) in vivo reprogramming for regenerative medicine and autologous immunotherapies.	
6. Data Science		
6.1	Deep learning for Robust Analysis of Medical Scans The doctoral project aims to develop a deep learning system for automated analysis of medical imaging scans such as X-rays, CT, and MR scans. The system will utilise deep learning models trained on large datasets of scans for different medical tasks. Students can conduct research on medical deep learning projects which includes: • Object detection in medical scans • Computer vision for medicine and population health • Medical segmentation, diffusion, reconstruction, and classification • Deep learning for the analysis of multi-modal medical dataset • Large language models for the analysis of medical imaging dataset • Large foundation models for medicine	Asst Prof Yeo Si Yong siyong.yeo@ntu.edu.sg Website https://medvisailab.github.io/research/
6.2	Systematically Investigating Molecular Mechanisms Underlying Aging-Related Human Diseases through Multi-Omics Profiling Aging is a complex biological process characterized by a gradual decline in physiological functions, which increases susceptibility to diseases and death. This process is influenced by a myriad of genetic, environmental, and lifestyle factors. To better	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)

	understand aging and study the relationship between aging and aging-related diseases, our research group is focused on building predictive models using machine learning techniques. The model is to integrate multi-omics datasets, focusing specifically on gut microbiome and metabolomics data. The comprehensive analysis of these multi-omic datasets aims to unveil crucial molecular indicators, intricate biological pathways, and influential regulatory circuits that play a role in the aging process and the pathogenesis of age-associated disorders. Such an understanding is likely to be helpful in the development of innovative therapeutic interventions to promote healthy aging and to address the onset and progression of neurodegenerative conditions such as Alzheimer's and Parkinson's diseases.	
6.3	Comprehensive Multi-omics Analysis of Human Aging Using the Large Language Module based Functional Module Annotation Multi-omic methods provide great opportunities to systematically reveal the critical molecular alterations of aging from a multidimensional perspective, while matching and investigating the biological information and functions from multi could be a heavy subjective work. Large Language Models (LLMs) has shown high efficiency and accuracy in repetitive search and collection work, which will help us to extensively and quickly investigate potential research objects and validate them with published works to prove their roles and molecular mechanism. So in this project, we aim to build up a tool utilizing LLM, such as GPT4, to accelerate and improve the biological investigation in multi-omics data for aging research.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
6.4	Data-driven Approaches for Mitigating Climate-related Health Risks As climate change and extreme weather events become more frequent worldwide, understanding their impact on public health is crucial. This research aims to investigate the relationship between climate-induced hazards and health outcomes. A key example is the 2022 malaria outbreak in Pakistan, the worst in 50 years. This outbreak followed severe flooding that	Dr Michele Nguyen michele.nguyen@ntu.edu.sg Website www.drnichelenguyen.com

	damaged homes, infrastructure, and crops. Using comprehensive data, advanced statistical modelling, and simulations, we will explore the connections between hazard intensity, conducive environmental conditions (for example, for mosquito breeding), and the incidence of disease. By linking these factors to health outcomes in the population and healthcare facilities, our findings will provide valuable insights for emergency management and hospital resource planning.	
6.5	Discovery of Gut Microbiome-Metabolized Bioactive Compounds from Traditional Chinese Medicine We propose to culture human gut microbiomes with Traditional Chinese Medicine (TCM) extracts and apply a novel computational algorithm to identify new bioactive compounds metabolized by the microbiota. This integrative platform enables systematic discovery of microbiome-derived metabolites from natural products, uncovering mechanisms underlying TCM efficacy and revealing potential therapeutic agents. Beyond discovery, we aim to construct a comprehensive atlas of gut microbiome-metabolized TCM and natural products. This resource will serve as a foundation for drug development and precision therapeutics based on host–microbe–metabolite interactions.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
6.6	Explaining Medical Imaging with Clinically Meaningful Explanations with XAI This PhD project, titled "Explaining Medical Imaging with Clinically Meaningful Explanations with XAI," aims to bridge the gap between artificial intelligence (AI) in medical imaging and clinical practice by developing advanced explainable AI (XAI) techniques that provide interpretations directly aligned with clinical understanding. The project will focus on designing XAI models that generate explanations using clinically meaningful concepts, such as anatomical features, pathology characteristics, and diagnostic criteria, making the explanations transparent and actionable for clinicians. Methods will include feature attribution, concept-based explanations, and multimodal fusion to enhance interpretability. The project targets applications in radiology, dermatology, and ophthalmology.	Asst Prof Fan Xiuyi xyfan@ntu.edu.sg

6.7	Irregular Time Series in Medical AI This PhD project, titled "Irregular Time Series in Medical AI," focuses on developing advanced machine learning models capable of handling irregular time series data, a common challenge in medical settings. Irregular time series occur when data points are collected at inconsistent intervals, such as patient vital signs recorded at varying times or sporadic medical test results. The project aims to design novel algorithms that can effectively learn from such data, leveraging techniques like temporal interpolation, attention mechanisms, and neural differential equations. These methods will be applied to medical domains, including patient monitoring, disease progression prediction, and personalized treatment planning.	Asst Prof Fan Xiuyi xyfan@ntu.edu.sg
6.8	Metabolic feature-based functional module analysis based on the large language model We propose to develop featureFMA, a novel large language model (LLM)-guided computational framework for metabolic feature-based functional module analysis in LC-MS untargeted metabolomics. Traditional pathway analysis lacks specificity and coverage for metabolomics data. featureFMA will integrate metabolite annotation, metabolic network modeling, and LLM-based functional interpretation to identify dysregulated modules linked to biological functions and diseases. This project includes software development (R package, Shiny app, and cloud platform), multi-species validation, and diverse case studies (e.g., enzyme mutation and gut microbiome). featureFMA will provide a scalable, intelligent solution for interpreting complex metabolomics data and accelerating functional discovery in systems biology.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
6.9	Sustainable Precision Healthcare: Predictive Modelling and Global Strategies for Environmentally Linked Diseases Precision healthcare promises to transform disease prevention, diagnosis, treatment and prognosis by tailoring interventions to individual risk profiles. However, its adoption faces challenges of cost, feasibility, and contextual relevance. This research	Dr Michele Nguyen michele.nguyen@ntu.edu.sg Website www.drnichelenguyen.com Co-Supervisor:

6.10	addresses these gaps by: (1) developing and evaluating predictive modelling frameworks for environmentally dependent diseases including respiratory illnesses; (2) quantifying the incremental predictive and clinical value of biomarkers, molecular signatures, phenotypes, endotypes, and external determinants including environmental exposures and socio-economic risks; and (3) assessing implementation feasibility and implications across high-income and low- and middle-income countries. The findings will provide evidence to guide equitable and sustainable precision healthcare strategies globally. The "Burden of Evidence" in Respiratory and Infectious Medicine: Quantifying the Impact of Low-Quality Research on Health Equity and AI Integrity <i>Remarks: Project may be supported by scholarship funding</i> The annual output of MEDLINE-indexed articles now exceeds one million, creating a paradox where more information often leads to less clarity. Medical knowledge increasingly reaches clinicians through fragmented feeds designed for engagement rather than accuracy. This phenomenon has created a "burden of evidence." Analogous to the "burden of disease," this concept measures the systemic prevalence of low-quality, biased, and redundant research. This burden is not merely a waste of resources; it is an active pollutant in the healthcare ecosystem that distorts clinical guidelines, threatens health equity, and poisons the datasets used to train the next generation of medical Artificial Intelligence (AI). To address this, we must shift from celebrating research volume to interrogating its integrity. This PhD project aims to quantify and characterize the burden of evidence specifically within Respiratory and Infectious Diseases—a field critically impacted by rapid, high-volume publication cycles. The research will proceed in two objectives: (1) Primary Research Assessment: Systematically evaluate the prevalence of "high risk of bias" in pivotal randomized controlled trials and observational studies within the field. (2) Synthesis quality assessment: Determine the proportion of evidence summaries (systematic reviews and meta-analyses) that are proved as low-certainty evidence to	Assoc Prof Sanjay Chotirmall Asst Prof Liang Yao Dr Liang Yao Liang.yao@ntu.edu.sg Website https://www.liamyao.com/ Co-Supervisor: Asst Prof Michele Nguyen Assoc Prof Sanjay Chotirmall
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	form conclusions. (3) Impact and uptake analysis: Trace the downstream penetration of this low-quality evidence by quantifying how frequently these flawed studies are cited in major clinical guidelines and policy documents. By mapping the extent of this "evidence burden" this project will provide a framework to decontaminate clinical decision-making and ensure that future health policies and AI tools are built upon a foundation of trustworthy data.	
6.11	Physio-Climate Heat Warning for Population Health and Heat Resilience <i>Remarks: Project may be supported by scholarship funding</i> This PhD project offers an exciting opportunity to develop a new physio-climate heat warning framework for climate adaptation and public health. The student will work across climate science, heat physiology, epidemiology, and urban health, using a biophysical model and physio-climate indices to understand how much heat different groups of people can safely tolerate. By combining data from France, Hong Kong, and Singapore, the project will build more precise, population-sensitive heat warning systems for humid and warming cities. This programme is well suited for students interested in climate and health, heat resilience, environmental epidemiology, physiological modelling, and data-driven adaptation policy.	Asst Prof Huang Tao tao.huang@ntu.edu.sg Webpage: https://dr.ntu.edu.sg/entities/person/Huang-Tao
6.12	Heat, Chronic Illness, and Climate Adaptation in Singapore <i>Remarks: Project may be supported by scholarship funding</i> This PhD project will investigate how rising heat exposure affects people living with chronic illnesses in Singapore and identify effective strategies for heat-health adaptation. The student will work at the intersection of climate science, epidemiology, chronic disease, and public health, using local health and environmental data to quantify heat-related risks across cardiovascular, respiratory, renal, and metabolic conditions. The project will examine multiple dimensions of heat exposure, including air temperature, humidity, radiation, and wind, assess variation by age and gender, and evaluate how future warming may alter risks. It will also explore awareness, healthcare use, productivity impacts, and trusted interventions to protect vulnerable populations.	Asst Prof Huang Tao tao.huang@ntu.edu.sg Webpage: https://dr.ntu.edu.sg/entities/person/Huang-Tao

6.13	Quantifying Zoonotic Spillover Risk from Wildlife through Integrated Exposure and Transmission Modelling Zoonotic diseases pose a growing global threat as environmental change, land-use intensification, and biodiversity loss increase human-wildlife contact and spillover risk. Preventing future outbreaks requires quantitative approaches that move beyond retrospective analyses. This project estimates zoonotic infection potential from mammalian wildlife using an integrated modelling framework. It will model human-wildlife interactions based on shedding events, pathogen concentrations, wildlife distributions, and human exposure pathways; infer dose-response relationships for novel pathogens from epidemiological data and similarities with known pathogens; and assess the role of reverse zoonosis in sustaining wildlife reservoirs. The research will advance zoonotic risk science, inform evidence-based policy, and support One Health surveillance and pandemic preparedness. Interested candidates are encouraged to apply for the Interdisciplinary Graduate Programme (IGP) at NTU as well.	Asst Prof Michele Nguyen michele.nguyen@ntu.edu.sg Webpage: www.drnichelenguyen.com Co-sup: Assoc Prof Janelle Thompson
7. Cancer Discovery & Regenerative Medicine		
7.1	The role of microtrauma in human hair regrowth and regeneration Androgenetic alopecia (or male pattern baldness) affects more than half of men by the time they reach middle age, whereby hair follicles miniaturise over time. We currently do not understand the mechanism of the human hair cycle, or how to reverse miniaturization. The popularity of treatments like microneedling suggest that subclinical wounding (ie. Microtrauma) has a role in allowing hair follicle stem cells and their microenvironment to regenerate. Our team is focused on understanding the basic mechanisms of microtrauma on human skin and hair follicles, and	Co-Supervisor: Asst Prof Etienne Wang etienne@nsc.com.sg

7.2	translating these findings into exciting new treatments for hair loss. In-vivo functional genetic screen to identify novel modulators of Non-Alcoholic Fatty Liver Disease (NAFLD) <i>Remarks: Project may be supported by scholarship funding</i> The project focuses on employing in-vivo mouse models that resemble and recapitulate human disease to study NAFLD disease progression. Our preliminary results have identified several shRNAs that confer a negative or positive effect on the regenerative capacity of the hepatocytes. Further approach will be focused on validation of these shRNAs, such as their cell migration and cell proliferation characteristics using various in-vitro assays, followed by selection of the top performing shRNAs for in-vivo validation. In addition, combined transcriptomic and proteomic approaches will be undertaken to unravel new insights with the aim of identifying targets for therapeutic intervention and treatment of the disease.	Assoc Prof Torsten Wuestefeld Torsten.Wuestefeld@ntu.edu.sg
7.3	Identification of novel senolytic targets for improving liver regeneration <i>Remarks: Project may be supported by scholarship funding</i> The project focuses on conducting in vivo & in vitro functional genetic screens to identify targets to eliminate senescent cells. Senescent cells are known to drive inflammaging attenuating the regenerative capacity of the liver. Through a negative selection screen in senescent cells we can identify vulnerabilities of these cells. The goal is to identify novel senolytic targets for therapeutic purposes.	Assoc Prof Torsten Wuestefeld Torsten.Wuestefeld@ntu.edu.sg
7.4	Identifying novel biomarkers in liquid biopsy derived exosomes <i>Remarks: Project may be supported by scholarship funding</i> The project focuses on identifying novel blood-based biomarkers for liver disease. Mouse models of chronic	Assoc Prof Torsten Wuestefeld Torsten.Wuestefeld@ntu.edu.sg

7.5	liver disease will be used, exosomes will be isolated from the blood and the content will be analyzed by transcriptomic and proteomic approaches. The same approach will be applied for liver patient derived blood samples. The goal is to identify novel conserved biomarkers for liver disease. Countering Cancer's Therapeutic Resistance Using Synthetic Lethality CRISPR Screen Therapeutic resistance is one of the major causes of treatment failure and poor prognosis in cancer. With the advent of CRISPR screen technology, we are now able to identify the novel genetic weaknesses of cancers that developed resistance to conventional treatments such as chemo-/radio-therapy and targeted therapy. To identify and specifically target the 'Achilles' heels' of these obstinate cancers, the PhD candidate will perform state-of-the-art in vitro and/or in vivo CRISPR screens followed by validation and mechanistic studies. Upon successful validation of the screen hits and the elucidation of the underlined mechanism, the candidate will test the findings in animal model or patient derived xenograft/ organoid models to provide pre-clinical insights that could potentially guide clinical practice. Other than identifying novel genetic dependences (weaknesses) from scratch, the PhD candidate can also choose to work on countering already identified genetic dependences in obstinate cancer. In this case, developing therapeutic strategies countering these weaknesses will become the overarching objective of the PhD thesis. The candidate will be testing out this possibility by re-purposing the FDA approved medications or exploiting various drug development strategies including but not limited to in silico drug/ natural product screen, antisense oligonucleotide (ASO) design, AI facilitated peptide/ peptidomimetics design, and proteolysis-targeting chimera (PROTAC) development.	Asst Prof Hongbin Yang Hongbin.yang@ntu.edu.sg
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7.6	Identifying Key Determinants and Regulators of Metastasis Using in vivo CRISPR Screen Cancer-related deaths are partly due to distant metastases and our current inability to eliminate them. Therefore, one possible approach to reduce cancer death is to target the key factor(s) required for metastasis so as to restrain tumour cells to their primary site for surgical removal. For already metastasized tumour, it is also possible to restrain further progression if weaknesses of metastatic cancer cells are identified and therapeutically targeted. Increasing evidence showed that metastasis is a combinational outcome of not only cancer cells' own efforts but also the facilitations from the non-cancerous cells in the microenvironment. The currently reported CRISPR screens aiming to identify metastasis-mediating factors were all in vitro, therefore, fell short of recapitulating such tumour-microenvironment interaction. The PhD candidate will have the opportunity to optimize and conduct a novel in vivo CRISPR screen specifically designed to identify key determinants and regulators of metastasis. This in vivo screen will not only potentiate the cancer-microenvironment crosstalk, but also provide all realistic routes, destinations, and challenges for metastatic process at organismal level. Upon successful validation of the screen hits and the elucidation of the underlined mechanism, the candidate will test the findings in animal model or patient derived xenograft/ organoid models to provide implications for treatment development.	Asst Prof Hongbin Yang Hongbin.yang@ntu.edu.sg
7.7	Ageing of bone microenvironments Our skeletons play a crucial role in regulating key physiological processes, including mineral homeostasis, energy metabolism, and blood cell production. The presence of multiple blood vessel (BV) subtypes and the distinct microenvironments they support contribute to the skeleton's multifaceted functions. Vascular aging is a key factor in the age-related functional and physical changes observed in	Assoc Prof Saravana Kumar Ramasamy saravana.kr@ntu.edu.sg

7.8	the skeleton. Understanding vascular niches and their age-related alterations could help target specific functional niches for managing age-related bone and blood diseases. In this study, we aim to identify and characterize bone vascular microenvironments and their functions. Leveraging cutting-edge techniques developed in our laboratory—including high-resolution 3D imaging, single-cell and spatial transcriptomics, metabolic analysis, and advanced mouse genetics—the candidate will have the opportunity to: • Characterize different types of microenvironments in bone. • Understand how blood vessels support these niches. • Identify strategies to replace or target aging blood vessel subtypes specifically. Metabolic control of bone marrow microenvironments The mammalian skeletal system undergoes continuous remodelling throughout life, intricately interacting with whole-body physiology. Metabolic changes significantly influence bone health by altering the cellular composition and functional dynamics of bone tissue. However, the cellular and molecular mechanisms underlying these dynamic changes remain poorly understood. In this study, we investigate the impact of metabolism on the mesenchymal composition of bone microenvironments. Specifically, the student will 1. Map and characterize the distribution patterns of mesenchymal cell subtypes in bone. 2. Explore how metabolic conditions such as diabetes, modulate mesenchymal cell composition	Assoc Prof Saravana Kumar Ramasamy saravana.kr@ntu.edu.sg
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7.9	3. Identify metabolic targets to modulate mesenchymal cell differentiation and composition. The student will employ advanced techniques, including confocal and intravital imaging, single-cell and spatial transcriptomics, metabolic profiling, and state-of-the-art mouse transgenics. Overall, this study aims to uncover the mechanisms driving bone pathology in metabolic diseases like diabetes, providing a foundation for targeted therapeutic strategies. Understanding the tumor microenvironment: High-resolution 3D and multiplex imaging approach for deciphering cancer progression Endothelial cells are pivotal architects of blood and lymphatic vessel integrity, forming the inner lining that regulates inflammation, immune cell trafficking, and organ-specific vascular functions. Perivascular and mesenchymal stromal cells dynamically shape vascular microenvironments, playing essential roles in tissue homeostasis and disease. In cancer, the tumor microenvironment (TME) drives disease progression by orchestrating a complex interplay among cancer cells, vascular networks, and stromal components. This dynamic milieu enhances metastatic potential and contributes to therapeutic resistance. Central to this process is epithelial-mesenchymal transition (EMT), which equips cancer cells with invasive properties. Critically, stromal and vascular cells are key enablers of EMT and therapy resistance, making them highly attractive targets for innovative therapeutic strategies. Despite their significance, the complexity, heterogeneity, and spatial interactions of tumor stroma and vasculature remain poorly understood across different stages of cancer progression. This knowledge gap limits the development of precision therapies. To address this challenge, we propose leveraging cutting-edge high-resolution light-sheet microscopy and multiplex imaging to define, at an unprecedented level, the spatial interactions between vascular, stromal, and cancer cells throughout disease	Assoc Prof Anjali Parmanand Kusumbe anjali.pkusumbe@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp02539
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7.10	progression. Our approach focuses on three malignancies with distinct clinical and biological challenges: head and neck cancers, glioblastoma, and breast tumors. This study aims to illuminate the spatial interactions within the TME, providing a foundation not only for the development of targeted interventions to disrupt the stromal-vascular axis in cancer progression but also for precise diagnostic and prognostic strategies throughout the course of the disease. Modeling Tertiary Lymphoid Structures in Solid Tumors: Unveiling Immune Modulation and Therapeutic Potential This PhD project aims to model tertiary lymphoid structures (TLS) in solid tumors to investigate their influence on the tumor microenvironment and response to cancer therapy. Using advanced in vitro techniques, the project will create a robust model system that mimics TLS formation, allowing us to explore interactions between immune cells and tumor cells. The student will gain experience with cutting-edge technologies in immunology and cancer biology and contribute to crucial discoveries in the tumor immune landscape. This research will offer new insights into TLS functions in cancer, with potential applications in developing more effective cancer treatments.	Asst Prof Andrea Pavesi Andrea.pavesi@ntu.edu.sg www.pavesilab.com
7.11	Modeling Tumor-Immune Interactions in Glioblastoma Join our lab to develop an advanced glioblastoma (GBM) model that integrates the blood-brain barrier and immune components to better understand tumor-immune interactions. This PhD project focuses on investigating the role of tertiary lymphoid structures (TLS) within the GBM microenvironment and exploring immunotherapy strategies targeting both GBM and TLS. This interdisciplinary project offers hands-on experience in cutting-edge cancer biology techniques, advanced model development, and preclinical testing—ideal for students passionate about driving	Asst Prof Andrea Pavesi Andrea.pavesi@ntu.edu.sg www.pavesilab.com

	innovation in cancer immunotherapy and tumor microenvironment research.	
7.12	Defining the roles of spindle dynamics in pluripotent stem cell fate decisions A fundamental question in developmental biology is how cells interpret intrinsic and extrinsic cues to make fate decisions. While the roles of transcription factors and niche-derived signals are well characterized, recent work has identified the mitotic spindle as an unexpected mechanical regulator of cell fate, coupling cytokinesis with transcriptional reprogramming in adult systems^{1–5}. However, in early embryogenesis—where a homogeneous population of pluripotent stem cells must generate heterogeneity and undergo symmetry breaking—the mechanisms initiating these processes remain poorly understood. This PhD project will test the hypothesis that the mitotic spindle acts as an intracellular mechanical orchestrator of fate specification during early development. Specifically, whether the spindle-dependent processes integrate intracellular biochemical cues (e.g., intracellular pH dynamics) with intercellular communication (e.g., cytoplasmic bridges) to drive fate diversification. By dissecting this link between mechanics and biochemistry, this work could redefine paradigms of cell fate determination, with broader implications for regenerative medicine and cancer biology—where aberrant spindle mechanics and pH dysregulation are hallmarks of disease progression.	Asst Prof Yi Liu yi.liu@ntu.edu.sg Website https://liulab.myportfolio.com/
7.13	Decoding the intracellular pH-sensing pathway that specifies regenerative intestinal stem cells Stem cell-mediated regeneration is essential for tissue repair, and understanding this process is critical for advancing regenerative medicine. In the intestinal epithelium, regeneration following injury is driven by Clusterin-positive (Clu⁺) stem cells⁶, which remain quiescent under homeostasis but activate upon damage. Despite their therapeutic potential, the	Asst Prof Yi Liu yi.liu@ntu.edu.sg Website https://liulab.myportfolio.com/

	regulatory mechanisms controlling Clu⁺ stem cell fate specification remain poorly understood. Our previous work demonstrated that decreasing intracellular pH (pHi) expands the Clu⁺ cell population and that pHi-dependent Clu expression inversely correlates with reduced expression of AP-1 components, suggesting a regulatory crosstalk, and highlighting decreasing pHi as a non-invasive approach to elicit a regeneration response. Given that AP-1 integrates multiple differentiation signals and is modulated by PARP1-mediated ADP-ribosylation, this PhD project will test the hypothesis that PARP1-AP-1-CLU is a cytosolic pathway mediating pHi-dependent stem cell differentiation. This project will define the mechanistic connections between PARP1, AP-1, and Clu⁺ stem cell behavior, leveraging genetic, biochemical, and cell biology approaches in physiologically relevant human intestinal organoids as well as <i>in vivo</i> animal models. By resolving this novel model wherein, the PARP1-AP-1-CLU axis transduces pHi signals to orchestrate stem cell differentiation during regeneration, it will not only advance fundamental understanding of pHi-regulated stem cell fate decisions but also provide actionable insights for enhancing regenerative therapies. References 1. Zhong, T. & Zhou, J. Orientation of the Mitotic Spindle in the Development of Tubular Organs. <i>J of Cellular Biochemistry</i> 118, 1630–1633 (2017). 2. Snippert, H. J. <i>et al.</i> Intestinal Crypt Homeostasis Results from Neutral Competition between Symmetrically Dividing Lgr5 Stem Cells. <i>Cell</i> 143, 134–144 (2010). 3. Hu, D. J.-K. & Jasper, H. Control of Intestinal Cell Fate by Dynamic Mitotic Spindle Repositioning Influences Epithelial Homeostasis and Longevity. <i>Cell Reports</i> 28, 2807-2823.e5 (2019). 4. Sei, Y., Feng, J., Chow, C. C. & Wank, S. A. Asymmetric cell division-dominant neutral drift model for normal intestinal stem cell homeostasis. <i>American Journal of Physiology-Gastrointestinal and Liver Physiology</i> 316, G64–G74 (2019). 5. Bellaïche, Y., Gho, M., Kaltschmidt, J. A., Brand, A. H. & Schweisguth, F. Frizzled regulates localization of cell-fate determinants and mitotic spindle rotation during asymmetric cell division. <i>Nat Cell Biol</i> 3, 50–57 (2001).	
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7.14	6. Ayyaz, A. <i>et al.</i> Single-cell transcriptomes of the regenerating intestine reveal a revival stem cell. <i>Nature</i> 569, 121–125 (2019). Bat-inspired targets to fight human diseases and aging The objective is to learn from bats with exceptional disease resistance and healthy longevity, aiming to translate these lessons into new targets to fight human diseases and extend healthspan. The pioneering work in bat inflammation (<i>Nat Micro</i> 2019, <i>PNAS</i> 2020, <i>Nature</i> 2021, <i>Cell</i> 2023 and ongoing development of a new class of anti-inflammatory drugs) has helped establish bats as a great model to uncover new strategies to fight human diseases and has just scratched the surface of what we can learn from bats to benefit humans. The three different and synergistic approaches include 1) ‘unbiased’ multi-omics aging atlas of bats 2) ‘disease centric’ disease-free bat models including metabolic and neurological diseases and 3) ‘more targeted’ study of enhanced proliferation/regeneration and increased apoptosis as potential anti-aging/cancer mechanisms.	Asst Prof Ahn Matae matae.ahn@ntu.edu.sg https://dr.ntu.edu.sg/entities/person/Matae-Ahn
7.15	Direct cell reprogramming for biomedical applications <i>Remarks: Project may be supported by scholarship funding</i> The manufacture of advanced stem cell-based products and therapies through directed differentiation faces significant challenges in achieving efficient, reliable, and scalable production of specialized cell types especially in a cGMP setting. Cell differentiation approaches involve stepwise culture of (pluripotent) stem cells to direct their development into target cell types. However, current manufacturing methods are generally not fit for purpose - being often hampered by complex, lengthy and costly protocols, low cell yield, purity and/or quality, and inconsistent outcomes - limiting industrial applications. Direct (or forward) cell programming offers a promising alternative by enabling the direct conversion of one cell type into another by activating gene	Associate Prof Yen CHOO yen.choo@ntu.edu.sg

7.16	regulatory networks that determine cell identity. This approach has the potential greatly to streamline the manufacturing process, reduce the time and resources required, and improve the consistency and functionality of cellular products. As the advanced therapy field develops, establishing robust, scalable manufacturing technology platforms (such as by direct cell programming) will become key to the success of the regenerative medicine and cell therapy industry. Programming of cells using lineage control networks has the potential to transform how we make cell therapies and immunotherapies, develop regenerative medicines, and create cellular models for research. However, identifying specific combinations of master regulatory genes known as transcription factors (TFs) that lead to highly efficient conversion of a scalable starting cell (e.g. iPSC, fibroblast) into desired cell types for biomedical applications (e.g. T cell, b cell) remains a significant challenge and a longstanding, critical bottleneck in the field. In this programme we will use an innovative combinatorial screening technology to rapidly assess the effectiveness of thousands of combinations of TFs in programming various human cell types into specific lineages that enable high value biomedical applications. Cell types we may derive in this project have diverse applications, including in: 1) developing advanced cellular/tissue models for biomedical R&D, 2) cGMP manufacturing of cell and gene therapies, including allogeneic immunotherapies, and 3) in vivo reprogramming for regenerative medicine and autologous immunotherapies. Intracellular pH-regulated Epithelial-Mesenchymal Transition This project will define the role of intracellular pH (pHi) dynamics as a fundamental regulator of epithelial-mesenchymal transition (EMT), a process epithelial cells transform into mobile mesenchymal cells for enhanced cell migration. We hypothesize that cytoplasmic alkalinization mediated by the sodium-hydrogen exchanger 1 (NHE1) coordinately drives the transcriptional and morphological programs of EMT through a pHi-modulated ERK–AP1–Formins axis. To test this hypothesis, this project will first map temporal pHi dynamics during and correlate these changes with	Asst Prof Yi Liu yi.liu@ntu.edu.sg Website https://liulab.myportfolio.com/ https://www.ntu.edu.sg/medicine/research/research-programmes/cancer-discovery-regenerative-medicine
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7.17	quantitative metrics of morphological reprogramming and transcriptional reprogramming, including the expression of signature EMT transcription factors. Next, we will determine the pHi-sensing mechanism that regulates EMT. Finally, we will validate the physiological relevance of pHi-regulated EMT using a zebrafish larval fin-regeneration model, ensuring that our findings translate to complex in vivo contexts. Role of axon guidance molecules in intercellular lipid signalling Certain lipids are integrated into intercellular signalling circuitry, and have potent effects on cell migration, behaviour and tissue morphogenesis. For example, Sphingosine-1-Phosphate (S1P) controls the migration of lymphocytes into circulation and also activates fibroblasts and drives fibrosis. The mechanisms deploying S1P is not clear for all contexts. We have shown that mutation of the Slit-Robo axon guidance pathway leads to similar effects on fibroblasts as S1P loss. Robo signalling acts upstream of extracellular S1P generation¹. This project will utilise cell culture, multiomics and in vivo gene editing to identify the mechanisms regulating lipid signalling by the Slit-Robo pathway. ¹Mahabaleshwar, H, Asharani, PV, Loo, TY, Koh, SY, Pitman, MR, Kwok, S, Ma, J, Hu, B, Lin, F, Li Lok, X, Pitson, SM, Saunders, TE, and Carney, TJ. (2022). Slit-Robo signalling establishes a Sphingosine-1-phosphate gradient to polarise fin mesenchyme. <i>EMBO Rep</i> 23, e54464. 10.15252/embr.202154464	Assoc Prof Tom Carney tcarney@ntu.edu.sg
7.18	Role of GPCR, <i>gnai</i> and Src in fertility and tumour progression The GPCR, Par2 has multiple roles in development and is inappropriately activated by dysregulated protease activity, often found in aggressive cancers. It is reported to activate multiple downstream targets in cell culture but how many of these targets are relevant in vivo is unclear. It is difficult to test these in an in vivo setting, We have defined a role for Par2 in very early zebrafish embryos which allows for facile in vivo screening of activated pathways. We have preliminary data implicating <i>gnai</i> genes and phosphorylated Src. This project will test this axis downstream of Par2 activation through use of immunostaining, CRISPR targeting, and pharmacological inhibition such as Src inhibitor, pertussis toxin and constitutively activated Gai R179C constructs. To compliment these assays,	Assoc Prof Tom Carney tcarney@ntu.edu.sg

7.19	unbiased screening using a small molecule library to test for activators or inactivators of the pathway will be conducted. Together this project will use an extremely accessible novel in vivo assay combined with genetic and pharmacological methods to define relevant pathways activated by a potent protease receptor in vivo. We will then use bioinformatics to verify if this is activated in the tumour context in patients. Developing a platform for screening compounds which reconstitute the mevalonate pathway The mevalonate pathway is a fundamental generator of essential lipids in all animals. The final products include cholesterol and its derived steroid hormones (eg estrogen), dolichol (for N-glycosylation), Coenzyme Q, and farnesyl diphosphate for protein lipidation. This pathway is targeted by important drugs including the cholesterol lowering Statins and the osteoclast poisons, the bisphosphonates which inhibit the Farnesyl diphosphate synthase enzyme. Whilst there are benefits to bone density by the systemic inhibition of osteoclasts, there are medical side effects caused by the loss of the mevalonate pathway in certain tissues. It would be advantageous to reconstitute pathway species in the tissues that are negatively affected by bisphosphonates. To achieve this, this project will generate a screenable platform of Fdps loss by CRISPR knockout in zebrafish. We predict this to be lethal, and may show similarities to linear porokeratosis caused by <i>FDPS</i> mutation. Once the knockout has been established, it will be fully characterized and then compared to bisphosphonate inhibition. Lipidomics will be performed to demonstrate loss of mevalonate species. We will then use the strength of larval zebrafish to screen for compounds and formulations that can rescue the phenotype. We will additionally use fluorescently labelled bisphosphonates to observe their absorption and distribution in vivo.	Assoc Prof Tom Carney tcarney@ntu.edu.sg
8. Microbiome Medicine		

8.1	Investigating the role of gut microbiome in cardiometabolic diseases In recent years, it has become evident that the gut bacteria living in our intestine significantly impact health and disease. This influence extends beyond intestinal disorders like inflammatory bowel disease to encompass a wide range of conditions including obesity, diabetes, and neurodegenerative diseases. Our laboratory has previously reported that certain gut bacteria contributes to the progression of cardiovascular disease (PMID: 30397344, 37279756). This PhD project focuses on gut microbiota and lipid metabolism, employing state-of-the-art technologies such as anaerobic culture systems, mouse models, and next-generation sequencing to advance research in this field.	Asst Prof Kazuyuki Kasahara kazuyuki.kasahara@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp02039 https://kasaharalab.com
8.2	Systematically Investigating Molecular Mechanisms Underlying Aging-Related Human Diseases through Multi-Omics Profiling Aging is a complex biological process characterized by a gradual decline in physiological functions, which increases susceptibility to diseases and death. This process is influenced by a myriad of genetic, environmental, and lifestyle factors. To better understand aging and study the relationship between aging and aging-related diseases, our research group is focused on building predictive models using machine learning techniques. The model is to integrate multi-omics datasets, focusing specifically on gut microbiome and metabolomics data. The comprehensive analysis of these multi-omic datasets aims to unveil crucial molecular indicators, intricate biological pathways, and influential regulatory circuits that play a role in the aging process and the pathogenesis of age-associated disorders. Such an understanding is likely to be helpful in the development of innovative therapeutic interventions to promote healthy aging and to address the onset and progression of neurodegenerative conditions such as Alzheimer's and Parkinson's diseases.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)

8.3	Comprehensive Multi-omics Analysis of Human Aging Using the Large Language Module based Functional Module Annotation Multi-omic methods provide great opportunities to systematically reveal the critical molecular alterations of aging from a multidimensional perspective, while matching and investigating the biological information and functions from multi could be a heavy subjective work. Large Language Models (LLMs) has shown high efficiency and accuracy in repetitive search and collection work, which will help us to extensively and quickly investigate potential research objects and validate them with published works to prove their roles and molecular mechanism. So in this project, we aim to build up a tool utilizing LLM, such as GPT4, to accelerate and improve the biological investigation in multi-omics data for aging research.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
8.4	Modulation of digestive enzyme activity as a safe approach to improve metabolism and health This project aims to design new therapeutic targets, with structure-function lead optimisation of compounds that inhibit luminal carbohydrate enzymes. Guided by naturally occurring plant-based compounds, this project involves side-chain modifications to improve enzyme inhibition selectivity and specificity. From chemistry to biology, this project will continue with the characterization of luminal carbohydrate digestion modulation on the recipient host. Investigations will include an assessment of intestinal health, alterations in gut microbiome, impact on immunology and finally carbohydrate metabolism and homeostasis.	Assoc Prof Yusuf Ali Yusuf.ali@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00609 Assoc Prof Zaher Judeh (Co-sup)
8.5	Gut-brain neurobiology: microbiome control of neural circuits and behaviour The trillions of bacteria living in our body encode over 46 million genes – suggesting tremendous functional capacity (by contrast, the human genome has less	Asst Prof Hwei-Ee TAN hweeee.tan@ntu.edu.sg Website

8.6	than a thousandth of that). Moreover, emerging evidence suggests that the gut microbiota profoundly influences host physiology and behaviour. In this project, we will investigate the fundamental biological basis of “gut-feelings”, how microorganisms and chemicals in the gut signal to brain to modulate neural substrates that control physiology and behaviour. We employ a range of experimental techniques in mice to study the mammalian gut-brain axis including sequencing, metabolomics, in vivo neural imaging/recording, and genetically-guided functional interrogation. Deciphering the Role of Atypical LPS and MAMPs in Gut Barrier Dysfunction and MASLD The gut barrier is a critical defense system, preventing harmful microbes and toxins from entering circulation while supporting a balanced relationship with gut bacteria. When this barrier is compromised, it contributes to a cascade of chronic diseases. One of the most pressing concerns is Metabolic-Associated Steatotic Liver Disease (MASLD), a leading cause of chronic liver disease worldwide, which is increasingly linked to gut microbial imbalances. This PhD project will explore how microbe-associated molecular patterns (MAMPs), specifically classical and atypical lipopolysaccharides (LPS), influence gut barrier integrity via Angiopoietin-like protein 4 (Angptl4), a key regulator of lipid metabolism and inflammation. However, the precise molecular mechanisms by which these LPSs regulate Angptl4 remain unknown. Using cutting-edge microbiome analysis, biochemical characterization, and in vivo models, you will uncover how microbial signals shape gut-liver communication. The candidate will analyze bacterial LPS, assess receptor activation and gut permeability, and utilize germ-free mouse models. Why Join This Project? You'll gain expertise in host-microbe interactions, molecular biology, and immunology, with opportunities for clinical collaborations. Who Should Apply? We welcome applications from motivated candidates with a background in microbiology, molecular biology, immunology, bioinformatics, or a related field. A passion for host-microbe interactions and translational medicine is essential. Join us in uncovering how the gut	tanlab.science  Assoc Prof Andrew Tan Nguan Soon nstan@ntu.edu.sg https://dr.ntu.edu.sg/cris/rp/rp00393
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	microbiome influences metabolic disease and paving the way for microbiome-based therapeutics! References: Low, ZS, Chua, D., Cheng, H.S. et. al (2024). The LIDPAD Mouse Model Captures the Multisystem Interactions and Extrahepatic Complications in MASLD. Adv. Sci. 11(35): e2404326.	
8.7	Discovery of Gut Microbiome-Metabolized Bioactive Compounds from Traditional Chinese Medicine We propose to culture human gut microbiomes with Traditional Chinese Medicine (TCM) extracts and apply a novel computational algorithm to identify new bioactive compounds metabolized by the microbiota. This integrative platform enables systematic discovery of microbiome-derived metabolites from natural products, uncovering mechanisms underlying TCM efficacy and revealing potential therapeutic agents. Beyond discovery, we aim to construct a comprehensive atlas of gut microbiome-metabolized TCM and natural products. This resource will serve as a foundation for drug development and precision therapeutics based on host-microbe-metabolite interactions.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org)
8.8	Metabolic feature-based functional module analysis based on the large language model We propose to develop featureFMA, a novel large language model (LLM)-guided computational framework for metabolic feature-based functional module analysis in LC-MS untargeted metabolomics. Traditional pathway analysis lacks specificity and coverage for metabolomics data. featureFMA will integrate metabolite annotation, metabolic network modeling, and LLM-based functional interpretation to identify dysregulated modules linked to biological functions and diseases. This project includes software development (R package, Shiny app, and cloud platform), multi-species validation, and diverse case studies (e.g., enzyme mutation and gut microbiome). featureFMA will provide a scalable, intelligent solution for interpreting complex metabolomics data and accelerating functional discovery in systems biology.	Asst Prof Shen Xiaotao xiaotao.shen@ntu.edu.sg Website Shen Lab (shen-lab.org) Assoc Prof Sunny Wong

8.9	Precision and Digital Medicine in Gastrointestinal Diseases: Integrating Multi-Modal Data for Disease Classification and Characterization This project aims to advance precision medicine in gastrointestinal diseases through integration of clinical, genomic, microbiome, environmental, and digital health data. The candidate will analyse large-scale datasets, including electronic health records, physiological signals, and molecular profiles, using machine learning and advanced computational approaches. The goal is to identify disease subtypes, predictive biomarkers, and mechanistic pathways underlying gastrointestinal disorders. This work sits at the interface of clinical medicine, data science, and systems biology. Candidates with backgrounds in bioinformatics, clinical informatics, data science, preferably with some biomedical or clinical exposure, are strongly encouraged to apply.	sunny.wong@ntu.edu.sg Website https://dr.ntu.edu.sg/entities/person/Sunny-Wong
8.10	Exploring Gastrointestinal Interoception, Microbiome, and Diets in Disorders of Gut-Brain Axis This project investigates how dietary factors, gut microbiota, and gastrointestinal physiology interact with brain function, including mood, resilience, and gut-brain disorders. The work combines wet lab and dry lab approaches, including microbiological culture, histology, murine models, and molecular data analysis. The candidate will explore mechanistic pathways linking gut signals to neurobehavioral outcomes. Applicants should have interest and experience in both experimental biology and computational analysis, and be motivated to work across disciplines.	Assoc Prof Sunny Wong sunny.wong@ntu.edu.sg Website https://dr.ntu.edu.sg/entities/person/Sunny-Wong
8.11	Microbiome and Gut Barrier Physiology in Digestive Cancers This project focuses on the role of the microbiome and gut barrier in gastric and colorectal cancer development and therapeutic response. The candidate will investigate how microbial communities and barrier integrity influence carcinogenesis including that of different cancer subtypes. The work will involve both experimental and computational approaches,	Assoc Prof Sunny Wong sunny.wong@ntu.edu.sg Website https://dr.ntu.edu.sg/entities/person/Sunny-Wong

8.12	including animal models, organoid systems, microbial sequencing, and integrative bioinformatics analyses. This project aims to uncover mechanistic insights and identify potential therapeutic targets. Candidates with backgrounds in microbiology, molecular biology, cancer biology, or bioinformatics are encouraged to apply. Gut Microbiome, Dietary Patterns, and Metabolic and Digestive Diseases in a Multi-Ethnic Asian Population Singapore's multiethnic population, comprising Chinese, Malay, and Indian communities, exhibits diverse dietary patterns that may influence the gut microbiome and risk of metabolic and digestive diseases. This project aims to investigate the interplay between diet, microbiome, and disease through a combination of human recruitment, nutritional and digital data collection, and biological sample collection and processing. The candidate will also perform data analyses to identify disease-associated patterns and mechanisms. The findings will inform culturally relevant nutritional and microbiome-targeted interventions. Candidates with backgrounds in nutrition or biomedical sciences, and an aptitude for data analytics or informatics, are preferred.	Assoc Prof Sunny Wong sunny.wong@ntu.edu.sg Website https://dr.ntu.edu.sg/entities/person/Sunny-Wong
9. Medical Education		
9.1	Climate and health – mapping the impacts towards positive action This PhD is located within a wider multidisciplinary project NTU “Climate Transformation Program” that seeks to map and model impacts of climate change. World Health Organization (WHO) emphatically noted that the risks of the climate crisis to human health extend way beyond physical impact(s) to mental health and called for intervention(s), mitigation and adaptation. The evidence however on mental health impacts in Singapore and Southeast Asia is limited. The PHD project will integrate evidence synthesis and	Assoc Prof Konstadina Griva Konstadina.griva@ntu.edu.sg https://earthobservatory.sg/research/climate climate-transformation-programme Co-supervisor: A/P Steve Yim

	observational mixed methods approached to identify mental health risks and at risk populations.	
10. Others		
10.1	<u>Chemistry and Bioengineering</u> Modulation of digestive enzyme activity as a safe approach to improve metabolism and health This project aims to design new therapeutic targets, with structure-function lead optimisation of compounds that inhibit luminal carbohydrate enzymes. Guided by naturally occurring plant-based compounds, this project involves side-chain modifications to improve enzyme inhibition selectivity and specificity. From chemistry to biology, this project will continue with the characterization of luminal carbohydrate digestion modulation on the recipient host. Investigations will include an assessment of intestinal health, alterations in gut microbiome, impact on immunology and finally carbohydrate metabolism and homeostasis.	Assoc Prof Yusuf Ali Yusuf.ali@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00609 Assoc Prof Zaher Judeh (Co-sup)
10.2	<u>NIE, Exercise Physiology</u> Nutritional intervention and the impact on muscle health in elderly health This project aims to molecularly dissect pathways that are altered under (i) intermittent fasting conditions and (ii) plant-based nutritional intake. These dietary interventions are increasingly being suggested as disease-modifiers, but the molecular	Assoc Prof Yusuf Ali Yusuf.ali@ntu.edu.sg Website https://dr.ntu.edu.sg/cris/rp/rp00609 Assoc Prof Steven Burns

	mechanisms that support these claims are still not well-defined. With a focus on insulin sensitivity, immunology and metabolic organ homeostasis and health, the candidate will undertake a series of in vitro and in vivo experiments to understand the role of intracellular lipid regulation response to both dietary interventions. In collaboration with exercise physiologists from the National Institute of Education, candidate will also undertake a human study to validate translation and clinical relevance.	(Co-sup)
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