

Highlights from the WisSing Symposium

22 May 2026

PARTNERS

Genome Institute of Singapore
A*STAR GIS
DukeNUS Medical School
Nanyang Technological University Singapore
Lee Kong Chian School of Medicine
NHG Health
NUS National University of Singapore
Wisconsin University of Wisconsin–Madison

The Wisconsin-Singapore Comparative Study of Microbiome and Mental Health (WisSing)

Different populations. Shared science.
Better mental health for all.



The Collaboration: Cross-Continental and Cross-Discipline

GLOW
Gut Linked Outcomes in Wellbeing

- >6,000 participants in Singapore (Chinese, Malay, Indian)
- Clinical recruitment across IMH, TTSH & NHGP
- Leading research institutes & integrated data analysis platforms

LUCIDA

- 1,500 participants in the US
- Leading institutions for mental health research
- Wisconsin Institute for Discovery
- Center for Healthy Minds
- University of Wisconsin-Madison

SAMPLES

- Microbiome (stool, oral, skin)
- Human (DNA, metabolites)
- Digital Phenotyping

SURVEYS

- Questionnaires & clinical assessments
- Lifestyle & environmental factors

Integrated analysis to identify human and microbial biomarkers, and digital signatures associated with mental health conditions.

A Multi-omics, Multi-modal Approach Leveraging Complementary Expertise from Singapore and the US

- Digital Phenotyping
- Metagenomics
- Clinical Psychology
- Gut Biology
- Mechanistic Metabolomics
- Machine Learning
- Data Analysis
- Neuroscience

A Shared Vision & Outputs



Planned Scientific Outputs

1. Factors shaping microbiome composition in Singapore and the US
2. Microbiome Markers associated with Mental Health Conditions
3. Metagenomic Profiles of Oral & Gut Microbiomes in individuals with Mental Health Conditions
4. Multimodal Characterisation of Mental Health Subtypes

Event Programme

20–21 May, 2026

WisSing Strategic Meeting

Wisconsin - LUCIDA

1. Prof Jo Handelsman
2. Prof John Denu
3. Prof Earlise Ward
4. Prof Mark Craven
5. A/Prof Simon Goldberg
6. Asst Prof Ross Jacobucci
7. Dr Margaret Thairu

Singapore - GLOW

1. Prof Patrick Tan
2. Prof John Chambers
3. A/Prof Niranjan Nagarajan
4. A/Prof Jimmy Lee
5. A/Prof Sunny Wong
6. Asst Prof Sabrina Wong
7. Asst Prof Marie Loh
8. Asst Prof Max Lam
9. Dr Seow Shih Wee
10. Dr Dorrain Low
11. Dr Pan Jingwen
12. Dr Konstanze Tan
13. Dr Ng Hong Kiat
14. Dr Gloria Tso
15. Ms Penny Tan
16. Ms Dayan Nurul AsyiqinBinte Mustafa

22 May, 2026

WisSing Symposium

Lee Kong Chian School of Medicine
Toh Kian Chiu Annex Lecture Theatre, HQ Building, Level 1
11 Mandalay Road, Singapore 308232

Opening remarks
By Professor Patrick Tan

Introduction to Gut Linked Outcomes in Wellbeing (GLOW)
By Prof John Chambers

The Microbiome and Well-Being
By Prof Jo Handelsman

Bridging the Awareness Gap: Digital Phenotyping's Role in Mental Health
By Asst Prof Sabrina Wong

Communication Between the Gut Microbiome and the Epigenome
By Prof John Denu

Uncovering Hidden Genetic Diversity in Asian Gut Microbiomes through Hybrid Metagenomics
By A/Prof Niranjan Nagarajan

Interpretable Machine Learning for Prediction and Discovery in the WisSing Project
By Prof Mark Craven

Foreword

In both Western and Eastern medicine, the connection between the gut and the mind has been recognised for centuries. Yet it is only recently that science has begun to be able to explain why, armed with modern tools like genomics, metabolomics, computational biology and digital phenotyping. It is fitting, then, that the WisSing collaboration brings the best of Wisconsin and Singapore together, uniting scientists from the US-based LUCIDA Project and Singapore's Gut Linked Outcomes in Wellbeing (GLOW) in a uniquely interdisciplinary international effort.

The field of microbiome and mental health research demands more than just a single lab's isolated efforts. By integrating Singapore's multi-ancestry genomic cohorts and robust computational frameworks with the mechanistic insights brought by our colleagues at the University of Wisconsin-Madison, we are moving past the historic limitations of siloed data and narrow disciplinary boundaries. The WisSing collaboration allows us to distinguish between what is unique to a specific population and what is universal to human physiology, essentially providing a much clearer lens through which to view human health.

Mental health remains one of the most challenging areas of medicine, defined far too often by a frustrating, protracted process of trial-and-error treatments. Behind the data are real individuals and families navigating invisible struggles. By utilizing high-dimensional data, we are finally beginning to map the patterns that were once hidden beneath the noise of environment, genetics, and microbial influence.

This partnership has set a standard for how we should approach complex disease. It demonstrates that when we pool our intellectual resources across oceans, we gain the perspective needed to translate basic science into actual patient care. We are only in the early stages, but the path forward is clear: if we intend to address the most pressing healthcare challenges of our time, we must continue to build these bridges, ensuring that our progress is as global and inclusive as the challenges we face.



Prof Patrick Tan

Executive Director
PRECISE

Dean and Provost's Chair
Cancer and Stem Cell Biology,
Duke-NUS Medical School

A Cross-Continental Conversation



Prof John Chambers
GLOW –
Lead Principal Investigator

In epidemiology, we see that international comparisons are vital;

for instance, South Asian populations face a 1% risk of diabetes at a healthy BMI of under 20,whereas Europeans only hit that same risk profile at a BMI of 30. To truly understand the rising tide of mental health conditions, we need massive, population-scale data.



Prof Jo Handelsman
LUCIDA –
Lead Principal Investigator

I couldn't agree more, John. While descriptive epidemiology gives us trends across large populations, the US team focuses on moving from correlation to mechanistic causality. In our lab, we are transferring microbiome samples from depressed human adolescents into entirely germ-free mice.

We have hints that some mouse behaviors that are similar to markers of depression in people may be altered as a result of the microbes they receive.

That mechanistic validation is exactly what makes this partnership a twin-track engine. Singapore brings a highly concrete data ecosystem via our **PRECISE SG100K infrastructure**, capturing 30 years of electronic health records and whole-genome sequencing across major Asian ancestries. Through our **GLOW** sub-study, we've rapidly mapped this diversity, gathering over 5,200 stool samples from a multi-ancestry cohort to dissect how this 'second genome' operates at scale.

That scale is exactly what our behavioral interventions need. In the US, we have decades of neurobiological research showing how mindfulness physically alters brain structures—like increasing gray matter in the hippocampus.Through our free **Healthy Minds Program (HMP)** smartphone app, we've deployed a scalable digital therapeutic that is already clinically proven to reduce depression scores



What is fascinating to us is how we can pair that digital phenotype with biology.

By integrating Singapore's genomic frameworks with your digital intervention data, we are moving past the historic limitations of isolated, Western-centric datasets. We can now track how continuous real-world sensor data matches subtle molecular shifts in the Asian gut microbiome.



And our data shows the biology is incredibly plastic We found that an average of just five minutes of daily engagement with the HMP app triggers rapid, specific shifts in microbial structures.

Amazingly, patients who respond strictly to cognitive lectures show entirely different microbiome changes than those who participate in active meditation, revealing completely distinct underlying pathways.

Ultimately, pairing the LUCIDA Project with the GLOW study allows us to build predictive algorithms that have never existed before. We are finally poised to discover which features of depression are universally hardwired into human biology, and which are unique to regional geography, ancestry, and culture—shifting the entire timeline of clinical psychiatric care globally.

Meet the Symposium Speakers

Bridging the Awareness Gap: Digital Phenotyping's Role in Mental Health



Asst Prof Sabrina Wong

Deputy Director
Clinical Research Unit,
NHG Polyclinics

Clinical Director
Primary Care and Family Medicine,
Lee Kong Chian School of Medicine, NTU

Expertise

As a primary care physician, Wong's expertise sits at the intersection of family medicine, clinical operations, and digital health technology, focusing heavily on bridging the awareness gap in mental healthcare.

Presentation Highlights

- **The HELIOSBEAM study:** An integrated digital phenotyping platform designed to gather longitudinal mental health insights.
- **Digital phenotyping innovation:** Quantifies human phenotypes in real-world settings using personal digital devices. This combines **active inputs** (validated surveys like PHQ-9 and GAD-7) with **passive inputs** (continuous sensor data tracking heart rate, sleep cycles, step counts, and screen interactions).
- **Mitigating clinical bias:** Traditional episodic psychiatric care biases (such as memory gaps/recall bias or social desirability bias) can be overcome by capturing continuous, objective baseline data.
- **Privacy-by-Design framework:** Incorporates advanced data privacy technologies, including End-to-End Encryption (E2EE), differential privacy (geo-indistinguishability via Laplace mechanism) for location tracking, and strict Trusted Research Environments (TRE) to completely safeguard participant anonymity.

> **"Passive digital tracking and smartphone data can help connect real-world behavioral responses with biological measurements to better understand the gut-brain connection."**

Meet the Symposium Speakers

Communication Between the Gut Microbiome and the Epigenome



Expertise

A leading molecular biologist and biochemist, Denu is an expert in epigenetics, metabolic signaling, and microbial ecology, focusing heavily on deciphering the molecular communication pathways between the gut microbiome and host physiology.

Presentation Highlights

- **The epimetabo-centric framework:** Investigates how nutrition and the gut microbiota-derived metabolome dictate host health, moving beyond pure correlation to map exact biochemical mechanisms.
- **Chromatin modification & gene expression:** How specific microbial metabolites act as signaling molecules that chemically modify chromatin structure, directly impacting host gene transcription and downstream systemic biology.
- **Metabolite-mediated communication:** The functional pathways of key gut microbiota-derived metabolites—such as short-chain fatty acids (SCFAs) and trimethylamine N-oxide (TMAO)—can influence host physiological states.
- **Mechanistic modeling in the gut-brain axis:** Contributes foundational molecular insights to the broader joint partnership, bridging the gap between computational microbial data and biological reality to explain how gut health drives host neural and metabolic outcomes.

Prof
John Denu

Professor
Biomolecular Chemistry,
School of Medicine and Public Health

Director
AI Precision Health Hub

Co-director
Wisconsin Nathan Shock Center,
University of Wisconsin-Madison

“Supplementing mice with short-chain fatty acids can alter host histone acetylation and reprogram gene expression, restoring epigenetic signaling patterns.”

Meet the Symposium Speakers

Uncovering Hidden Genetic Diversity in Asian Gut Microbiomes through Hybrid Metagenomics



Expertise

The main focus of Nagarajan's research is the development of cutting-edge genome analytic tools for studying the function of diverse microbial communities and their impact on human health. His lab was one of the first to develop hybrid assembly tools for genome-resolved metagenomics.

Presentation Highlights

- **Hybrid metagenomic assembly:** Pioneering methods that combine short-read and long-read sequencing technologies can reconstruct complete, high-quality microbial genomes, effectively uncovering hidden diversity within complex biological samples.
- **Decoding complex microbial communities:** Computational and analytical frameworks are needed to profile dense microbial populations, mapping how diverse bacterial species interact and coexist within the human gut.
- **Functional pathway analysis:** Specialised bioinformatic pipelines to interpret genomic data, moving beyond simple species identification to analyze the specific metabolic and functional pathways that microbes utilize to interact with their host.
- **Data-driven insights:** Translating massive, multi-dimensional genomic datasets into structured biological insights is necessary to link microbiome profiles to host health and mental well-being outcomes.

A/Prof Niranjan Nagarajan

Associate Director, AI and Compute
Genome Institute of Singapore, A*STAR

Associate Professor
Department of Biochemistry, Yong Loo Lin School of Medicine, NUS

"Combining techniques such as short-read and long-read sequencing technologies with Hi-C chromosome conformation capture data is giving deep insight into gut microbial diversity across Asia."

Meet the Symposium Speakers

Interpretable Machine Learning for Prediction and Discovery in the WisSing Project



Expertise

As a senior data scientist and machine learning expert, Craven's expertise sits at the intersection of artificial intelligence, computational biology, and clinical informatics, focusing heavily on developing transparent models that bridge the gap between raw data and interpretable insights.

Presentation Highlights

- **Interpretable machine learning:** The "black-box" nature of traditional predictive algorithms can be addressed by employing interpretability methods that provide explanations of model outputs, making complex data-driven predictions accessible to researchers.
- **Demystifying complex scientific datasets:** Novel computational methods to analyze high-dimensional, multi-modal biomedical data, extracting meaningful, high-level abstractions rather than just correlation patterns.
- **Building clinician trust:** Both local (patient-specific) and global (system-wide) explanations for algorithmic decisions help to ensure that machine learning insights are verifiable and trusted by medical professionals.
- **Facilitating scientific discovery:** Turning massive datasets into clear, structural hypotheses allows biological and clinical investigators to pinpoint the exact variables, and interactions among them, driving predictive outcomes.

Prof Mark Craven

Professor
Department of Biostatistics and Medical Informatics,
Department of Computer Sciences,
University of Wisconsin-Madison

Director
Computation and Informatics, Biology and Medicine (CIBM) Training Programme

> **"Models must not only be multi-modal, incorporating 'omics, digital phenotyping and other data, but should also be transparent and predictable to gain trust."**