A*STAR RESEARCH

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A*STAR Skin Research Labs (A*SRL)
Advanced Remanufacturing and Technology Centre (ARTC)
Bioinformatics Institute (BII)
Bioprocessing Technology Institute (BTI)
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Genome Institute of Singapore (GIS)
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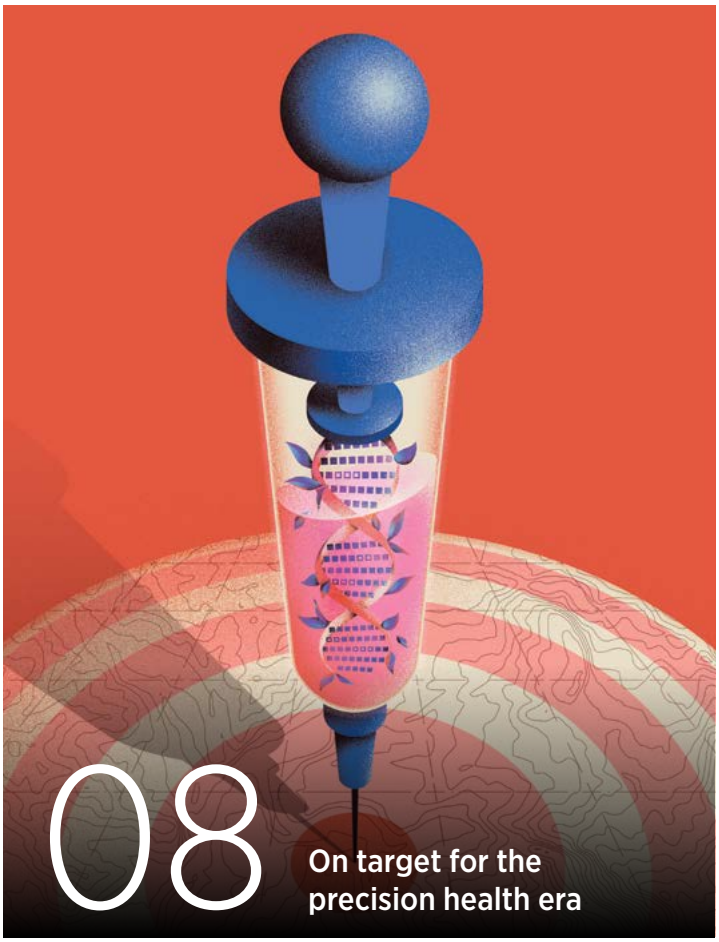

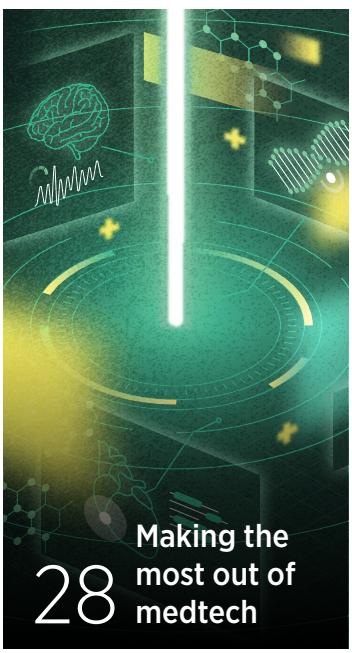

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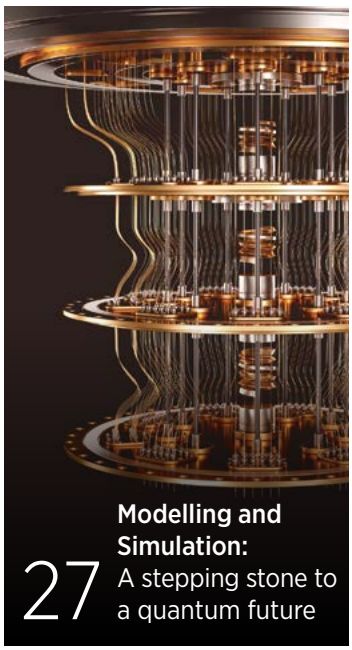
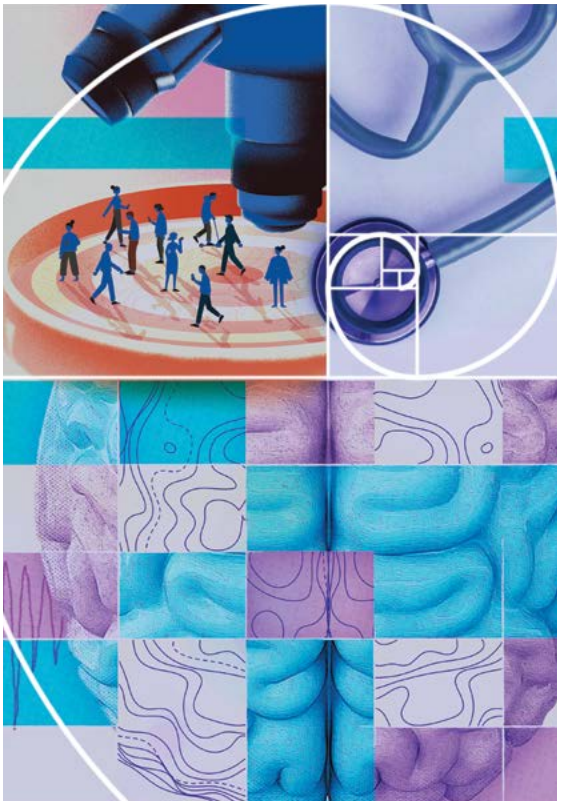


EDITORIAL NOTES



Each of us carries a unique copy of the human genetic code. For better or worse, the quirks within that code that differentiate us from one another can shape our lives from infancy to old age.

With sequencing technologies becoming more affordable, scientists can now examine patterns of disease risk in the genomes of entire populations. Insights from these risks, coupled with the effects of lifestyle and the environment on our health, are giving rise to an era of precision medicine—healthcare interventions tailored to meet individual needs.

In this issue's cover story, 'On target for the precision health era (p. 08)', we look at efforts by A*STAR researchers and collaborators to address gaps in precision medicine research. Through Singapore's National Precision Medicine (NPM) programme, multidisciplinary teams are conducting some of Southeast Asia's most comprehensive population genomics studies, translating big data insights to advanced models of treatment and prevention.

Beyond our genetic codes, gene expression patterns also vary between cells and individuals. In our first feature, 'The mind cartographer (p. 18)', A*STAR researcher Jinyue Liu discusses how her work in spatial transcriptomics charts the complex connections within the human brain, helping scientists develop targeted treatments for neurological disorders.

To translate medical research from the lab to the clinic, health technologists bring seemingly disparate disciplines together. In our second feature, 'Making the most out of medtech (p. 28)', A*STAR scholar Daryl Jude Lawrence shares his journey from materials science to medicine, combining expertise in both fields to create simple, cutting-edge devices for complex conditions.

Elsewhere, A*STAR research institutes continue to expand scientific frontiers in fields ranging from sustainable electronics to nanosurface engineering. For more on these, turn to 'Breathing new life into e-waste (p. 24)' and 'Nanofluids draw more oil from stone (p. 34)'.

For more of the latest developments from A*STAR researchers, visit our website at **research.a-star.edu.sg**. You can also stay up-to-date by following us on Twitter at **@astar_research**, LinkedIn at **A*STAR Research** and Telegram at **A*STAR Research**.

On the cover
Through targeted insights from population genomics and environmental data, precision medicine is set to revolutionise Singapore's healthcare landscape.

For the latest on A*STAR's COVID-19 research, please scan the QR code or visit: https://research.a-star.edu.sg/tag/covid-19/

COVID-19

Going with the flow

Researchers blend the physics of particle dynamics with complex computational simulations to gauge the risk of catching COVID-19 in different social settings.

Just as the fluid nature of air carries planes to their destinations, it also sends virus-laden droplets from coughs and sneezes drifting toward others with startling efficiency. This is why when a new airborne virus emerges, public health authorities must find ways to optimally curb the spread of infections from person to person.

Chin Chun Ooi, a Research Scientist at A*STAR's Institute of High Performance Computing (IHPC), said science-backed public health measures have been vital for minimising case numbers, particularly during the early days of the pandemic. However, social distancing and wearing masks are not one-size-fits-all solutions. Instead, their effectiveness depends on many variables in real-world settings.

In collaboration with Singapore's Ministry of Health, National Centre for Infectious Diseases, and Land Transport Authority, Ooi led a study on new methods for assessing infection risks in various indoor settings.

"Critical questions such as the minimum viral dose required for infection; the viral load emitted when individuals cough, talk, or exercise; and the impact of both on infection risk needed to be answered," said Ooi. To that end, Ooi and his colleagues

Photo credit: zydeaosika / Pexels

Using live and mathematical simulations, Ooi's team assessed the relative risk of COVID-19 transmission in a typical double-decker bus from an infected individual in different everyday scenarios.

"Critical questions such as the minimum viral dose required for infection; the viral load emitted when individuals cough, talk, or exercise; and the impact of both on infection risk needed to be answered."

designed a two-pronged approach to build their risk assessment framework, combining measurements of how droplets move in air with advanced computational simulations.

The researchers used an everyday situation as their test case: a ride home on a double-decker public bus. First, they collected data on how particles circulated on board with the help of a fog machine and a small fleet of particle detectors. They then modified the setup to simulate unique environmental conditions, such as with the windows closed, the air conditioning turned on, and the COVID-19-infected individual placed in different locations.

The study's results support the importance of mask-wearing: the chances of transmission were greatly reduced for those who masked up. Interestingly, seat choice also influenced the chances of catching COVID-19. Passengers seated behind an infected individual were at higher risk due to the movement of air in the enclosed environment.

According to Ooi, these results highlight risk assessment models as vital tools for protecting vulnerable communities against viral threats. "We propose a risk stratification framework that is simple, intuitive and easily interpretable to facilitate communication and decision-making," explained Ooi.

The virus has evolved since the study was conducted, sprouting multiple variants of concern with higher transmission rates and prompting the need for updates to the existing risk framework, noted Ooi.

"The viral load thresholds are specific to early variants and will need to be updated with data collected about how more recent variants spread," said Ooi, adding that these efforts could help to refine and enhance the accuracy of their risk assessment methodology under current circumstances. ★

Researcher
Chin Chun Ooi, IHPC

IN BRIEF
The researchers' model could improve public health measures by providing simpler, more intuitive assessments of COVID-19 transmission risk in community spaces.

1. Ooi, C.C., Suwardi, A., Ou Yang, Z.L., Xu, G., Tan, C.K.I., *et al*. Risk assessment of airborne COVID-19 exposure in social settings. *Physics of Fluids* **33**, 087118 (2021).

COVID-19

How variants have loosened their grip

A deletion in the genome of SARS-CoV-2 variants makes resulting infections milder and could also be a target for future COVID-19 treatments.

Another year into pandemic life and most of us have settled into a new normal. While masking and vaccinations continue to help keep COVID-19 case numbers down, the gradual de-escalation of the public health threat it poses may be partly thanks to a curious quirk of viral evolution—the 'accidental birth' of weaker variants.

Despite being more transmissible than the original virus, certain genetic variants of SARS-CoV-2 tend to cause milder disease symptoms with less inflammation throughout the body. Experts attribute this shift to a 'mutational hotspot' in a region of the virus's genome called ORF8.

"The ORF8 region encodes one of SARS-CoV-2's most rapidly mutating proteins," said Siew-Wai Fong, a Research Scientist at the A*STAR Infectious Diseases Labs (ID Labs). "Since the beginning of the pandemic, we've seen different ORF8 mutations in multiple variants of concern (VOCs), including Alpha, Gamma, Delta and Omicron."

Fong explained that for viruses, random mutations are essential to adapt to host defences and keep replicating. While some mutations might boost a variant's transmission speed, or lead it to induce more life-threatening symptoms, the luck of the genetic draw might also dull a variant's infective edge.

Notably, some of the more benign SARS-CoV-2 variants carry genomes with sections deleted from ORF8. Fong and Lisa Ng, Executive Director at ID Labs, co-led a pioneering study of how a local variant with a large 382-base deleted section in ORF8, known as △382 SARS-CoV-2, caused an altered immune system response versus the original (or wildtype) virus.

"Understanding the natural biology of host immune responses after infection with these SARS-CoV-2 variants will provide important insights into preventive and therapeutic strategies," said Fong.

The researchers recruited a cohort of 66 patients with COVID-19 in Singapore, 19 of whom had been infected with the △382 variant. They then extracted genetic material from the participants' blood samples and analysed them with RNA sequencing technology. This approach enabled the team to tease out molecular differences in the immune responses between wildtype SARS-CoV-2 and △382 infections.

The team found a potential explanation for the milder symptoms: with its ORF8 proteins disabled by the missing section of RNA, the △382 variant set off stronger and more immediate immune responses compared to the wildtype. The researchers' data also revealed a surge in T cell activity and a decrease in inflammatory cytokine production, as well as faster antibody responses.

Fong said that these results put ORF8 in the spotlight as a previously unexplored target for future COVID-19 vaccines and antiviral treatments. However, ORF8 isn't the only mutation hotspot in play for SARS-CoV-2; mutations affecting the virus's spike protein may also influence infection severity and transmission speed.

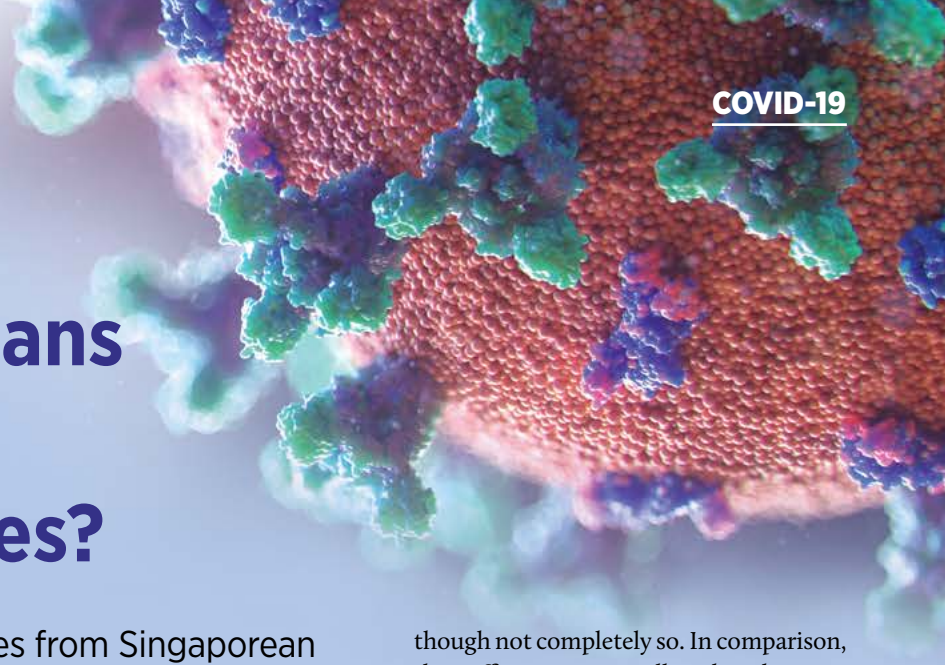
"The asymptomatic or mild disease symptoms attributed to ORF8's absence, in tandem with enhanced infectivity from spike mutations, may explain the high transmissibility of VOCs that became dominant over the pandemic's course," concluded Fong, adding that ORF8 mutation monitoring would be a focal point of the team's ongoing studies. ★

Photo credit: Victor He / Unsplash

Researcher
Siew-Wai Fong,
ID Labs

IN BRIEF
Infections by △382 SARS-CoV-2, a variant with an impaired ORF8 protein, cause more robust immune responses compared to those by the original virus.

1. Fong, S.-W., Yeo, N.K.-W., Chan, Y.-H., Goh, Y.S., Amrun, S.N., *et al*. Robust Virus-Specific Adaptive Immunity in COVID-19 Patients with SARS-CoV-2 △382 Variant Infection. *Journal of Clinical Immunology* **42**, 214-229 (2022).



COVID-19

Are Singaporeans vulnerable to evolving viruses?

A profile of the immune responses from Singaporean patients recovered from COVID-19 has revealed an urgent need to update vaccines against new viral variants.

The global COVID-19 vaccine rollout was a remarkable victory in a war against a pandemic that left no country untouched. While timelines for drug discovery and approval often drag on for years, the first mRNA vaccines against the SARS-CoV-2 virus were rolled out with FDA authorisation within months of testing, potentially saving millions of lives.

Unfortunately, SARS-CoV-2 remains an evolving foe in the medical arms race. "RNA-based viruses like SARS-CoV-2 constantly mutate," explained Laurent Rénia, a Senior Fellow and Principal Investigator at the A*STAR Infectious Diseases Labs (ID Labs). "This has been shown to allow some variants of these viruses to escape the immune system."

COVID-19 vaccines train an immune system to produce antibodies against the virus, similar to what a body would naturally do when recovering from a real infection. These antibodies often rely on binding to a specific protein on viral particles, known as the spike (S) protein, to neutralise them.

However, if certain mutations alter the S protein, they can prevent antibodies from doing their job. Experts are interested to find out whether people who recovered from the first pandemic wave might retain immune protection against emerging viral strains which, thanks to lucky (or unlucky) mutations, might have different S protein shapes from that of the original virus.

On the hunt for answers, Rénia and Cheng-I Wang, a Principal Investigator at A*STAR's Singapore Immunology Network (SIgN), worked with colleagues to collect blood samples from 57 Singaporean patients who had experienced mild, moderate or severe COVID-19 infections early in the pandemic. The team then analysed how well the antibodies from these samples could neutralise the original SARS-CoV-2 isolate alongside two variant strains: Alpha and Beta.

Using an S protein flow cytometry-based (SFB) assay, the researchers mixed modified cells expressing each strain's S proteins with antibody-rich plasma extracted from patient samples. They then measured how well those antibodies bound to each type of S protein, simulating their actions against live viral counterparts.

"The SFB assay can be applied to any proteins expressed on the surface of a range of pathogens, including other viruses, bacteria and even parasites," said Rénia, adding that they also used the technique for malaria studies.

As expected, antibody samples from study participants were most effective against the original coronavirus isolate, though not completely so. In comparison, their efficacy was partially reduced against the Alpha variant, B.1.1.7, and even more so against the Beta variant, B.1.351.

Rénia said that these results exposed a growing critical weakness in the COVID-19 vaccines originally rolled out in 2021: "These vaccines are only partially protective against reinfection by the original strain they were developed from, and sometimes not at all against variants." This finding is particularly concerning for people with weak immune systems such as the elderly and patients on certain medications, Rénia added.

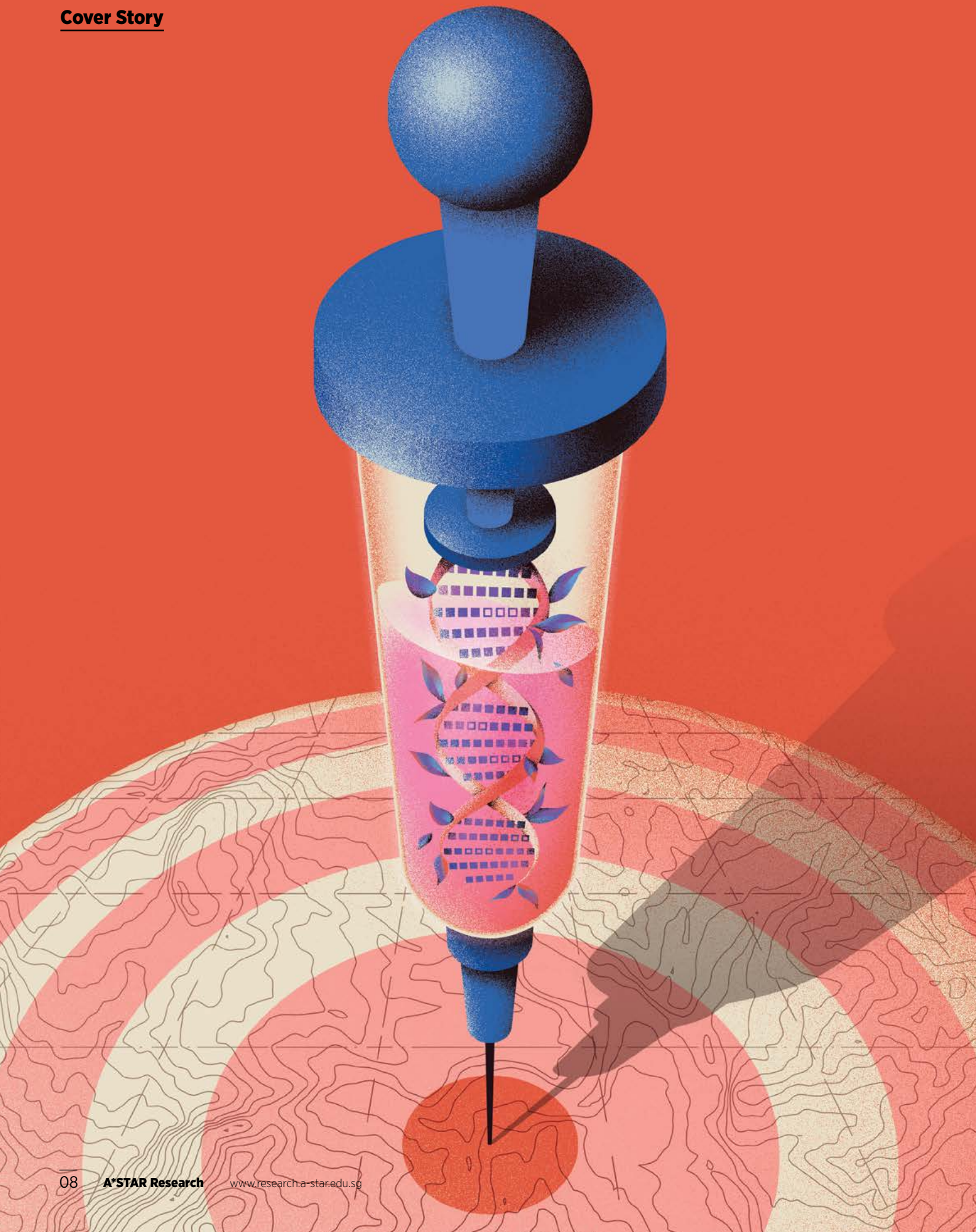
Moving forward, Rénia said the team would continue to study the emergence and immune evasion abilities of new SARS-CoV-2 variants, as they see this as an important jumping-off point for developing, designing and implementing future 'variant-proof' COVID-19 vaccines. ★

Researchers
Laurent Rénia and Cheng-I Wang, ID Labs

IN BRIEF
Antibodies from the original SARS-CoV-2 virus only partially protect against reinfection by the same strain, and may not protect against new variants with altered spike proteins.

1. Wang, B., Goh, Y., Prince, T., Ngoh, E., Salleh, S., *et al.* Resistance of SARS-CoV-2 variants to neutralization by convalescent plasma from early COVID-19 outbreak in Singapore. *NPJ Vaccines* **6** (1), 125 (2021).

Photo credit: Fusion Medical Animation / Unsplash



ON TARGET FOR THE PRECISION HEALTH ERA

Multidisciplinary efforts across A*STAR are paving the way toward Singapore's precision medicine vision.

Singapore is one of Asia's most rapidly ageing societies. While longer lifespans are generally considered a positive sign of progress, the quality of those lives also matters. However, health experts predict that a growing proportion of Singapore's elderly is at risk of chronic lifestyle diseases such as hypertension and diabetes, and will thus put increasing and unsustainable pressure on the healthcare system.

For these concerns about the economics of healthcare, precision medicine could be a promising solution. Where conventional medicine relies on a one-size-fits-all approach—with diagnosis and treatment based on generalised constellations of symptoms and health indicators—precision medicine accounts for the myriad of genetic, environmental and lifestyle differences that exist between individuals. Using this data, early disease detection and intervention will also be possible.

"Precision medicine promises to transform healthcare for groups and individuals through early disease detection, refined diagnoses and tailored treatments, but its most significant impact may be at the population level," said Patrick Tan, Executive Director of the Genome Institute of Singapore (GIS) at A*STAR, adding that precision medicine could support early interventions to reduce the incidence of late-stage diseases and improve overall population health.

With genetics proposed as the root of up to 30 percent of healthcare outcomes, a key enabler of precision medicine is the availability of individual genomic profiles. However, Asian genomes are underrepresented in genomic research projects and public databases, with most existing discoveries in the field based on populations of European ancestry.

Recent efforts by international consortiums such as the Genome Aggregation Database (gnoMAD) and the Trans-Omics for Precision Medicine (TOPMed) programme have attempted to generate more diverse cohorts. Even so, less than 10 percent of individuals within these two databases are of Asian ancestry, Tan explained.

Tan also highlighted a more concerning point: "None of these studies focus on Southeast Asia, a region with a total population of over 670 million people and of considerable genomic and cultural diversity." He added that the lack of specific data for Southeast Asia presents a significant barrier to the practice of precision medicine in the region.

In response, the Singapore government is taking large steps to address this gap in genomic and precision medicine research, with A*STAR being an agency well-positioned to support these efforts.

SCANNING A NATION'S GENOMIC LANDSCAPE

The Singapore government has displayed a commitment to the advancement of precision medicine across the country. As part of its efforts, precision medicine was designated as a priority area of development for Human Health and Potential, one of four domains of strategic importance in the government's RIE2025 Plan.

A key goal under this domain is the expansion of the country's National Precision Medicine (NPM) programme, a 10-year roadmap to accelerate biomedical research, improve health outcomes and enhance economic opportunities.

Given Singapore's genetically diverse population of around 6 million, which includes the three major Asian ethnic groups of Malay, Chinese and Indian, the country's demographics also make it a natural fit for research aimed at creating similarly diverse genomic datasets for precision medicine.

"The availability of an all-Singaporean database to capture data specific to our multiancestral population could help develop more accurate algorithms for prediction and fine-tuned interpretative tools for genetic composition analysis," said Tan. He also noted that this molecular data could reveal novel disease mechanisms and potential drug targets specific to Asian populations.

However, meeting the NPM's goals will be no easy feat. In a commentary published in *Frontiers in Digital Health* in May 2022, a group of Singapore-based experts including A*STAR researchers suggested that the success of the nation's precision medicine efforts would require "appropriate data collection, data processing and interpretation", and highlighted the benefits of a multidisciplinary effort to realise the NPM's visions.

This is where A*STAR's wide-ranging expertise across scientific disciplines is valuable. For example, GIS's Precision Medicine and Population Genomics arm—a core focus of the institute since its founding in 2000—is dedicated to supporting precision medicine initiatives in the country. According to Tan, GIS's strength in genomics and data analytics, as well as knowledge of data infrastructure requirements to host, process and securely store genomic data, positions it as a key contributor to the nation's precision medicine landscape.

"In addition, other A*STAR research institutes such as the Bioinformatics Institute (BII), the Institute for Infocomm Research (I^2R) and the Institute of High Performance Computing (IHPC), with their capabilities in artificial intelligence (AI) and data federation know-how, would also be instrumental in driving data-driven healthcare solutions that harness new insights from Asian genomes to improve patient outcomes," he shared.

PRECISION SUPPORT THROUGH PARTNERSHIPS

Just as A*STAR's academic and research strengths are bringing Singapore's precision medicine vision to fruition, the agency's relationships with industry partners are playing a similarly crucial role. A*STAR maintains that strong public-private partnerships are key enablers in the agency's mission to translate science into real-world impact, a stance particularly evident in how it has supported the NPM's different phases to date.

Headlining the NPM's first phase was the Singaporean 10,000 Genomes (SG10K) project, which saw the collection of whole-genome sequences from 10,000 consenting and healthy Singaporean volunteers from Malay, Chinese and Indian ethnic backgrounds. By the end of this first phase in 2021, these genomes were used to establish the Singapore Reference Genome, the largest Asian database of whole genomes to date.

"The availability of an all-Singaporean database to capture data specific to our multiancestral population could help develop more accurate algorithms for prediction and fine-tuned interpretative tools for genetic composition analysis."

— Patrick Tan, Executive Director
at A*STAR's Genome Institute of Singapore (GIS)

A*STAR's joint lab partnership with genomic company NovogeneAIT Genomics proved an invaluable asset in this endeavour. "The partnership provided access to the latest Illumina HiSeq X-based whole genome sequencing (WGS) and bioinformatics analysis. Their centre devoted a significant portion of its sequencing capability to support the programme, and its proximity to GIS also sped up logistics arrangements for samples and data transfer, enabling the timely completion of the 10,000 genomes," said Tan.

Through a new multi-year partnership with Illumina, NovogeneAIT Genomics will also carry out genome sequencing for the NPM's ongoing second phase, which expands Phase I's scope more than tenfold. Phase II aims to provide whole-genome sequences for 100,000 healthy Singaporeans and an additional 50,000 people with specific diseases to create Southeast Asia's most comprehensive consented population genomics study, SG100K. Through new insights into the Asian genome and data-driven healthcare solutions, NPM Phase II intends to transform healthcare in Singapore and improve patient outcomes.

Tan, who also heads Precision Health Research, Singapore (PRECISE)—the government's central coordinating entity for Phase II's implementation—believes that the partnership with NovogeneAIT Genomics will allow local sequencing companies to benefit from training and certification in the use of Illumina's proprietary platforms, allowing those companies to access new regional and international markets.

Alongside these partnerships, A*STAR's GIS and BII will continue to support SG100K with their genomics and bioinformatic capabilities. GIS, for instance, has set up a high-throughput automated DNA extraction lab to ensure high-quality DNA is extracted from SG100K samples.

REFINING DATA INTO TARGETED INSIGHTS

With an increasingly large pool of genomic data to sift through, researchers are turning to the computational powers of bioinformatics to make the data useful. Sebastian Maurer-Stroh, Executive Director of BII, explained that bioinformatics can process, visualise and interpret data systematically and on a large scale, revealing patterns usually indecipherable by traditional analytical tools.

"The methods we have developed and continue to improve on at BII are well suited to interpret changes in genomic information collected through the NPM programme," said Maurer-Stroh.

As with all precision medicine endeavours, data processing is equally as important as its collection: specifically, the processing of vast datasets produced by projects such as SG10K and SG100K, encompassing the integrated genomic and phenotypic data of tens of thousands of individuals.

In this area, a crucial A*STAR contribution to the NPM programme's first phase was the establishment of

a new national service called Genomic Web Services. From the SG10K_Health web portal, users can query the SG10K dataset for information on a range of factors such as protein-drug interactions, polygenic risk scores (PRS) and allele frequencies. To date, the platform offers five services to help researchers distil health insights from SG10K, through invaluable contributions from GIS, BII, I²R and IHPC.

Among the services provided through SG10K_Health is the PRS Web Service, developed by I²R researchers. The team established pipelines for preprocessing and feature engineering to integrate and analyse data from WGS, consumer wearables and questionnaire responses. They then used the data to develop calculation pipelines for PRS—a metric that measures one's genetic disease risk—of the three major Asian populations within SG10K.

Similarly, IHPC researchers developed SG10K_Health's Imputation Server, optimising its codes and pipelines to reduce running times for genotype imputation—the process of estimating missing genotypes—for genome-wide association studies (GWAS) based on the same cohort.

A third key service within the portal is one developed at BII together with GIS: SNPdrug3D, which Maurer-Stroh describes as "providing the first complete map of single-nucleotide polymorphism (SNP)-drug 3D interactions both across the human proteome and at a population-wide level".

SNPs vary widely across individual human genomes; by mapping them to protein structures, SNPdrug3D allows the exploration of how SNP variants affect proteins at sequential and structural levels. These deeper dives, especially into variants involved in protein-drug binding, might in turn shed light on how they impact drug dosing and response in different people.

Using SNPdrug3D and other datasets, researchers at BII have already made some fascinating breakthroughs. "Collectively, we have mapped approximately 5.8 million unique SNP variants from over 80,000 individuals—including around 10,000 from Singapore—to protein structures related to around 6,000 drugs," shared Maurer-Stroh. From this data, BII researchers have found and experimentally validated previously undefined SNP variants that affect how drugs bind to metabolic enzymes and drug targets.

Creating new insights from the available data will only get faster and more efficient. BII researchers have also since used the data to build a machine learning-based prediction tool that identifies SNP variants that may affect drug metabolism. Insights such as these further pave the way towards Singapore's precision medicine vision of better and more tailored treatment strategies for patient groups.

SHARING THE GENOMIC DATA

Besides making sense of big data, A*STAR's safe and efficient data sharing also facilitates collaborations with other A*STAR research institutes. For instance, A*STAR's Centre for Big Data and Integrative Genomics (c-BIG) is a multi-institutional effort by BII, GIS, IHPC and I²R to address the challenges of big data analytics and integrative genomics for precision medicine in Singapore.

Coordinated by Nicolas Bertin of GIS's Genome Research Informatics and Data Science Platform, c-BIG combines an extensive genomics data hub with data science and high-performance computing capabilities to develop infrastructure and conduct research projects that support Singapore's genomics ecosystem. These range from broader genomics reference resources to specific areas such as cancer genomics and toxicity prediction.

Some c-BIG endeavours include CELLHUB, a cellular human body map of one million single-cell transcriptomes, and POLARIS, a development team for clinical-grade genomics software. Notably, c-BIG is also involved in the A*STAR Data Analytics Exchange Platform (A*DAX) for federated data, which facilitates safe data sharing and advanced analytics.

FROM CALCULATIONS TO CLINICS

Together with ecosystem partners from industry, academia and other government agencies, A*STAR's efforts to advance precision medicine have been paying off, with game-changing research findings in recent years.

In one instance, a team of researchers from GIS and A*STAR's Bioprocessing Technology Institute (BTI)

"Collectively, we have mapped approximately 5.8 million unique SNP variants from over 80,000 individuals—including around 10,000 from Singapore—to protein structures related to around 6,000 drugs."

— Sebastian Maurer-Stroh, Executive Director at A*STAR's Bioinformatics Institute (BII)

collaborated with the Singapore Eye Research Institute (SERI) to sequence DNA over 20,000 participants across 14 countries—including 1,200 Singaporeans—to uncover a gene that could cause blindness among the elderly. The proverbial needle in a haystack of over 18,000 genes turned out to be *CYP39A1*.

Meanwhile, working with public hospitals and universities across Singapore, A*STAR researchers from GIS, the Institute of Molecular and Cell Biology (IMCB) and the Institute of Medical Biology (IMB) sequenced the genes of 275 patients and their families recruited from the Singapore Undiagnosed Disease Programme, aiming to speed up diagnoses and improve treatment for those with suspected but unconfirmed genetic disorders.

Within A*STAR, the translation of research into solutions to address national challenges remains a priority. For precision medicine, breakthroughs in A*STAR labs have led to better treatments in the field and more lives saved.

In one example, the A*STAR scientists turned 'accidental entrepreneurs' behind MiRXES capitalised on research using miRNA as biomarkers for early disease detection. Building on a decade's worth of research on overlooked genetic material in blood, urine and tears, this spinoff company now makes highly sensitive biopsy test kits that detect gastric cancer early enough to improve patient survival rates and quality of life.

Another A*STAR spinoff, Nuevocor, is similarly built on years of basic research in genetically-linked heart diseases such as dilated cardiomyopathy. Now in its preclinical stage, the biotech company hopes to roll out gene therapies designed to stop heart disease-causing mutations in the LMNA gene and restore cardiac function in at-risk patients.

Nalagenetics, another biotech company with roots in A*STAR, is focused on personalised disease screening and interventions in Southeast Asia. The company aims to provide accessible end-to-end genetic testing alongside clinical decision support software for physicians and local healthcare systems.

Finally, A*STAR's Health and Medical Technologies Horizontal Technology Coordinating Office (HMT HTCO) is also developing a 'diabetes clinic of the future' in partnership with SingHealth to tackle Asia's diabetes epidemic. The clinic will use data from the country's largest diabetes registry, which covers 200,000 patients across a decade of historical data. Given the genetic and cultural differences underlying a predisposition to diabetes, the clinic hopes to thoroughly evaluate and improve the state of diabetes care.

All in all, these examples show how far precision medicine research has come on a national scale, while providing a glimpse of its further potential with the right technology, talent and data. As the NPM programme sets its sights on targeting up to one million Singaporean genome sequences and incorporating more complex social and environmental data, it is certain that A*STAR—with its network of research institutes, trained researchers, and public and private partnerships—will be a valuable source of support on the road ahead. ★

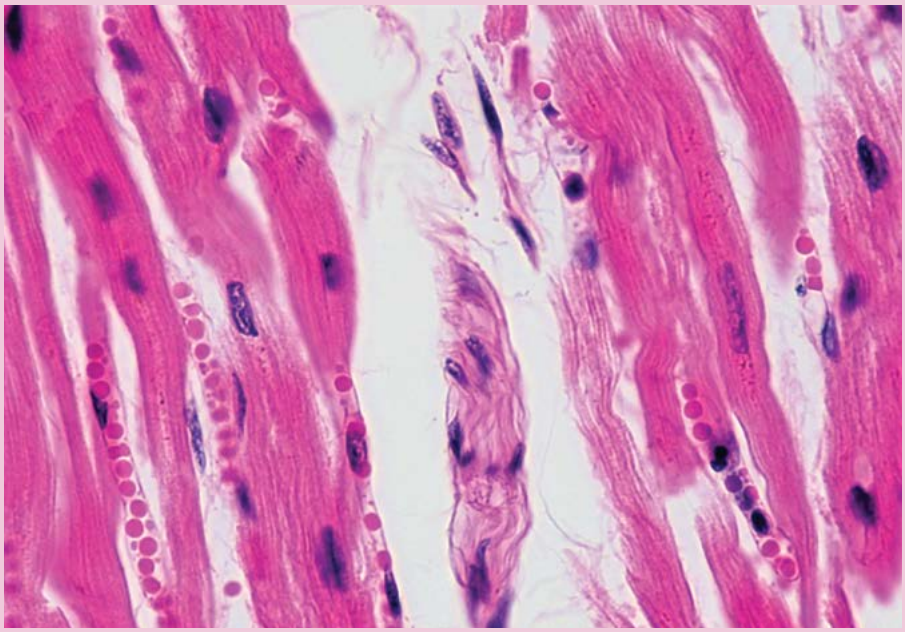
In addition to those previously mentioned, the following research and clinical partners are acknowledged for the Precision Medicine work mentioned in the cover feature:

- A*STAR's Singapore Institute for Clinical Sciences (SICS)
- KK Women's and Children's Hospital (KKH)
- Lee Kong Chian School of Medicine, Nanyang Technological University (NTU)
- National Healthcare Group (NHG)
- National Supercomputing Centre (NSCC) Singapore
- National University Health System (NUHS)
- National University Hospital (NUH)
- National University of Singapore (NUS)
- Singapore Eye Research Institute (SERI)
- SingHealth Duke-NUS Institute of Precision Medicine (PRISM)
- SingHealth Duke-NUS Academic Medical Centre
- Tan Tock Seng Hospital (TTSH)

GENE THERAPY

Remedy for a fragile heart

Experimental gene therapy promises a new lease of life for patients with genetic heart disease.



Whether relaxing by the pool or sweating on a treadmill, every heartbeat involves a perfectly orchestrated sequence of electrical impulses and cellular activity. A dizzying array of proteins work in unison to initiate contractions, and the functional loss of even one can have devastating consequences.

One example is lamin A, a structural protein found in heart cells. In dilated cardiomyopathy (DCM), mutations in the gene encoding lamin A cause the heart's chambers to weaken, severely compromising cardiac function. Notably, lamin A is a particularly difficult therapeutic target—over 450 different lamin A-associated gene mutations have been reported in DCM patients.

Colin Stewart, a Research Director at the A*STAR Skin Research Labs (A*SRL), has been studying lamins for over three decades and was among the first to establish the proteins' role in congenital heart disease. In a recent breakthrough, Stewart's team found a promising lead for DCM therapy.

Using a genetically engineered mouse model lacking the *LMNA* gene, which encodes for lamin A protein, the researchers found that the absence of the protein triggered a spike in another structural protein called SUN1. Animals with elevated SUN1 levels died of cardiac failure around a month after birth. The team then developed an experimental gene therapy that suppresses SUN1 and administered it to the mice with unexpected results.

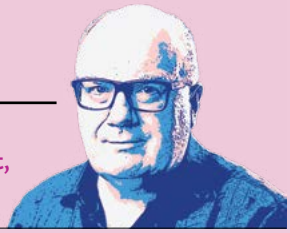
"Mice that received the gene therapy lived for over a year, instead of a month, and showed good to normal contractile function and reduced tissue scarring."

"To our immense surprise, we found that the loss of SUN1 made the mice healthier because they lived much longer. It also took longer for the heart and skeletal defects to develop," said Stewart. The researchers hypothesised that blocking SUN1 prevents the weakened heart cells from being subjected to mechanical stress as the heart contracts.

"Mice that received the gene therapy lived for over a year, instead of a month, and showed good to normal contractile function and reduced tissue scarring," said Stewart. These findings put SUN1 in the spotlight as an attractive target for treating DCM patients.

Meanwhile, Stewart helped co-found Nuevocor, a spinoff company that raised US$24 million in funding to bring their DCM gene therapy to the clinic. Stewart says ongoing efforts aim to refine the gene therapy's viral delivery platform.

"We intend to test these new variants in non-human primate models to ensure the gene therapy is delivered to the heart cells and expressed at sufficient levels to be of therapeutic value," shared Stewart. ★



Researcher
Colin Stewart, A*SRL

IN BRIEF
Treatments targeting the SUN1 gene could help patients with dilated cardiomyopathy (DCM) live longer and slow the formation of heart and skeletal defects.

1. Chai, R.J., Werner, H., Li, P.Y., Lee, Y.L., Stewart, C.L., *et al.* Disrupting the LINC complex by AAV mediated gene transduction prevents progression of Lamin induced cardiomyopathy. *Nature Communications* **12**, 4722 (2021).

Photo credit: Berkshire Community College Bioscience Image Library / Flickr

MOLECULAR MEDICINE

Striking a balance in healthy skin

Fine-tuning the levels of three skin cell metabolites could be the key to unlocking treatments for psoriasis and ageing skin.

Handstands are the ultimate test of balance—even the slightest weight shift can topple the pose. Similarly, healthy skin involves a delicate balance of cell renewal and cell death. As skin cells gradually move from the inner to outer layers of our skin, they divide, differentiate into hardy forms, and eventually die to form our body's protective barrier against the elements.

However, in hyperproliferative skin disorders such as psoriasis, skin cells can multiply up to 10 times faster than usual, often resulting in itchy, scaly and inflamed patches. Researchers studying the skin's mysteries have uncovered new details about the root of this uncontrolled proliferation: a balancing act between a triad of metabolites known as polyamines.

"Polyamines are a family of metabolites that are essential for normal cellular function in all cells," explained Leah Vardy, Covering Executive Director at the A*STAR Skin Research Labs (A*SRL). Polyamine levels have previously been observed to be lowered in ageing skin and elevated in hyperproliferative skin, showing the importance of tight control of their levels.

To better understand the factors affecting this triad of polyamines in our skin, Vardy and colleagues focused on a polyamine regulator protein called adenosylmethionine decarboxylase 1, or AMD1. In particular, the research group was interested in how AMD1 influenced gene expression patterns in skin cells, and how these changes impacted the skin's overall ability to act as a protective barrier.

First, the researchers took a closer look at patterns of AMD1 expression within the various layers of healthy human skin. They found that the AMD1 protein was least expressed in the deepest or basal layers of the epidermis, where skin cells normally focus on dividing themselves. Moving outwards, however, AMD1 expression gradually increased, peaking in the outermost skin layers where cells were most differentiated. They also found that AMD1 promoted high levels of spermine (Spm), a polyamine essential for the cell differentiation process.

Taking these two findings together, the researchers suggested AMD1 helps skin cells shift their behavioral gears—stopping division and starting differentiation—by gradually altering the balance of the three polyamines in different skin layers.

In follow-on cell culture experiments, the team blocked AMD1 activity in differentiating skin cells and found that this threw off the balance between Spm and two other polyamines, putrescine (Put) and spermidine (Spd), resulting in skin cells that behaved much like they would in patients with psoriasis. However, adding Spd and Spm into the culture 'rescued' skin cell differentiation, restoring a robust epidermal barrier.

Moving forward, Vardy said the team plans to explore the possibility of using AMD1 as a treatment target to tackle hyperproliferative skin disorders and ageing-related skin conditions.

"Our findings have demonstrated the importance of fine-tuning the levels and ratios of the three polyamines," Vardy commented, adding that they identified AMD1 as being central to maintaining this equilibrium. "We need a better understanding of how these polyamine ratios change in hyperproliferative conditions, as any therapeutic methods would need to control them to be effective." ★

Photo credit: Evgeniy Kalinovskiy / Shutterstock

Researcher
Leah Vardy,
A*SRL

IN BRIEF
The AMD1 protein helps shift the ratio of gene-regulating polyamines, controlling how rapidly cells multiply across different skin layers.

1. Rahim, B.A., Lim, H.K., Tan, C.Y.R., Jia, L., Leo, V.I., *et al.* The polyamine regulator AMD1 upregulates spermine levels to drive epidermal differentiation. *Journal of Investigative Dermatology* **141** (9), 2178-2188 (2021).

NEUROSCIENCE

The dark side of brain radiotherapy

Non-invasive imaging technology reveals how radiation exposure in the brain, particularly early in life, damages delicate brain tissue.

The Hippocratic oath of "do no harm" remains the cornerstone of modern medical ethics. Unfortunately, not all clinical interventions for cancer patients completely align with this age-old philosophy. Take radiotherapy for example, which uses strong beams of energy to destroy tumours but also leaves serious and lasting imprints on patients' lives: many adults and almost all children who receive radiotherapy experience learning and memory problems after receiving radiotherapy.

While neuroscientists have documented these functional changes, the consequences of brain radiation exposure on a cellular level have remained unclear. For Bhanu Prakash, a Principal Investigator at A*STAR's Bioinformatics Institute (BII), imaging technologies that allow scientists to look inside the brain non-invasively in real time may hold the key.

"Magnetic resonance imaging, or MRI, allows us to look into brain development systematically," Prakash explained, speaking on a study he led using MRI to track the effects of radiation exposure in mice. "We can see how the brain structure and networks change in the same cohort of animals over a certain period."

In collaboration with the Singapore Nuclear Research and Safety Initiative, Prakash and his team worked towards developing novel MRI-based biomarkers of brain damage to better monitor the long-term effects of early life radiation exposure.

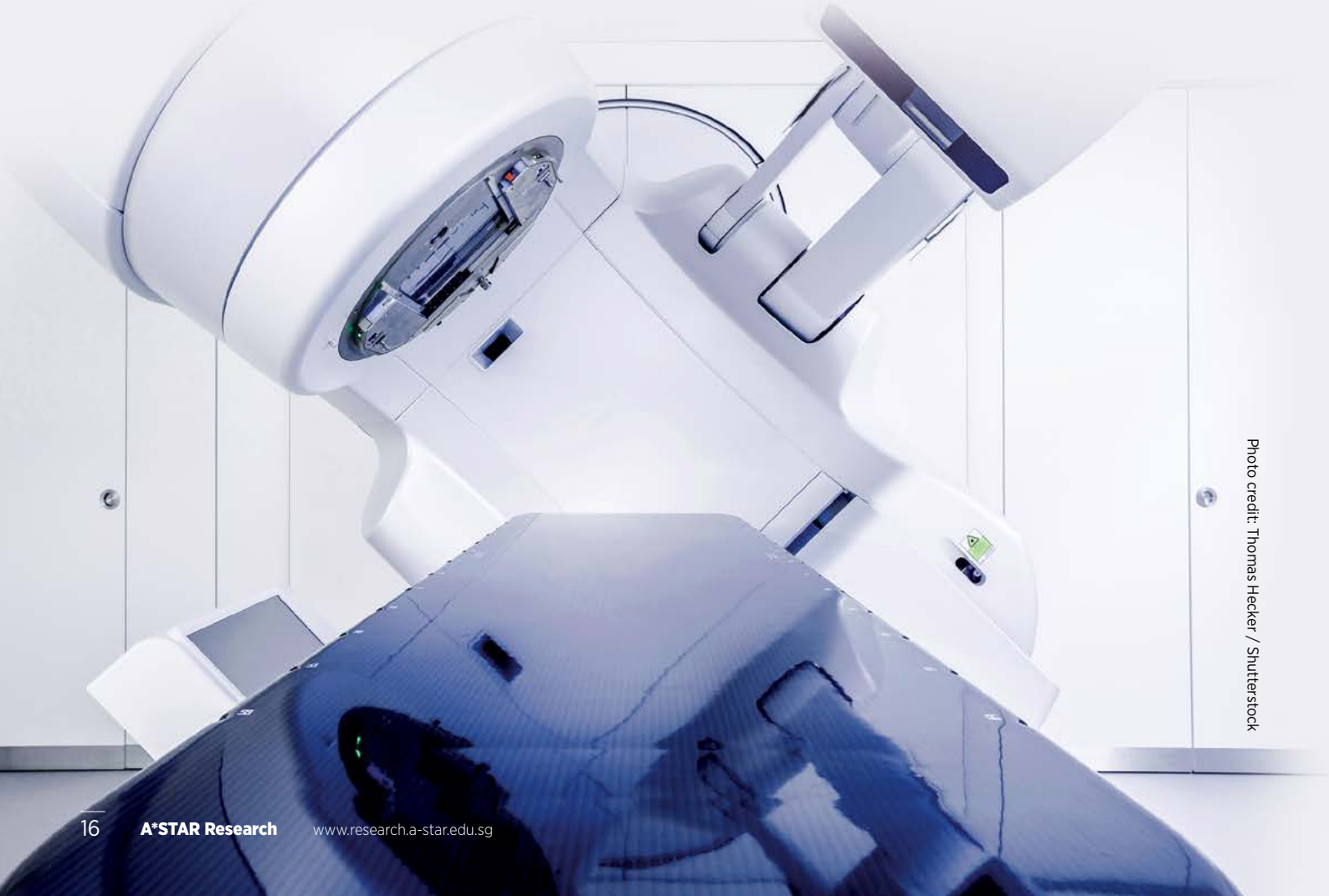


Photo credit: Thomas Hecker / Shutterstock

"This approach allows us to not only identify brain structures affected by radiation, but also understand the strength and duration of radiation exposure at which the structural changes become irreversible."

Animals were divided into separate groups that received a single radiation dose at three, 10 or 21 days after birth. The researchers then performed MRI scans at 13 months or the 'middle age' in the life cycle of mice.

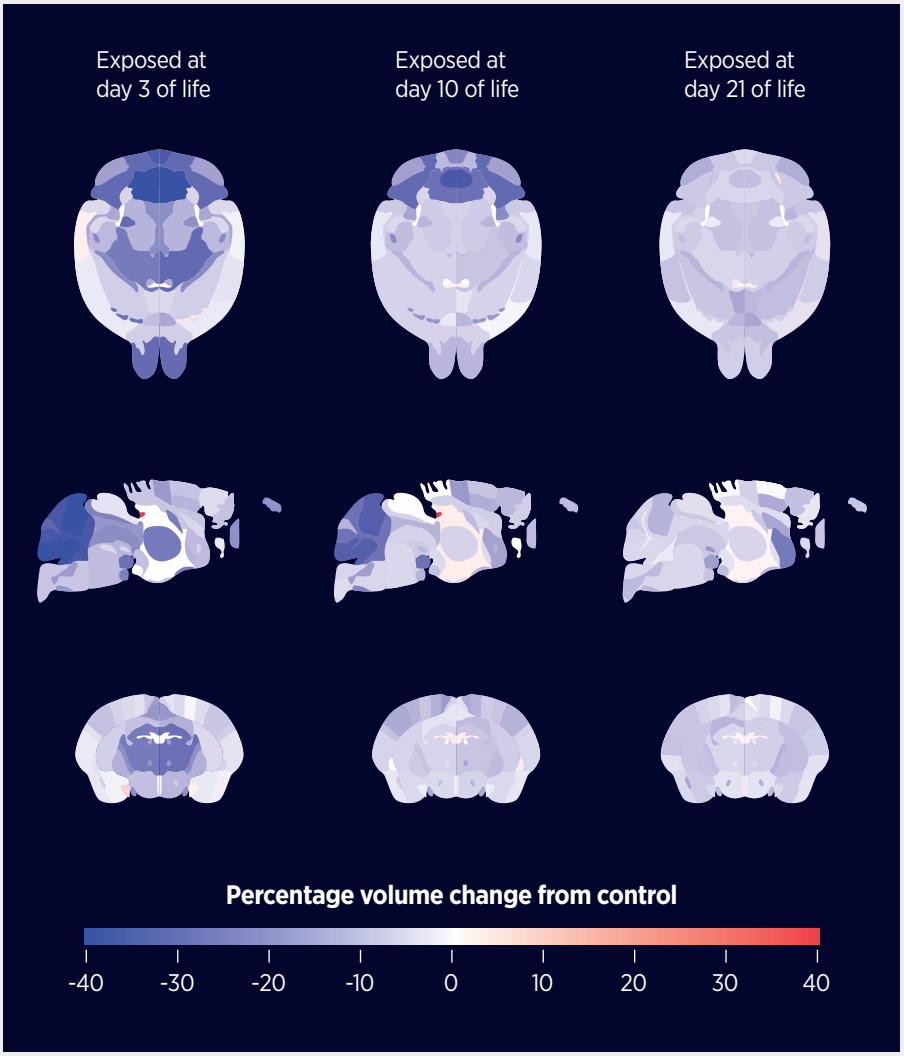
The team used a custom in-house bioimaging pipeline to precisely align the MRI scans to a reference atlas of the mouse brain. The innovative technology significantly sped up image analysis by automatically labelling regions of the brain and calculating any changes in brain volume.

"This approach allows us to not only identify brain structures affected by radiation, but also understand the strength and duration of radiation exposure at which the structural changes become irreversible," said Prakash.

The data collected revealed widespread brain shrinkage and neuron death in multiple regions including the cerebellum, which maintains balance and movement, and the hippocampus, the brain's memory centre.

Furthermore, the researchers found that the earlier the exposure took place, the greater the extent of the structural damage in the brain—mice exposed to radiation three days after birth showed the highest impact, findings that lined up with previous clinical studies.

Prakash said that this proof-of-concept study highlights MRI-based approaches as reliable, non-invasive alternatives to current biopsy-based analytical methods. "We established that MRI can give very similar insights to the results obtained at the microscopic or histological level." ★



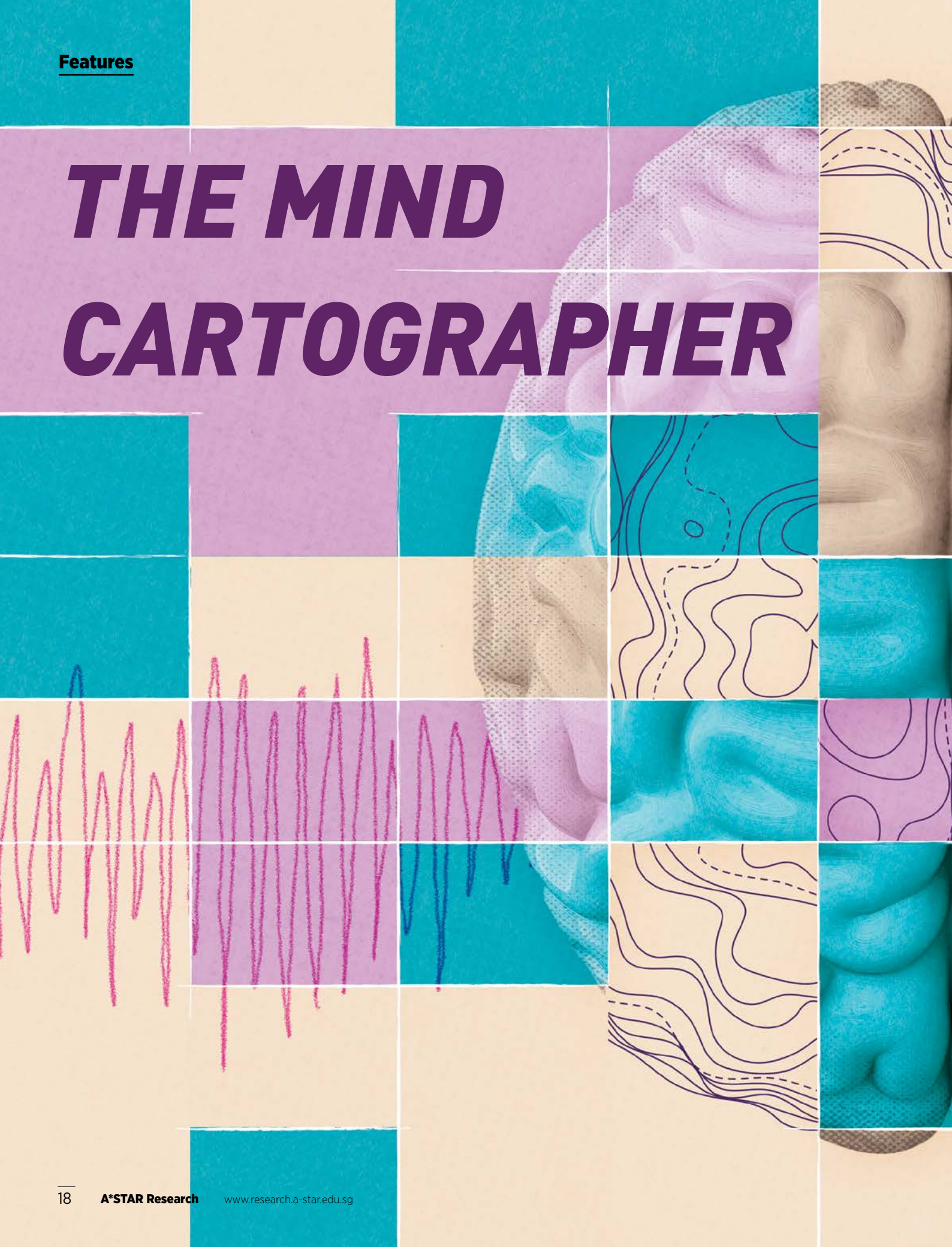
After 13 months, MRI scans found mice exposed to acute radiation at an earlier age had lower volumes of brain tissue in multiple regions compared to unexposed individuals.

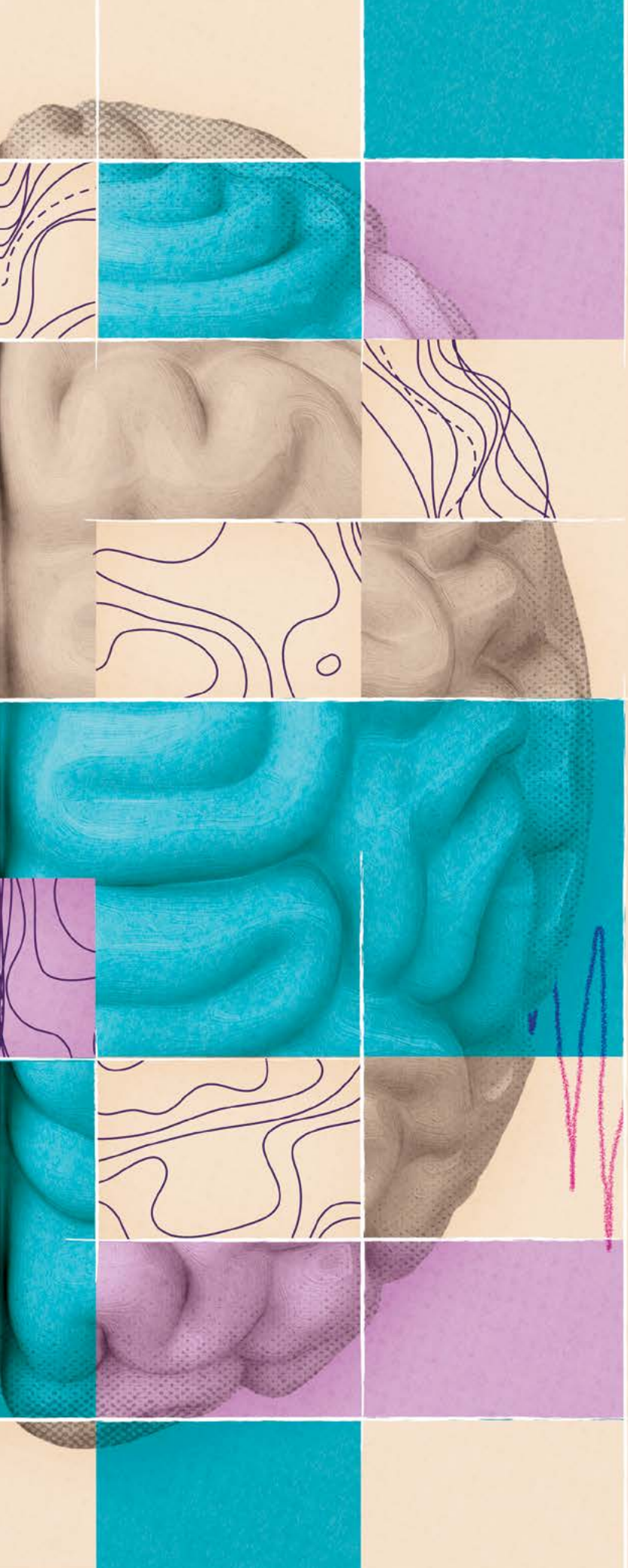
Researcher
Bhanu Prakash, IBB

IN BRIEF
Under MRI scanning, young mice exposed to radiation showed impaired brain structures in middle age, including regions affecting movement and memory.

1. Ren, B.X., Huen, I., Wu, Z.J., Wang, H., Duan, M.Y., *et al.* Early postnatal irradiation-induced age-dependent changes in adult mouse brain: MRI based characterization. *BMC Neuroscience* **22**, 28 (2021).

THE MIND CARTOGRAPHER





Through innovative molecular technologies, Jinyue Liu is building maps of the brain's circuitry to better understand how these connections go awry in disease.

Anyone setting out to explore a new holiday locale would likely turn to a map application on their smartphone for their navigational needs. Whether in quaint towns or bustling cities with elaborate railways, digital maps today serve as trusty sidekicks to visualise and pinpoint the best routes to reach one's destination.

Similarly, the human brain carries a rich and complicated topography. Across its convoluted landscape, 'highways' and 'towns' of neurons and their supporting cells endlessly convey and process information. The networks of pathways between these cells give rise to the complex functions of our minds, such as vision, memory and behavioural control.

However, this labyrinth of cellular connections can be confusing to navigate even to trained eyes. Much of this complexity boils down to how cells activate their genes differently across developmental periods and brain regions. These variations not only influence individual functions, but also govern the connections that the cells make to form brain circuits.

Jinyue Liu, a Principal Investigator at A*STAR's Genome Institute of Singapore (GIS), is on a mission to make sense of the intricacies of these brain networks and decipher how various disorders alter their connections. But doing so will require having a map of the underlying gene activation patterns.

As the Head of the Laboratory of Single-Cell Spatial Neuromics at GIS, Liu works with her team to build comprehensive maps of the brain by harnessing spatial transcriptomics approaches. This emerging class of molecular techniques involves charting gene expression patterns and their relative locations in a given tissue. Molecular 'guidebooks' based on these could help scientists precisely trace the brain's circuits on a molecular level, helping them develop new treatments that target disrupted connections in neuropsychiatric disorders.

Q: WHAT DRIVES YOUR INTEREST IN NEUROBIOLOGY?

All of us are unique on so many levels, whether in the ways we think and act, the circumstances that affect our health, or the DNA that makes us. I'm particularly interested in how individual brain circuits are assembled. The process of brain wiring is governed by some common rules. However, the brain cells that participate in each circuit and their levels of activity distinguish each one of us. Brain disorders often arise when these circuits malfunction, though their severity may vary from person to person.

My research aims to understand both the individuality and the commonalities between different people and translate them into something purposeful in the clinic. For example, in personalised psychiatry, doctors could select the most appropriate treatment strategies based on the unique neural circuitry underlying each person's condition. By investigating unique and common features among patients, we can better tackle different neurological disorders and start to find new and more targeted treatments.

Q: HOW DID THE A*STAR SCHOLARSHIP SHAPE YOU AS A RESEARCHER?

During my PhD training at Harvard University under A*STAR's National Science Scholarship, I got to witness first-hand the rise of the genomics revolution. My colleagues and I were adopting newly emerging technologies—from microarrays to bulk RNA sequencing and single-cell RNA sequencing—to examine the role of our genes in building the nervous system. These efforts led to the discovery of many new types of cells that differ in the genes they express.

It dawned on me that the next big gap in knowledge is how these diverse cells converse with one another to give rise to higher-order functions. I thus sought ways to understand how cells are organised in space within tissues and arrived at spatial transcriptomics for the next phase of my research.

We were fearless and tactful in embracing new technologies to break new frontiers and the experience proved incredibly valuable in setting me up to become an independent researcher. Moreover, I saw how my mentors and seniors were able to anticipate the next 'big thing' in the field. That kind of insight is a soft skill that can't be learned from textbooks, yet it was critical in my development as a scientist.

"By investigating unique and common features among patients, we can better tackle different neurological disorders and start to find new and more targeted treatments."

— Jinyue Liu, Principal Investigator at A*STAR's Genome Institute of Singapore (GIS)

Q: WHY DOES SPATIAL TRANSCRIPTOMICS MATTER IN STUDYING BRAIN DEVELOPMENT AND DISORDERS?

As the saying goes, "no man is an island". Similarly, no cell is an island. The interactions between cells determine the functions of the tissues they belong to, and may contribute to how diseases occur. To study these interactions, it's important to look at where and how individual cells express their genes. Spatial transcriptomics allows us to do just that.

This class of molecular profiling techniques involves quantifying and locating the expression of numerous genes within an area of intact tissue. Preserving tissue context enables us to see how our brain is organised and how it becomes disorganised in diseases. In recent years, spatial transcriptomics has been used to address important biological questions about brain development, ageing and neurodegeneration.

Q: HOW MIGHT YOUR TEAM'S WORK TRANSLATE TO NEW CLINICAL APPLICATIONS?

Our research focuses on identifying the key cell-to-cell interactions that underlie various brain disorders by using patient-derived stem cells and other model systems.

In studying autism spectrum disorder (ASD), for example, we used three-dimensional tissue structures called organoids to emulate the developing brain. We found that some cells were misplaced in the autism organoid model compared to those seen in normal brain development. These misplaced cells may go on to make abnormal connections later in life, potentially accounting for the behavioural symptoms seen in individuals with autism.

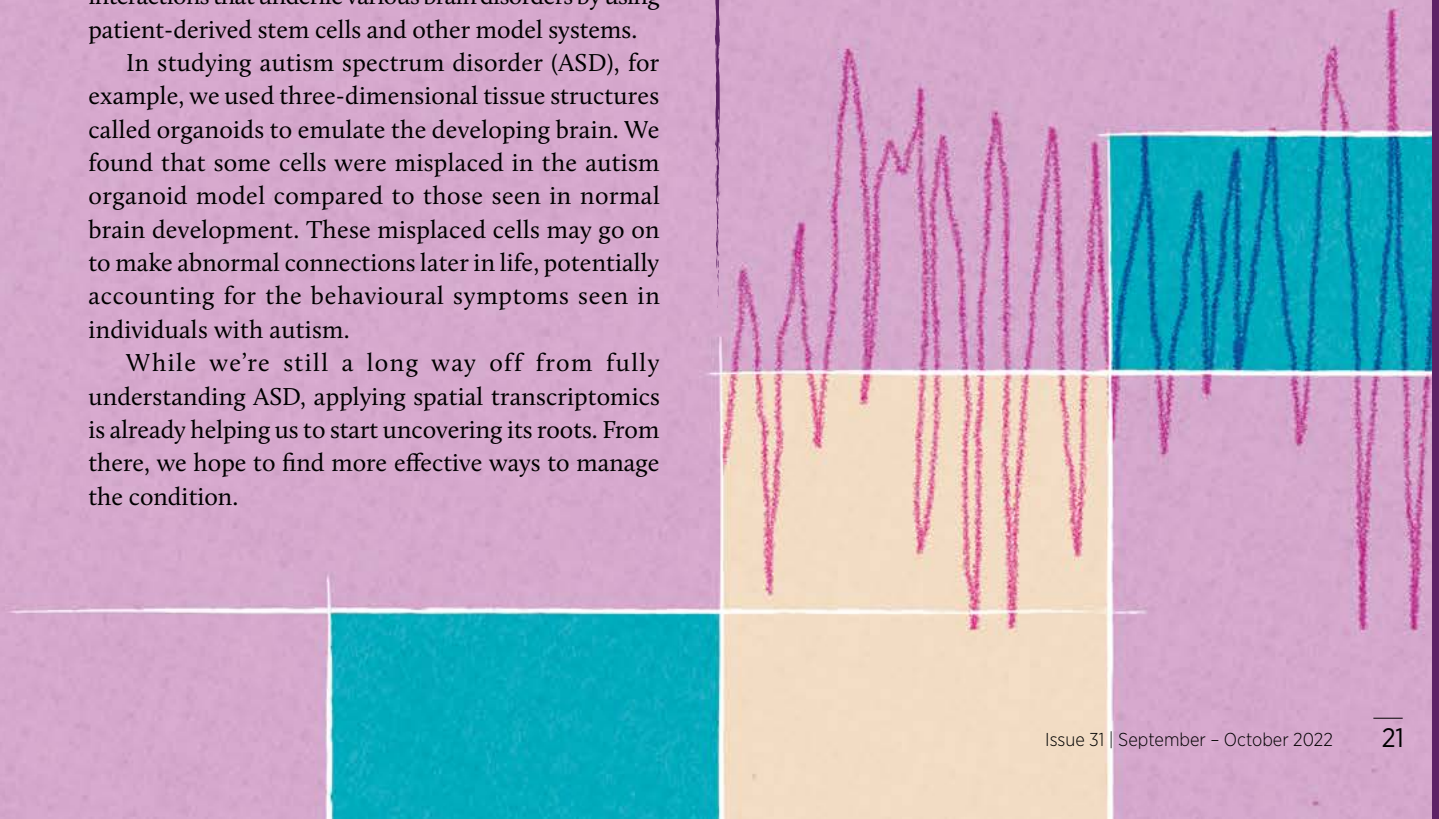
While we're still a long way off from fully understanding ASD, applying spatial transcriptomics is already helping us to start uncovering its roots. From there, we hope to find more effective ways to manage the condition.

Q: HOW HAS A*STAR SUPPORTED YOUR DEVELOPMENT AS A PRINCIPAL INVESTIGATOR?

A*STAR has equipped us with the resources and a talented team to make exciting research happen. At GIS, we have a strong core of diverse scientists who are investigating DNA and RNA to address human diseases. Such an environment truly facilitates interdisciplinary and impactful research. Moreover, A*STAR has provided a home for building my laboratory. Pursuing research is no doubt challenging, but I feel very fortunate to have the space to develop my lab, pursue my scientific interests and nurture my team.

Q: WHAT ADVICE WOULD YOU SHARE WITH YOUNGER COLLEAGUES ON PURSUING RESEARCH?

Be clear about your motivations for pursuing research. It is a long journey, and you will need a lot of perseverance. Science is constantly evolving, so it's important to keep up with the latest discoveries to stay inspired and relevant. Invest in teamwork, as research is a collaborative activity. Learn to see the big picture, and stay open-minded and curious. That way, we'll be able to see the next step before it unfolds, and be the ones to drive science forward. ★



MACHINE LEARNING

The catalyst cookbook

A purpose-built machine learning platform takes the guesswork out of catalyst formulations for green energy generation.

Catalyst chemistry is a lot like cooking in a fine dining kitchen. Just as chefs spend hours adjusting recipes for palate perfection, chemists likewise spend time painstakingly tweaking catalysts (chemical reaction boosters) for optimal results.

"Figuring out an optimised catalyst is a formidable task when there's a vast space of possibilities to explore," said Joyjit Chattoraj, a Research Scientist from A*STAR's Institute of High Performance Computing (IHPC). "You need to play around with a wide array of parameters, ranging from preparation methods and operating conditions, to the presence and concentration of base and promoter metals."

The good news is that catalyst chemists now have a secret weapon in their kitchens: machine learning, or ML. Through ML, computational models can help automate the trial-and-error nature of catalyst optimisation, which Chattoraj said speeds things up tremendously.

However, existing ML models are only as good as the data they're trained with. Just as even a good kitchen appliance with bad ingredients makes poor dishes, a good ML model with bad data makes bad predictions. For example, without incorporating a basic knowledge of physics, some of today's purely data-driven models sometimes start bending the laws of thermodynamics by predicting catalytic conversion efficiencies over 100 percent.

To figure out a model with more realistic predictions, Chattoraj and Teck Leong Tan led a team of A*STAR scientists from IHPC and collaborators from the Institute of Sustainability for Chemical, Energy and Environment (ISCE^2) who aim to build better ML frameworks for hydrogen fuel technology, a greener energy alternative to fossil fuels.

The team focused on ML-driven catalyst optimisation for the water-gas shift (WGS) reaction, a key process that eliminates toxic carbon monoxide (CO) produced from hydrogen fuel cells.

They started with a cleanup of an open-source WGS dataset used in previous models to ensure all data points in it adhered to chemical reaction principles. Next, they added physical and chemical data tags (known as 'fingerprints') to the dataset to facilitate new catalyst discovery. They leveraged this spruced-up data to develop a new-and-improved, physics-guided ML framework more likely to obey the laws of thermodynamics.

"Our state-of-the-art model can establish complex relationships between catalyst synthesis parameters through forward modelling: a training process more accurate and reliable than its conventional counterparts in predicting CO conversion," said Chattoraj. "This paves the way for reliable inverse modelling, allowing us to search for potential catalyst candidates based on optimal compositions and reaction conditions."

With this ML-powered catalyst cookbook under their belts, the researchers are now working on applying their model to discover next-generation WGS catalysts that stay effective even at low reaction temperatures, which could benefit many industries with stakes in fuel cell technology.

Again, getting the ingredients right is part of the challenge; the current training dataset for their model has limited experimental data on low-temperature reactions, said Chattoraj. "Overcoming this would require more data and a better understanding of how catalyst properties affect CO conversion, which will only be possible if knowledge is shared across different research domains." ★

Researchers
Joyjit Chattoraj, Luwei Chen and Teck Leong Tan,
IHPC

IN BRIEF
With cleaner reaction data, improved data structure and added physics-based guidance, a new ML framework could uncover better catalysts for removing toxic CO from hydrogen fuel systems.

1. Chattoraj, J., Hamadicharef, B., Kong, J.F., Pargi, M.K., Zeng, Y., *et al.* Theory-Guided Machine Learning to Predict the Performance of Noble Metal Catalysts in the Water-Gas Shift Reaction. *ChemCatChem* **14** (16), e202200355 (2022).

Photo credit: Rafael Classen rcphotostock.com / Pexels

BIOINFORMATICS

Digital crystal ball flags problematic proteins

A user-friendly online computational platform helps researchers scour complex datasets to predict how likely food proteins are to trigger allergic reactions.

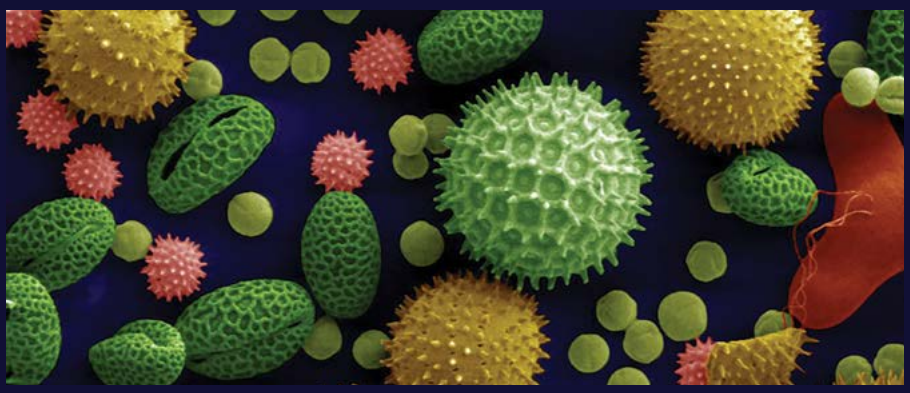


Photo credit: Image Catalog / Flickr

Making sense of big data can empower us to 'look' into the future. Take the weather app on your phone, for instance; it forecasts rainy days based on atmospheric patterns, historical weather trends and real-time meteorological data.

Similarly, scientists have been working on a 'weather app' to forecast protein allergens: substances in everyday foods and other consumables that might, in an unlucky minority of people, cause immune system flare-ups. Also known as allergic reactions, these flare-ups can range from mild but irritating rashes to life-threatening breathing problems.

Whether you're a food producer, regulator or consumer, having access to tools to predict a protein's allergenicity—how likely it is to trigger a bad immune response—would be hugely beneficial. Existing computational platforms for mapping and predicting allergenicity are, however, notoriously unreliable, with estimated accuracy levels between 51 to 73 percent at best.

According to Sebastian Maurer-Stroh, Deputy Executive Director at A*STAR's Bioinformatics Institute (BII), data is the key to bumping up the dependability of these predictive platforms. With that in mind, Maurer-Stroh and colleagues built AllerCatPro 2.0, a computational platform that may set a new gold standard for allergenicity prediction.

"AllerCatPro 2.0 predicts a protein's allergenic potential based on the most comprehensive international databases of proteins reliably associated with allergenicity," said Maurer-Stroh, listing examples such as the WHO/International Union of Immunological Societies (WHO/IUIS) and the Comprehensive Protein Allergen Resource (COMPARE).

What sets the platform apart from its predecessors is its ability to crunch data from large, multidimensional datasets that include amino acid sequences and 3D protein structures, thereby boosting its accuracy when pinpointing potentially problematic proteins.

In their study, the international team of researchers deployed AllerCatPro 2.0 to compile a list of nearly 5,000 known protein allergens, including 165 human proteins with links to autoimmune diseases. They also identified 162 safer protein options with low allergenic scores. When tested, AllerCatPro 2.0 significantly outperformed other benchmark platforms in terms of reliability, scoring an impressive 84 percent accuracy.

"AllerCatPro 2.0 can be used as the first step in food safety assessments to find potential new allergens that might warrant further evaluation," explained Maurer-Stroh, adding that the team is working with industry collaborators to continually update the platform as new allergens are identified.

Usability was also a priority in designing the platform, which is currently freely accessible as a web server. "We created a user-friendly interface with updated features that provides detailed results on potential cross-reactivity, protein information, functionality, clinical relevance and information relating to similar allergens," Maurer-Stroh said.

The team is currently expanding the platform's capabilities for detecting allergens in specific fish species, and is also working together with academic and industrial collaborators on a project to assess food safety risks in Singapore's urban aquaculture industry. ★

Researcher
Sebastian Maurer-Stroh, BII

IN BRIEF
Researchers created AllerCatPro 2.0, a web server that can predict a protein's potential allergenicity with more accuracy and detail than existing computational platforms.

1. Nguyen, M.N., Krutz, N.L., Limviphuvadh, V., Lopata, A.L., Gerberick, G.F., *et al.* AllerCatPro 2.0: a web server for predicting protein allergenicity potential. *Nucleic Acids Research* **50** (W1), W36-W43 (2022).

SUSTAINABILITY

Breathing new life into e-waste

Researchers identify an easy-to-recycle plastic alternative for use in electronics, making strides towards a circular economy.

Whenever eyes are glued to the latest release of a sparkly new feature-heavy gadget, much less thought is given to the fate of our old, soon-to-be-replaced electronic devices. Unfortunately, the vast majority of Singapore's electronic waste (or e-waste) is destined for the landfill, where their slowly degrading plastic components wreak environmental havoc.

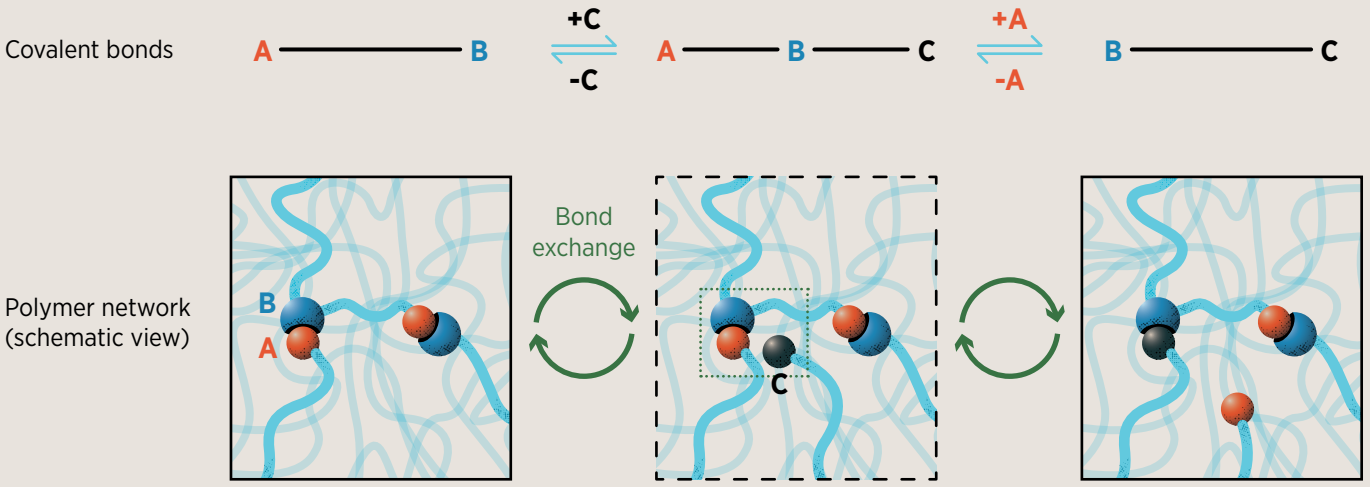
"In Singapore, about 60,000 tons of e-waste are produced every year—but only a mere six percent is recycled," said Jie Zheng, a Research Scientist at A*STAR's Institute of Sustainability for Chemicals, Energy and Environment (ISCE²).

Zheng says plastic components within electronics' inner workings are to blame for this troubling statistic. "Metal components in electronics are typically bound to strong, durable and chemically resistant plastics called thermosets, which makes them extremely difficult to separate for recycling."

Swapping out these 'bad' plastics for more sustainable alternatives could move e-waste out of landfills and back onto production lines. With this in mind, Zheng led a collaborative endeavour with researchers from the National University of Singapore (NUS) and Nanyang Technological University (NTU) to focus on finding greener plastics for use in one of the most common applications for thermosets—thermoelectric generators (TEGs).

TEGs scavenge heat to generate electricity and have protruding metal structures, called 'legs', that bridge the electrical flow between components. Traditionally, legs are insulated by thermosets which are difficult to strip from

Photo credit: Pixabay / Pexels



Vitrimers are networks of crosslinked plastic polymers. These links (covalent bonds) are dynamically associated, allowing them to be reversibly broken and reformed under heat, light, chemicals or other external stimuli.

the underlying metal, making recycling highly inefficient.

Zheng and colleagues saw a solution in a different class of plastics called vitrimers. These polymers are not only easy to recycle, but also remarkably strong and flexible, so as not to compromise on functionality when replacing thermosets.

"Vitrimers owe their flexibility to their inherent chemical structure, which contains dynamic covalent polymer networks (DCPNs)," explained Zheng. "Such networks can be decomposed on demand when subjected to an external stimulus such as heat or the presence of chemicals; they're living, reprogrammable and self-healing."

To test their theory, the researchers simulated e-waste recycling by submerging vitrimer-encapsulated TEGs into warm solvents. As anticipated, the plastic coating on the component's legs melted away with ease, revealing electrical components that can be further reprocessed and reused.

Next, the researchers used the recycled components to build a new TEG from scratch, which excitingly, performed as well as its parent device, further validating the reliability of their technique.

Zheng said these results demonstrate how vitrimers could spark a circular economy in the electronics industry. Recyclable thermoelectric devices are just the start—vitrimers could also be used in everything from cooling components to powering electronic screens.

"Such networks can be decomposed on demand when subjected to an external stimulus such as heat or the presence of chemicals; they're living, reprogrammable and self-healing."

Moving forward, Zheng plans to grow the green polymer toolkit further, with more diverse options for sustainable electronics. "For instance, some materials which contain light-sensitive polymer networks can be degraded by simply exposing them to light, which initiates the recycling process," said Zheng. ★

Researchers
Jie Zheng, Zibiao Li and Ady Suwardi, ISCE² and IMRE

IN BRIEF
Recyclable vitrimers used in place of conventional plastics can be easily melted away from metal components without compromising on device performance.

1. Zheng, J., Solco, S.F.D., Wong, C.J.E., Sia, S.A., Tan, X.Y., *et al*. Integrating recyclable polymers into thermoelectric devices for green electronics. *Journal of Materials Chemistry A* **10**, 19787-19796 (2022).

ARTIFICIAL INTELLIGENCE

Giving handheld devices a computing edge

A new compression method developed at A*STAR shrinks energy and hardware requirements for complex computational platforms on everyday devices.

When it comes to computing, size matters. Hardware dimensions typically line up with computers' capabilities, with big tasks in artificial intelligence (AI) such as machine learning algorithms usually needing more extensive and bulky computing servers. However, emerging technologies could one day put supercomputing in the palms of our hands; specifically, through our edge devices.

Ranging from our smartphones to internet-enabled home appliances, edge devices are devices that can act as interfaces between networks and the real world to collect and communicate information, said Zhehui Wang, a Research Scientist at A*STAR's Institute of High Performance Computing (IHPC).

Edge devices have the potential to run sophisticated computing functions such as convolutional neural networks (CNNs), but their small batteries and consumer-level hardware can hold them back.

"If they're running 'energy-hungry' computing processes like those involved in traditional CNNs, they'll run out of power quickly," explained Tao Luo, a fellow Research Scientist at IHPC, whose team works on innovative approaches towards small but mighty next-generation edge devices.

Wang, Luo and colleagues developed EDCompress, a CNN model compressor that adapts and optimises CNN processes to be more energy efficient when used in compact, battery-powered hardware. "Think of it as creating a zipped file on your computer," said Wang. "EDCompress analyses the hardware features of the device running the CNN model, and shrinks the model's architecture and energy requirements to suit."

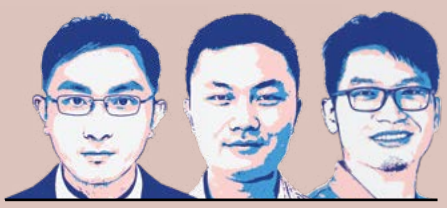
Using reinforcement learning techniques—similar to how a chess AI is 'taught' optimal strategies by playing thousands of games—Luo's group designed EDCompress to find the best combination of quantisation (making data values less precise) and pruning (removing less important parameters) that would speed up CNN processes, reduce energy consumption and still generate reasonably accurate and precise results.

"CNNs are well-suited for tasks such as classifying, detecting and segmenting images and objects. If edge devices could run CNNs on their own, they could do these tasks offline, without relying on a back-and-forth with external networks," Wang added. "This would improve data privacy, reduce server workloads and speed up data processing."

Validation experiments using EDCompress on three existing CNN architectures proved successful, with the team demonstrating remarkable energy efficiency boosts with only a negligible accuracy loss. They found that EDCompress was 17 to 26 times more energy-efficient and was intuitive, automatically picking the optimal dataflow to conserve energy consumption.

"With EDCompress, we can reach lower latencies that let applications run closer to real-time on edge devices while lowering energy and hardware costs," commented Luo. "There's a wide range of possibilities to explore. Imagine a smartwatch that could monitor your heart without needing frequent recharging, or a smartphone that could identify objects in real-time."

Applications that demand more intelligence, computing power and advanced services at the network edge, such as medical wearables, could benefit greatly from EDCompress' capabilities. Wang added that EDCompress also contributes to a 'green AI' future, driving down carbon emissions associated with advanced computing. The team hopes to collaborate with other research institutes and external partners to further develop its application in real-use spaces. ★



Researchers
Zhehui Wang, Tao Luo and Joey Tianyi Zhou,
IHPC

IN BRIEF
EDCompress makes convolutional neural networks more energy efficient, enabling small, battery-powered edge devices to use powerful computing abilities without relying on large central computers.

1. Wang, Z., Luo, T., Goh, R.S.M. and Zhou, J.T. EDCompress: Energy-Aware Model Compression for Dataflows. *IEEE Transactions on Neural Networks and Learning Systems* 1-13 (2022).

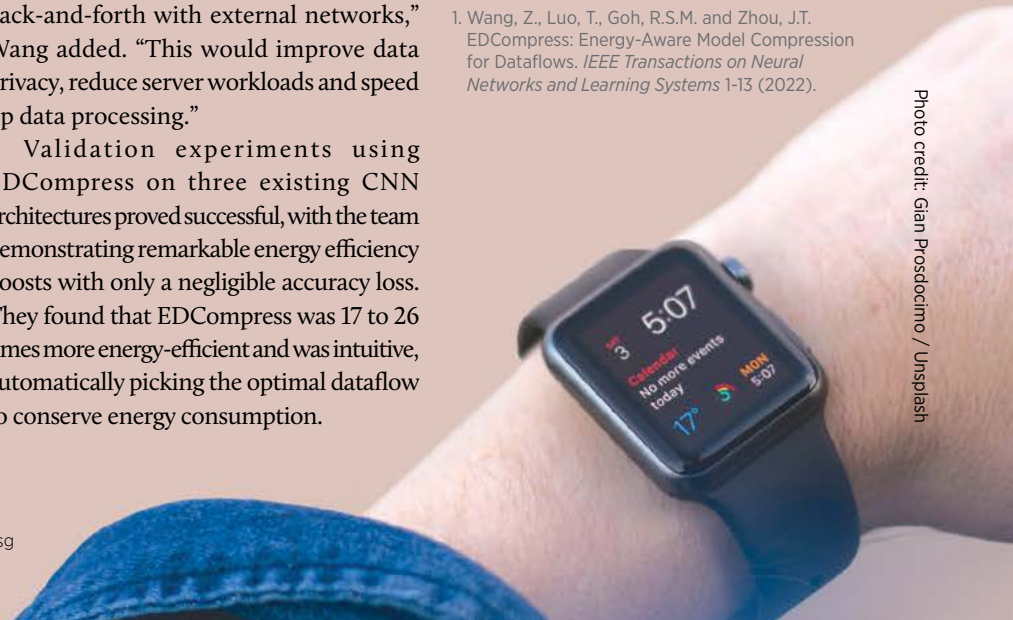


Photo credit: Gian Prosdocimo / Unsplash

MODELLING AND SIMULATION

A stepping stone to a quantum future

A*STAR researchers develop a first-of-its-kind quantum algorithm that co-opts classical computers to solve complex engineering problems.

We're at an exhilarating point in the Silicon Age, where computers seem to have the answers for everything from the mysteries of the human genome to starting colonies on faraway planets. However, the evolution of computing hardware still lags behind the evolution of our data needs; while researchers have crafted equations that could answer more complex questions, today's computers may struggle to process them.

For computer scientists, quantum computers may be the answer. Where classical computing uses a binary system of ones and zeroes to encode information in units called bits, quantum computing uses subatomic particles such as electrons or photons, which can exist in multiple states at the same time. The result? Computing power in quantum units, or qubits, that (at least in theory) can effortlessly solve large-scale calculations that would take classical computers millions of years.

However, currently available quantum computers are still difficult to use for real-world engineering problems such as simulating electromagnetism, explained Wei-Bin Ewe, a Senior Researcher from A*STAR's Institute of High Performance Computing (IHPC). For one, slight environmental changes can affect the hardware, causing 'noise' or calculation errors; for another, today's most advanced machines still only contain a relatively low number of qubits.

One solution may be cloud-based variational quantum algorithms (VQAs); hybrid techniques that pair up classical and quantum computers, splitting the computing work to either machine based on what either does best.

To investigate their potential, Ewe and his team designed a VQA based on a quantum linear system algorithm (QLSA) to simulate electromagnetic waves travelling through a metallic waveguide. Such wave problems are regularly tackled by engineers as an integral part of designing microwave circuits—key components in telecommunications devices ranging from radars to radios.

"QLSAs can solve linear equations faster and represent N data using $\log(N)$ qubits, both of which speed up the solving of large electromagnetic problems," commented Ewe.

In their study, the team first broke down a waveguide into grids of tiny cells before they computed the possible frequencies of electric and magnetic waves across all cells with VQAs. To reduce the amount of quantum processing power required, the grid was decomposed further into smaller tables.

With this new approach, the researchers were able to reproduce results derived from hybrid quantum-classical algorithms more efficiently, with minimal quantum resources required. Ewe said that this demonstrates the almost limitless potential VQAs could have in the industry. "It is the first VQA to solve such problems and could be adapted to other problems in engineering," explained Ewe.

However, technical barriers remain to its commercial applications. The team is working on noise mitigation schemes to enhance VQA accuracy while searching for other problems in electronics and photonics that could benefit from VQAs. "I hope that the ideas from our work will inspire more research in the use of VQAs to solve real-world problems," Ewe said.★

"It is the first variational quantum algorithm to solve such problems and could be adapted to other problems in engineering."

Researcher
Wei-Bin Ewe, IHPC

IN BRIEF
By combining quantum and classical computing capabilities, Variational Quantum Algorithms (VQAs) might help overcome the constraints of current-generation quantum machines, bringing them a step closer to real-world applications.

1. Ewe, W.-B., Koh, D.E., Goh, S.T., Chu, H.-S. and Png, C.E. Variational Quantum-Based Simulation of Waveguide Modes. *IEEE Transactions on Microwave Theory and Techniques* **70** (5), 2517-2525 (2022).

Photo credit: Bartlomiej K. Wroblewski / Shutterstock

MAKING THE MOST OUT OF MEDTECH

To fully realise the potential of medical technology, A*STAR scholar Daryl Jude Lawrence explains why scientists should move beyond the lab and experience the inner workings of industry-level production and entrepreneurship.

When someone mentions they are a scientist, one might picture the stereotype of a reclusive genius who spends long days and nights in a lab by themselves, pouring all their time and energy into a niche, narrow field of expertise.

However, science isn't just about conducting experiments and publishing papers. Researchers are now more aware of and involved in the process of translating their research from the lab bench into real-world applications that highly benefit the public.

This is especially important for more application-oriented fields like medical technology, or medtech, where new technologies, no matter how innovative or groundbreaking the research behind them may be, will not achieve their true potential unless they reach their intended users in the real world.

For A*STAR scholar Daryl Jude Lawrence, this lesson came to him during his undergraduate years at Imperial College London in the UK. While wrapping up his degree in materials science and engineering, he realised that his research project—a graphene-based device that screens for cancer by detecting tiny particles secreted from cells—could very well languish in libraries and in the pages of scientific journals.

To translate his diagnostic device from concept to technology, Lawrence understood that he would need to progress from proof-of-concept studies into the clinic. There were practical barriers, too: how would he mass-produce the device? Where would the materials come from? Could he convince hospitals to begin using his device on patients? Who would fund this venture?

Lawrence has since moved on from his graphene project, but these questions continue to guide him through his career as he works toward a PhD degree at the University of California (UC) Berkeley, US.

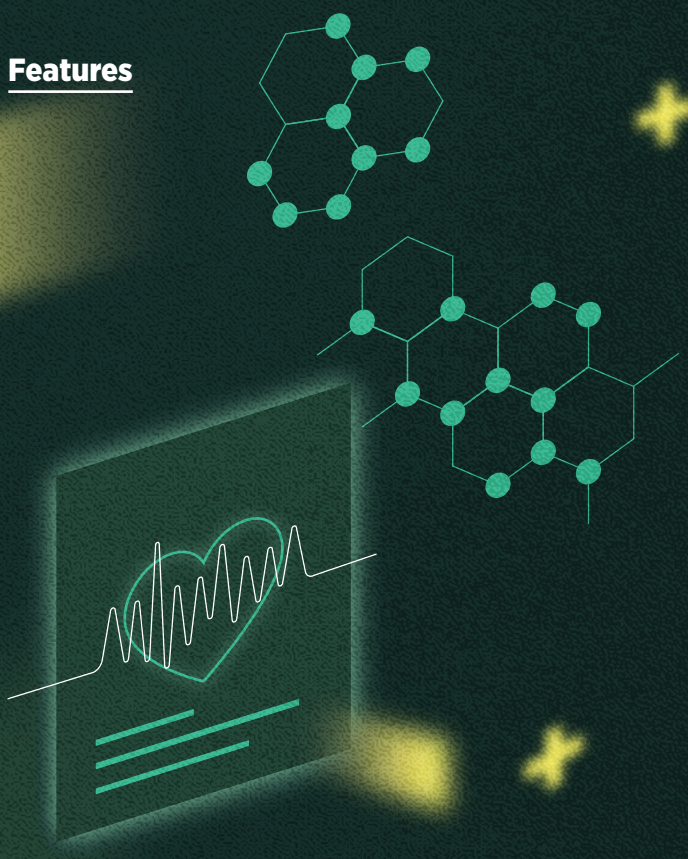
In this interview with *A*STAR Research*, Lawrence looks back on the moment when it all began and shares his journey to becoming a scientist-entrepreneur.

Q: WHAT INSPIRED YOU TO APPLY FOR THE A*STAR SCHOLARSHIP?

I've always been interested in math and science. In my fourth year at NUS High School, I joined a friend's team for a programme that allowed us to conduct research projects in a research lab. We worked in a Materials Science lab at Republic Polytechnic and got to fabricate our own thin films—I loved it! Despite our limited knowledge, we had a say in the trajectory of the research project which was very exciting for me as a secondary school student.

At the end of the project, we still had many ideas to try, so we reached out to as many labs as we could find online. Many rejections later, we received an acceptance email from a lab at Nanyang Technological University (NTU), and we were off to the races.

I was captivated by the entire process of relentless iteration for innovation. I also enjoyed sharing my results and new ideas with fellow researchers at conferences and research fairs. Motivated by this experience, it was an easy decision to apply for the A*STAR scholarship.



Q: WHAT LED YOU FROM MATERIALS SCIENCE TO MEDTECH?

Having been exposed to research projects in the lab, I decided to pursue a degree in Materials Science and Engineering at Imperial College London. This was a major change as I'd been living in Singapore my whole life. It was especially difficult when a close family member passed away while I was overseas. It gave me an added drive to make the most of my time in the UK and inspired me to delve into medtech.

During the final year of my studies, I had the opportunity to work on graphene electrodes for the detection of exosomal biomarkers of disease. This was my first foray into the exciting world of medical diagnostics.

After graduating, I wanted to learn more about commercialisation, and my subsequent attachment at A*STAR's Institute of Bioengineering and Bioimaging (IBB) provided the perfect opportunity to do so. I collaborated with researchers at the National University of Singapore (NUS) to develop market reviews, business models and pitch decks for a novel biophotonic sensor developed by IBB.

I learned how to switch between a research and business-development mindset. The ability to find connections between consumer needs and technology deliverables has proven to be a very useful skill.

Q: HOW DID YOUR TIME AS A PROJECT MANAGER AT A*STAR SHAPE YOUR VIEWS ON MEDTECH INNOVATION AND DEVELOPMENT?

Initially, I was supposed to begin my PhD studies after my stint at IBB. However, due to the severity of the pandemic at the time, coupled with visa and other logistical issues, I decided to defer my studies for a year.

This turned out to be a blessing in disguise as I was able to join the incredible team at the Diagnostics Development Hub (DxD Hub). I worked on quality assurance and regulatory approval processes, which are crucial for bringing medical devices to market.

That experience gave me insights into the actual behind-the-scenes work in ensuring a product goes from concept to market-ready. It also deepened my knowledge of the inner workings of industry-level production and opened my eyes to the many processes needed to ensure a product meets the quality and safety standards set by regulatory bodies for consumer use.

Q: COULD YOU TELL US MORE ABOUT YOUR CURRENT RESEARCH FOCUS AS A PHD CANDIDATE?

My PhD work is a unique blend of machine learning (ML), signal processing, neuroscience and clinical logistics. Along with an incredible team of surgeons, clinicians, engineers and neuroscientists at UC Berkeley and UC San Francisco, I am developing a closed-loop system that can stimulate the brain only when it needs to.

This technology will be particularly relevant to patients with Parkinson's disease, who are typically implanted with 'neural pacemakers' to control symptoms such as tremors or dyskinesia. While these devices are effective, the constant and continuous amount of deep brain stimulation that is typically administered can result in negative side effects. In contrast, my work involves developing ML models that only activate stimulation when necessary.

The team and I are also implementing new ways to make this new technology more accessible in lower-resource settings through wearable devices and telehealth.

"New technologies must be validated by clinicians and certified as compliant in addition to providing quantifiable clinical benefits."

— Daryl Jude Lawrence, A*STAR National Science Scholarship recipient

Q: WHAT ARE YOUR PLANS AFTER COMPLETING YOUR PHD?

I love the idea of using simple devices to assess complex medical conditions. For example, sensor 'patches' over the stomach are being used to assess gastrointestinal conditions while watches can non-invasively measure blood glucose levels. I'm passionate about using advanced sensors with ML models to attain a more holistic view of consumer health.

Medtech innovation, however, is a multi-faceted endeavour as there are many moving parts. New technologies must be validated by clinicians and certified as compliant in addition to providing quantifiable clinical benefits.

I'm also learning how these systems work in the San Francisco Bay Area so that I can find potential solutions that may apply to Singapore.

Q: CAN YOU SHARE SOME ADVICE WITH ASPIRING A*STAR SCHOLARS?

Be open to new opportunities. It can be daunting to explore a new field or to switch fields altogether, but the change will be worth it if that's where your passion lies. My suggestion is to do an honest review of the boundaries of your knowledge in areas you feel are relevant. Then, fill in those gaps at your own pace. ★

MATERIALS SCIENCE

Making metasurfaces

A new hybrid metasurface created by researchers opens doors to exciting new aerospace, defence and biomedical optical applications.

A scene from a sci-fi movie plays out—the hero dons their invisibility cloak just in time to escape the clutches of a fast-approaching villain. Believe it or not, materials with the invisibility cloak's optical properties aren't just the stuff of movies.

Metamaterials are specially engineered structures that defy the natural laws of physics, giving them unique optical properties such as 'invisibility'. Their surfaces are made of nanostructures smaller than the wavelength of light, which allow them to bounce inbound light waves off much like a mirror's reflection.

Metamaterials are being used in some real-world applications in the aerospace and defence industries, although experts say manufacturing challenges limit their potential in other spheres. "A wider range of applications can be realised if more design dimensions are provided from material and fabrication perspectives to allow dynamic control of light," explained Hong Liu, Head of the Nanofabrication Department at the Institute of Materials Research and Engineering (IMRE).

"Through the hybrid design of nanopatterning the PCMs on top of the silicon metasurfaces, we created a single device that is tunable and multifunctional."

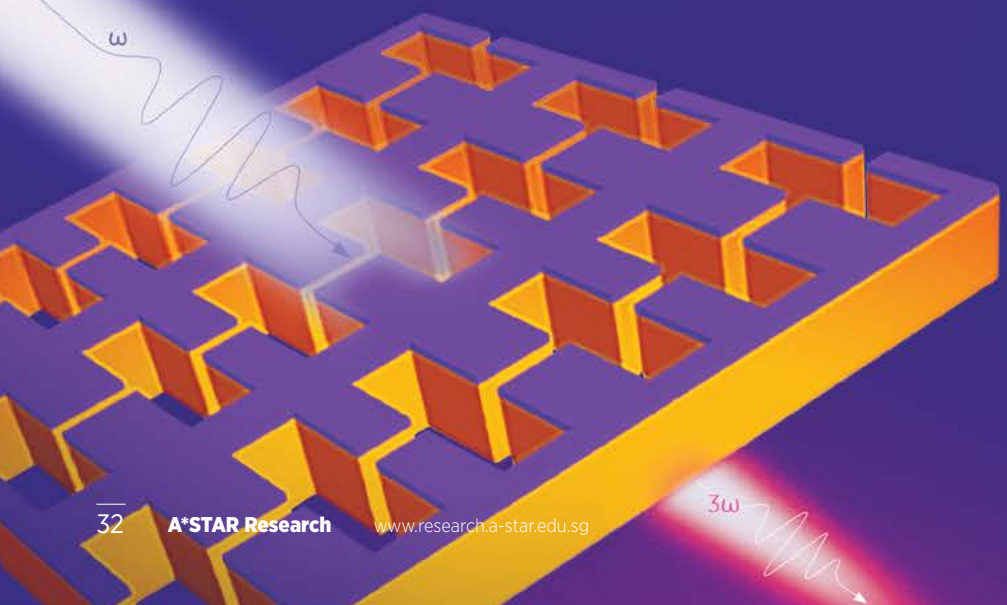
Liu co-led a collaborative effort with researchers from Nanyang Technological University to overcome these hurdles by creating a next-generation class of high-efficiency, tunable metasurfaces. The researchers combined metamaterials principles with optical phase-change materials (PCM)—a group of materials that possess large changes in optical properties—to create a hybrid silicon metasurface.

"We incorporated PCMs such as germanium-antimony-tellurium (GST), which can rapidly switch its state from amorphous to crystalline when heated, offering a precise approach to control its light emission," added Liu. "Through the hybrid design of nanopatterning the PCMs on top of the silicon metasurfaces, we created a single device that is tunable and multifunctional."

Liu added that silicon was specially selected as it offers strong light-matter interaction, which enables highly efficient third-harmonic generation, an optical phenomenon where light hitting the metasurface can be manipulated.

The researchers further refined their innovation by optimising the GST layer's thickness, a key step in mitigating the material's optical losses. Their optimal device design was found to be 32 times more efficient than reported metasurfaces, paving the way for many advanced applications in quantum photonics, spectrometry and lasers.

Liu's team has plans to continue developing their hybrid metasurface by focusing on a reversible tuning strategy, a novel technique that could enable powerful nanophotonic devices with unprecedented light emission and control. "We are also seeking funding support to develop these hybrid metasurfaces for ultraviolet light applications, as the current state of the technology hinders its practical usage," Liu said. ★



Researcher
Hong Liu,
IMRE

IN BRIEF
Silicon-GST metasurfaces could produce stronger, more efficient and controllable light emissions for advanced nanophotonic devices.

1. Abdelraouf, O.A.M., Anthur, A.P., Dong, Z., Liu, H., Wang, Q., *et al.* Multistate Tuning of Third Harmonic Generation in Fano-Resonant Hybrid Dielectric Metasurfaces. *Advanced Functional Materials* **31** (48), 2104627 (2021).

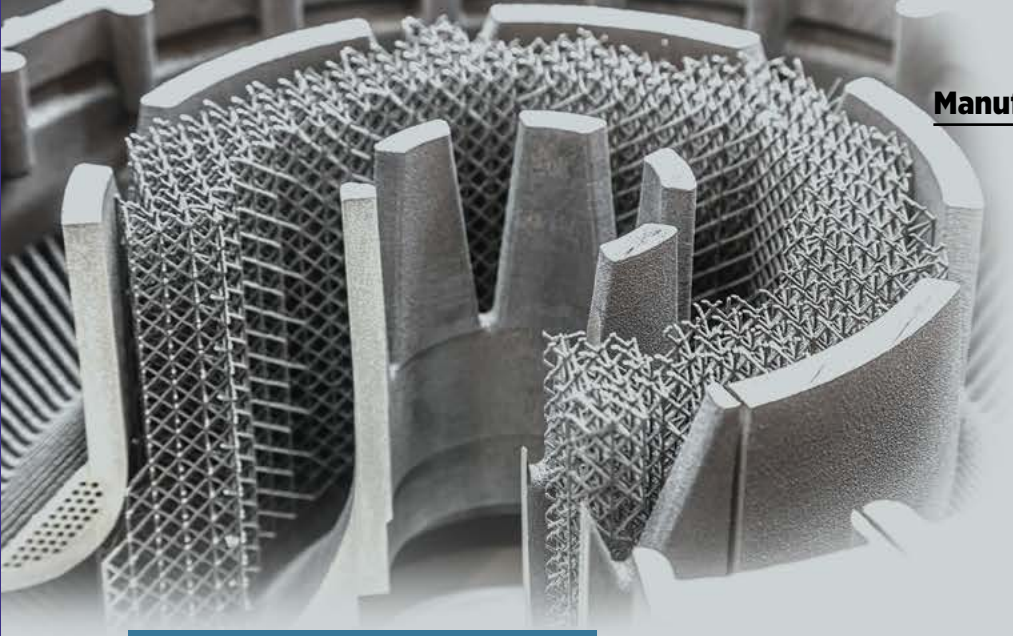


Photo credit: OlegDoroshin / Shutterstock

ADDITIVE MANUFACTURING

Ironing out kinks for laser-sharp precision

An algorithm inspired by nature guides metal-depositing lasers for faster, more precise component manufacturing.

The forging of metals into weapons, jewellery and utensils is one of the oldest trades in human civilisation. Archaeological evidence suggests that skilled blacksmiths have been heating metals and hammering them into their desired shapes for thousands of years.

Today, lasers have replaced hammers. With laser-aided additive manufacturing (LAAM), layers of metal powders are melted and deposited by a high-energy laser beam, fabricating intricate shapes such as medical implants or aerospace components with unprecedented speed and precision.

Compared to traditional top-down manufacturing approaches, lasers in the LAAM process deposit metals from the bottom up by following manually guided routes called toolpaths. These toolpaths can range from simple parallel lines to more complicated contours that fill each layer in puzzle-like segments. However, common infill toolpath strategies often don't fully account for geometrical kinks that may happen in the fabrication process.

"With complicated geometrical shapes, current LAAM approaches tend to form undesirable bead and track features such as voids—awkward regions too narrow to fit another path in, leaving an irregular gap," explained Youxiang Chew, a Research Scientist at the Singapore Institute of Manufacturing Technology (SIMTech). "These flaws give rise to defects that can degrade the mechanical performance of the final product."

For engineers, planning and testing more efficient paths can be time-consuming and tedious. In response, Chew collaborated with fellow researchers Ning Liu from the Advanced Remanufacturing and Technology Centre (ARTC) and Yunfeng Zhang from the National University of Singapore (NUS) to develop an advanced algorithm that would help automate the planning process.

The team's new technique builds on previous path-planning approaches by using artificial intelligence (AI) to streamline the segmentation process. A genetic evolutional algorithm—a framework inspired by Darwin's Theory of Evolution—automatically divides the blueprint for a target object into multiple optimised sections. This approach allows the laser to deposit metal in the most efficient way possible while minimising void formation.

"We based our approach on a genetic algorithm as it is more capable of 'looking at the big picture' to search for high-quality solutions to a complex problem like path-planning in LAAM," said Liu.

The team found that the new algorithm was 90 percent faster than the current best approaches and produced consistently high-quality metal parts at higher deposition efficiency rates. These could translate to a significant reduction in LAAM operating and labour costs, making the technology more viable in other applications such as repair, remanufacturing and 3D printing.

The researchers are currently exploring how other AI techniques such as deep learning could further optimise the segmentation process. "These 'learn-to-optimise' techniques could provide near real-time optimisation results to improve the evolutional algorithm currently used," concluded Chew. ★

Researchers
Youxiang Chew and Ning Liu, SIMTech

IN BRIEF
A genetic algorithm helps automate and optimise path-planning in laser-aided additive manufacturing, improving product quality, process efficiency and overall costs.

1. Liu, N., Ren, K., Zhang, W., Zhang, Y.F., Chew, Y.X., *et al.* An evolutional algorithm for automatic 2D layer segmentation in laser-aided additive manufacturing. *Additive Manufacturing* **47**, 102342 (2021).

SURFACES AND INTERFACES

Nanofluids draw more oil from stone

Researchers show how small amounts of nanoparticles can significantly boost crude oil extraction from rocks.

It's tough to wean the world off its reliance on fossil fuels. Despite the global push towards cleaner, sustainable energy sources, estimates point to the current demand of 100 million barrels of oil per day. Moreover, green economies still need fossil fuels—they're used as building blocks for other materials such as plastics.

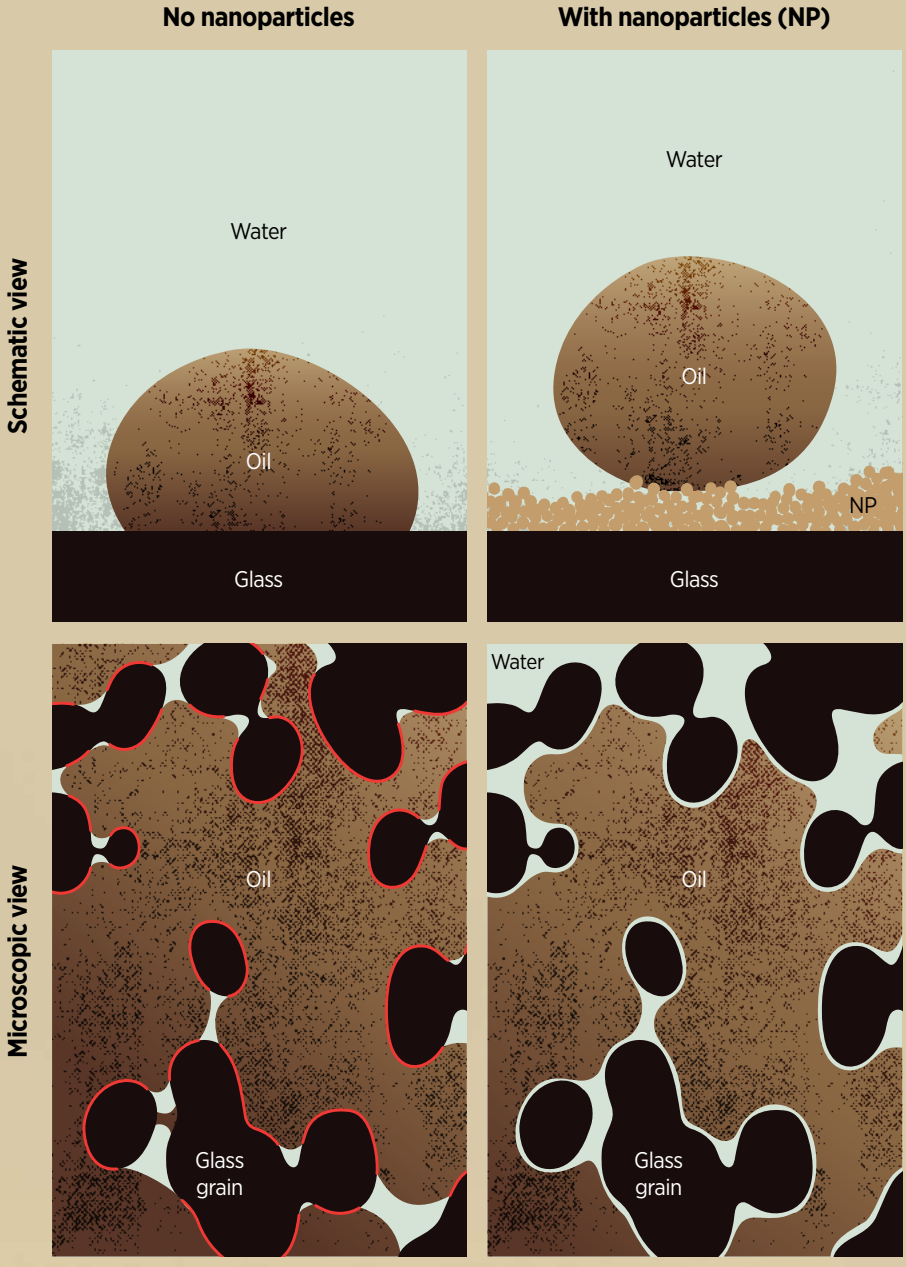
Where there's room for improvement, however, is in the crude oil extraction process. "Being able to extract 20 percent more oil from oil reservoirs worldwide will translate to billions of barrels of oil," said Dan Daniel, a Research Scientist at A*STAR's Institute of Materials Research and Engineering (IMRE).

"Just as detergent molecules allow us to dislodge dirt and oil from our clothes, nanoparticles greatly reduce adhesion of oil to rocks, allowing us to extract oil from the rock network more easily."

Recent advances in nanotechnology have created a buzz in the field, with nanoparticles hypothesised as being a viable means of drawing out more oil trapped within porous rocks. Suspensions of silica nanoparticles, also known as nanofluids, are thought to alter the wettability of oil reservoirs, thereby enhancing the oil recovery process. However, until now, there has been no robust way of measuring just how much nanofluids help.

Researchers from IMRE and A*STAR's Institute of Sustainability for Chemicals, Energy and Environment (ISCE^2) dove deeper into this topic using innovative visualisation approaches. Besides Daniel, the team included Shidong Li, a Research Scientist with the then-Institute of Chemical and Engineering Sciences at A*STAR, and Ludger Paul Stubbs, formerly of ISCE^2 and now a Senior Research Scientist at A*STAR's Singapore Institute of Food and Biotechnology Innovation (SIFBI).

Photo credit: wirestock / Freepik



Silica nanofluids reduced the contact area between oil droplets and simulated rock (etched glass) by forming a thin film of nanoparticles (NP) and water between the two surfaces.

The researchers used an array of microscopy techniques to visualise and quantify the effects of nanofluids in oil extraction simulations. They found that adding even trace amounts of nanoparticles to oil droplets improved the surface wettability and reduced the adhesion of oil to rocks by over 400 times.

Daniel likens these effects to doing a load of laundry. "Just as detergent molecules allow us to dislodge dirt and oil from our clothes, nanoparticles greatly reduce adhesion of oil to rocks, allowing us to extract oil from the rock network more easily."

The findings demonstrated that silica nanofluids could improve oil recovery rates by eight percent under laboratory conditions, a process that the team plans to optimise for use in industry settings.

"By understanding the mechanism by which the nanoparticles enhance extraction processes, we are now planning to perfect our nanoparticle 'recipe' for even better oil recovery," said Daniel. ★

Researcher
Dan Daniel, IMRE

IN BRIEF
By using microscopy to examine how nanofluids extract oil, the researchers found that silica nanofluids improved oil recovery rates.

1. Li, S., Sng, A., Daniel, D., Lau, H.C., Torsæter, O. *et al.* Visualizing and quantifying wettability alteration by silica nanofluids. *ACS Applied Materials & Interfaces* **13**, 41182–41189 (2021).

NEXT ISSUE

Here's a sneak peek of the material covered in the next issue of *A*STAR Research*

COVID-19

CALMING THE CYTOKINE STORM

A stem cell-based treatment for psoriasis might also be the answer to easing life-threatening COVID-19 symptoms.

MATERIALS SCIENCE

A PERFECT PAIR MAKES SPARKS FLY

Researchers match materials to create the first high-efficiency thermoelectric generator that turns waste heat into electricity.

IMMUNOLOGY

HITTING THE ANTIBODY MANUFACTURING SWEET SPOT

Scientists create a platform for reliably customising antibody molecular structures, opening the door to more potent and effective antibody medicines.

COMPUTER VISION

GHOST-BUSTER ALGORITHM KEEPS WATCH

Computer scientists develop an algorithm that tracks moving objects faster and more accurately than current platforms.

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REIMAGINE RESEARCH

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