A*STAR and King's College London PhD Studentships October 2022 Entry

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A*STAR and King's College London PhD Studentships

When choosing a project from this catalogue in the funding section & research proposal section of the online application form, please enter the funding code that corresponds to the theme of your first project choice:

1. Cells, Molecules and the Basis of Health and Disease: **THEME1_2022**
2. Neuroscience and Mental Health: **THEME2_2022**
3. Biomedical Engineering and Medical Imaging: **THEME3_2022**

Important dates:

Date	**Application Stage**
Deadline for application	Sunday 10th April 2022, midnight
Application Outcome	By 20 May 2022
Interviews	Week commencing Monday 6th June 2022
Interview Outcomes	By Friday 10th June 2022
Acceptance of studentship offer	By 24th June 2022
Start Date	October 2022

The 2022/23 studentships will commence in October 2022. For further information or queries relating to the application process, please contact: doctoralstudies@kcl.ac.uk.

Projects listed in this catalogue are subject to amendments, candidates invited to interview will have the opportunity to discuss projects in further detail.

THEME1: Cells, Molecules and the Basis of Health and Disease

1.1 Using single cell sequencing to map vascular smooth muscle cell heterogeneity in vascular calcification.

Co-Supervisor 1A: Professor Catherine Shanahan

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Co-Supervisor 1B: Professor Roger Foo

Research Institute: GIS

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Project Description:

Vascular calcification is the deposition of calcium salts in the vessel wall and is a well established risk factor for cardiovascular morbidity and mortality. It is associated with vascular stiffening as well as rupture of atherosclerotic plaques and heart attacks. Vascular calcification is highly prevalent in the ageing population and accelerated in diabetes and chronic kidney disease. It is mediated by vascular smooth muscle cells (VSMCs) which undergo osteogenic differentiation to become bone-like cells. Despite the current state of knowledge there are currently no treatment options and lack of comprehensive data on the key mechanisms of VSMC change. This project will take an unbiased approach to identify early and novel pathways leading to vascular calcification and will validate these pathways in human disease. Ultimately this will enable the identification of novel therapeutic targets for the treatment of this detrimental and prevalent pathology.

Two representative publications from supervisors:

Runx2 (Runt-Related Transcription Factor 2) Links the DNA Damage Response to Osteogenic Reprogramming and Apoptosis of Vascular Smooth Muscle Cells.Cobb AM, Yusoff S, Hayward R, Ahmad S, Sun M, Verhulst A, D'Haese PC, Shanahan CM. Arterioscler Thromb Vasc Biol. 2021 Apr;41(4):1339-1357. doi: 10.1161/ATVBAHA.120.315206.

Tan, W. L. W., Anene-Nzelu, C. G., Wong, E., Lee, C. J. M., Tan, H. S., Tang, S. J., . . . Foo,R. S. Y. (2020). Epigenomes of human hearts reveal new genetic variants relevant for cardiac disease and phenotype. Circ Res, 127(6), 761-777. doi:10.1161/CIRCRESAHA.120.317254

2.1 Exploring a novel therapeutic approach to the treatment of renal and skin ischemia through targeting Connective Tissue Growth Factor (CTGF) and Connexin 43 (Cx43).

Co-Supervisor 1A: Professor Christer Hogstrand

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Co-Supervisor 1B: Dr NG Yi Zhen

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Project Description:

During an injury many organs suffer a temporary deprivation of oxygen followed by a restoration of blood flow; referred to as ischemia reperfusion injury. Paradoxically, both the ischemia and the reperfusion cause damage. When the initial ischemia is brief, the injury can be transient with some cell death, but when it is extended, even for as little as 45 minutes, there can be an ongoing injury. This can be seen in unresolving scarring to the skin or in the kidney, where the acute injury can develop into a chronic disease, even resulting in kidney failure. The identification of the molecular signalling causing the development of chronic disease may facilitate the development of novel treatments. The hypothesis underlying this project is that an axis is created linking the extracellular matrix via CTGF/CCN2, to a multifunctional protein that mediates cell-cell communication Connexin 43. This concept is germane to the ability of cells to sense their environment and pass this communication onto neighbouring cells. In this project the student will develop skills in primary human cell culture, molecular biology techniques such as gene silencing and quantitative gene expression. The student will learn live cell microscopic imaging, visualising the intracellular changes in real time. The nature of this collaborative project will allow a student to spend time in 2 leading international research centres, uniquely combining the expertise present in each. Both CCN2/CTGF and Connexin 43 are seen as therapeutic targets, consequently this project has real potential for providing novel approaches to prevent chronic disease.

Two representative publications from supervisors:

Taylor KM, Muraina IA, Brethour D, Schmitt-Ulms G, Nimmanon T, Ziliotto S, Kille P, Hogstrand C. (2016) Zinc transporter ZIP10 forms a heteromer with ZIP6 which regulates embryonic development and cell migration. Biochem J. 2016 Aug 15;473(16):2531-44.

Ng, Y.Z., Lacina, L., Lunny, D.P., Benny, P.B., Gerdes, A.M., Broesby-Olsen, S., Martin, L., Parmentier, L., Ebzery, C., Goodwin, A. and Hohl, D., 2016. Cytological and transcriptomic analysis reveals new features of multiple self-healing squamous epithelioma (MSSE). Journal of Dermatological Science, 84(1), p.e48.

3.1 Molecular mechanisms of the genetic predisposition of acne.

Co-Supervisor 1A: Professor Michael Simpson

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Co-Supervisor 1B: John Common

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Project Description:

Genetics explains a large proportion the variation of why some individuals develop acne and others don't. Our recent large-scale genome wide association study has identified 43 regions of the genome at which specific genetic variation is associated with developing acne. It has been established that therapeutics that mimic the effect of genetic variation that is protective for a disease are likely to be effective in treating disease. The aim of this project is to establish the molecular and cellular mechanisms through which genetic variation influences acne susceptibility. The resulting insights will be critical for the potential development of therapeutics that mimic these genetic effects on the biological system. The project is based in two of the leading acne research laboratories in the world and will provide training in contemporary approaches to human genetics, functional genomics and cellular biology. The first year based at KCL will provide training in computational and statistical methodologies to utilise the vast array of large-scale functional genomic data to identify putative causal genes, pathways and cell types in acne. In years 2 and 3, located at A*STAR the project will focus on specific cellular investigations of a small number of putative causal genes to understand the molecular mechanisms through which genetic variation is influencing disease risk at the cellular level. The final year based a KCL will seek to further establish the therapeutic potential of these casual genes including genetically informed on target safety analysis.

Two representative publications from supervisors:

Genome-wide meta-analysis implicates mediators of hair follicle development and morphogenesis in risk for severe acne. Petridis C, Navarini AA, Dand N, Saklatvala J, Baudry D, Duckworth M, Allen MH, Curtis CJ, Lee SH, Burden AD, Layton A, Bataille V, Pink AE; Acne Genetic Study Group, Carlavan I, Voegel JJ, Spector TD, Trembath RC, McGrath JA, Smith CH, Barker JN, Simpson MA. Nat Commun. 2018.

What does acne genetics teach us about disease pathogenesis? Common, J.E.A.,# Barker, J.N., van Steensel, M.A.M. British Journal of Dermatology. 2019.

4.1 Identification of molecular mechanisms underlying response and resistance to BCL-2 inhibition in NPM1 mutated Acute Myeloid Leukaemia.

Co-Supervisor 1A: Dr Richard Dillon

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Research Institute: Genome Institute of Singapore

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Project Description:

We are performing a clinical trial for patients with acute myeloid leukaemia (AML). In this study patients are randomly assigned to be treated either with intensive chemotherapy or with a new and much less toxic treatment called venetoclax - low dose cytarabine. In this study, we observe a whole range of responses to both treatments, in spite of the fact that all patients in the study have the same gene mutation profile. In this PhD project, we would like to use the samples that will be taken as part of this trial and perform detailed analysis to try to identify markers which can predict which patients will be cured with this new treatment and which patients still need to have intensive chemotherapy. The analysis will use profiling performed on the whole sample (in London) and more advanced profiling done on individual cells (in Singapore) and will be performed at multiple time points throughout treatment. We hope to use these results to understand why some patients do not respond well to treatment and to try to find ways to overcome this.

Two representative publications from supervisors:

Dillon R, et al, Molecular MRD status and outcome after transplantation in NPM1-mutated AML. Blood 2021. 2020 Feb 27;135(9):680-688. doi: 10.1182/blood.2019002959.

Sharma et al…and R DasGupta* (2020). “Onco-fetal reprogramming of endothelial cells drives immunosuppressive macrophages in Hepatocellular Carcinoma”. Cell S0092-8674(20)31082-5.

5.1 Spatiotemporal modulation of tumour-immune interaction within organotypic models of pancreatic ductal adenocarcinoma through targeted gene delivery by optoporation.

Co-Supervisor 1A: Dr Ciro Chiappini

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Research Institute: Singapore Immunology Network

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Project Description:

This project develops a vascularized model of pancreatic ductal adenocarcinoma (PDAC) to study the interactions within the tumour-immune microenvironment for immunotherapy. We will use optoporation to deliver mRNA to selected macrophages within a vascularised PDAC tumor spheroid. The mRNA will alter the phenotype of those macrophages ultimately regulating their pro- and anti-tumour polarization. The extreme space and time resolution of optoporation will control individual macrophages at desired locations and times, providing a sophisticated regulation of their interactions with the tumour. Using high content-imaging and spatial transcriptomics we will dissect complex microenvironmental interactions providing crucial information for the development of new therapies. The student will acquire a transdisciplinary expertise in nanomedicine, oncoimmunology, gene delivery, high content imaging and spatial transcriptomics. Year 1 develops magrophages optoporation. Year 2 develops optoporation in the PDAC model. Year 3 establishes the imaging and transcriptomics workflow. Year 4 dissects complex tumour-immune interactions upon optoporation.

Two representative publications from supervisors:

C. Chiappini, E. DeRosa, J.O. Martinez, X. Liu, J. Steele, M. Stevens, E. Tasciotti, Biodegradable silicon nanoneedles delivering nucleic acids intracellularly induce localized in vivo neovascularization, Nature Materials 14, 532-539 (2015).

Lee SWL, Adriani G, Ceccarello E, Pavesi A, Tan AT, Bertoletti A, Kamm RD, Wong SC. Characterizing the Role of Monocytes in T Cell Cancer Immunotherapy Using a 3D Microfluidic Model. Frontiers in Immunology. 9:416 (2018).

6.1 Why do identical twins occur? Characterizing a lifelong epigenetic signatures of identical twins towards identification of early developmental factors that influence the twinning process.

Co-Supervisor 1A: Dr Jordana Bell

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Project Description:

Human identical twins, or monozygotic twins, occur when the early embryo splits to give rise to two genetically identical embryos. Why and how this process occurs remains an enigma in human biology. Although MZ twins are relatively rare events, they have been invaluable in genetic studies of human disease and are currently widely studied in human genomics, therefore understanding the developmental process of MZ twinning is a major research area. Our joint work recently contributed to a large-scale collaboration identifying a lifelong molecular signature of identical twins (van Dongen et al. 2021, Nature Communications). The results developed a molecular predictor that can be used to retrospectively diagnose if a person was conceived as a monozygotic twin. However, what remains unknown is whether this molecular signature is the cause and consequence of the twinning process itself. The novel predictor can now be applied to large-scale existing molecular data from human populations to help identify dissect the molecular drivers of monozygotic twinning in early development. The proposed project will explore this research question using a combination of inter-disciplinary approaches, spanning computational analysis human population based genomic and multi-omic datasets, together with experimental molecular techniques in cell models, to identify early life factors that influence the twinning process in identical twins.

Two representative publications from supervisors:

Dr Bell: Min JL*, Hemani G*, Hannon E, Dekkers KF, Castillo-Fernandez J, Luijk R, Carnero- Montoro E, Lawson DJ, Burrows K, Suderman M, Bretherick AD, Richardson TG, Klughammer J, Iotchkova V, Sharp G, Al Khleifat A, Shatunov A, Iacoangeli A, McArdle WL, Ho KM, Kumar A, S¨oderh¨all C, Soriano-T´arraga C, Giralt-Steinhauer E, Kazmi N, Mason D, McRae AF, Corcoran DL, Sugden K, Kasela S, Cardona A, Day FR, Cugliari G, Viberti C, Guarrera S, Lerro M, Gupta R, Bollepalli S, Mandaviya P,

Zeng Y, Clarke T-K, Walker RM, Schmoll V, Czamara D, Ruiz-Arenas C, Rezwan FI, Marioni RE, Lin T, Awaloff Y, Germain M, A¨ıssi D, Zwamborn R, van Eijk K, Dekker A, van Dongen J, Hottenga J-J, Willemsen G, Xu C-J, Barturen G, Catal`a-Moll F, Kerick M, Wang C, Melton P, Elliott HR, Shin J, Bernard M, Yet I, Smart M, Gorrie-Stone T, BIOS Consortium, Shaw C, Al Chalabi A, Ring SM, Pershagen G, Mel´en E, Jim´enez-Conde J, Roquer J, Lawlor DA, Wright J, Martin NG, Montgomery GW, Moffitt TE, Poulton R, Esko T, Milani L, Metspalu A, Perry JRB, Ong KK, Wareham NJ, Matullo G, Sacerdote C, Panico S, Caspi A, Arseneault L, Gagnon F, Ollikainen M, Kaprio J, Felix JF, Rivadeneira F, Tiemeier H, van IJzendoorn MH, Uitterlinden AG, Jaddoe VWV, Haley C, McIntosh AM, Evans KL, Murray A, R¨aikk¨onen K, Lahti J, Nohr EA, Sørensen TIA, Hansen T, Schmidt Morgen C, Binder EB, Lucae S, Ramon Gonzalez J, Mariona Bustamante M, Sunyer J, Holloway JW, Karmaus W, Zhang H, Deary IJ, Wray NR, Starr JM, Beekman M, van Heemst D, Slagboom PE, Morange P-E, Tr´egou¨et D-A, Veldink JH, Davies GE, de Geus EJC, Boomsma DI, Vonk JM, Brunekreef B, Koppelman GH, Alarc´on-Riquelme ME, Huang R-C, Craig Pennell C, van Meurs J, Ikram MA, Hughes AD, Tillin T, Chaturvedi N, Pausova Z, Paus T, Spector TD, Kumari M, Schalkwyk LC, Visscher PM, Davey Smith G, Bock C, Gaunt TR, Bell JT*, Heijmans BT*, Mill J*, Relton CL*. 2021. Genomic and phenomic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 53: 1311-1321, https://doi.org/10.1038/s41588-021-00923-x **Joint first and joint senior authors.*

Dr Reversade: Guoliang Chai, Ph.D., Emmanuelle Szenker-Ravi, Ph.D., Changuk Chung, Ph.D., Zhen Li, Ph.D., Lu Wang, Ph.D., Muznah Khatoo, B.S., Trevor Marshall, B.S., Nan Jiang, Ph.D., Xiaoxu Yang, Ph.D., Jennifer McEvoy-Venneri, B.S., Valentina Stanley, B.S., Paula Anzenberg, B.S., Nhi Lang, B.S., Vanessa Wazny, B.S., Jia Yu, Ph.D., David M. Virshup, M.D., Rie Nygaard, Ph.D., Filippo Mancia, Ph.D., Rijad Merdzanic, M.D., Maria B.P. Toralles, M.D., Paula M.L. Pitanga, M.Sc., Ratna D. Puri, M.D., Rebecca Hernan, M.Sc., Wendy K. Chung, M.D., Ph.D., Aida M. Bertoli-Avella, M.D., Ph.D., Nouriya Al-Sannaa, M.D., Maha S. Zaki, M.D., Ph.D., Karl Willert, Ph.D., **Bruno Reversade***, Ph.D., and Joseph G. Gleeson*, M.D. 2021. **N Engl J Med** 2021; 385:1292-1301 https://www.nejm.org/doi/full/10.1056/NEJMoa2033911 **Joint senior authors.*

7.1 Rapid screening of microbes by spectroscopic imaging to accelerate natural antibiotic discovery.

Co-Supervisor 1A: Dr Ka Lung Andrew Chan

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Co-Supervisor 1B: Lim Yee Hwee

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Project Description:

There is an urgent need to find new, more effective antibiotics as antibiotic resistance is becoming a major issue in clinics, with devastating consequences. Advanced synthetic biology and genomic technologies have enabled the discovery of many new promising natural compounds, produced by modified bacteria, with potent antimicrobial effects. However, there is a crucial lack of high-throughput analytical methods to characterise these compounds for their optimisation, which is a persistent bottle-neck in antibiotic discovery. The aim of this project is to tackle this problem by developing advanced Fourier transform infrared spectroscopic (FTIR) imaging technology, which can measure thousands of spectra in minutes, into a mass screening tool for the analysis of large libraries of new microbials. This will accelerate the discovery of optimal bacterial strains and new antibiotics. The project will allow the student to gain multidisciplinary skills, including advanced synthetic biology, gene editing technologies, advanced bioanalytical methods (liquid chromatography mass spectrometry (LCMS), FTIR imaging, microfabrication and 3D printing). Overarching objectives: Y1: To establish the protocol for FTIR measurements of bacteria in the solid and suspension states. Y2: To develop the protocol for the editing/design of bacteria and their characterisation using LCMS and traditional FTIR. Y3: To develop a methodology to produce large libraries (hundreds) of bacteria of different strains and growth conditions and characterise them. Y4: To develop a microfabricated device for the high-throughput FTIR measurement of bacteria, established in Y2/3, using the imaging system.

Two representative publications from supervisors:

W. Terakosolphan, A. Altharawi, A. Poonprasartporn, R. D. Harvey, B. Forbes and K. L. Andrew Chan*, “In vitro Fourier transform infrared spectroscopic study of the effect of glycerol on the uptake of beclomethasone dipropionate in living respiratory cells” International Journal of Pharmaceutics, 2021, 609, Art no. 121118, DOI: 10.1016/j.ijpharm.2021.121118.

Wan Lin Yeo, Elena Heng, Lee Ling Tan, Yi Wee Lim, Kuan Chieh Ching, De-Juin Tsai, Yi Wun Jhang, Tsai-Ling Lauderdale, Kak-Shan Shia, Huimin Zhao, Ee Lui Ang, Mingzi M. Zhang, Yee Hwee Lim* and Fong Tian Wong*, Biosynthetic engineering of the antifungal, anti-MRSA auroramycin, Microb. Cell Fact., 2020, 19, 3. https://doi.org/10.1186/s12934-019-1274-y.

8.1 Development of a multi-omics pipeline to target unconventional epitopes via immunotherapies in Head and Neck cancer and beyond.

Co-Supervisor 1A: Dr Michele Mishto

Research Division/Department or CAG: School of Immunology & Microbial Sciences Centre for Inflammation Biology and Cancer Immunology (CIBCI) & Peter Gorer Department of Immunobiology

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Co-Supervisor 1B: Dr Jinmiao Chen

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Website: https://www.a-star.edu.sg/sign/people/principal-investigators/jinmiao-chen

Project Description:

The project aims to develop research strategies tcombining bioinformatics and biology to identify novel targets of immunotherapy against cancer. These strategies will be applied to Head & Neck cohort of cancer samples and can lead to potential clinical applications in this form of cancer (and others) in the next decade. The student will learn both bioinformatics and molecular biology and immunology techniques. The work of the student will be embedded in a transnational scientific hub led by Dr. Mishto and colleagues, which provides a great support for the new generations of scientists. The project is highly multi-disciplinary and range from artificial intelligence tools to clinical potential applications. It is strongly supported by a collaboration network, which is one of the strength of KCL (and other linked London-based entities such as CRUK – Centre of London) and A*STAR. The supervisors of the project have a transnational approach to science, which will support the student both from the science angle and his/her wellbeing. The student will also benefit from the presence of other PhD students with similar fellowships such as KCL-NUS in the supervisors' labs.

Two representative publications from supervisors:

Liepe J, Marino F, Sidney J, Jeko A, Bunting DE, Sette A, Kloetzel PM, Stumpf MP, Heck AJ, Mishto M. A large fraction of HLA class I ligands are proteasome-generated spliced peptides. Science 2016 Oct; 354(6310): 354-358. DOI: 10.1126/science.aaf4384.

Li M, Zhang X, Ang KS, Ling J, Sethi R, Lee NYS, Ginhoux F, Chen J. DISCO: a database of Deeply Integrated human Single-Cell Omics data. Nucleic Acids Res. 2022 Jan 7;50(D1):D596-D602. doi: 10.1093/nar/gkab1020.

THEME2: Neuroscience and Mental Health

1.2 Dissecting the relationship between cognition and psychiatric disorders using genetics.

Co-Supervisor 1A: Professor Cathryn Lewis

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Co-Supervisor 1B: Jianjun Liu

Research Institute: Genome Institute of Singapore

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Project Description:

Cognition plays a key role in psychiatric disorders. In schizophrenia, cognitive impairment is a core feature, with cognitive deficits often predating the onset of psychosis. In depression, cognitive impairment is observed during depressive episodes, but may continue life-long, impacting quality of life even after recovery from depression. This project will disentangle the clinical, social and genetic features of cognition in depression and schizophrenia. Genetic tools will be used to discriminate the shared and non-shared contributions across cognition and psychiatric disorders, further considering the role of mediators such as educational attainment. The student will have access to large psychiatric disorder genetic studies (UK Biobank, Psychiatric Genomics Consortium) across ancestry groups, contributing to crucial efforts to expand genomic studies worldwide, across population groups. Year 1 (KCL): Analysis of UK Biobank data for depression and cognition, identifying unique genetic predictors and the relationship with educational attainment. Year 2 (A*STAR): Year 2 (A*STAR): Assess the relationship between schizophrenia, education attainment and cognition using cross-ancestry genetic methodologies. Year 3 (A*STAR): Build polygenic risk prediction models to estimate the probability of treatment-resistant schizophrenia. Year 4 (King's): Using new cognitive data to be collected in UK Biobank, build predictive models for cognitive decline (10-15 years) using depression diagnoses and genomics signals for disorders and cognition. The student will be trained in multi-disciplinary skills for analysis of clinical, epidemiological and genetic studies. Cutting-edge skills in programming, statistics and genomics will equip the student for future roles within genetics, computational biology and data science, filling a major skills shortage.

Two representative publications from supervisors:

Fabbri C, Hagenaars SP, John C, Williams AT, Shrine N, Moles L, Hanscombe KB, Serretti A, Shepherd DJ, Free RC, Wain LV, Tobin MD, Lewis CM. Genetic and clinical characteristics of treatment-resistant depression using primary care records in two UK cohorts. Mol Psychiatry. 2021 Jul;26(7):3363-3373. doi: 10.1038/s41380-021-01062-9. Epub 2021 Mar 22. PMID: 33753889; PMCID: PMC8505242.

Lam M, Chen CY, Li Z, Martin AR, Bryois J, Ma X, Gaspar H, Ikeda M, Benyamin B, Brown BC, Liu R, Zhou W, Guan L, Kamatani Y, Kim SW, Kubo M, Kusumawardhani AAAA, Liu CM, Ma H, Periyasamy S, Takahashi A, Xu Z, Yu H, Zhu F; Schizophrenia Working Group of the Psychiatric Genomics Consortium; Indonesia Schizophrenia Consortium; Genetic REsearch on schizophreniA neTwork-China and the Netherlands (GREAT-CN), Chen WJ, Faraone S, Glatt SJ, He L, Hyman SE, Hwu HG, McCarroll SA, Neale BM, Sklar P, Wildenauer DB, Yu X, Zhang D, Mowry BJ, Lee J, Holmans P, Xu S, Sullivan PF, Ripke S, O'Donovan MC, Daly MJ, Qin S, Sham P, Iwata N, Hong KS, Schwab SG, Yue W, Tsuang M*, Liu J*, Ma X*, Kahn RS*, Shi Y*, Huang H*. Comparative genetic architectures of schizophrenia in East Asian and European populations. Nat Genet. 2019 Dec;51(12):1670-1678. doi: 10.1038/s41588-019-0512-x. Epub 2019 Nov 18. PMID: 31740837 * Joint senior author.

2.2 Motivation to model others' minds: the importance of cognitive motivation for mental state understanding in early adolescence.

Co-Supervisor 1A: Dr Caroline Catmur

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Co-Supervisor 1B: Dr Yuen Siang Ang

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Project Description:

Understanding others' mental states allows individuals to obtain the social support necessary for mental wellbeing. But some people struggle to understand others. Early adolescence is a period of intense social change, making this a crucial developmental period for mental state understanding. Identification of factors influencing mental state inference during adolescence may lead to improved predictors and treatments for mental ill-health in later life. The factors impacting upon individuals' motivation to engage in mental state understanding are not well understood, and few measures of this motivation exist. This project combines the first supervisor's research into how humans model others' minds, with the second supervisor's expertise in cognitive motivation, to measure motivation to engage in mental state inference. Following development and validation of the 'Motivation to Model Minds' measure (months 1-12, London), the student will assess this ability in the GUSTO cohort of 13-14-year-old youths (months 13-33, Singapore). We will capitalise on the exceptionally rich datasets that have been collected from this cohort, allowing us to identify early-life factors which impact on the motivation to model others' minds in adolescence, along with measuring associations during adolescence between the motivation to model minds and other social and cognitive abilities, and mental wellbeing. Months 34-48, in London, will focus on writing up the thesis and disseminating the project results. This project involves methodologies from experimental psychology and computational modelling, along with big data analysis techniques. This makes it an exciting opportunity for the student to develop a range of highly transferable skills as part of their studies.

Two representative publications from supervisors:

Conway, J. R., Coll, M. P., Cuve, H. C., Koletsi, S., Bronitt, N., Catmur, C., & Bird, G. (2020). Understanding how minds vary relates to skill in inferring mental states, personality, and

intelligence. Journal of Experimental Psychology: General, 149(6), 1032–1047. https://doi.org/10.1037/xge0000704.

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THEME3: Biomedical Engineering and Medical Imaging

1.3 Cardiac blood flow simulation for patients with heart failure and atrial fibrillation HF-AF.

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Project Description:

Heart failure and atrial fibrillation are two common cardiovascular diseases that commonly co-exist. However, there are many aspects of treating atrial fibrillation in the presence of heart failure that are still unknown. One of these aspects is the effect of the two commonly atrial fibrillation used treatments, i.e., rate control and rhythm control on the blood pumped by the heart during each heartbeat. During this project, the student will learn how to simulate the blood flow in the heart undergoing rate and rhythm control treatments. The simulation results will be used to determine the favourable and adverse effects of each treatment on heart performance. We will test if these simulations can be used to predict patient outcomes. We will use a high-performance computation to predict the results and then validate them against the patients' data. By working on this project, the student will learn how to define a research question, collect and analyse patient-specific data, use a multidisciplinary approach to model the phenomenon mathematically, computationally simulate the blood flow, and translate the results in a medically relevant guideline. Besides the technical skills, the student will be trained to communicate clearly with the scientific community, think critically, identify current challenges, and find research opportunities in their field of interest. e prospective student will benefit from the world-class computational facilities and mentoring by prominent scientists during this international collaboration between KCL and A*STAR.

Two representative publications from supervisors:

De Vecchi, A., Marlevi, D., Nordsletten, D.A., Ntalas, I., Leipsic, J., Bapat, V., Rajani, R. and Niederer, S.A., 2018. Left ventricular outflow obstruction predicts increase in systolic pressure gradients and blood residence time after transcatheter mitral valve replacement. Scientific reports, 8(1), pp.1-11.

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