IGS

INSTITUTE FOR GENOME SCIENCES

Insider

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UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES

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DIRECTOR'S CORNER

A New Vision for the Institute for Genome Sciences

Elana J. Fertig, PhD, FAIMBE
Director, Institute for Genome Sciences

To learn more about Dr. Fertig's vision for IGS, read this [Q&A] on the UMSOM website

Dear All:

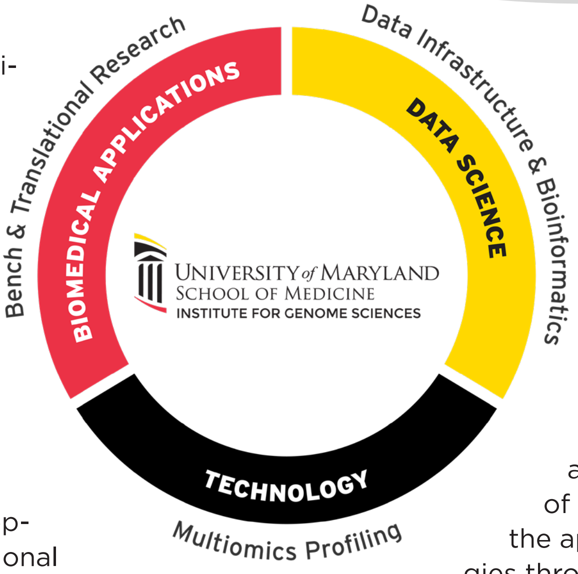
Last year at this time, I was just getting ready to become IGS Director when I attended "Breaking Ground and Blazing Trails" the celebration honoring Claire Fraser, PhD, the Founding Director of the Institute for Genome Sciences (IGS), upon her retirement. There, I learned about the 18-year history of IGS as part of the University of Maryland School of Medicine—built on an even older foundation with many of our faculty playing a founding role in genomic sequencing prior to coming to IGS with Dr. Fraser from The Institute for Genomic Research (TIGR) in Rockville, Maryland.

There are few opportunities in one's career where a woman can walk in the footsteps of scientific heroines, and it's been truly humbling to take on the reins as Director of the Institute for Genome Sciences. IGS has a rich history pioneering genomic technologies and bioinformatics, bringing these tools to mainstays of modern biomedical and clinical leadership.

I'd like to honor that history and the hard work of all who have built IGS, building on its history in pioneering genomic technologies and bioinformatics to continue to advance biological and biomedical sciences. In many ways, for me personally, this research represents a homecoming to the University of Maryland system where I completed my PhD. But, as a graduate student in applied mathematics, I could only begin to dream of adapting the same techniques I was then applying to leverage satellite data in weather forecasting to genomics data for the modern paradigm of predictive medicine.

Under my leadership, I look forward to furthering the group's development of the next generation of single-cell and spatial molecular technologies. These new approaches are expanding at a rate unprecedented even in the early days of the genome project, that is IGS's legacy. Now we can go beyond genes to measure in space each individual cell, its molecular function, and genetic fingerprint to uncover the fundamental nature of biology. We know that biology and human disease are complex, evolving systems, that include molecular, cellular, tissue, population, and environmental factors changing over time. By expanding our use of multiomic technologies—such as spatial transcriptomics and single-cell sequencing—we will enable more innovative scientific discovery within IGS. In addition, with this new concentration on computational biology and AI, we can interpret these data in entirely new ways and even develop virtual cells or genes that can be estimated entirely from computer systems.

CLICK HERE or
SCAN the **QR Code**
to **Support IGS**!



Over the last several years, multiomics has advanced from basic science tools to mainstays of modern biomedical research and clinical practice. Now as Director at IGS, I look forward to expanding our collaborations across the University of Maryland system, as well as to partnering with outside organizations to apply these technologies to advance medical care. I am fortunate to have also had the opportunity to undertake an additional role as **Associate Director of Quantitative Sciences for the University of Maryland Greenebaum Comprehensive Cancer Center** to further develop our research and clinical applications to cancer genomics. Applying the new technologies developed in IGS with the translational cancer research in the cancer center will provide unprecedented opportunities to discover new therapeutic targets and biomarkers that can better predict a patient's outcome to care. There are further opportunities to expand this opportunity across diseases, building on the plentiful disease-specific expertise of IGS faculty and the enhanced digitized data and health-based AI offered in the growing Institute for Health Computing. This will add to our current portfolio that focuses on women's and infant health through our new Center for Microbiome Research and Innovation (CAMRI—see **page 4**) led by our former Interim Director Jacques Ravel, PhD; infectious and parasitic diseases, and neuroscience, as well as bacterial and human genomics. His partnership has been instrumental in collaborating to build a rich program that spans all biological scales of human health.

Education will remain at the core of the IGS mission. Our formal programs have spanned from elementary school through postdocs with additional training workshops targeted to anyone who wants to learn bioinformatics or transcriptomic or microbiome analysis. We plan to further develop our educational offerings to become the hub of genomic education, enhancing the applications of these technologies throughout the University of Maryland system.

These are trying times, but by working together, IGS will answer the call, as it always has. We will leverage our cutting-edge infrastructure to build grand-challenge clinical genomics problems that can advance internal and external partnerships. Together, these initiatives will enable us to expand the next generation of technology-driven bench and bedside research. Ultimately, my vision is for an invigorated, multiomics- and analytics-driven IGS that becomes a competitive global leader known for integrating bioinformatics, genomics, and computational biology in its robust research program—leading to new clinical knowledge, treatments, prevention, and cures that can be applied across all human diseases.

Thank you for the warm welcome and your support of IGS,

Elana

Elana J. Fertig, PhD, FAIMBE

Director, Institute for Genome Sciences
Associate Director for Quantitative Science in the Marlene and Stewart Greenebaum Comprehensive Cancer Center (UMGCCC)
University of Maryland School of Medicine

CAMRI

NEW Microbiome Research Center Established at the Institute for Genome Sciences

Probiotics are all the rage. Everyone from influencers to your best friend raves about the amazing benefits for overall wellness. Companies tout less bloating, better digestion, relief of brain fog, and mood enhancement when balancing the gut microbiome.

The truth, however, is that probiotics are not regulated by the Food and Drug Administration (FDA) and using them to treat conditions could cause other health issues, says Jacques Ravel, PhD, Director of the new Center for Advanced Microbiome Research and Innovation (CAMRI) at the University of Maryland School of Medicine (UMSOM). The gut microbiome's role in infant health is just one area of research that Ravel and his colleagues study at CAMRI.

CAMRI officially launched in March at the Mid-Atlantic Microbiome Meet-Up hosted by CAMRI on the University of Maryland, Baltimore (UMB) campus and attended by microbiome scientists from the D.C.-Delaware-Virginia-Maryland area. Wide-ranging microbiome science was discussed, from the environmental microbiome of the Chesapeake Bay to non-human microbiomes from cheetahs to cheeses, and, of course, the human microbiome—the specialty of CAMRI's faculty.

CAMRI's establishment recognizes the extensive expertise in microbiome science and microbial genomics long held within the Institute for Genome Sciences (IGS) at UMSOM. CAMRI now serves as a hub for pioneering microbiome research—bridging foundational science with translational applications to improve health outcomes.

Why Study the Microbiome?

Dr. Ravel and CAMRI's nine faculty members study the microbiome's role in vaginal health, sexually transmitted infections, and maternal and infant birth outcomes, as well as the role of the gut microbiome in infant health and organ transplantation.

The microbiome is a community of microorganisms such as bacteria, fungi, or viruses that live in the human body—the gut, mouth, and vagina—and on the skin. Disruptions or imbalances of these communities are often implicated in diseases, such as irritable bowel syndrome, sexually transmitted infections (STIs), or tooth decay. Microbiome health also has been linked to systemic health issues, such as heart disease, cancer, preterm birth, and poor mental health. However, the "right" microbiome can offer protection from these outcomes.

The popularity of microbiome centers has grown throughout the United States in recent years, with more than 80 located at universities and national laboratories. The growth recognizes that studying the microbiome's impact on people and the environment is core to the life sciences.

CAMRI's History

"Although we have recently formalized as a center, our history of innovating in research goes back 30 years to the sequence of the first free-living organism—*Haemophilus influenza*—by our IGS colleagues Claire Fraser and Owen White that launched the field of microbial genomics," Ravel says.

At that time, Fraser and White worked at a now-defunct organization called The Institute for Genomic Research (TIGR) in Rockville, Md., that established the world's first Microbial Sequencing Center. In 2007, Fraser brought many colleagues to UMSOM to launch IGS, including Ravel who had joined TIGR five years earlier.

In the first year of IGS, the National Institutes of Health (NIH) established the Human Microbiome

Project (HMP) with the mission of generating resources to characterize the human microbiome and analyze its role in human health and disease. IGS received funding through HMP for multiple projects and established the HMP Data Analysis and Coordination Center under White's leadership. The team followed with many more NIH-funded microbiome grants and impactful discoveries to establish its leadership in the field.

Global Leadership in Research

In the 18 years since its establishment at UMSOM, IGS researchers have become global leaders in microbiome science, especially the vaginal microbiome. The media often seeks the expertise of the now-CAMRI faculty to comment on or advocate for issues involving the microbiome.

For example, in a unique interdisciplinary collaboration, Dr. Ravel and Diane Hoffman, JD, the Jacob A. France Professor of Health Law at the University of Maryland Francis King Carey School of Law, and colleagues from UMSOM and the University of Maryland School of Pharmacy, called for federal regulation of direct-to-consumer microbiome tests in a commentary in ***Science***. One key point they make is that the tests to check your gut or vaginal microbiome are not regulated or clinically validated, and the companies' recommendations could lead some to make harmful dietary changes or become overdependent on supplements.

In an interview with ***Nature***, Dr. Ravel pointed out that parents relying on these tests to change an infant's or child's microbiome without the supervision of a medical practitioner is particularly frightening.

"Excessive reliance on supplements could interfere with natural growth and development," he says.

Other CAMRI faculty also share their expertise in the media. Rebecca Brotman, PhD, MPH, has been sought out for her science on understanding bacterial vaginosis (BV). In a commentary in ***JAMA Network Open***, she advocated for a medication used in Europe to be better studied in the United States. Women's ***Health*** and ***Scientific American*** interviewed Johanna Holm, PhD, on what the vaginal microbiome can tell a woman about her overall health. The article states: "Holm also hopes for more research. Menopause and conditions like BV, fibroids, and endometriosis—which affect hundreds of millions of women every year—currently have received less than 0.1 percent of federal dollars for research."

Innovation in Therapeutic Development

One area that sets CAMRI research apart from many other academic-led microbiome centers is its work on leveraging its microbiome research to develop live biotherapeutic drugs with the potential to prevent recurrence of BV, thus eliminating other obstetric complications.

"The first step is to understand what constitutes healthy or dysbiotic microbiomes—whether the vaginal, gut, mouth, or skin's—and then to develop a therapeutic that goes through rigorous testing and approval by the Food and Drug Administration," Dr. Ravel says.

His research has translated into a startup biotechnology company he founded in 2019, LUCA Biologics. LUCA's first product, constructed using its UMB-owned patented technology, was licensed to SEED Health. This California-based company manufactures and sells VS-01, a vaginal probiotic that has shown significant benefits in restoring and maintaining a healthy vaginal microbiome in clinical trials.

"CAMRI, with the support of the Gates Foundation, is also working on developing a unique live biotherapeutic drug specifically designed to treat BV in African women," Ravel says. "We're grateful to have CAMRI as an established center within IGS at UMSOM to support our efforts so we can find treatments for many diseases caused by microbiome disruption." **IGS**

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BREAKING GROUND & BLAZING TRAILS

Celebrating Claire Fraser's Retirement

The Institute for Genome Sciences (IGS) said good-bye last year to its retiring Founding Director Claire Fraser, PhD, with a day of about 20 talks and tributes from current and former colleagues, distinguished guests, and trainees who came from around the world to celebrate her science.

A timeline of Dr. Fraser's accomplishments spanned from 1977 when she received her Bachelor of Science in Biology from Rensselaer Polytechnic Institute to her retirement and being named Professor Emerita in 2024—and multiple accolades and accomplishments along the way.

Other highlights included when, as President of The Institute for Genomic Research (TIGR), she and her team completed the first genome sequence of a free-living organism, *Haemophilus influenzae* in 1995 launching the field of microbial genomics to coming to the University of Maryland School of Medicine to launch IGS in 2007. Elections to elite organizations included being named to the National Academy of Medicine in 2011 to serving a three-year term—one as President—at the American Association for Advancement of Science in 2019 and her election to the National Academy of Sciences in 2023.

Enjoy these highlights:

Photo courtesy of the William J. Clinton Presidential Library.

Claire Fraser appears with President Bill Clinton, then NIH Director Francis Collins, and his wife Diane Baker at the First Survey of the Human Genome event at the White House held on June 26, 2000. Photo courtesy of the William J. Clinton Presidential Library.

> **"My favorite Frost poem is The Road Not Taken. It's a great metaphor for my career and particularly meaningful in the context of retirement. We all make choices throughout our lives and that precludes exploring all paths, but there can be wonderful opportunities around every bend in every road."**
>
> —Claire M. Fraser, PhD

The State of Maryland

Governor of the State of Maryland, to

FOUNDING DIRECTOR CLAIRE FRASER, PHD , **Greetings:**

Be it Known: *Because of your demonstration of high integrity and ability, meriting our great trust and respect, we are most pleased to award you the*

Governor's Citation

in appreciation of your outstanding services to the citizens of this State

Given *Under My Hand and the Great Seal of the State of Maryland,*
this 8th *day of* October
Two Thousand and twenty-four

Governor

Aruna Miller
Lt. Governor

Susan C. Lee
Secretary of State

City of Baltimore

Certificate of Recognition

On behalf of the citizens of Baltimore, I am pleased to present this certificate to

Claire M. Fraser, PhD

in recognition of your groundbreaking work as founding Director of the Institute for Genome Sciences at the University of Maryland School of Medicine. Your innovation and dedication has changed the lives of millions and furthered our understanding of human genomes. On behalf of the people of Baltimore, I offer my sincere thanks for your dedication and wish you a long, happy, and well-deserved retirement!

October 8, 2024

Brandon M. Scott
Mayor

Maryland Governor Wes Moore has awarded Claire Fraser the Governor's Citation for the State of Maryland stating, "Because of your demonstration of high integrity and ability, meriting our great trust and respect, we are most pleased to award you a Governor's Citation in appreciation of your outstanding services to the citizens of this state."

Baltimore Mayor Brandon Scott has recognized Claire Fraser's contributions to science and the city writing, "Your innovation and dedication has changed the lives of millions and furthered our understanding of human genomes. On behalf of the people of Baltimore, I offer my sincere thanks for your dedication and wish you a long, happy, and well-deserved retirement!"

Claire Fraser and team sequence her dog, Shadow and publish in *Science*: The Dog Genome: Survey Sequencing and Comparative Analysis

To honor the legacy of Claire Fraser, PhD, on her retirement, The Institute for Genome Sciences (IGS) has created **The Claire M. Fraser Fund for Graduate Education in Genomic Sciences**.

The fellowship will support various needs of graduate students doing 'omics research at IGS, such as travel to conferences, sequencing and analysis costs, and lab supplies. Please consider a donation at this **link** or by using the QR code here.

MARYLAND GENOMICS Launches New Technology Development Hub Focused on Spatial Biology

Spatial biology isn't as out-of-this world as the name suggests. Rather, it gets deeper into the world of cells, and how they interact within tissues.

The growing use of spatial biology technologies in scientific research is why Maryland Genomics has launched its new Technology Development Hub.

"We have significantly expanded our capacity to support spatial multiomics projects to characterize the cellular and molecular landscape in tissues," says Luke Tallon, Senior Executive Director of Maryland Genomics and Associate Director of Core Services at the Institute for Genome Sciences (IGS). "We offer researchers two of the most advanced spatial biology platforms in the world, the Nanostring CosMx Spatial Molecular Imager and the 10X Genomics Visium HD System."

In addition to these platforms, Maryland Genomics will broaden its capabilities by evaluating and implementing the newest spatial and single-cell technologies on the market.

"We've also started a new initiative aimed at streamlining access to these technologies for investigators on the UMB campus," adds Mike Humphrys, Technical Director of Maryland Genomics. "It's a partnership with the Pathology Biorepository Core to coordinate tissue and slide preparation for all spatial platforms. This will give researchers a more seamless experience when using the services of both cores."

Anyone with questions about how to use spatial or other genomic technologies can contact the Maryland Genomics team here. **IGS**

> ***We have significantly expanded our capacity to support spatial multiomics projects to characterize the cellular & molecular landscape in tissues.***
>
> Luke Tallon

Australian Pharmaceutical Company & CVD Team Up with Maryland Genomics for Clinical Trial

Joining forces with the University of Maryland School of Medicine's (UMSOM) Center for Vaccine Development and Global Health (CVD) once again, Maryland Genomics will collaborate on a clinical trial testing a drug to prevent severe respiratory illness in at-risk populations.

The drug developer, ENA Respiratory, based in Melbourne, Australia, tapped CVD and Maryland Genomics to conduct the 2a (Proof of Concept) clinical trial. The multicenter study will be a randomized, double-blind, and placebo-controlled study to test the drug INNA-051 in healthy adults who are at increased risk for viral respiratory infections.

Maryland Genomics, along with Tracy Hazen, PhD, faculty with IGS's CAMRI, will support the study through patient enrollment and self-collection sampling, as well as providing technical laboratory services using respiratory diagnostic assays for genomic sequencing.

"We're very excited to support CVD and ENA Respiratory in this important trial," says Mike Humphrys, Technical Director of Maryland Genomics. "We have contributed to several trials with CVD and other partners, and we're looking forward to participating in more clinical trials both within UMSOM and globally."

The trial begins in October and is expected to conclude at the end of the winter respiratory illness season.

FACULTY SPOTLIGHT

Julie Dunning Hotopp Named MPower Professor

Julie C. Dunning Hotopp, PhD
Professor Microbiology & Immunology

Several years ago, Julie Dunning Hotopp, PhD, got feedback on a grant submission strongly suggesting she find an expert in the biology of sex of nematodes before resubmitting. She found the perfect collaborator in Eric Haag, PhD, at the University of Maryland College Park. That collaboration has now led her to receive an MPower Professorship.

MPower Professors must show collaboration on strategic research that would be difficult to achieve on either the University of Maryland, Baltimore or University of Maryland College Park campuses without a partnership with someone from the other campus. They also must embrace MPower's mission to collectively strengthen and serve the state of Maryland and its citizens. Each professor receives $150,000 over three years to support their salaries or research activities.

Dr. Dunning Hotopp, a scientist at the Institute for Genome Sciences and Professor of Microbiology and Immunology at the University of Maryland School of Medicine, and Dr. Haag, a Professor in the Department of Biology and the Director of the Biological Sciences Graduate Program, collaborated on a project to better understand the processes that lead to the formation of a new Y chromosomes on filarial nematodes and how the genes on that chromosome become properly regulated. Dr. Dunning Hotopp had already been part of a team that discovered two new Y chromosomes on filarial nematodes that cause tropical diseases, such as river blindness, and kill or disable millions of people globally.

Drs. Dunning Hotopp and Haag now co-mentor a student who uses resources on both campuses, including the computational infrastructure at IGS to work on this research project.

"We have really had a lot of synergy in this work and are looking forward to expanding it even further," Dr. Dunning Hotopp says. "I've had other collaborations with College Park professors which have also been great examples of team science."

> ***We have really had a lot of synergy in this work and are looking forward to expanding it even further.***
>
> Julie C. Dunning Hotopp, PhD

One of those other collaborations was with Iqbal Hamza, PhD, who had technology at College Park that she needed for an experiment. She used his biolistics machine—commonly called a 'gene gun'—that is used to introduce DNA or other genetic material into cells. Dr. Hamza is now in the same building at UMB as Dr. Dunning Hotopp and is an affiliate faculty member at IGS.

Dr. Dunning Hotopp also is the leader of IGS's first T32 training grant of $1.9 million called "Systems-Level Research in Microbial Pathogenesis." Students learn how a "systems-level" approach applies to both the type of research the trainees will undertake and the style of education they will receive. Systems level means that it's necessary to understand how the parts of a whole interact, interconnect, interrelate, and often influence each other.

"In many ways the T32 and MPower Professorship align perfectly in that both involve collaboration on basic science, both teaching it and doing it," Dr. Dunning Hotopp says. "I am very grateful for both opportunities." **IGS**

IGS Holds First Hackathon to Increase Knowledge of Spatial Transcriptomics

Everyone was a winner at the Institute for Genome Science's first hackathon. Four teams gathered on July 31 to present how they spent the prior week tackling a problem on cell typing with spatial transcriptomic data.

For those who aren't familiar, a hackathon is an event where people collaborate intensely over a short period of time to find solutions to a specific challenge. The teams then come together to discuss what they've discovered.

The IGS teams included a mixture of faculty, students (including one UMD undergrad), postdocs, and staff from Bioinformatics and Maryland Genomics.

The teams had one week to work on their challenge before presenting to the wider group. Their challenge was to look at spatial transcriptomic data generated from 10x Genomics's VisiumHD on colorectal cancer to determine if the cell-type annotation worked. Teams used the statistical method known as Robust Cell Type Decomposition (RCTD) to sort cell types from the spatial data. Then, they were able to validate their data using a set from the Human Tumor Atlas Network, an initiative designed to construct three-dimensional atlases of dynamic cellular and molecular features of cancer as it develops from a precancerous lesion to advanced disease stages.

"I think hackathons are important because they foster innovation, promote cross-team collaboration, and allow people to use techniques and technologies that they have not used before," says Dmitrijs Lvovs, PhD, a Research Associate at IGS and the Department of Medicine at the University of Maryland School of Medicine (UMSOM). "Best of all, a hackathon is a risk-free version of real project work that team members may need to do in the future."

Each team approached the challenge using different tools, including benchmarking studies, gene enrichment validation, synthetic data generation, and proteomics. Some teams divided up the challenge so that each member took on one aspect of the challenge, while other teams worked on the problem together. (Check out the winning categories on the right!)

IGS Director Elana J. Fertig, PhD, says that events like the hackathon that work across labs, as well as with different technologies, is part of expanding IGS's focus on technology development and working with large-scale data sets in research.

"The spatial transcriptomic focus of this hackathon was particularly important because I'd love to see more of our colleagues working with spatial technologies," Dr. Fertig says. "Many of the individuals on the teams had never even worked with spatial technology before."

Some team members also had never participated in a hackathon before.

"It was my first hackathon, and I really enjoyed the experience," says Evelina Mocci, PhD, Research Associate at IGS and in the Department of Medicine at UMSOM. "It gave me a great chance to try out a new method. I learned a lot by listening to my colleagues' approaches."

Even several summer interns took on the extra work of trying to figure out the challenge.

"This was an amazing experience," says Daniel Pintard, a summer intern in the lab of IGS Affiliate Faculty Member Alex Xu, PhD, Assistant Professor of Bioengineering in the Fischell Department of Bioengineering at University of Maryland, College Park. "I think it is highly beneficial to have hackathons for crowdsourcing ideas that can help us in working with new data modalities!"

In addition to learning more about spatial transcriptomics, participants learned more about the work their team members do at IGS.

"Discussing with peers having different expertise while learning in a friendly way and solving the problems in science is the best part of the hackathon that I liked," says Bharath Swargam, a volunteer in Seth Ament's lab at IGS. "I would recommend all the colleagues irrespective of the background to participate in hackathon." **IGS**

HERE ARE YOUR WINNERS!

UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES

****WINNER****

Best Data Quality Assessment

First Summer Hybrid Hackathon @IGS • July 31st, 2025

This Certificate is Proudly Presented to

Bharath Swargam, Christopher Holt, & Daniel Pintard

As a Member of the Winning Team

TEAM #2

For Their Focused Work on Evaluating Spatial Transcriptomics Data Using Marker Gene Analysis, Spatial Homogeneity Metrics, and Synthetic Data Generation

Dmitrijs Lvovs
Dmitrijs Lvovs
Hackathon Coordinator

Elana J. Fertig
Elana J. Fertig
Director, IGS

UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES

****WINNER****

Best Methodological Innovation

First Summer Hybrid Hackathon @IGS • July 31st, 2025

This Certificate is Proudly Presented to

Herve Tettelin, Kathleen Noller, Kranthi Vavikolanu, & Yang Son

As a Member of the Winning Team

TEAM #1

For Proposing a Decision Tree for Cell Typing Method Selection Using Benchmarking Studies, and Exploring Multiple Annotation Methods Despite Technical Constraints

Dmitrijs Lvovs
Dmitrijs Lvovs
Hackathon Coordinator

Elana J. Fertig
Elana J. Fertig
Director, IGS

UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES

****WINNER****

Best Technical Tool Integration

First Summer Hybrid Hackathon @IGS • July 31st, 2025

This Certificate is Proudly Presented to

Aditi Biswas, Adonis D'Mello, Ankit Dwivedi, & Kathleen Trang

As a Member of the Winning Team

TEAM #4

For their Comparative Analysis of Localization Models and Proteomics Tools, and Proposing Innovative Bin-based Consensus Functions for Cell Type Identification.

Dmitrijs Lvovs
Dmitrijs Lvovs
Hackathon Coordinator

Elana J. Fertig
Elana J. Fertig
Director, IGS

UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES

****WINNER****

Best Multi-Track Exploration

First Summer Hybrid Hackathon @IGS • July 31st, 2025

This Certificate is Proudly Presented to

Daniel Bergman, Evelina Mocci, Sushma Nagaraj, & Varun Rao

As a Member of the Winning Team

CRYPTKEEPERS

For Running Four Parallel Analytical Tracks: Integrating Foundation Models, Gene Enrichment Validation, Visualization Tools, and Cell Cycle Analysis.

Dmitrijs Lvovs
Dmitrijs Lvovs
Hackathon Coordinator

Elana J. Fertig
Elana J. Fertig
Director, IGS

NEW GRANT

NIH Awards $14.5 million Grant to IGS to Develop a Data Center for the Human Virome Program

The National Institutes of Health (NIH) has announced that it is launching a new research program to understand how the viruses that live within the human body or on the skin—known as the human virome—can impact a person's health.

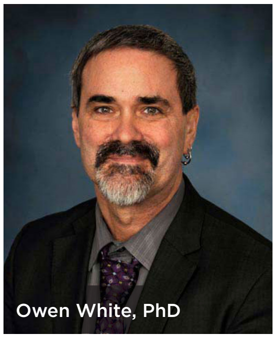
As a critical part of NIH's new Human Virome Program, the Institute for Genome Sciences at the University of Maryland School of Medicine will receive $14.5 million over five years to establish a comprehensive and cutting-edge data center. The Consortium Organization and Data Collaboration Center (CODCC) will house and analyze data for the program. Owen White, PhD, Associate Director at IGS and Professor in the Department of Epidemiology and Public Health at UMSOM will lead the CODCC.

Like the better understood microbiome—composed of bacteria, viruses, and other microorganisms—the human virome contains millions of viruses that impact health both positively and negatively. The new program—made possible through the NIH's Common Fund—provides funding to 16 locations to study the impact of viruses across ages, sex, ancestry, and geographic locations.

"Most current technologies and tools can only help us understand a small portion of the virome, so this award will enable us to close the scientific knowledge gap through a combination of experimental, computational, and data-generation activities," Dr. White explained. "We will develop new analytics tools and a user-friendly portal, so researchers can easily access the data generated by our counterparts in the program. IGS has an extensive background in working with data from other NIH projects so we are excited to use our expertise once again to better the field."

Those data collaborations between IGS and NIH include the Human Microbiome Project, the Neuroscience Multiomic Data Archive (NeMO), the Single Cell Opioid Responses in Context of HIV Program (SCORCH), and the Common Fund Data Ecosystem.

The IGS team will develop and maintain a searchable Human Virome Reference Dataset that will benefit scientists and be publicly accessible. As part of this virome data portal, they will standardize, store, and disseminate data. Key to this will be the creation of a toolkit for virome analysis and visualization, along with developing new methods to integrate multiomics into the understanding of the virome's interaction within the body.


Owen White, PhD


Michelle G. Giglio, PhD

To develop all the tools needed within the COCCC, IGS scientists will also work with researchers from the Broad Institute, Harvard T.H. Chan School of Public Health, Washington University in St. Louis, Baylor College of Medicine, and Lawrence Berkely National Laboratory. One key collaborator is Curtis Huttenhower, PhD, Professor of Computational Biology and Bioinformatics at the Harvard T.H. Chan School of Public Health who will work with the IGS team to develop and optimize cloud-based data analysis pipelines specifically tailored to the needs of each site in the HVP consortium.

"Another key aspect of this grant is developing training programs for our counterparts on the grant, as well as educating other scientists and the public about our findings," said Michelle Giglio, PhD, a co-investigator on the grant, and Associate Director for Education and Outreach at IGS. The consortium held their first meeting in Rockville, Maryland in mid-January.

"We know a great deal about harmful viruses as well as commensal viruses that live in a host without harming or helping it. Now it's critical to understand what constitutes a beneficial human virome so that we can harness it to help people, especially considering our aging population," said Mark Gladwin, MD, Dean of UMSOM and the John Z. and Akiko K. Bowers Distinguished Professor, and Vice President for Medical Affairs, University of Maryland, Baltimore. IGS

NEW GRANT

Ament Lab Awarded National Microgrant to Help Baltimore Confront the Opioid Crisis

IGS's Seth Ament Lab is helping Baltimore become more informed about the opioid crisis in the city. Spearheaded by Post-Docs and PhD students, the lab won a $2,000 Research!America Civic Engagement Microgrant to host a community symposium and panel discussion about the crisis.

The Ament Lab was one of only 24 awards given nationwide in recognition of scientists who work to bridge the gap between science and the public. Working in partnership with the Kahlert Institute for Addiction Medicine, the event—called How Science and Politics Save Lives in the Opioid Epidemic—brought together scientists, policymakers, and public health leaders to address communication gaps that may hinder progress in combating opioid addiction.

The symposium drew 57 participants and fostered a lively discussion around how research, public policy, and community engagement can unite to save lives.

"Our goal was to spark a dialogue between the local public, the scientific community, and public health officials to fill the communication gaps regarding the opioid epidemic in Baltimore," said one of the Project Leaders Sterling Arjona, PhD. "By connecting science with lived experience, we can better understand the opioid epidemic and respond with compassion and evidence-based action."

Following the panel presentations, guests enjoyed a catered dinner accompanied by smaller group discussions—further enriching the experience. In addition, they received free Narcan kits from the Naloxone Project, and the Maryland Addiction Consultation Service (MACS) provided on-site resources and support. **IGS**

> ***Our goal was to spark a dialogue between the local public, the scientific community, and public health officials to fill the communication gaps regarding the opioid epidemic in Baltimore...***
>
> Sterling Arjona, PhD

MEDIA HIGHLIGHTS

Even media from around the world have taken an interest in IGS! The *Greek City Times* wrote about a study on the soil microbiome of Crete that IGS scientists Lynn Schriml, PhD, and Johanna Holm, PhD led; *The Munich Eye* picked up the story about the work of IGS Director Elana Fertig, PhD, in simulating cancer cell behavior; and two French publications—*Le Monde* and *Liberation*—have interviewed CAMRI Director Jacques Ravel about his work on understanding the vaginal microbiome.

CHECK OUT ALL OF THE IGS COVERAGE!

GenomeWeb

Computational Model Predicts Tissue-Specific Cell Activity Over Time

Genetic Engineering & Biotechnology News

Cell Activity Predicted Using Plain-Language "Hypothesis Grammar"

Technology Networks

Scientists Simulate Cancer Cell Behavior Researchers have developed a method to predict cancer cell activity in tissues over time.

The Munich Eye

Researchers Develop Innovative 'Virtual Cell Laboratory' for Future Cellular Research

Greek City Times

Historic One-Day Island-Wide Soil Microbiome Study Completed on Crete University of Maryland School of Medicine Researchers Contribute to Unexpected Discoveries

Le Monde

The vaginal microbiota, the little-known ecosystem that regulates women's health

Science Magazine

AI Holds Promise for Predicting Health Outcomes, But Should Not Be the Sole Method

InnoReports:

AI's Role in Health Predictions: A Balanced Approach

Medscape:

Study Reveals Sexual Transmission of Bacterial Vaginosis

Science News:

These scientists have a plan to demystify the vaginal microbiome

Medscape:

Bacterial Vaginosis Subtype Increases Risk for *Chlamydia* Infection and Reinfection

Liberation:

Women's Health: Vaginal Microbiota, a Crucial Subject "From a Scientific, Health and Societal Perspective"

Medscape:

Women's health: the vaginal microbiota, a crucial subject "on scientific, health and societal levels"

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Nature:

Microbiome interventions for children raise the ethical stakes

News Medical Life Sciences:

Discovery of leptin-responsive neurons offers new hope for obesity treatment

Neuroscience News:

New Appetite Regulating Neurons Discovered

Science Blog

Scientists Discover Novel Brain Cells That Control Appetite

Nature

The secrets of an optimal vaginal microbiome

Women's Health

What Your Vaginal Microbiome Can Tell You About Your Overall Health

The Guardian

Personalising stuff that doesn't matter': the trouble with the Zoe nutrition app

Forbes

Experts Call For More Regulation Of At Home Microbiome Test Kits

The Microbiologist

Researchers call for regulation of direct-to-consumer microbiome tests

Medscape

US Researchers Call for Robust Studies Into Dequalinium, a Bacterial Vaginosis Therapy Common in Europe

Forbes

Microbiome Science Company Hones In On Vaginal Health With New Launch

The Microbiome Times

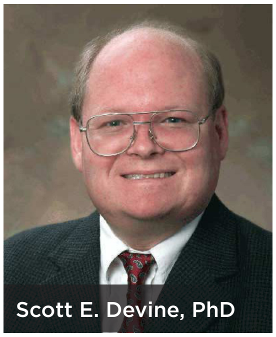
Women's Health: The Next Microbiome Frontier

Public News Service

MD scientists create Latino genetic database for medical research

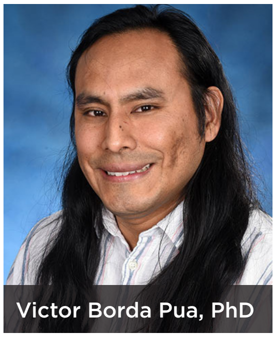
MEDIA SPOTLIGHT

Two Team Research Studies—That Include IGS Researchers—Get Attention in *Stat News*



Scott E. Devine, PhD

Timothy D. O'Connor, PhD



Victor Borda Pua, PhD

In academia, middle authors on a paper easily can be passed over. They may, however, be a major link to not only getting the science done, but taking the steps to make big breakthroughs.

That's why it's important to call attention to our IGS scientists who have contributed to groundbreaking discoveries—despite not being first, last, or corresponding authors.

Two recent papers gained national press and the renowned health and science publication *Stat News* covered both. IGS's Scott Devine, PhD, and Jonathan Crabtree, MS, contributed to the *Nature* paper published in July: **Complex genetic variation in nearly complete human genomes**. While Timothy O'Connor, PhD, and Victor Borda, PhD, were authors on **Subcontinental genetic variation in the *All of Us* Research Program: Implications for biomedical research** published in June in the *American Journal of Human Genetics*.

Stat News—the award-winning online publication covering science, medicine, and biotech—said both papers moved forward the understanding of genomics. Its articles that covered the papers were: **Researchers sequence complex parts of the human genome, expanding the future of precision medicine** and **Massive NIH study challenges use of race as a proxy for genetic ancestry in research**.

Dr. Devine, also an Associate Professor of Medicine at the University of Maryland School of Medicine (UMSOM) and Jonathan Crabtree, a Lead Bioinformatics Software Engineer at IGS, contributed to the sequencing of the samples used to decode the DNA from regions of the genome that had previously been missing. Altogether, the consortium used data from 65 human samples spanning five continents and 28 different population groups to fill in gaps in the genome.

"Our contributions included samples sequenced at IGS's **Maryland Genomics**, as well as doing some follow-up analysis on the samples for the consortium," says Dr. Devine. "It's really a great feeling to participate in such a landmark paper that shows genomic variation across ancestries—commonly called a pangenome—to a level that has never been completed before."

Dr. O'Connor, an Associate Professor of Medicine at UMSOM and Dr. Borda, a Research Associate at IGS, participated in the analysis of the genomes of more than 200,000 participants in the All of Us cohort. The study concluded that self-reported race is markedly different than genetic make-up.

"It's been a tough concept for people, even scientists, to grasp the difference between race—a social construct—and genetics—which is biologically determined," says Dr. O'Connor. "For the first time, this groundbreaking work shows us that even the term "ancestry" might be too narrow to use, especially when studying health outcomes or disease risk. That should be assessed individually for better precision."

One example the authors gave is that people from West Africa are predisposed to have high Body Mass Indexes (BMI), while those from East Africa tend to have a lower BMI. Still, both those groups are lumped together as having "African ancestry."

Dr. O'Connor added that he agrees with the comment that the paper's lead author, Charles Rotimi, PhD, Distinguished Investigator at the National Institutes of Health (NIH) told an IGS audience when he spoke at its Fifteenth Anniversary Celebration and repeated in *Stat News*: "Trying to use genetics to define race is like slicing soup. You can cut it all you want, but it's going to stay mixed." **IGS**

FACULTY SPOTLIGHT

Michelle Shardell, PhD, on Researching Aging & Becoming An ASA Fellow

"Aging is something we all get to do—if we're lucky!" That positive take is why Michelle Shardell, PhD, chose to focus her research on aging—healthy aging specifically.

"I chose aging rather than a disease-specific option because it just seemed more hopeful," says Dr. Shardell, a faculty member of IGS's CAMRI and Professor of Epidemiology and Public Health at the University of Maryland School of Medicine. "Specifically, I try to identify modifiable factors at most the individual and contextual level that can be intervened on to promote healthy aging."

Her journey to aging research wasn't direct. In fact, she began her academic career as an accounting major. "Then I couldn't stop taking math and statistics classes, so I switched to a math major and statistics minor," she says. "I took a course in biostatistics and loved how math can be used to benefit the public's health."

Rather than working directly with research participants, Dr. Shardell develops new statistical methods and analyzes secondary data to help obtain accurate answers to scientific questions about what interventions can enhance a healthy lifespan in older adults. Her work, she says, simultaneously respects data generated by others and looks for ways to affect health.

"So much time, hard work, and resources are used to generate high-quality biomedical data," she explains. "I see rigorous biostatistics as a way of honoring the investments made in generating these data. In my work, I enhance and adapt different biostatistical approaches and apply them to biomedical data in pursuit of reliable results that can positively impact health."

One of her favorite projects in recent times was known as **PROVIDO** for **PR**oject on **O**ptimal **VI**tamin **D** in **O**lder adults and was published in ***The American Journal of Clinical Nutrition***.

Michelle Shardell, PhD
Professor Epidemiology
& Public Health

"My colleagues and I harmonized five large epidemiologic cohorts to identify and validate thresholds of circulating vitamin D concentrations that best predicted incidence of slow walking speed in older adults," Dr. Shardell says. "Not only did this project involve developing and applying some cool statistical methods, but we also addressed major challenges in vitamin D research in older adults."

The main challenge involved the ongoing debate about the recommended amount of vitamin D for optimal bone health, physical function, and independent living. Recent studies had not shown a beneficial effect in some adults—but previous research had not answered the question about why that was the case.

"We developed a general workflow that can be implemented for the next high-profile supplement or vitamin before resources are allocated to studies of participants who might not benefit," she says.

All her work in statistics paid off as she was named a Fellow of The American Statistical Association (ASA).

"I am grateful for my supporters for nominating me for this recognition," she says. "Notably, ASA only elects up to one-third of one percent of the total association membership as fellows each year, so this is a real honor."

If she weren't a scientist, she says she would be a personal trainer or jewelry maker. But being part of IGS has continued to fuel her passion for biostatistics.

"Being part of IGS means working with top-notch scientists who keep me on top of my game!" she says. "Not only do we have high standards and access to the best resources, but we also have a culture of collaboration and shared benefits. It's great to be a part of that." **IGS**

Welcome New Faculty Joining IGS

(IN ALPHABETICAL ORDER)

Daniel Bergman, PhD

Adding together math plus cancer research equals the emerging field of mathematical oncology. That's the specialty of Daniel Bergman, PhD, who has joined the Institute of Genome Sciences faculty from Johns Hopkins University where he was a postdoctoral fellow in Oncology.

"I use mathematics to understand cancer," says Dr. Bergman, who is also Assistant Professor in the Department of Pharmacology and Physiology. "I build mathematical models of tumor growth, particularly in the presence of an immune response."

In his research, Dr. Bergman uses agent-based modeling (ABM)—a computational approach that simulates the behavior of a system by modeling individual interactions of agents within a defined environment. In this case, the system is cancer, and the agents are the cells. The model provides insight into how cells interact and respond to therapy.

"ABMs help us understand biological systems better and may someday translate to clinical decision making," Dr. Bergman says. "We are building toward a 'digital twin' of a patient to enable precision treatments."

Dr. Bergman received his MS and PhD in Mathematics from the University of California, Irvine. He served as a Postdoctoral Assistant Professor in Mathematics at the University of Michigan in Ann Arbor before his fellowship in Oncology at Johns Hopkins.

Dmitrijs "Dima" Lvovs, PhD

Dima Lvovs, PhD, took a winding road to the Institute for Genome Sciences. He has worked various jobs around the world including as an engineer, a financial analyst, head of risk management, and a consultant for the International Atomic Energy Agency. That last position took him to countries including Malta, Mozambique, and Montenegro.

Most recently, Dr. Lvovs was a Research Associate in the Oncology Center-Quantitative Sciences at the Johns Hopkins School of Medicine.

Now a Research Associate at IGS, Dr. Lvovs's research focuses on spatial transcriptomics and machine learning. In part, he is supported by a grant from the Break Through Cancer Foundation where he will work on spatial molecular bioinformatics analysis. He also directed IGS's first hackathon (see page 10).

Dr. Lvovs received his BSc in Mechanical Engineering and his MSc in Medical Physics from Riga Technical University in Latvia. He completed his PhD in Bioinformatics at the Institute for Information Transmission Problems in Moscow.

Mustafa Özçam, PhD

More than 33 million Americans suffer from food allergies, and they've also become more deadly in recent years. According to the Food Allergy Research and Education Organization, anaphylactic food reactions have increased by almost 400 percent since 2007.

While there are many theories, a single cause for the disturbing increase in food allergies has not been identified. That's why Mustafa Özçam, PhD, researches the gut microbiome's role in immune tolerance with a focus on food allergies.

Dr. Özçam has joined IGS's Center for Advanced Microbiome Research and Innovation (CAMRI) at the University of Maryland School of Medicine (UMSOM) where he has set up and is Principal Investigator in the Translational Microbiome & Immune Tolerance Laboratory. He also is an Assistant Professor in the Department of Microbiology and Immunology at UMSOM.

"Our lab's focus is to understand how early-life diet shapes gut microbial functional capacity, immune development, and the risk of allergic disease, especially in food allergies," says Dr. Özçam. "We apply multiomic microbiome profiling of human birth cohorts to uncover microbial and metabolic predictors of food allergy development that can be targeted to reduce allergic disease risk. Our mission is to translate these insights into therapies and, ultimately, prevention strategies for food allergies."

Prior to joining CAMRI, he earned his PhD at the University of Wisconsin–Madison and completed his postdoctoral training at the University of California San Francisco. Dr. Özçam also worked in the probiotic industry to develop microbiome-based interventions for clinical use between his PhD and postdoctoral trainings. **IGS**

> "
> ***Our lab's focus is to understand how early-life diet shapes gut microbial functional capacity, immune development, and the risk of allergic disease, especially in food allergies.***
>
> Mustafa Özçam, PhD
> "

Welcome New Affiliate Faculty Joining

(IN ALPHABETICAL ORDER)

Wei Li, PhD

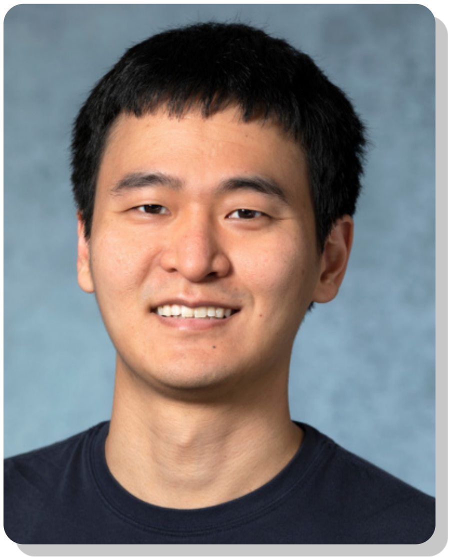
Wei Li, PhD, holds a unique position at the University of Maryland School of Medicine—or, you might say five positions.

Dr. Li's appointment is the first in a collaboration between five different entities at UMSOM, including the Institute for Genome Sciences, where he serves as an affiliate faculty member and the Department of Pharmacology and Physiology where he is Assistant Professor. He also works withthe University of Maryland—Institute for Health Computing; the University of Maryland Greenebaum Comprehensive Cancer Center; and the University of Maryland Medicine Institute for Neuroscience Discovery (UM-MIND).

Dr. Li brings his expertise in computational biology, CRISPR gene editing, and AI/ML modeling in genomics to UMSOM from Children's National Hospital and George Washington University.

"I have a passion for understanding how the human genome functions through using innovative AI, gene editing, and genomics technologies," Dr. Li says. "Right now my lab studies many types of cancer, as well as infectious and genetic diseases."

Dr. Li received his bachelors and masters degrees in Computer Science from Tsinghua University in Beijing, China and his PhD in Computer Science from the University of California, Riverside.



Alex Xu, PhD

Alex Xu, PhD, has a rabbit named Peanut, plays the viola, and loves competitive cooking shows. But perhaps his biggest passion is all things related to spatial biology.

Dr. Xu is an Assistant Professor of Bioengineering in the Fischell Department of Bioengineering at University of Maryland, College Park. He also has affiliated appointments in Computational Biology, Bioinformatics, and Genomics; the Biophysics Program; the Applied Math, Statistics, and Scientific Computer Program; the Marlene and Stewart Greenebaum Comprehensive Cancer Center; and the Department of Pathology at the University of Maryland Baltimore.

Now, he has added yet another affiliation to his resume: Affiliated Faculty at the Institute for Genome Sciences.

"I work on bioinformatic pipelines to analyze spatial omics data to generate predictive biomarkers and candidate therapies for cancers," Dr. Xu says. "That's why I'm looking forward to collaborating with the scientists and bioinformaticians at IGS to expand and enhance my research."

Dr. Xu earned his PhD in Materials Science and Engineering from Stanford University where he worked on developing nanostructured tools for intracellular delivery with Nicholas Melosh. His postdoc with Jim Heath spanned two institutions,

IGS

> *I work on bioinformatic pipelines to analyze spatial omics data to generate predictive biomarkers and candidate therapies for cancers.*
>
> Alex Xu, PhD

Caltech and the Institute for Systems Biology in Seattle, where he developed tools for single-cell multiomics. Prior to joining UMD/UMB, he was an instructor at Cedars-Sinai Medical Center.

“Currently, I’m working on constructing systems-level understanding of the complex interactions within human tissue, especially cancer,” says Dr. Xu. “Spatial tells us so much about biology, and the ‘where’ of it all is so important to the ultimate questions of ‘how’ and ‘why’.”

You can learn more about Dr. Xu by visiting his website **here**. **IGS**

How to Become an IGS Affiliate Faculty Member

Becoming an IGS Affiliate Faculty member is open to University of Maryland faculty who will promote the basic research, collaboration, and teaching missions of the Institute for Genome Sciences. Appointments are evaluated for renewal every three years. To apply to become an Affiliate Faculty Member, please read the full requirements and fill out this **application**. Applications are reviewed by a committee that makes recommendations to the IGS Director. **IGS**

Innovative CT Scan Technique Could Improve Prognosis and Treatments for Head and Neck Cancers, New Research Suggests

Data collected in pre-treatment CT-scans may provide important imaging biomarkers to better predict patient prognosis, and potentially customize treatment strategies

by Katie Ghiardi

Cancers occurring in the mouth, nose, and throat are on the rise in the U.S., especially in younger people. About 60,000 new cases are diagnosed every year with one in five cases occurring in people younger than 55, according to the American Cancer Society. A new study provides insights that may eventually help oncologists better predict how the disease will respond to certain therapies, leading to improved survival outcomes for patients.

The findings were recently published in the journal *Scientific Reports*. A team of researchers from the University of Maryland School of Medicine (UMSOM) Department of Radiation Oncology and the University of Maryland Marlene and Stewart Greenebaum Comprehensive Cancer Center (UMGCCC) analyzed the pre-treatment CT scans of patients with head and neck squamous cell carcinoma (HNSCC) to locate radiomic biomarkers that can be used to predict the aggressiveness of the disease and its response to treatment.

CT scans are a standard pre-treatment diagnostic tool for patients with HNSCC and are used by oncologists to create individualized treatment plans. In this study, researchers took a closer look at the data collected by these scans in 203 patients from UMGCCC and 77 patients from the MD Anderson Cancer Center dating back to 2003. Using radiomics, advanced mathematical and statistical algorithms, they identified tumor features that are not otherwise visible to the human eye. These biomarkers were then used to develop predictive models for treatment, focusing on the likelihood of progression-free survival after treatment. Researchers concluded that the identification of these radiomic biomarkers offer valuable insights into who will be most likely to benefit from certain treatments.

> ***Our Institute for Genome Sciences team played a crucial role in this study by helping to acquire the clinical data necessary for analysis, as well as evaluating & validating the obtained results.***
>
> Daria A. Gaykalova, PhD

"Integrating prognostic and predictive biomarkers into clinical care could help to provide more targeted therapies, leading to improved survival outcomes for patients," said the study's Senior Author, Lei Ren, PhD, Professor of Radiation Oncology and Associate Chief of Physics Research in the Department of Radiation Oncology at UMSOM. "The findings from this study pave the way for future investigations through larger clinical trials to further evaluate the clinical efficacy of radiomics biomarkers for progression-free survival prediction in HNSCC patients."

Despite advancements in surgical techniques and other therapies, the 5-year survival rate for HNSCC remains around 50 percent. Tobacco smoking and alcohol consumption significantly increase the risk of HNSCC, as well as certain strains of Human Papillomavirus (HPV).

Typical treatment for these cancers may include surgically removing the tumor, administering radiation to the affected area, or giving the patient a regimen of chemotherapy, immunotherapy, or a combination of therapies. These treatments can cause potentially permanent side effects impacting a patient's ability to see, swallow, or speak. Researchers found that the use of radiomic biomarkers in treatment planning may also allow oncologists to recommend less invasive treatment protocols, therefore reducing the risk of lasting side effects.

“This research is reflective of our goal at UMGCCC to improve outcomes and reduce side effects for patients with HNSCC and other forms of cancer,” said William F. Regine, MD, the Isadore and Fannie Schneider Foxman Professor and Chair of the University of Maryland Department of Radiation Oncology. “Exacting imaging biomarkers from standard-of-care CT scans offers a noninvasive approach without additional costs to patients.”

“Our Institute for Genome Sciences team played a crucial role in this study by helping to acquire the clinical data necessary for analysis, as well as evaluating and validating the obtained results,” said Daria Gaykalova, PhD, Associate Professor of Otorhinolaryngology at UMSOM and researcher at IGS. “We are proud to contribute to research in head and neck and other forms of cancer to learn more about causes and treatments.”

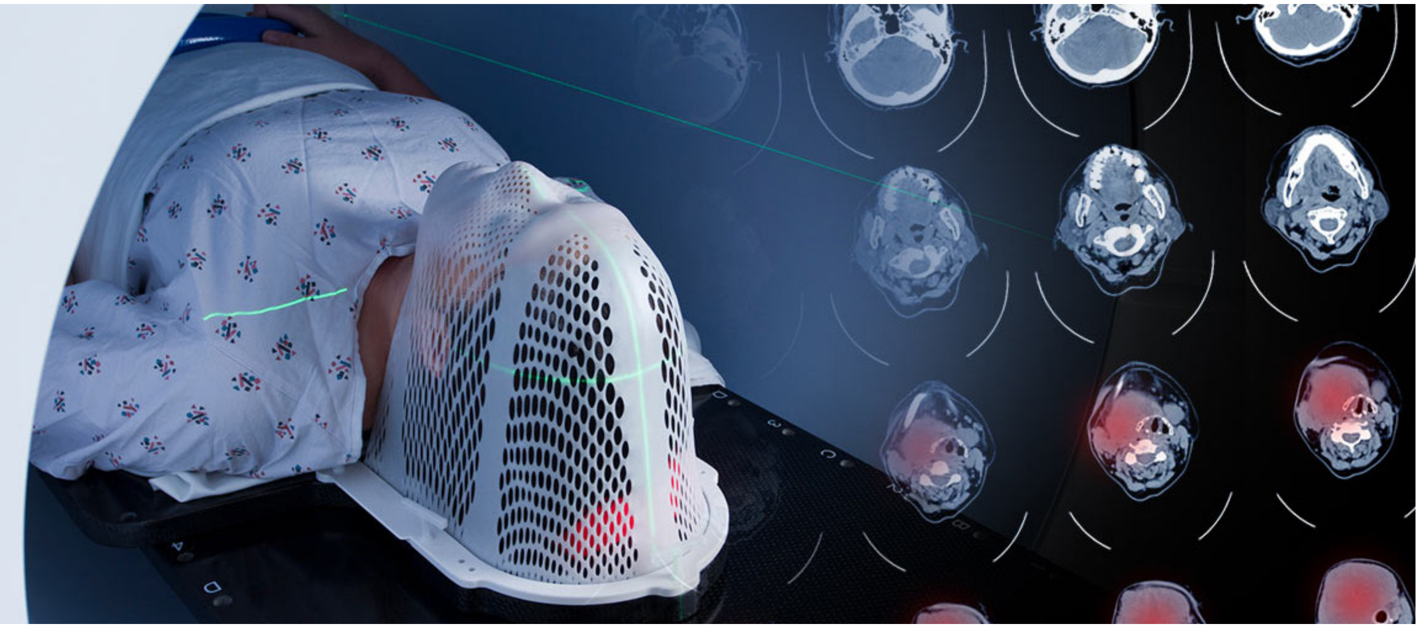
In future studies, researchers hope to gain a better understanding of these imaging biomarkers and their underlying meaning and validate their findings in data from other institutions. This research will need to be completed before a prospective clinical trial could be offered to patients for treatment intervention based on the imaging biomarkers and prognosis prediction. For example, patients with imaging biomarkers associated with less aggressive disease might be offered a decreased radiation protocol.

“While preliminary, this study offers a promising path forward to learn about novel predictors of response and to develop a non-invasive tool to personalize different treatment options for head and neck cancers,” said Taofeek K. Owonikoko, MD, PhD, Executive Director of UMGCCC and the Marlene and Stewart Greenebaum Distinguished Professor of Oncology at UMSOM.

Daria A. Gaykalova, PhD
Associate Professor
Otorhinolaryngology-Head & Neck Surgery

The study was funded in part by the National Institutes of Health (NIH) grants R01DE033426 and U54CA273956, and the National Institute of Dental and Craniofacial Research (NIDCR). NIDCR’s stated mission is to improve oral, dental, and craniofacial health through research, research training, and the dissemination of health information. **IGS**

Originally published on the UMSOM website.



UNDER the MICROSCOPE

A Look at IGS Featured Research

New Research Simulates Cancer Cell Behavior

Researchers at the University of Maryland School of Medicine Invent Software Fueled by Genomics into Mathematical Models to Predict Cancer Cell Behavior

Published In: ***Cell***

Lead IGS Autyhors: Jeanette Johnson, PhD; Elana Fertig, PhD, FAIMBE; Daniel Bergman, PhD

In the same vein as weather forecast models that predict developing storms, researchers now have developed a method to predict the cell activity in tissues over time. The new software combines genomics technologies with computational modeling to predict cell changes in behavior, such as communication between cells that could cause cancer cells to flourish.

Researchers at the University of Maryland School of Medicine's (UMSOM) Institute for Genome Sciences (IGS) co-led the study that published online on July 25 in the journal *Cell*. It is the result of a multi-year, multi-lab project at the interface of software development with important collaborations between bench and clinical team science researchers. This research eventually could lead to computer programs that could help determine the best treatment for cancer patients by essentially creating a "digital twin" of the patient.

"Although standard biomedical research has made immeasurable strides in characterizing cellular ecosystems with genomics technologies, the result is still a single snapshot in time—rather than showing how diseases, like cancer, can arise from communication between the cells," said Jeanette Johnson, PhD, a Postdoc Fellow at the Institute for Genome Sciences (IGS) at UMSOM and co-first author of this study. "Cancer is controlled or enabled by the immune system, which is highly individualized; this complexity makes it difficult to make predictions from human cancer data to a specific patient."

What makes this research unique is the use of a plain-language "hypothesis grammar" that uses common language as a bridge between biological systems and computational models and simulates how cells act in tissue.

Paul Macklin, PhD, Professor of Intelligent Systems Engineering at Indiana University led a team of researchers who developed the grammar to describe cell behavior. This grammar allows scientists to use simple English language sentences to build digital representations of multicellular biological systems and enabled the team to develop computational models for diseases as complex as cancer.

"As much as this new 'grammar' enables communication between biology and code, it also enables communication between scientists from different disciplines to leverage this modeling paradigm in their research," said Daniel Bergman, PhD, a scientist at IGS and Assistant Professor of Pharmacology and Physiology at UMSOM and co-leading author with Dr. Johnson.

Dr. Bergman and his colleagues at IGS then combined this grammar with genomic data from real patient samples to study breast and pancreatic cancer, with technologies such as spatial transcriptomics.

In breast cancer, the IGS team modeled an effect where the immune system cannot curtail tumor cell growth and instead promotes invasion and cancer spread. They adapted this computational modeling framework to simulate a real-world immunotherapy clinical trial of pancreatic cancer.

Using genomics data from untreated tissue samples of pancreatic cancer, the model predicted that each virtual "patient" had a different response to the immunotherapy treatment—showcasing the importance of cellular ecosystems for precision oncology. For example, pancreatic cancer is a difficult cancer to treat, in part, because it is often surrounded by a dense structure of non-cancerous cells called fibroblasts. The team used new spatial genomics technology to further demonstrate the ways fibroblasts communicate with tumor cells. The program allowed the scientists to follow the growth and progression of pancreatic tumors to invasion from real patient tissue.

"What makes these models so exciting to me as someone who studies immunology is that they can be informed, initialized, and built upon using both laboratory and human genomics data," said Dr. Johnson. "Immune cells are amazing and follow rules of behavior that can be programmed into one of these models. So, for instance, we can take data and treat it as a snapshot of what the human immune system is doing, and this framework gives us a sandbox to freely investigate our hypotheses of what's happening there over time without extra costs or risk to patients."

> **"*Ever since my transitioning from my training in weather prediction at the University of Maryland, College Park into computational biology, I have believed that we could apply the same principles to work across biological systems to make predictive models in cancer.*"**
>
> Elana J. Fertig

"Ever since my transitioning from my training in weather prediction at the University of Maryland, College Park into computational biology, I have believed that we could apply the same principles to work across biological systems to make predictive models in cancer. I am struck by how many rules of biology we don't yet know," said Elana J. Fertig, PhD, Director of IGS, Associate Director of Quantitative Sciences for the Greenebaum Comprehensive Center, and Professor of Medicine and Epidemiology at UMSOM and a lead author on the study. "Adapting this approach to genomics technologies gives us a virtual cell laboratory in which we can conduct experiments to test the implications of cellular rules entirely in silico."

Dr. Fertig calls the research "a tapestry of team science" with additional validation of the computational models coming from clinical collaborators at Johns Hopkins University and Oregon Health Sciences University.

The new grammar is open source so that all scientists can benefit from it. "By making this tool accessible to the scientific community, we are providing a path forward to standardize such models and make them generally accepted," said Dr. Bergman.

To demonstrate this generalizability, Genevieve Stein-O'Brien, PhD, the Terkowitz Family Rising Professor of Neuroscience and Neurology at Johns Hopkins School of Medicine (JHSOM) led researchers in using this approach in a neuroscience example in which the program simulated the creation of layers as the brain develops.

"With this work from IGS, we have a new framework for biological research since researchers can now create computerized simulations of their bench experiments and clinical trials and even start predicting the effects of therapies on patients," said Mark T. Gladwin, MD, Vice President for Medical Affairs at the University of Maryland, Baltimore, the John Z.

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and Akiko K. Bowers Distinguished Professor and UMSOM Dean. “This has important applications to enable digital twins and virtual clinical trials in cancer and beyond. We look forward to future work extending this computational modeling of cancer to the clinic. **IGS**”

The team of senior authors on this study include, Paul Macklin, PhD, Associate Dean for Undergraduate Education and Professor of Intelligent Systems Engineering at the Indiana School of Informatics, Computing and Engineering at Indiana University, Genevieve Stein-O’Brien, Bloomberg Assistant Professor of Neuroscience and Assistant Director Single-Cell Training and Analysis Center (STAC) at Johns Hopkins University, and Dr. Fertig are continuing efforts to disseminate this software and extend its integration with genomics data for automatic model formulation through the National Cancer Institute (NCI) Informatics Technology in Cancer Research Consortium, who funded this study. Additional benchmarking of this study and applications of the software to breast and pancreatic cancer are supported from numerous NCI grants, the Jayne Koskinas Ted Giovanis Foundation, the National Foundation for Cancer Research, the Cigarette Restitution Fund Program from the State of Maryland, and the Lustgarten Foundation.

First Ever One-Day Island-Wide Soil Microbiome Study Completed on Crete

Researchers from the University of Maryland School of Medicine Among the Scientists to Make Surprising Findings on the Record-Setting Day

Published In: ***Environmental Microbiome***

Lead IGS Authors: Johanna Holm, PhD; Lynn Schriml, PhD

Additional IGS Authors: Mike Humphrys, Apaala Chatterjee

It was nothing short of “groundbreaking” research—literally. Scientists conducted the first-ever study of an island’s soil microbiome—on Crete—all in one day—a major challenge since the Greek island is about 160-miles long and rises more than 8,000 feet above sea level.

The genomic sequencing and analysis of more than 435 samples taken that day have just been published in *Environmental Microbiome*.

A microbiome is the community of organisms—bacteria, fungi, viruses—that live together in one space, such as the in the gut, on the skin, or in water or soil. A healthy soil microbiome is critical for maintaining a thriving ecosystem, including mitigating climate change, sustaining plant health, and balancing carbon dioxide in the atmosphere.

“It was a history-making day—the first large-scale, island-wide sampling ever conducted on Crete, and the first comprehensive survey of its soil microbiome. From coastal beaches to mountain peaks, the Island Sampling Day captured a snapshot in time,” said the study’s lead author Johanna Holm, PhD, a researcher at the Center for Advanced Microbiome Research and Innovation (CAMRI) and Assistant Professor at the University of Maryland School of

Lynn Schriml, PhD on site in Crete, Greece.

Medicine (UMSOM). “Most importantly, by collecting the soil samples all on the same day, we minimized variation from weather fluctuations, seasons, and land usage.”

During the annual meeting of the Genomic Standards Consortium (GSC) on June 15, 2016, scientists and citizen volunteers sampled soil across 72 locations throughout Crete.

The GSC is an international group of scientists whose mission is to develop metadata standards for reporting genomic data so that it is easily discoverable and interoperable to researchers across different countries. The GSC developed strict sampling protocols, ensuring the collection was standardized and scientifically rigorous.

Some of the results surprised the researchers. For example, they discovered that microbes in the Crete soil remained highly diverse throughout the island.

“We thought that perhaps the elevation might reduce the microbial diversity due to more extreme conditions,” said Lynn Schriml, PhD, the study leader, Professor, and scientist at UMSOM’s Institute for Genome Sciences (IGS) and GSC President. “We found that it was a combination of environmental factors, soil moisture, and nitrogen that drove microbial diversity across ecozones.”

In addition to creating a new framework for comparing ecosystems by collecting all samples in one day, the GSC has made this data openly available for reuse, encouraging future studies. Data can be accessed here. **IGS**

In Two Commentaries, Researchers Say AI Could Be the Game Changer in Predicting Health Outcomes, But It Should Not Be the Only Method

Virtual Cells for Predictive Immunotherapy

Published In: ***Nature Biotechnology***

Lead Authors: Elana J. Fertig, PhD, FAIMBE; Daniel Bergman, PhD;

Balancing Ethical Data Sharing and Open Science for Reproducible Research in Biomedical Data Science

Lead IGS Authors: Elana J. Fertig PhD, FAIMBE; Dmitrijs Lvovs, PhD

Additional IGS Authors: Anup Mahurkar, PhD; Owen White, PhD

Published In: ***Cell Reports Medicine***

With the advent of artificial intelligence (AI), predictive medicine is becoming an important part of healthcare, especially in cancer treatment. Predictive medicine uses algorithms and data to help doctors understand how a cancer might continue to grow or react to specific drugs—making it easier to target precision treatment for individual patients.

While AI is important in this work, researchers from University of Maryland School of Medicine (UMSOM) say that it should not be relied on exclusively. Instead, AI should be combined with other

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> ***With a mathematical model, we could create virtual cancer cells and healthy cells and write a program that would mimic how those cells interact and evolve inside of a tumor with different types of treatments.***
>
> Daniel Bergman, PhD

(continued from page 27)

methods, such as traditional mathematical modeling, for the best outcomes.

In a commentary published in Nature Biotechnology, Elana J. Fertig, PhD, FAIMBE, Director of the Institute for Genome Sciences (IGS) and Professor of Medicine at UMSOM and Daniel Bergman, PhD, an IGS scientist argue that mathematical modeling has been underestimated and under-used in precision medicine to date.

All health computational models need three key components to work: datasets, equations, and software. Then, after generating data comes leveraging it to improve early diagnoses, discover new treatments, and aid understanding of the diseases.

In a second commentary, out in *Cell Reports Medicine*, Dr. Fertig and IGS colleagues Dmitrijs Lvovs, PhD, Anup Mahurkar, PhD, and Owen White, PhD, address how to ethically share health data and methods to create reproducible science.

Taken together, the two commentaries set a foundational approach to generating, analyzing, and ethically sharing data to benefit both patients and science.

Explaining the argument of the *Nature Biotechnology* commentary Dr. Fertig said, "AI and mathematical models differ dramatically in how they arrive at an outcome. AI models first must be trained with existing data to make an outcome prediction, while mathematical models are directed to answer a specific question using both data and biological knowledge."

That means that when data is sparse—as it often is in newer cancer treatments such as immunotherapy—AI can over generalize, resulting in biased or inaccurate outcomes that cannot be reproduced by other scientists. Mathematical modeling, on the other hand, uses known biological mechanisms, learned from scientific experiments, to explain how it arrived at an outcome.

"For example, with a mathematical model, we could create virtual cancer cells and healthy cells and write a program that would mimic how those cells interact and evolve inside of a tumor with different types of treatments," said Dr. Bergman, Assistant Professor at IGS and UMSOM's Department of Pharmacology, Physiology, and Drug Development. "At this time, AI cannot give us that type of specificity."

The authors state that in addition to using both types of models in "computational immunotherapy," using a breadth of populations, and making datasets publicly available are critical for the most accurate outcomes.

"Data breadth and accuracy are key. Artifacts in the dataset, or even a simple typo in computer code, can throw off the accuracy of either type of model," added Dr. Fertig. "Therefore, for any analysis pipeline to work correctly, it must be reproducible and that can only be assured by open science—giving access to other researchers whose work can confirm the models will get the right treatment to the right patient."

However, reproducibility remains a critical challenge in science. In a 2016 article in Nature surveying more than 1500 scientists, more than 70% of researchers said they have tried and failed to reproduce another scientist's experiments, and more than half have failed to reproduce their own experiments.

"Reproducible research enables investigators to verify that the findings are accurate, reduce biases, promote scientific integrity, and build trust," explained Dmitrijs Lvovs, PhD, Research Associate at IGS and first author on the Cell Reports Medicine commentary. "Because data science is computationally driven, all results should be transparent and automatically reproducible from the same dataset if the analysis code is readily available through open science."

While that sounds simple enough—and there are best practices in place—the challenge, the authors argue, is how to share data while protecting patient privacy and blocking unauthorized data breeches. Genomic data, when combined with personal health information (PHI), could lead to re-identification of patients, a privacy violation.

The authors say that creating ethical open science data sharing means: 1. Getting detailed informed consent from patients; 2. Ensuring data quality when collecting and processing data by mitigating errors; 3. Harmonizing and standardizing data collected from disparate sources; 4. Using and creating resources and platforms, such as multiomic, clinical, public health, and drug discovery repositories; and 5. Working with vetted pipelines, such as open source analysis tools and software platforms.

“Ethical and responsible data sharing democratizes research, supports the advancement of AI, and informs public health policies,” said Dr. Lvovs. “With ethical and responsible data sharing, the biomedical research community can maximize the benefits of shared data, accelerate discovery, and improve human health.” **IGS**

A Previously Unknown Population of Neurons in the Hypothalamus Could Lead to New Obesity Treatments

Leptin-activated Hypothalamic BNC2 Neurons Acutely Suppress Food Intake

Published in: ***Nature***

IGS Author: Brian Herb, PhD

Obesity affects a staggering 40 percent of adults and 20 percent of children in the United States. While some new popular therapies are helping to tackle the epidemic of obesity, there is still so much that researchers do not understand about the brain-body connection that regulates appetite. Now, researchers have discovered a previously unknown population of neurons in the hypothalamus that regulate food intake and could be a promising new target for obesity drugs.

In a study published in Nature, a team of researchers from the Laboratory of Molecular Genetics at Rockefeller University in New York, the Institute for Genome Science (IGS) at the University of Maryland School of Medicine (UMSOM) in Baltimore, as well as New York and Stanford Universities discovered a new population of neurons that is responsive to the hormone leptin. Leptin responsive neurons are important in obesity since leptin is sent to the brain from the body’s fat stores to suppress hunger.

“We’ve long known that the hypothalamus—located deep in the brain—plays a role in hunger, hormone levels, stress responses, and body temperature,” said Brian Herb, PhD, a scientist at IGS and a Research Associate of Pharmacology, Physiology, and Drug Development at UMSOM. His research published in 2023 in *Science Advances* was the first time that scientists used single-cell technology to map the cells in the developing hypothalamus in humans, from precursor stem cells to mature neurons.

“Since our earlier research showed that unique regulatory programs in genes give rise to specialized neuronal populations—it makes sense that this new research discovered a previously unknown set of neurons that regulate energy and food intake,” Dr. Herb added

Through several experiments with mice, the researchers found that this previously unknown neuronal population that express both receptors for leptin and the BNC2 gene not only helps suppress hunger, but also responds to food-related sensory cues, such as food palatability and nutritional status. For example, the researchers used CRISPR-Cas 9 to knock out the leptin receptor (LEPR) in these BNC2 neurons. Those mice ate more and gained more weight than control mice. In addition, researchers added fluorescence to the BNC2 neurons and noticed when they fed mice after fasting, the BCN2 neurons activated, whereas previously known neuronal populations in the hypothalamus did not react.

“These findings add a critical new component to our understanding of how neurons impact appetite and obesity,” Dr. Herb said. “This could be a future target for obesity treatment, such as by activating these neurons to reduce weight or suppress hunger.” **IGS**

Summer in the Lab

Faculty at the Institute for Genome Sciences worked with 39 students throughout the summer. Of those, Michelle Giglio, PhD, and Joe Receveur, PhD, guided 17 high school students participating in the IGS High School Summer Bioinformatics Program that included classes and field trips to learn more about genomics, bioinformatics, and Python programming.

Also, 22 summer interns worked in the lab or on analytical projects with their faculty mentors. Some came from other programs and collaborations throughout the University of Maryland system, including the University of Maryland Scholars Summer Research Program (UM Scholars), Supporting Undergraduate Members in Microbiology and Immunology Research (SUMMIR), Nathan Schnaper Intern Program in Translational Cancer Research (NSIP), National Foundation for Cancer Research Summer Internship (NFCR), and the Bridges to the Doctorate program (B2D).

The interns who worked on research projects, in alphabetical order, are:

Maryam Ali

Mentor: Daniel Lesperance, MS

Project Title: *Gearing Up for Collaboration: Datasets, Outreach, and Expression*

Worked on understanding how the well-established Hearing gEAR could be applied to a new platform, Cancer gEAR. Uploaded multiple datasets to both platforms to promote collaboration. Learned that both platforms are interactive tools to explore gene expression, can analyze single and multi-genes at the same time, look at gene expression changes over time, and discovered that more outreach is needed for Cancer gEAR to promote visibility, usage, and awareness, as well as to understand the potential for collaborative data and discovery.

Dana Aument

Mentor: Scott Devine, PhD

Project Title: *Constructing a Plasmid to Track L1 Retrotransposons*

Worked to generate a plasmid that could be used to test the mobilization activity of a specific LINE-1 element in humans. LINE-1 elements are active transposable elements found in the human genome that can generate mobile element insertions at new sites in the human genome. She tested an element on chromosome 14 (chr14) to determine how active it is in HeLa cells compared to positive and negative LINE-1 test plasmid controls. Using techniques including cloning and sequencing, she successfully generated the chr14 test plasmid.

Janice Baffoe Bonnie

Mentor: Vincent Bruno, PhD

Project Title: *Lomentospora prolificans in Human Cells*

Studied the various reactions of human cells when infected with *Lomentospora prolificans*.

Lina Berhaneyessus, UM Scholars

Mentor: Bing Ma, PhD

Project Title: *Investigating Immune Markers Correlated with Neonatal Leaky Gut*

Discovered that neonates—babies in the first 28 days of life—who had a high abundance of TGF-β1 (Transforming Growth Factor beta-1) with high intestinal perforation (IP), that it could be physiological response to gut barrier weakness and injury.

Aryaan Duggal

Mentor: Elana Fertig, PhD

Project Title: *Applying KRAS Regulatory Logic to the Loveless SC Atlas*

Discovered the Loveless Single-Cell Atlas that offers single cell expression from pancreatic ductal adenocarcinomas (PDACS) to evaluate transferability and biological insight of the pipeline.

Harsha Gandluri

Mentor: Daria Gaykalova, PhD

Project Title: *The Role of TMEM14C in Racial Disparities in HPV-Negative Head and Neck Squamous Cell Carcinoma (HNSCC)*

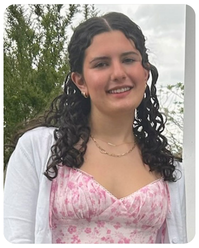
Discovered that TMEM14C is significantly upregulated in Black patients compared to White HNSCC patients. The high expression of TMEM14C correlates with significantly worse overall survival in Black patients. This may be potentially linked to specific cell cycle changes that support proliferation.

Margaret Kato, UM Scholars

Mentor: Bing Ma, PhD

Project Title: *Genomic Specialization of Bifodobacterium for Human Milk Oligosaccharide Utilization in Preterm Gut Maturation*

Characterized, annotated, and performed pangenome functional and phylogenomic analysis on 15 *B.. breve* strains isolated from early preterm infants and revealed extensive strain-specific genomic contents underlying maternal milk metabolizing capabilities and postnatal gut barrier development. This resulted in a prerequisite for developing targeted live biotherapeutics to promote gut maturation to reduce the risk from leaky gut.



Ella Longman

Mentor: Elana Fertig, PhD

Project Title: *Agent-Based Model of PDAC Tumor Suppression*

Worked on a rules-based framework and hypothesis grammar for agent-based modeling of pancreatic ductal adenocarcinoma (PDAC) and ran the model through different hypotheses to better understand its progression.

Sophie Miller

Mentors: Isaac Chaudry; Lindsay Rutt, MS; Jacques Ravel, PhD

Project Title: *Purifying Proteins from Harmful Bacteria*

Worked on purifying virulent proteins from potentially harmful bacteria in the vaginal microbiome to enable in vitro studies.

Christopher Moore

Mentor: Isaac Chaudry; Lindsay Rutt, MS; Jacques Ravel, PhD

Project Title: *Purifying Proteins from Harmful Bacteria*

Worked on purifying virulent proteins from potentially harmful bacteria in the vaginal microbiome to enable *in vitro* studies.

Lucy Murr, SUMMIR Program

Mentor: Vincent Bruno, PhD

Project Title: *Candida Albicans and Human Cells*

Studied the various reactions of human cells when infected with *Candida albicans*.

Joshua Naranjo, B2D

Mentor: Elana Fertig, PhD

Project Title: *Developing An Agent-Based Model of the Pancreatic Ductal Adenocarcinoma Microenvironment and Host Immune Resistance*

Ran a model that showed both immune response and suppression, explosive growth of cancer cells in the environment and proved that agent-based modeling is a powerful tool for modeling disease.

Daniel Pintard, UMCP

Mentor: Alex Xu, PhD

Project Title: *Spatial Transcriptomics for the Investigation of Precursor Lesions in High-Grade Serous Ovarian Cancer*

Looked at Serous Tubal Intraepithelial Carcinomas (STICs) using spatial transcriptomics data. STICs are a precancerous lesion to high grade serous ovarian cancer, which is the most lethal and common form of ovarian cancer. Evaluated gene expression in fallopian tube sections containing STICs, with an aim in characterizing STIC gene expression patterns.

Lynijah Russell, NSIP

Mentors: Elana Fertig, PhD, and Daniel Bergman, PhD

Project Title: *Modeling Pancreatic Cancer and Precancer Microenvironments Using PhysiCell Agent-Based Simulations*

Developed a prototype pipeline to automate integration of multiomics data into agent-based models to create digital twins of pancreatic ductal adenocarcinoma (PDAC).

Anushka Shome, SUMMIR

Mentor: Franck Dumetz, PhD

Project Title: *Gain-of-Function Analysis and Genome Assembly in Trypanosomatids*

Researched the *Trypanosoma brucei* that is a parasitic species that is present in sub-Saharn Africa and is inhabits the blood plasma and body fluids.

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It causes deadly vector-borne diseases, such as sleeping sickness. She also participated to a submitted manuscript about RNA secondary structure prediction in *Leishmania donovani.*

Hamza Siddiqui

Mentor: Daniel Bergman, PhD

Project Title: *Cell Merger Capabilities in PhysiCell*

Developed a prototype pipeline to automate integration of multiomics data into agent-based models to create digital twins of pancreatic ductal adenocarcinoma (PDAC).

Brian Temu

Mentor: Victor Felix, MS

Project Title: Virgil: Grid Monitoring System

Achieved performance improvements on Virgil—a real-time web-based monitoring system for high-performance computing, including significantly faster dashboard response times, enhanced real-time data processing capabilities, and scalable architecture supporting larger grid environments.

Isaac Uy, NFCR

Mentors: Elana Fertig, PhD; Dmitrijs Lvovs, PhD

Project Title: *Subsampling Datasets for Spatial Transcriptomics*

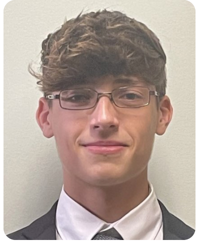
Used spatial transcriptomics to measure gene expression throughout tissue. Learned this can be integrated with other types of tissue analysis.

Cameron Westlake, NSIP

Mentor: Daria Gaykolova, PhD

Project Title: *Investigating the Functional Role of UBASH3B Isoforms in HPV-Negative Head and Neck Squamous Cell Carcinoma*

Among the findings, identified that the UBASH3B-1 isoform is associated with enhanced cell cycle progression, increased cellular proliferation, and migration, indicating its oncogenic potential.



Cameron Yeagle, NSIP

Mentors: Elana Fertig, PhD & Daniel Bergman, PhD

Project Title: *Agent-based Modeling of the Ductal Structure in Pancreatic Precancer*

Developed a model of the ductal structure of pancreatic cancer precursor lesions to identify key biophysical interactions that mediate early carcinogenesis.

Samiatu Yussuf, SUMMIR

Mentors: Julie Dunning Hotopp, PhD and Robin Bromley

Project Title: *Epitranscriptomics: Developing a Rapid Diagnostic to Identify Single-Based CRISPR-induced Deletions in Drosophila melanogaster*

Worked on developing an assay to detect the mutation to help breed flies to generate a population that only has the mutation to generate future homozygous lines.

IGS Summer Program Helps High School Students Become Scientists

by Claire Ravel

Many scientific research organizations only take college students as summer interns, but the Institute for Genomic Sciences (IGS) welcomes exceptional high school students every summer as well. Two past high school interns reflected on their experiences at IGS.

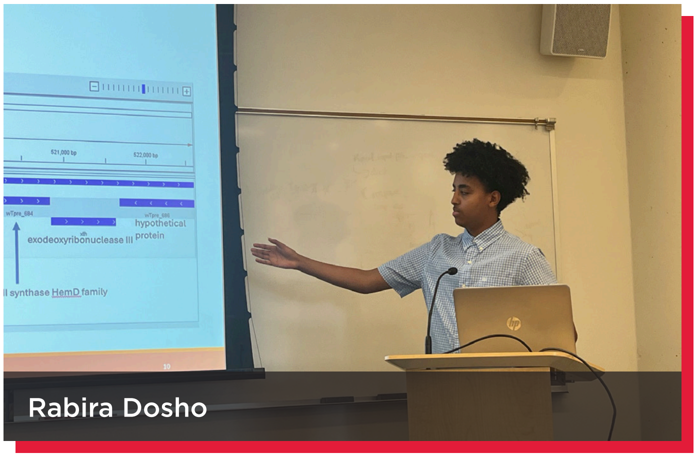
Rabira Dosho and Thomas Ludecke each spent summers doing scientific research at IGS. Rabira worked in the Julie Dunning Hotopp, PhD, lab and Thomas spent one summer working with Michelle Giglio, PhD, and the next with Franck Dumetz, PhD, and Joana Carneiro da Silva, PhD.

"It was a great way to learn about different types of research and get an introduction to the professional world of research," says Rabira, who graduated from Montgomery Blair High School in Silver Spring, MD, and started at Columbia University this fall, majoring in Engineering. "You meet tons of great people, with backgrounds from all across the world. As long as you are interested in learning, you can't lose with the experience."

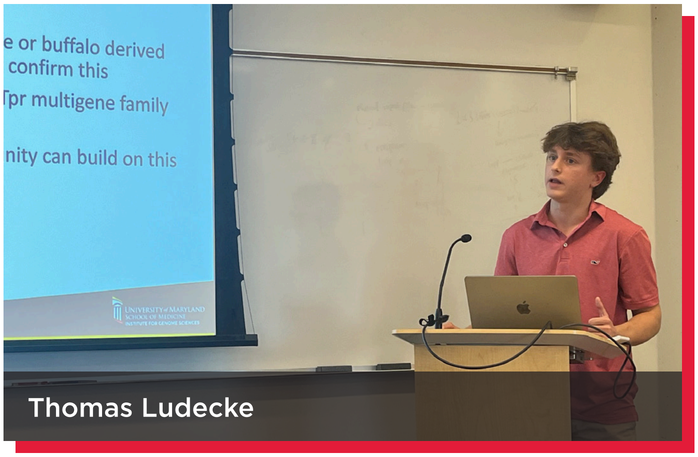
One highlight, Rabira recalls was attending the seminar series to learn about different types of research. For Thomas, the highlight was working in the lab, gaining valuable laboratory skills that he will use in his upcoming graduate studies, including how to navigate the scientific method, reiterating and refining his approach to address new questions. After graduating last spring from St. Andrews Episcopal School in Potomac, Maryland, he is attending the Massachusetts Institute of Technology majoring in Biotechnology.

"It changed a lot about what I want to do with my career," he says. "It's a really great experience and the responsibility of being a scientist as a high schooler was really meaningful. Anyone who is considering it should do it." **IGS**

> **_It was a great way to learn about different types of research & get an introduction to the professional world of research_**
>
> Rabira Dosho



Rabira Dosho



Thomas Ludecke

City Sampling Day Tracks Microbes Across Subways

Scientists collected 26 samples from subway platforms and train cars during this year's **City Sampling Day**, targeting high-touch areas such as seats, railings, escalator handrails, elevator buttons, and tile floors. Samples were gathered from **three trains and three stations**, with negative controls taken at the start and end of the effort.

The samples, collected globally on **June 20–21**, will be analyzed at the **MetaSUB Chris Mason Lab at Weill Cornell Medicine in New York**. They will be sequenced alongside the past five years of data to track the microbiome communities that thrive in urban transit systems.

Previous findings, published in *Cell* in 2021, revealed that cities each harbor their own distinct microbial fingerprints and uncovered more than **10,000 novel viral genomes** (study link). The 2024 sampling map and dataset are publicly available (map link). **IGS**

The team sampling subways from IGS included Lynn Schriml, PhD; Claudia Sanchez-Beato Johnson; IGS summer intern Margaret Kato; and Isaac Fertig.

Three Cheers

Promotions, Awards & Accolades Around IGS!

- **Jacques Ravel, PhD**, Director of IGS's Center for Advanced Microbiome Research and Innovation has been named Assistant Dean for Research Advancement, University of Maryland School of Medicine (UMSOM).

- **Andrew Neuwald, PhD**, IGS Affiliate Faculty and former IGS Faculty has been designated as Professor Emeritus in the Department of Biochemistry & Molecular Biology at UMSOM. This prestigious designation recognizes Dr. Neuwald's significant contributions to the academic community and his distinguished scholarship. The Emeritus status honors his commitment to excellence throughout his career.

- In the past year, three IGS faculty members have been promoted to full Professor. Congratulations to:

  Michelle Giglio, PhD, Professor of Medicine at UMSOM and Associate Director, Education and Outreach, IGS, and Associate Director, Analysis, Informatics Resource Center, IGS.

  Vincent Bruno, PhD, Professor of Microbiology and Immunology at UMSOM and a scientist at IGS.

  Lynn Schriml, PhD, Professor of Epidemiology and Public Health at UMSOM and a scientist at IGS.

- Shout out to **Anup Mahurkar, MS**, for his promotion to Associate Professor, Epidemiology and Public Health at UMSOM. Mahurkar also serves as Chief Information Officer at IGS and Executive Director of Software Engineering and IT at IGS's **Maryland Genomics**.

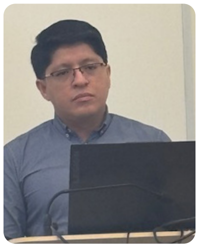
- IGS remains a foundational training ground for new genomic scientists. **Congratulations to those who defended their PhDs this year!**

Chris Holt, PhD
The Dunning Hotopp Lab
Genome Enabled Analyses of Onchocercidae Filarial Nematodes.

Bern Monari, PhD
The Ravel Lab
Characterizing the Composition, Structure, and Functional Capacity of the Vaginal Microbiota of Transmasculine Individuals Using Gender-Affirming Care

Riley Risteen, PhD
The Bruno Lab
Unraveling Host-Pathogen Interactions in Pulmonary Mucormycosis

Ryan Scalsky, PhD
The Silva Lab
Characterization of Putative Protective Parasite Targets of a Whole Organism Malaria Vaccine



Diego Veliz-Otani, PhD
The O'Connor Lab
Unifying Population Structure and Relatedness Analysis through a Coalescent Approach.

Kaylee Watson, PhD
The Dunning Hotopp Lab
Epitranscriptomics: Advancing RNA Modification Detection with ONT Direct RNA Sequencing.

GOOD TIMES AROUND IGS!

↑ **The Ament Lab** had a wonderful time at the wedding of two lab members this past summer. Congrats to Yumna Ahmed, MS, and Bobby Lease, who held a traditional Pakistani reception the day after their private wedding ceremony where Yumna wore an altered version of her mom's original wedding outfit. While many people were traveling for summer break, about half the lab was able to make it!

↑ Walk down Pearl Street and check out a picture of a lamp created by Owen White, PhD. The actual lamp lives in his IGS office, while the gallery features pictures of his invention.

↑ Several IGS faculty and staff members attended the Stand Up for Science Rally in Washington, DC on March 7, 2025 to protest cuts to science research positions and federal grants.

← Franck Dumetz, PhD, Research Associate at IGS and Graduate Student Susweta Roy from the IGS O'Connor Lab gave a talk for the Science Slam at Baltimore Underground Science Space (BUGSS) on genomic science last spring. Dr. Dumetz returned to BUGGS this summer to hold a conversation with students on Oxford Nanapore Sequencing and its usages in genomic science.

This summer, IGS faculty, staff, friends, pets, and family came together for an annual picnic. From bubbles for kids to relaxed conversations, good food and drink. It was a hot day but everyone had a sizzling good time!

Diversity 2025 Dinner & Celebration

IGS members, including Director Elana Fertig, PhD, attended UMSOM's annual Diversity Dinner & Celebration. The event supports the University's mission by broadening opportunities and resources essential to cultivating a truly inclusive and thriving environment and for the betterment of our vibrant and interconnected communities.

SAVE THE DATE

Nov. 4–7, 2025

Transcriptome Analysis

This workshop will introduce transcriptome sequencing and analysis techniques. It will include instruction on the use of different analytical tools, relevant file formats, reference genomes, reference-based alignment, and differential gene expression. Bulk, single-cell, and spatial approaches will be covered. The workshop will employ hands-on exercises using complete analytical pipelines on test datasets. Learn more and register **HERE**.

Dec. 8–12, 2026

Biology 039 Epigenetics

Join IGS faculty member **Daria Gaykalova, PhD**, Associate Professor, Department of Otorhinolaryngology-Head and Neck Surgery, University of Maryland School of Medicine, for this in-person workshop on the NIH campus. This workshop will address the basic principles of epigenetics, the role of epigenetic mechanisms in normal development and human disease, and the development of epigenetically effective drugs. **REGISTER HERE**.

Feb. 26, 2026

Frontiers in Genomics Lecture

Dissecting the Signaling Networks of Cellular Communities Driving Trajectories of Alzheimer's Disease and Brain Aging

Philip De Jager, MD, PhD, Chief, Division of Neuroimmunology; Co-Director, Multiple Sclerosis Center; Deputy Director, Taub Institute for Research on Alzheimer's Disease and the Aging Brain; Director, Center for Translational and Computational Neuroimmunology; Weil-Granat Professor of Neurology (in the Taub Institute for Research on Alzheimer's Disease and the Aging Brain), Columbia University.

Spring 2026, Stay Tuned!

Microbiome Analysis Workshop

This workshop will provide attendees with in-depth training on analysis of bacterial community sequence data, both whole metagenome shotgun and 16S. Tools for community profiling, gene clustering, and annotation will be explored. Learn more **HERE**.

New Grants for Our IGS Faculty

(IN ALPHABETICAL ORDER)

Seth Ament, PhD

National Institutes of Mental Health

Dissecting the Role of Ca2+ Channel Dysfunction in the Pathgenesis of Neurodevelopmental Disorders

Total Award: $570,515

Goal: Since disrupted calcium channel dynamics may be a common feature in a larger subset of Neurodevelopmental Disorders (NDD), studying the impact of these CaV1.2 mutations on neuronal function will help us understand the role of calcium signaling in NDD.

Seth Ament, PhD

National Institutes of Health

Internal Dynamics of the Postsynaptic Density

Total Award: $238,490

Goal: To assess previously unexplored features of brain synapses that may allow their performance to be adjusted in unexpected ways and will help understand the biological basis of forming memories. Also, since mental illness frequently arises from aberrant synapse function, these experiments will help determine the origin and potential treatments for diseases including schizophrenia and depression.

Seth Ament, PhD

Maryland Stem Cell Research Fund-Discovery

Convergent Effects of Genetic and Inflammatory Risk Factors for Autism Spectrum Disorders on the Development of Human Purkinje Cells

Total Award: $345,000

Goal: To study the central hypothesis that genetic risk factors for Autism Spectrum Disorder (first-hit) and early-life exposure to inflammation (second-hit) have convergent effects on the maturation of Purkinje cells.

Sterling Arjona, PhD

Maryland Stem Cell Research Fund-Fellowship

Implication of SETD1A Loss-of-Function in DNA Replication Stress During Neural Induction

Total Award: $130,000

Goal: To understand how impacts of histone modifiers on DNA replication and DNA damage contribute to the pathogenesis of neurodevelopment diseases using SETD1A as a model.

Vincent Bruno, PhD

National Institute of Allergy and Infectious Diseases

Therapeutic Targeting the Host Hypoxia-Response Pathway to Treat Mucormycosis

Total Award: $3,882,359

Goal: To discover novel therapies to treat mucormycosis, a deadly invasive fungal infection with limited treatment options, no vaccines, and a mortality rate greater than 50 percent.

Vincent Bruno, PhD

Lundquist Institute/National Institutes of Health

Deciphering Immunopathogenesis of MUCORmycosis to ADVANCE Risk Stratification Diagnosis and Management of the Disease

Total Award: $3,016,356

Goal: To perform all of the sequence generation and computational analysis for this research.

Joana Carneiro da Silva, PhD

National Institutes of Allergy and Infectious Diseases

Genomic Surveillance for Artemisinin Resistance in Africa

Total Year-One Award: $34,497 year one (out years TBD)

Goal: To provide proof-of-concept for a phenotype-independent genomic surveillance approach to detect selection in populations sampled over time in genes involved in parasite functions implicated in artemisinin resistance

New Grants for Our IGS Faculty

(IN ALPHABETICAL ORDER)

Elana Fertig, PhD

Break Through Cancer

Break Through Cancer Scientist: Dima Lvovs

Total Award: $232,746

Goal: To support Dima Lvovs as a Break Through Cancer Scientist working with the Break Through Cancer Data Science Hub.

Elana Fertig, PhD

Break Through Cancer

Break Through Cancer: Data Science Hub

Total Award: TBD; First Year: $128,859

Goal: To unify leading data science investigators into a collaborative network that will accelerate and maximize the research and discovery objectives of BTC.

Tracy Hazen, PhD

ENA Respiratory

ENA Study Agreement

Total Award: $591,834

Goal: Conduct a validation study to evaluate the room temperature stability of respiratory pathogens in a transport buffer system.

Brian Herb, PhD

National Institute on Drug Abuse

Joint Decomposition of SCORCH Multiomic Data to Explore the Impact of Substance Use Disorder (SUD) and HIV on Reward Circuitry and Neuroinflammation

Total Award: $2,709,959

Goal: To establish a SUD/HIV focused data ecosystem with SCORCH data as its foundation and expand the collection to include historical, current, and future relevant non-SCORCH datasets to help identify characteristic biological signatures of SUD/addiction and HIV in the brains of non-human models and to dissect compound signals in human patients with varied genetic and medical backgrounds. These harmonized datasets and signatures of addiction/HIV will be made available to the greater neuroscience community through NeMO Analytics, which will act as a genomics analysis hub for the field.

Tim O'Connor, PhD

Rush University/National Institute on Aging

Mexican Teachers Cohort Study: Genetics and Cognitive Function

Total Award: $759,285

Goal: To contribute nearly 20,000 GWAS and 5,000 whole genome sequences to the Alzheimer's Disease Sequencing Project (ADSP) from participants of the "Estudio de la Salud de las Maestras" (Mexican Teachers Cohort), to detect novel genetic drivers of cognitive function in this large Mexican cohort, in combination with existing ADSP cohorts.

Jacques Ravel, PhD

Gates Foundation

The Vaginal Microbiome Research Consortium (VMRC) Shared Data Portal

Total Award: $371,417

Goal: The VMRC Data Portal will be a valuable resource dedicated to collecting and disseminating all standardized and harmonized VMRC omics data and metadata currently stored elsewhere. Future features will include data ingestion and transfer to cloud-based computational infrastructure, among others. The VMRC Data Portal will provide online training to all VMRC members on how to use the VMRC Data Portal to maximize the value of the resource.

David Serre, PhD

National Institute of Allergy and Infectious Diseases

Characterization of Plasmodium Falciparum Long Non-coding RNAs and Their Roles in Gene Regulation

Total Award: $445,488

Goal: To rigorously and comprehensively examine the role of long non-coding RNAs (lncRNAs) in regulating *P. falciparum* gene expression and parasite development using a unique combination of genomic and bioinformatic approaches and state-of-the-art molecular parasitology assays.

New Grants for Our IGS Faculty

(IN ALPHABETICAL ORDER)

David Serre, PhD

National Institutes of Health

Investigating the Mechanisms Underlying Mosquito Infectiousness in Malaria

Total Award: $70,437

Goal: To conduct bioinformatic analyses and interpretation of genomic data that the project generates.

Hervé Tettelin, PhD

University of Maryland College Park

Cellular Mechanisms by Which Neisseria Gonorrhoeae Infects the Female Reproductive Tract

Total Award: $933,000

Goal: To oversee all spatial transcriptomics data generation and analyses, as well as the integration of these data with other experimental data this project generates.

Hervé Tettelin, PhD

National Institutes of Health

Cardiac Microlesion Formation During Invasive Pneumococcal Disease

Total Award: $712,109

Goal: Oversee all large scale bGWAS analyses and follow-up *in silico* gene function prediction analyses, all *in vivo* NanoString-based targeted transcriptomics data generation and analysis activities, and all Illumina-based whole genome sequencing of novel isolates associated with cardiac damage or for the verification of mutants generated over the course of the proposed studies.

Owen White, PhD*

National Heart, Lung, and Blood Institute

A Consortium Facilitation, Coordination and Data Management Center for the Human Virome Program

Total Award: $14,592,185

Goal: To establish a Consortium Organization and Data Collaboration Center (CODCC) dedicated to providing technical and administrative support for researchers and endeavors within the Human Virome Program consortium. Our goal is to develop a CODCC characterized by fairness, responsiveness, efficiency, and cutting-edge computational analysis capabilities.

*Read More About This Project on **Page 12**

Owen White, PhD

National Institute of Drug Abuse

NeMO Archive: SCORCH Support, Coordination and Outreach—Renewal

Total Award: $8,483,770 total

Goal: To continue the operation of the NeMO-SCORCH data center which is the coordination center to analyze single cell and other molecular data sets generated by Single Cell Opioid Responses in the Context of HIV (SCORCH) and other NIDA-funded HIV and substance use disorder projects.

Owen White, PhD

National Institute of Mental Health

A BRAIN Initiative Resource: The Neuroscience Multi-omic Data Archive—Supplement

Total Award: $2,777,628

Goal: To further support the research community involved in the BRAIN Initiative given that, so far, the archive has collected five-fold more data than planned. The Neuroscience Multi-Omic Archive (NeMO Archive) is a data repository that is specifically focused on the storage and dissemination of omic data from the BRAIN Initiative and related brain research projects. The Archive has accumulated over 700 TB (~2.7 million files) of unrestricted transcriptomic and epigenetic sequence data from mouse, human, and marmoset of which users have performed cumulative downloads of over 380 TB.

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