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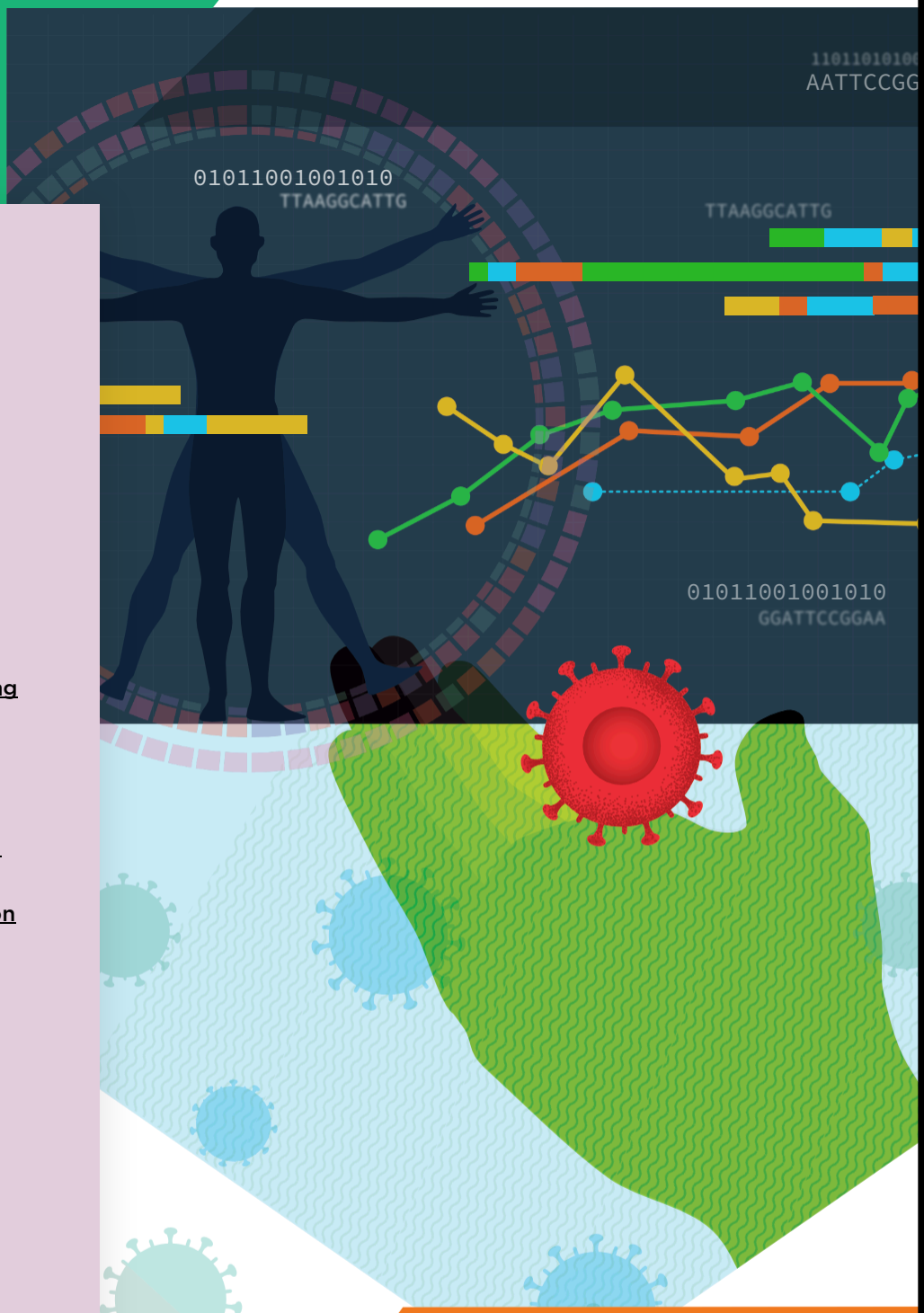
INSTITUTE FOR GENOME SCIENCES

Insider

WINTER 2024

UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES



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DIRECTOR'S CORNER

Dear All:

Happy 2024! While our Baltimore Ravens came up shy of heading to the Superbowl, we've had a lot to celebrate here at the Institute for Genome Sciences. This newsletter includes the research we've been tackling; the grants we've scored; our national media hits; and a great cheering section.

Seth Ament, PhD, received national media coverage for his research showing that inflammation in the brains of young children may cause autism or other mental health disorders. Check out the many articles in our Media Highlights on page 14.

Not only does our research continue to get media attention, but we continue to publish in top-tier journals, as you can read about in our Under the Microscope section on page 5. Our faculty and students spent last fall at various conferences and giving talks on campus, as well.

Of course, we also leave some time for fun as you will see on page 21 from a summer family to picnic to Halloween costume contests and our annual holiday celebration.

I hope you have fun catching up on all we're up to here at IGS.

Jacques Ravel, PhD

ACTING DIRECTOR, INSTITUTE FOR GENOME SCIENCES
PROFESSOR, MICROBIOLOGY & IMMUNOLOGY, AND MEDICINE
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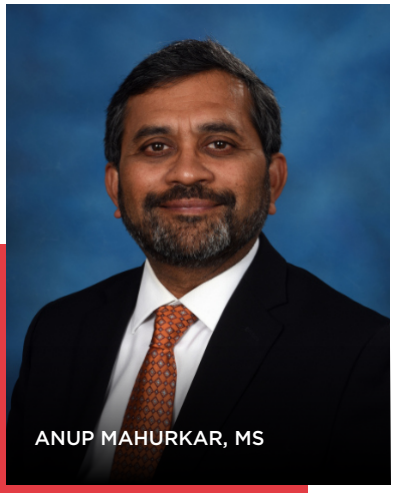
IGS' ANUP MAHURKAR DEVELOPS AN EASIER WAY FOR CLINICIANS TO ANALYZE DATA



ANUP MAHURKAR, MS

It's not uncommon for clinicians to ask themselves "What are the predictors of disease outcomes?" But often barriers—such as not being able to easily access, visualize, and analyze data—stands in their way of discovering the clues that ultimately might help their patients.

That's why Lisa Shulman, MD, Professor of Neurology, at the University of Maryland Medical School contacted Anup Mahurkar, MS, Executive Director, Bioinformatics Software Engineering, and the CIO at the Institute for Genome Sciences to create a simple solution.

The two, in partnership with Jonathan Crabtree, MS, created a new software program they dubbed POD-Vis—for Probing Outcomes Data with Visual Analytics—so that non-data scientists could visualize and analyze their own data.

POD-Vis
PROBING OUTCOMES DATA WITH VISUAL ANALYTICS

"POD-Vis uses simple language of predictors and outcomes so that it's easy to explore data," says Mahurkar. "The user can view relationships in clinical data, as well as generate hypotheses and preliminary data for a project."

Already, POD-Vis is being tested by researchers in the Intramural Branch at the National Institute on Deafness and Communication Disorders (NIDCD) to analyze audiology data on twenty-thousand patients across multiple NIH institutes, as well as for a multicenter trial on using statins after chemotherapy to prevent hearing loss. POD-Vis also is being deployed at the UM3 Institute for Health Computing (IHC) for researchers there to visualize and analyze large clinical datasets.

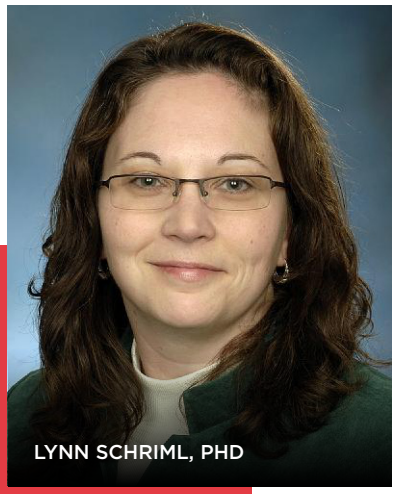
Learn more about POD-Vis at a Zoom seminar on March 28 from noon to 1 pm.

REGISTER HERE

> ***One user told us that POD-Vis makes data into a playground, Dr. Shulman says. That was the exact thing we were striving for: to make working with data easy and fun—though still relevant—for the non-trained person.***
>
> – LISA SHULMAN, MD

If you are interested in learning more about POD-Vis or have your clinical data loaded into POD-Vis please contact Dr. Shulman: lshulman@som.umaryland.edu or Mr. Mahurkar: amahurkar@som.umaryland.edu.

LYNN SCHRIML JOINS OMIC BON TO BETTER CLASSIFY BIODIVERSITY


LYNN SCHRIML, PHD

The newly formed Omic Biodiversity Observation Network (BON) has many goals, but one main purpose: to understand all forms of life at the molecular level and to use that knowledge for insight and action. That objective is what drew IGS's Lynn Schriml, PhD, to join the organization.

"As the current president of the Genomic Standards Consortium (GSC), I saw great synergies between our group and Omic BON to both align data and standardize descriptors," says Lynn Schriml, PhD, a scientist at IGS and Associate Professor in Epidemiology and Public Health at the University of Maryland School of Medicine. "GSC started a Biodiversity working group in 2009 to build intersections between the genomics and biodiversity communities, so this is perfect for us to collaborate to meet these goals."

> ***GSC started a Biodiversity working group in 2009 to build intersections between the genomics and biodiversity communities, so this is perfect for us to collaborate and meet these goals.***
>
> – LYNN SCHRIML, PHD

Omic BON is part of a larger umbrella organization known as GEO: Group on Earth Observations made up of hundreds of governments and organizations. Similarly, Omic BON has attracted members from around the world working as researchers, policy makers, and standards developers.

Omic BON plans to create a global omic meta-observatory that monitors biodiversity at the molecular level through the coordination and standardizing how the information is collected. It will focus on observing and monitoring biodiversity of organisms and environments by studying genes, transcripts, proteins, metabolites, and other biomolecules.

A meta-observatory is a distributed observatory to which anyone performing well-documented and metadata-rich observations—from citizen science initiatives to established long-term observatories—can contribute. The observations conducted independently across time and space are integrated into a coordinated body of observations.

In August, the group published its first paper in Gigascience to set forth its vision, mission, and goals: The founding charter of the Omic Biodiversity Observation Network

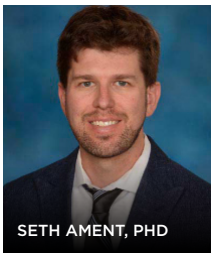
UNDER THE MICROSCOPE

A look at IGS featured research

1 Discovery: How Brain Inflammation in Children May Cause Neurological Disorders Such as Autism or Schizophrenia

LEAD RESEARCHER: Seth Ament, PhD

PUBLISHED IN: *Science Translational Medicine*


SETH AMENT, PHD

Severe inflammation in early childhood is a clinically known risk factor for developing autism and schizophrenia. Now, for the first time, scientists from the University of Maryland School of Medicine (UMSOM) have discovered that inflammation alters the development of vulnerable brain cells, and this could have mechanistic links to neurodevelopmental disorders. This finding could lead to treatments for many different childhood-onset neurodevelopmental disorders.

Using single-cell genomics to study the brains of children who died from inflammatory conditions—such as a bacterial or viral infections or asthma—along with those who died from a sudden accident, researchers from the University of Maryland School of Medicine led a study that found inflammation in early childhood prevents specific neurons in the cerebellum from maturing completely. The cerebellum is a brain region responsible for motor control and higher cognitive functions used in language, social skills, and emotional regulation.

Faculty from UMSOM's Institute for Genome Sciences (IGS), Department of Pharmacology, and the University of Maryland-Medicine Institute of Neuroscience Discovery (UM-MIND) conducted the research. The study appeared in the October issue of *Science Translational Medicine*. It is part of a collection of nearly 30 papers describing the development and diversity of cell types in the human brain. All of these studies were coordinated by the Brain Research Through Advancing Innovative Neurotechnologies (BRAIN) Initiative Cell Census Network, a multisite consortium funded by the National Institutes of Health.

Previous research has shown that babies born with abnormalities of the cerebellum frequently go on to experience neurodevelopmental disorders, and animal models exposed to inflammation before birth also develop these conditions.

"We looked at the cerebellum because it is one of the first brain regions to begin developing and one of the last to reach its maturity, but it remains understudied," said Seth Ament, PhD, IGS scientist and Associate Professor in the Department of Psychiatry at UMSOM who co-led the research with Margaret McCarthy, PhD, the James and Carolyn Frenkil Dean's Professor and Chair in Pharmacology and Director of UM-MIND. "With the fairly new technology of single-nucleus RNA sequencing we could look at the cell level to see changes in the brains."

Added Dr. McCarthy: "This has never been done before in this age group and in the context of inflammation. The gene expression in the cerebella of children with inflammation were remarkably consistent."

The researchers examined donated post-mortem brain tissues of 17 children who died when they were one to five years old, eight from conditions that involved inflammation and nine from accidents. None of the donors had been diagnosed with a neurological disorder prior to death. The two groups were similar in age, gender, race/ethnicity, and time since death. These

unique brain tissue specimens had been collected over many years by UMSOM researchers at the University of Maryland Brain and Tissue Bank, a tissue repository of the NIH NeuroBioBank, as well as the Maryland Brain Collection of the Maryland Psychiatric Research Center.

The study found that two specific, yet rare types of cerebellar neurons were most vulnerable to brain inflammation—the Golgi and Purkinje neurons. At the single-cell level, these two types of neurons showed premature disruption of their maturation.

"Although rare, Purkinje and Golgi neurons have critical functions," Dr. Ament said. "During development, Purkinje neurons form synapses connecting the cerebellum to other brain regions involved in cognition or emotional control, while Golgi neurons coordinate communication between cells within the cerebellum. Disruption of either of these developmental processes could explain how inflammation contributes to conditions like autism spectrum disorders and schizophrenia."

As with many diseases, both genetics and the environment—in this case, inflammation—likely contribute to the risk of developing these disorders. That's why it is crucial to understand the roles of specific cells within the brain regions—as well as how they interact with genes to influence brain function—to find treatments for brain disorders, like ASD and schizophrenia, as well as others including dementia, Parkinson's disease, or substance use disorders.

"This study is one of the first to show that gene expression changes during inflammation may set the stage for later cellular dysfunction, such as reducing synaptic connectivity or altering energy metabolism," said UMSOM Dean Mark Gladwin, MD, who is also Executive Vice President for Medical Affairs, UM Baltimore, and the John Z. and Akiko K. Bowers Distinguished Professor at UMSOM. "It's critical to understand these mechanisms and changes at the cellular level during brain development in the hope that someday we can develop treatments for neurodevelopmental disorders."

> ***This study is one of the first to show that gene expression changes during inflammation may set the stage for later cellular dysfunction, such as reducing synaptic connectivity or altering energy metabolism...***
>
> – UMSOM DEAN MARK GLADWIN, MD

The data from this study—along with all of the BRAIN Initiative papers—has been deposited in the Neuroscience Multi-Omic Archive (NeMO Archive)— a curated genomic data repository—housed at the Institute for Genome Sciences at UMSOM. Neuroscience researchers can access the archive's data through a user-friendly portal to transform their understanding of the complex workings of the brain.

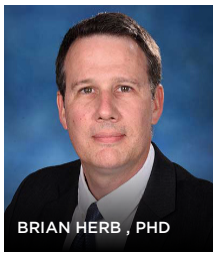
Additional authors from the Institute for Genome Sciences include Marcia Cortez-Gutierrez, Brian Herb, Evalina Mocci, and Carlo Colantuoni.

Hear more about this study from Dr. Ament on this video.

2 Discovery: New Research for the First Time Maps Neuron Development in Human Brain's Hypothalamus That Could Lead to New Treatments for Obesity, Sleep, and Mood Disorders

LEAD RESEARCHER: Brian Herb, PhD

PUBLISHED IN: *Science Advances*


BRIAN HERB , PHD

The small and complex hypothalamus located deep in the brain plays a critical role in regulating sleep, stress responses, hunger, body temperature, hormone levels, and memory—and can disrupt development, possibly leading to thyroid disease, obesity, anxiety, and depression later in childhood or well into adulthood.

Now, scientists at the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine (UMSOM), have mapped the cells in the developing prenatal hypothalamus in humans—from precursor stem cells to mature neurons and glia—giving science the first ever comprehensive view of human hypothalamus development at the cellular level. The research was published in *Science Advances*.

> ***Knowing about the number of medical issues caused by hypothalamus dysfunction motivated us to research its development***
>
> – BRIAN HERB PHD

"The hypothalamus is such an important part of brain function, and up until this study, nearly everything we knew about its development came from animal models," said Brian Herb, PhD, Research Associate at IGS, and the lead author on the study. "Knowing about the number of medical issues caused by hypothalamus dysfunction motivated us to research its development and to better understand it through the use of transcriptomics, or how each gene is active or inactive in every cell in the hypothalamus."

The research team used single-cell RNA sequencing on the hypothalamus of 11 prenatal samples—four female, seven male—ranging from six to 25 gestational weeks. In addition, they compared this with single-nucleus RNA sequencing on three healthy adult brains, as well as with previous mouse models, and previous research in forebrain development—the location of the hypothalamus.

"We discovered precursor cells develop into 170 distinct types of neurons in the human hypothalamus," said Seth Ament, PhD, IGS scientist and Associate Professor in the Department of Psychiatry at UMSOM, and corresponding author of the study. "This shows the development and diversity of neurons in this brain region in unprecedented detail."

In addition, when compared with mouse models, the team discovered much of the development trajectory and marker genes had been conserved through evolution. They found one big difference in the neurons—known as POMC (pro-opiomelanocortin)—that release amino acid neurotransmitters and play a big role in obesity. While humans and mice share some types, there is great difference in the genes those specific neurons use to function.

When compared with other forebrain regions, including the cortex, the researchers discovered gene expression differences showed at the earliest stages of development. This means that unique regulatory programs give rise to specialized neuronal populations.

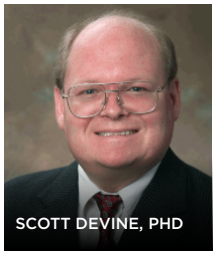
"The research shows that differentiation of the neuronal subtypes occurred mostly in the samples from the second trimester, with evidence that it may continue into the third trimester or even after birth," added Dr. Herb. "This research is a critical step in understanding brain development. An equally important next step will be to understand how particular environmental impacts at certain time points in development affect human health."

Additional authors from the Institute for Genome Sciences include Carlo Colantuoni and Seth Ament.

3 Discovery: Assembly of 43 diverse human Y chromosomes reveals extensive complexity and variation

CONTRIBUTING IGS AUTHORS:
Scott Devine, PhD, and Luke Tallon, as part of the Human Genome Structural Variation Consortium

PUBLISHED IN: ***Nature***


SCOTT DEVINE, PHD

Although the first human Y chromosome sequence happened about 20 years ago, repetitive sequencing made putting together the complete sequence elusive to scientists until recently. The implementation of long-read sequencing has allowed scientists to assemble Y chromosomes from males, representing the five continental groups from the 1000 Genomes Project.

This milestone will allow researchers to understand the full extent of human genetic variation and provides the starting point to associate Y-chromosomal sequences to specific human traits and more thoroughly study human evolution.


LUKE TALLON

This newly assembled dataset of 43 Y chromosomes therefore provides a view of genetic variation at the nucleotide level, across more than 180,000 years of human Y chromosome evolution. The time to the most recent common ancestor (TMRCA) is estimated to be approximately 182,900 years ago.

IGS scientists Scott Devine, PhD, and Luke Tallon serve on the Human Genome Structural Variation Consortium that contributed to this important research, as did a student working in Dr. Devine's lab at IGS at the time, Nelson Chuang.

"Our contributions include those males from a ***Science*** paper published in 2021 that were sequenced by IGS's technology core Maryland Genomics, as well as providing general input on the overall project," says Dr. Devine. "We sequenced about one-third of the original sequences, and the consortium used those several more times for follow up analysis."

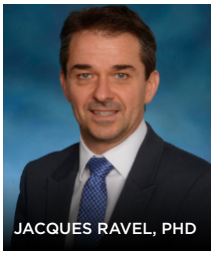
The availability of fully sequence-resolved Y chromosomes from multiple individuals provides a unique opportunity for identifying new associations of traits with specific Y-chromosomal variants and garnering insights into the evolution and function of complex regions of the human genome.

4 Discovery: New Research Uses Composition and Function to Identify Clinically Important Vaginal Microbiomes and could lead to precision treatments that protect women against STDs, HIV, and Preterm Birth

LEAD RESEARCHERS:
Johanna Holm, PhD and Jacques Ravel, PhD

PUBLISHED IN: *Microbiome*


JOHANNA HOLM, PHD


JACQUES RAVEL, PHD

Researchers have long known that the composition of microbes in the vagina plays a major role in women's genital health, such as susceptibility to sexually transmitted diseases such as HIV and preterm birth. What has not been well understood is exactly how those microbes function together to create a healthy and protective vaginal microbiome.

Now for the first time, researchers from the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine (UMSOM) have applied metagenomic sequencing to understand the function of the bacterial strain communities in the vagina. While genomics looks at the genetic content of a single strain of species, metagenomics looks at the DNA makeup of multiple strains and species at the same time—and can show how the strains of the same species work together to contribute to health or disease.

Understanding how these microbiome communities function could lead to new targets for treatment of vaginal infections, as well as new diagnostic strategies for conditions like bacterial vaginosis. The research has been published in the Nov. 30 issue of *Microbiome*.

"Vaginal microbiomes cluster by similar bacterial species compositions, but each species consists of different strain combinations. These combinations likely play a significant role in the susceptibility to—and the course of—an infection," said Johanna Holm, PhD, a scientist at IGS, Assistant Professor of Microbiology and Immunology at UMSOM, and the paper's lead author.

To capture the functional information, the researchers sequenced 1,890 vaginal metagenomes from more than one thousand women of reproductive age. They found 28 bacterial species common to the vagina. Within those species, they identified 135 distinct strain combinations—known scientifically as metagenomic subspecies.

It is the first time that scientists have identified different combinations of strains of bacteria within the vaginal microbiome. The researchers use these 135 combinations to develop a new functional classification of vaginal microbiomes which they call, "Metagenomic Community State Types" or mgCSTs. In addition, they built a software classifier with open source coding for other scientists to use to create consistency in the way researchers study the vaginal microbiome.

"Our research highlights a previously unknown amount of functional diversity in the vaginal microbiome, which has, for a long time, been considered of low diversity and simple." said Jacques Ravel, PhD, Acting Director of IGS, Professor of Microbiology and Immunology at

UMSOM, and the corresponding author on the paper. “These new categories—based on their functional diversity—will help scientists to better understand how vaginal microbiomes interact within women to affect their reproductive health. This new knowledge can help us develop novel approaches to keeping the vaginal microbiome optimally protected.”

However, even with a “good” microbiome—which previous research shows is dominated by the species *Lactobacillus*—each strain can be functionally different and provide varying levels of protection. This makes it critical for researchers to understand the community of strains, and what those strains are capable of doing in the vaginal microbiome.

In addition, the researchers identified functionally unique types of non-optimal vaginal microbiomes.

“We observed nine types of bacterial vaginosis-like communities, which research had previously characterized into only two groups. This presents an opportunity for improving treatment for bacterial vaginosis, through personalized treatment” said Dr. Holm.

“Our hope is that as more metagenomes are sequenced, other researchers use the mgCSTs to easily validate and reproduce their own studies,” added Dr. Holm. “Ultimately, our continuing work should reveal novel therapeutic targets to provide women protection against infections without using antibiotics that often lead to yeast infections, as well as finding ways to treat other vaginal and reproductive health challenges.”

> ***Ultimately, our continuing work should reveal novel therapeutic targets to provide women protection against infections…***
>
> – JOHANNA HOLM, PHD

Additional authors from the Institute for Genome Sciences include Michael France, Pawel Gajer, Bing Ma, Rebecca Brotman, and Michelle Shardell

WATCH A VIDEO THAT EXPLAINS THE RESEARCH

FACULTY FEATURE:

REBECCA BROTMAN, PHD, MPH RESEARCHING THE VAGINAL MICROBIOME

Growing up in a small South Texas community, Rebecca Brotman, PhD, MPH, witnessed firsthand the challenges of teenage pregnancy and the whispers about sexually transmitted infections among her peers.

These early experiences sparked her lifelong commitment to reproductive and sexual health research. Today, she is a Professor in the Institute for Genome Sciences, where her work focuses on the vaginal microbiome.

Her journey from teen to scientist wasn't a direct path, but always centered on reproductive health and public health policy.

"When I was an undergraduate at Washington University, I worked in an Obstetrics and Gynecology lab where we talked about global family planning policies while researching biochemistry associated with birth control," Dr. Brotman says. "This showed me that you could intertwine basic research with public health policy."

That undergraduate experience led her to a job as a research study coordinator for male contraceptive research at the University of Washington. That then catalyzed her to pursue an MPH and PhD at Johns Hopkins.

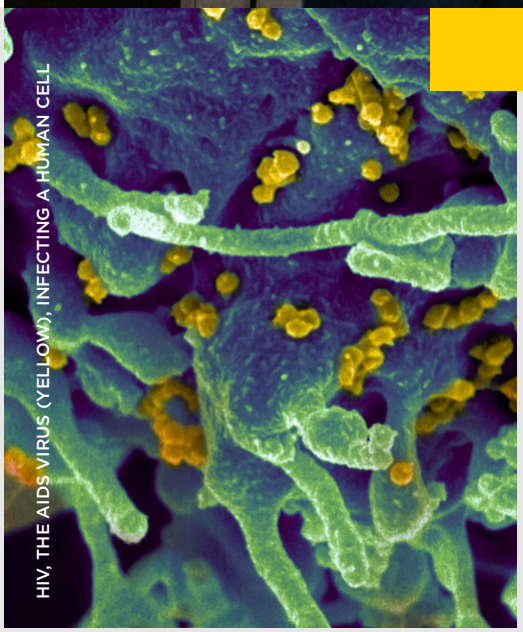
"That's where I learned about vaginal bacterial communities that are the unsung guardians against harmful pathogens, including HIV," she says. "Since 2000, my research has focused on many different aspects of the vaginal microbiome, including its influence on urogenital infections and menopause."

Her latest research—supported by an RO1—focuses on why chlamydia infections in half of all women will clear spontaneously on their own within a year. Her research revealed that bacterial vaginosis, a microbiota that has low levels of *Lactobacillus* species, is associated with persistence of chlamydia. Discovering how the vaginal microbiome helps clear chlamydia could lead to more approaches to prevent the infection.

> ***Our team dedicated years to assemble a dataset from an archived cohort study so we can understand the natural progression of sexually transmitted infections and determine how best to prevent infection...***
>
> – REBECCA BROTMAN, PHD, MPH

When she's not in her lab or crunching data, Dr. Brotman enjoys one-on-one mentoring. "It is deeply fulfilling to witness a student's journey from the genesis of an idea to its full realization," she says. "Guiding students from the birth of an idea to its fruition, through hypothesis formation, study design, and data analysis, to presentation and publication, is incredibly rewarding."

REBECCA BROTMAN, PHD, MPH *(right)*
RECEIVED THE AMERICAN SEXUALLY TRANSMITTED DISEASES ASSOCIATIONS ACHIEVEMENT AWARD FOR A MID-CAREER RESEARCHER



HIV, THE AIDS VIRUS (YELLOW), INFECTING A HUMAN CELL

Working at IGS, she says, has given her access to a highly collaborative community of passionate academics across multiple disciplines, leading to her ultimate goal: “I want to discover ways to optimize the health of the vaginal microbiome from reproductive age to menopause,” she says. “Understanding how the microbiome can provide protection against STI acquisition and preterm birth is a global health priority. We know the vaginal microbiome is the first line of defense, and right now, we are on the cusp of capitalizing on this natural defense.”

IGS'S MEDIA HIGHLIGHTS

The Institute for Genome Sciences faculty have had a banner few months being interviewed in the media for their expertise in everything from the vaginal microbiome to diversity in genomic databases. Read all articles here:

Giddy: Can Your Microbiome Impact Pregnancy Outcomes?

The Daily Beast: The Keys to Mental Illness May Be Hiding Within Amish Genes

The Baltimore Banner: What to know about the lethal strain of malaria contracted in Maryland

Newsweek: Neuroscientists Make 'Unexpected' Discovery Over Cause of Childhood Autism

The Washington Post: New 'brain atlas' maps the highly complex organ in dazzling detail

Health Day: New Clues to How Inflammation in Young Children's Brains Might Spur Autism

Science News: What a look at more than 3,000 kinds of cells in the human brain tells us

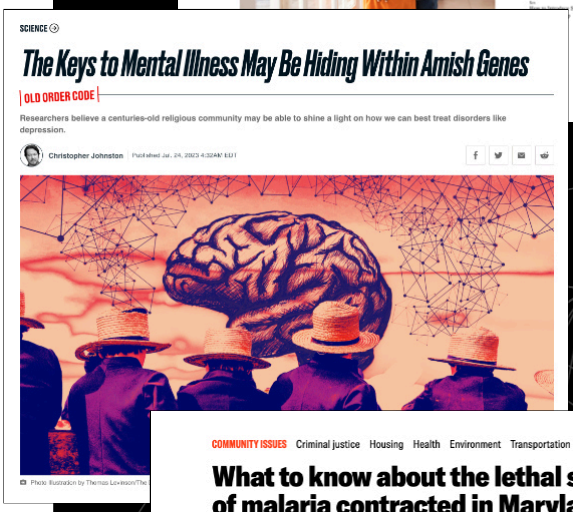
GenomeWeb: Brain Cell Features Detailed in Human Cell Atlas Research Collection

New Atlas: How inflammation in early childhood can lead to autism and schizophrenia

Spectrum News: Vast diversity of human brain cell types revealed in trove of new datasets

Scientific American: The Vaginal Microbiome Might Affect Health More than We Thought

Scientific American: How a Parasitic Worm Forces Praying Mantises to Drown Themselves



CHAMINDI SENEVIRATNE, MD, MOVES TO NIH

After nine years with IGS, Chamindi Seneviratne, MD, has left for a new role at the Medications Development Branch in the National Institute on Alcohol Abuse and Alcoholism (NIAAA) at the National Institutes of Health.

As a Health Scientist Administrator—better known as Program Officer—Dr. Seneviratne will advance medication development research and recommend new initiatives to support the institute's priorities.

"My first-hand experiences and the high standards of faculty I witnessed at IGS will help me serve a variety of researchers in this new position," she says. "IGS provided me a safe space to develop my scientific expertise and learn to use state-of-the-art technology to gain continuous NIH funding."

> ***My first-hand experiences and the high standards of faculty I witnessed at IGS will help me serve a variety of researchers in this new position...***
>
> – CHAMINDI SENEVIRATNE, MD

Dr. Seneviratne started at IGS in 2014 as an Assistant Professor in Psychiatry, and later joined the Department of Pharmacology. She will remain an Adjunct Assistant Professor in Pharmacology and affiliate IGS faculty for one year, in addition to her new role at NIAAA.

"One of my best memories at IGS was receiving the notice of my first R01 award as a PI in the first round of application submissions in 2018—something that happens rarely," Dr. Seneviratne says. "My favorite publication to date will be out soon. For the first time, the research showed common transcriptomic changes underlying binge drinking and placebo responses."

CHAMINDI SENEVIRATNE, MD

"IGS benefited from Dr. Seneviratne's work using transcriptomics, pharmacogenomics, and the placebo effect to understand alcohol use disorder," says Jacques Ravel, PhD, Acting Director of IGS. "We congratulate her on both her new position at the NIH and as an editor of a new book out on placebo effect research."

See page 20 for more information on the book that Chamindi Seneviratne, MD contributed to as an editor.

JOIN BOOK CLUB ON HOW TO USE POPULATION DESCRIPTORS IN GENOMIC RESEARCH

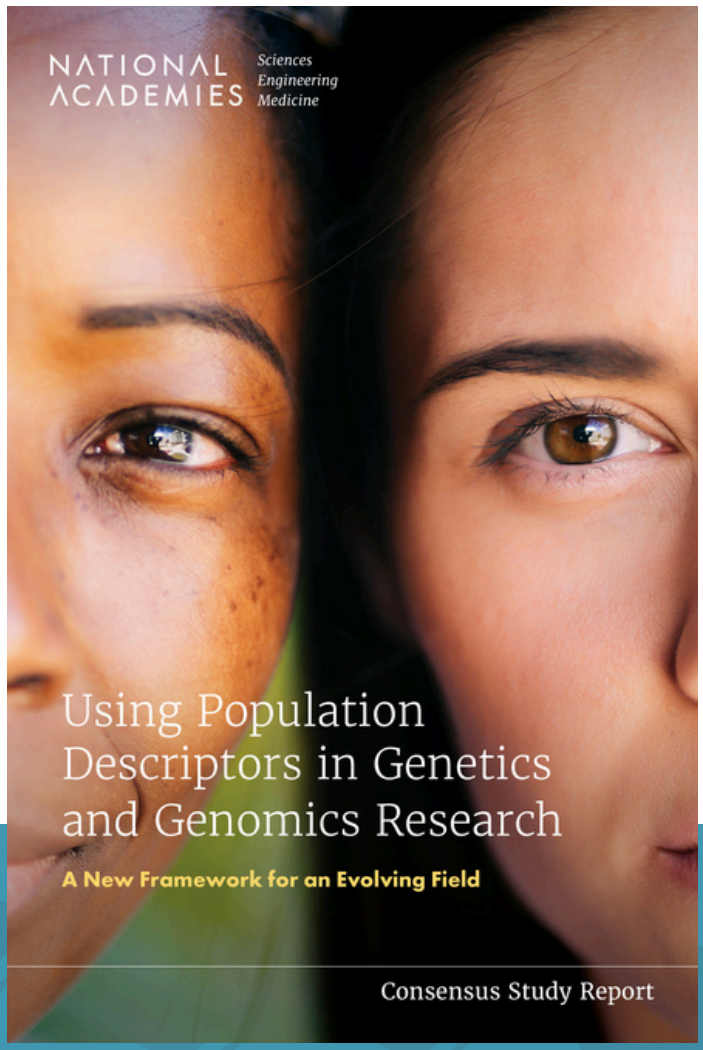
With genetic and genomic research crossing disciplines, population descriptors—such as race, ancestry, ethnicity—are often inconsistent or, even inappropriately, used. Even researchers who have long worked in science often do not describe their protocol's population correctly.

That's why the National Academies of Science, Engineering, and Medicine convened a committee to write a report on how to do it correctly. But reading the 240-page report—titled *Using Population Descriptors in Genetics and Genomics Research: A New Framework for an Evolving Field—can be daunting*.

"That's why I have started a book club to tackle the report chapter-by-chapter and have a great discussion around the issues the report raises," says Timothy O'Connor, PhD, Associate Professor of Medicine at the University of Maryland School of Medicine, faculty at the Institute for Genome Sciences, and Co-Director of the Program in Health Equity and Population Health. "It's critical that all scientists use these terms correctly."

The book club is open to everyone and takes place on Zoom from 10 am to 11 am on the first Thursday of each month. Individuals are welcome to join any or all of the meetings.

If you're interested to learn more—and to be on the mailing list for the Zoom link and in case the time and date changes—please email Erin Walton at Erin.Walton@som.umaryland.edu.



IGS FACULTY PARTICIPATE IN WIN-WIN COLLABORATIVE EVENTS

Five Institute for Genome Sciences (IGS) faculty members took part in Win-Win Collaborative Events geared at letting other scientists across campus learn more about specific research topics within the University of Maryland School of Medicine. Each event featured five, 5-minute talks on a research theme followed by an opportunity to network with potential collaborators.

Jacques Ravel, PhD, Acting Director of IGS, emceed the event on Genetics/Genomics.

Seth Ament, PhD, Associate Professor, Psychiatry, and IGS faculty, spoke on using single-cell technology in neurogenomics studies of human and rodent brains, as well as molecular adaptations in addiction, neurodegeneration, and brain injury.

Ramaswamy Iyer, PhD, D(ABMGG), FACMG, Associate Director, Translational Clinical Genomics, IGS, introduced attendees to the Maryland Genomics Translational and Diagnostics Laboratory. The CLIA-certified lab is available for research collaboration, as well as developing clinical testing for solid tumors, pharmacogenomics, and Non-Invasive Prenatal Testing.

RAMASWAMY IYER, PHD,D(ABMGG), FACMG

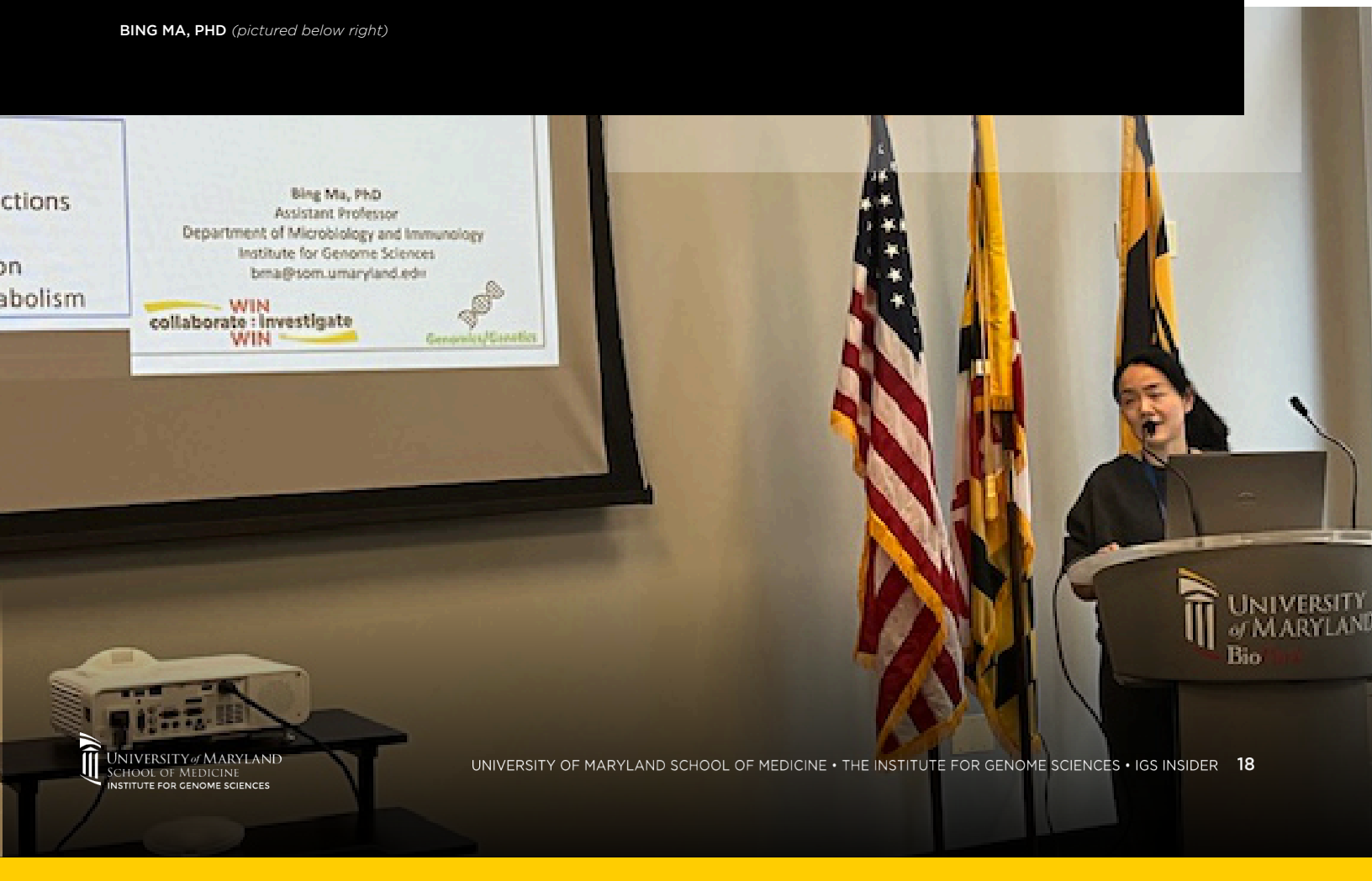
SETH AMENT, PHD

OWEN WHITE, PHD

Bing Ma, PhD, Assistant Professor, Microbiology and Immunology and IGS faculty, discussed the gut microbiome as an ecosystem for individual health, as well as how 'omics technology can be used in translational science. She talked about her ongoing research on the role of the gut microbiome in heart transplants and the role of the maternal milk in infant gastrointestinal health.

Owen White, PhD, Associate Director, Research Collaboration and Development, IGS, spoke at the Win-Win event featuring Big Data. He discussed the data ecosystems across the National Institutes of Health (NIH), focusing on the Neuroscience Multi-Omic Archive (NeMO Archive) a data repository built and housed at IGS that stores and disseminates 'omics data generated from various brain research programs at the NIH.

BING MA, PHD *(pictured below right)*



THREE CHEERS

BRUCE E. JARRELL, MD, FACS, CLAIRE FRASER, PHD, & MARK GLADWIN, MD

REBECCA BROTMAN, PHD, MPH

MIKE HUMPHRYS, MS

CHAMINDI SENEVIRATNE, MD

Claire Fraser, PhD, was one of eight faculty members named a University of Maryland, Baltimore Distinguished University Professor at the UMB Faculty Convocation on Sept. 14, 2023. She was presented a special medal by President Bruce Jarrell, MD, FACS, and University of Maryland School of Medicine Dean Mark Gladwin, MD, and presented a bouquet of flowers by Owen White, PhD, Associate Director of IGS. (Little known fact: Dr. Jarrell also crafted the medals given out that day!) Congratulations, Claire!

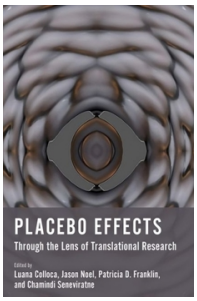
Speaking of Claire Fraser, ***Research.com, a leading academic platform for researchers, has ranked Dr. Fraser 196 in United States, and 309 in the world among the Top 1000 Female Scientists in the World***. They use the H-index metric obtained from various bibliometric sources to increase visibility for scientific achievements of women.

Mike Humphrys, MS, Maryland Genomics's Executive Director, Technical, has been awarded the prestigious Board of Regents Staff Award for "Exceptional Contribution to the Institution and/or Unit to Which a Person Belongs" for his work setting up and running a testing lab during the COVID-19 Pandemic. Mike was presented with a $2,000 check and award at the Board of Regents meeting at the University of Maryland Global Campus on Sept. 22, 2023. You can read more about Mike's award in last Summer's *IGS Insider* on page 11.

Rebecca Brotman, PhD, received the American Sexually Transmitted Diseases Association's

Achievement Award presented to a person at mid-career to acknowledge an outstanding body of work in sexually transmitted diseases or to an individual for a single major achievement in the field. Read more about Dr. Brotman's work in this issue of the *IGS Insider* on page 12.

Chamindi Seneviratne, MD, an IGS affiliate faculty member, is an editor of *Placebo Effects Through the Lens of Translational Research*—out in November from Oxford University Press. "In this interdisciplinary collaboration, our four editors and the contributing authors illuminate the intricate factors shaping our well-being and empowers us to design effective disease prevention and treatment strategies through the use of placebo effects," says Dr. Seneviratne. The book is the result of a conference held at the University of Maryland, Baltimore in 2021 on placebo effects in health. It was attended by 500 people from 25 countries. Dr. Seneviratne studies placebo effects relating to Alcohol and Substance Use Disorders (AUD, SUD). In addition, the book covers placebo effects relating to mental health, biomarkers and precision medicine, clinical practice, and various conditions, such as COVID-19. The book is free to download or can be ordered here.



Congrats to those on our IGS team who have received promotions:

Seth Ament, PhD, to Associate Professor with Tenure

Luke Tallon to Associate Director of Core Services, Institute for Genome Sciences; Senior Executive Director, Maryland Genomics; Research Associate, Microbiology and Immunology, University of Maryland School of Medicine

Ramaswamy Iyer, PhD, D(ABMGG), FACMG, to Associate Professor, Medicine, University of Maryland School of Medicine; Asscociate Director, Clinical Genomics, Institute for Genome Sciences

Victor Borda Pua, PhD, to Research Associate, Institute for Genome Sciences

Ankit Dwivedi, PhD, to Research Associate, Institute for Genome Sciences

Evelina Mocci, PhD, to Research Associate, Institute for Genome Sciences

Sarah Brown, PhD, to Postdoc, Institute for Genome Sciences

Gillian Mbambo, PhD, to Postdoc, Institute for Genome Sciences

Kevin Regan, MS, to Bioinformatics Software Engineer II, Institute for Genome Sciences

Olukemi Ifeonu, PhD, to Bioinformatics Analyst-Lead, Institute for Genome Sciences

Mahashweta Basu, PhD to Bioinformatics Analyst-Senior, Institute for Genome Sciences

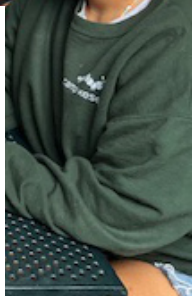
FUN TIMES @ IGS

"If people never did silly things, nothing intelligent would ever get done."

– Ludwig Wittgenstein

SUMMER PICNIC

From some killer games of volleyball, Uno, and cornhole to popsicles on the playground, everyone enjoyed the annual IGS Summer Picnic at Centennial Park...including Pearl, the dog!



HALLOWEEN COSTUME CONTEST

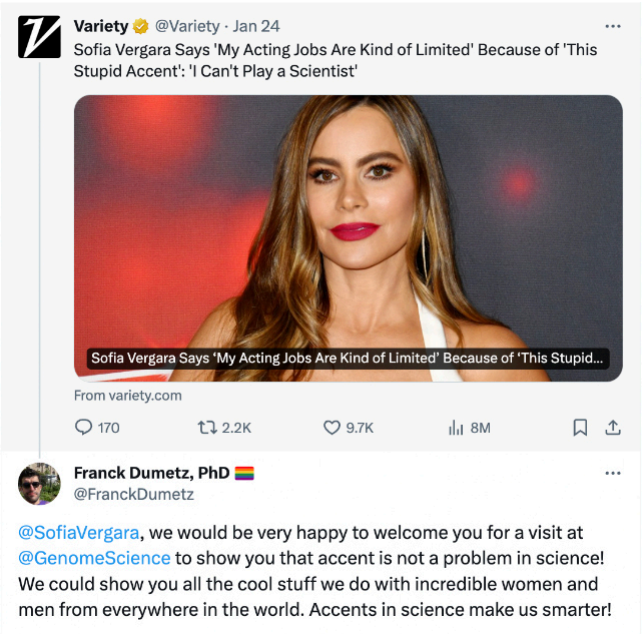
The yellow foosball team won...But everyone had fun dressing up!

JINGLE & MINGLE HOLIDAY PARTY

Ending 2023 on a good note, the IGS Annual Jingle & Mingle Holiday party included a Left/Right White Elephant Exchange and a Snowman Making Contest in which Stacy Holton crocheted her way to a win!

ANYONE KNOW SOPHIA VERGARA?

Our Franck Dumetz, PhD, has officially invited her to the Institute for Genome Sciences via X to learn about genomics and the microbiome – and to see that accents don't matter in science. We have researchers from France, Portugal, Brazil, China, Germany – and all around the world!



SAVE THE DATE

February 29, 2024

JANE CARLTON, PHD

Bloomberg Distinguished Professor at the Johns Hopkins Bloomberg School of Public Health and Johns Hopkins University Department of Biomedical Engineering, and director of the Johns Hopkins Malaria Research Institute

"It's a Parasite's World: Plasmodium, Trichomonas, and the Johns Hopkins Malaria Research Institute"

HSFIII, LECTURE ROOM 1010
11 AM TO NOON

March 14, 2024

MOSTAFA ZAMANIAN, PHD

Assistant Professor, Department of Pathobiological Sciences, University of Wisconsin-Madison

Revisiting Approaches to Anthelmintic Discovery in the Age of Resistance

HSFIII, LECTURE ROOM 1010
11 AM TO NOON

March 28, 2024

LISA SHULMAN, MD

Professor, Neurology, University of Maryland School of Medicine

ANUP MAHURKAR, MS

Chief Informatics Officer, Institute for Genome Sciences

SIMPLE VISUAL ANALYTICS TOOL: POD-VIS

See story on page 3 for more details.

ON ZOOM
12 PM TO 1 PM

REGISTER HERE

April 8, 2024

RODOLPHE BARRANGOU, PHD

Todd R. Klaenhammer Distinguished Professor, University Faculty Scholar, Department of Food, Bioprocessing and Nutrition Sciences, North Carolina State University

Manipulating the Microbiome using CRISPR Technologies

HSFIII, LECTURE ROOM 1010
11 AM TO NOON

May 1, 2024

SAVE-THE-DATE: IGS TOWN HALL

10 AM TO NOON

May 2, 2024

KERI MARTINOWICH, PHD

Lead Investigator, Lieber Institute for Brain Development; Associate Professor, Psychiatry and Neuroscience, Johns Hopkins University

HSFIII, LECTURE ROOM 1010
11 AM TO NOON

September 16-18, 2024

WORKSHOP:
INTRODUCTION TO R AND DATA VISUALIZATION FOR BIOINFORMATICS

SIGN UP HERE

CONFERENCES

Science Talks

IGS Faculty & Student Presentations at Conferences

@ASHG: American Society of Human Genetics

Jennifer French, MPH, Graduate Research Assistant in the lab of Timothy O'Connor, PhD, presented a poster titled: *Comparing Imputation Quality in Two Distinct Latin American Populations: Influence of Super Population Exclusion*. Her poster showed differences in imputation quality—identifying unknown genotypes—in two different Latin American populations when excluding European and African individuals from the reference panel.

Bing Guo, MD, Graduate Research Assistant, Institute for Genome Sciences in the lab of Timothy O'Connor, PhD, gave an oral presentation titled: *Tabular Encoding of Rare-Variant Genotype Data for Enabling Efficient Random Access in Memory and Analysis of Rare Allele Sharing* in which he and his colleagues created a way to encode rare variant genotype data in a table with each row representing the genotype call of a rare allele, significantly enhancing data storage and retrieval efficiency.

Victor Borda, PhD, Research Associate, Institute for Genome Sciences, working in the lab of Timothy O'Connor, PhD, gave a poster presentation titled: *Structural Variant Adaptation Between the Peruvian Andes and Amazon Using Long-Read Sequencing*. The team found strong allele frequency differences on two different genes when comparing the two populations. Notably, the Andean population exhibited a highly differentiated 30bp deletion on *JAK2*, a gene related to hypoxia tolerance. In contrast, the Amazonian population displayed a 3305bp insertion on gene *CASP8*, a gene that plays an important role in inflammatory cytokine production during bacterial infections.

JENNIFER FRENCH, MPH

BING GUO, MD


VICTOR BORDA, PHD

THE SETH AMENT, PHD, LAB AT THE SOCIETY FOR NEUROSCIENCE MEETING

JOE RECEVEUR, PHD, BIOINFORMATICS ANALYST, INSTITUTE FOR GENOME SCIENCES, DEMONSTRATES HOW THE NEUROSCIENCE MULTI-OMIC ARCHIVE (NEMO ARCHIVE) WORKS TO BENJAMIN GRISSOM, MS, FROM SETH AMENT, PHD'S LAB AT IGS. THE NEMO ARCHIVE IS A DATA REPOSITORY HOUSED AT IGS THAT STORES AND DISSEMINATES 'OMICS DATA GENERATED FROM VARIOUS BRAIN RESEARCH PROGRAMS AT THE NIH.


BRIAN HERB, PHD

@Society for Neuroscience

Brian Herb, PhD, Research Associate, Institute for Genome Sciences, presented his research: *Single-cell Genomics Reveals Region-specific Developmental Trajectories Underlying Neuronal Diversity in the Human Hypothalamus*. Learn more about this research on page 8.

NEW GRANTS TO OUR IGS FACULTY: 2023 WAS A STELLAR YEAR

The Institute for Genome Sciences had an abundant 2023 with research grants from multiple agencies, including the National Institute of Allergy and Infectious Diseases, National Institute on Aging, and the United States Department of Agriculture, as well as funders from Canada.

DAVID SERRE, PHD, NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASE

Multi-Omics Characterization of Plasmodium vivax Hypnozoites

Total Award: $2,778,702

Goal: To better understand the processes underlying the fate and development of liver-stage *P. vivax* parasites to develop better malaria vaccines and therapies.

JACQUES RAVEL, PHD, CANADIAN INSTITUTE OF HEALTH RESEARCH/ UNIVERSITY OF WESTERN ONTARIO

Neovaginal Health for Transfeminine People

Total Award: $248,350

Goal: To better understand the microbiome in people who have had vaginoplasty. Dr. Ravel's lab will perform microbiome analyses, as well as bioinformatic and statistical analyses of the data.

MICHELLE SHARDELL, PHD, NATIONAL INSTITUTE ON AGING

Methods to Test Biomarkers of Aging as Shared Determinants of Alzheimer's Disease and Related Dementias and Physical Disability

Total Award: $3,746,659

Goal: To test and discover biomarkers of aging to predict and explain the relationship between cognitive and physical risk factors beyond those already known. Identifying new biomarkers may be able to prevent and predict cognitive and physical disability in older adults.

VINCENT BRUNO, PHD, NATIONAL INSTITUTE OF DENTAL AND CRANIOFACIAL RESEARCH/UNIVERSITY OF PITTSBURGH

Host and Fungal Regulation of Type 17 Immunity to Oral Candidiasis

Total Award: $84,048

Goal: Dr. Bruno will perform bioinformatics analyses for this research to better understand the mechanisms of Type 17 Immunity to yeast infections in the mouth.

REBECCA BROTMAN, PHD, NATIONAL INSTITUTE OF DIABETES AND DIGESTIVE AND KIDNEY DISEASES/ JOHNS HOPKINS UNIVERSITY

Mechanisms of Successful Vaginal Estrogen Prophylaxis for Postmenopausal Women with Recurrent Urinary Tract Infections: Urogenital Microbiota and Host Immune Responses

Total Award: $164,165

Goal: Dr. Brotman will supervise data generation from extraction to sequencing and analysis for this research that seeks to understand how vaginal estrogen works to prevent urinary tract infections in post-menopausal women.

BING MA, PHD, EUNICE KENNEDY SHRIVER NATIONAL INSTITUTE OF CHILD HEALTH AND HUMAN DEVELOPMENT

Mucosal Immune Biomarkers to Detect Neonatal Leaky Gut

Total Award: $424,875

Goal: To provide new insights into the interplay between host immunity and gut microbiota dysbiosis that contributes to an increase in gut barrier injury in early life. Understanding this will allow clinical studies to discover interventions to prevent leaky gut and promote healthy intestinal barrier functions and newborn health.

OWEN WHITE, PHD, NATIONAL INSTITUTE OF MENTAL HEALTH/ BROAD INSTITUTE

Scalable Molecular Pipelines for FAIR and Reusable BICAN Molecular Data

Total Award: $2,540,558

Goal: To test pipelines, ingest and process multi-omics data and make it available in the NeMO Data Archive, and develop tools and dashboards, as well as establish standards for genomic data and metadata.

OWEN WHITE, PHD, NATIONAL INSTITUTES OF HEALTH DATA COMMONS FUND

University of Maryland NIH Data Commons Facilitation Center

One Year Award: $1,196,285

Goal: To support communication across stakeholders in the Common Fund Data Ecosystems meetings and to support quarterly data submissions. IGS researchers will lead the Ontology Working Group to support new data and maintain infrastructure.

DAVID SERRE, PHD, NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES/PASTEUR INSTITUTE CAMBODIA

Comprehensive characterizations of the Genetic Factors and the Host Immune Response Associated to Protection from Clinical Plasmodium vivax Malaria

Total Award: $752,821

Goal: Dr. Serre's laboratory will prepare RNA and DNA libraries from the nucleic acids extracted at the Pasteur Institute Cambodia and perform bioinformatic analysis to understand the genetics of the parasite and the host immune response.

JOANA CARNEIRO DA SILVA, PHD, UNITED STATES DEPARTMENT OF AGRICULTURE

Babesia caballi Genome Sequences and Annotation

Total Award: $24,000

Goal: Sequence this protozoan parasite to obtain its complete genome and gene sequences to predict lifecycle, adaptation to vertebrate and invertebrate hosts, as well as learning about how vaccination or chemotherapeutic treatments might prevent disease.

REBECCA BROTMAN, PHD, NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES/JOHNS HOPKINS UNIVERSITY

The Vaginal Microenvironment in Asymptomatic vs. Symptomatic Bacterial Vaginosis

Total Award: $115,256

Goal: Dr. Brotman will characterize the vaginal microbiome data in this study and guide analysis to better understand microenvironmental differences in women who have symptoms vs. those who do not when they have bacterial vaginosis.

MICHELLE GIGLIO, PHD, NATIONAL INSTITUTE OF HEALTH/UNIVERSITY OF CALIFORNIA SAN DIEGO

SPARC Engagement Plan with the Common Fund Data Ecosystem

Total Award: $79,982

Goal: Dr. Giglio will attend meetings and contribute to establishing project plans, a project registry, and relevant materials for the Common Fund Data Ecosystem. In addition, she will support the collection and evaluation of documentation, user profiles, success metrics, and gap analysis.

DAVID SERRE, PHD, NATIONAL INSTITUTES OF HEALTH/PASTEUR INSTITUTE CAMBODIA

Extent, Dynamics, and Mechanisms of Plasmodium vivax Immune Evasion Caused by PvDBP Gene Amplification

Total Award: $446,977

Goal: Dr. Serre's laboratory will be responsible for the sample preparation, sequencing, analyses, and interpretation of the genomic and transcriptomic data in this project.

SETH AMENT, PHD, NATIONAL INSTITUTES OF HEALTH/UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER

SOLAR-Eclipse Computational Tools for Imaging Genetics

Total Award: $439,690

Goal: To perform software engineering related to the development of the SOLAR-Eclipse platform and bioinformatics analysis to integrate brain imaging, genetics data, and functional genomics data.

PUBLICATIONS

1. Adediran, T. Y., G. L. Robinson, J. K. Johnson, Y. Liang, S. Bejo, S. Leekha, D. A. Rasko, O. C. Stine, A. D. Harris and K. A. Thom (2024). **"Factors associated with patient-to-healthcare personnel (HCP) and HCP-to-subsequent patient transmission of methicillin-resistant *Staphylococcus aureus*."** Infect Control Hosp Epidemiol: 1-7.

2. Alizadeh, M., N. Sampaio Moura, A. Schledwitz, S. A. Patil, H. El-Serag, J. Ravel and J. P. Raufman (2024). **"A Practical Guide to Evaluating and Using Big Data in Digestive Disease Research."** Gastroenterology 166(2): 240-247.

3. Alizadeh, M., N. Sampaio Moura, A. Schledwitz, S. A. Patil, J. Ravel and J. P. Raufman (2023). **"Big Data in Gastroenterology Research."** Int J Mol Sci 24(3).

4. Alizadeh, M., N. Sampaio Moura, A. Schledwitz, S. A. Patil, J. Ravel and J. P. Raufman (2024). **"Gastroenterology Fellowship and Postdoctoral Training in Omics and Statistics-Part I: Why Is It Needed?"** Dig Dis Sci 69(1): 18-21.

5. Alizadeh, M., N. Sampaio Moura, A. Schledwitz, S. A. Patil, J. Ravel and J. P. Raufman (2024). **"Gastroenterology Fellowship and Postdoctoral Training in Omics and Statistics-Part II: How Can It Be Achieved?"** Dig Dis Sci 69(1): 22-26.

6. Ament, S. A., M. Cortes-Gutierrez, B. R. Herb, E. Mocci, C. Colantuoni and M. M. McCarthy (2023). **"A single-cell genomic atlas for maturation of the human cerebellum during early childhood."** Sci Transl Med 15(721): eade1283.

7. Ament, S. A. and A. Poulopoulos (2023). **"The brain's dark transcriptome: Sequencing RNA in distal compartments of neurons and glia."** Curr Opin Neurobiol 81: 102725.

8. Bajracharya, R., J. M. Guralnik, M. D. Shardell, M. C. Hochberg, D. L. Orwig and J. S. Magaziner (2023). **"Predictors of mobility status one year post hip fracture among community-dwelling older adults prior to fracture: A prospective cohort study."** J Am Geriatr Soc 71(8): 2441-2450.

9. Baron, J. A., C. S. Johnson, M. A. Schor, D. Olley, L. Nickel, V. Felix, J. B. Munro, S. M. Bello, C. Bearer, R. Lichenstein, K. Bisordi, R. Koka, C. Greene and L. M. Schriml (2024). **"The DO-KB Knowledgebase: a 20-year journey developing the disease open science ecosystem."** Nucleic Acids Res 52(D1): D1305-D1314.

10. Baron, J. A. and L. M. Schriml (2023). **"Assessing resource use: a case study with the Human Disease Ontology."** Database (Oxford) 2023.

11. Bhavana, V. H., G. H. Hillebrand, K. P. Gopalakrishna, R. A. Rapp, A. J. Ratner, H. Tettelin and T. A. Hooven (2023). **"A group B *Streptococcus* indexed transposon mutant library to accelerate genetic research on an important perinatal pathogen."** Microbiol Spectr 11(6): e0204623.

12. Borgogna, J. C., S. G. Grace, J. B. Holm, T. Aviles Zuniga, H. Kadriu, X. He, S. R. McCoski, J. Ravel, R. M. Brotman and C. J. Yeoman (2023). **"Investigating the impact of condomless vaginal intercourse and lubricant use on the vaginal metabolome: a pre-post observational study."** Sex Transm Infect 99(7): 489-496.

13. Brown, S. E. and R. M. Brotman (2023). **Letter to the Editor on "A randomized trial on the effectiveness and safety of 5 water-based personal lubricants."**J Sex Med 20(10): 1257.

14. Brown, S. E., S. Tuddenham, M. D. Shardell, M. A. Klebanoff, K. G. Ghanem and R. M. Brotman (2023). **"Bacterial Vaginosis and Spontaneous Clearance of *Chlamydia trachomatis* in the Longitudinal Study of Vaginal Flora."** J Infect Dis 228(6): 783-791.

15. Burris, H. H., N. Yang, V. Riis, L. Valeri, E. C. South, J. Ravel and M. A. Elovitz (2024). **"The role of neighborhood deprivation in the cervicovaginal microbiota."** Am J Obstet Gynecol MFM 6(3): 101291.

PUBLICATIONS

16. Carey, M. E., Z. A. Dyson, D. J. Ingle, A. Amir, M. K. Aworh, M. A. Chattaway, K. L. Chew, J. A. Crump, N. A. Feasey, B. P. Howden, K. H. Keddy, M. Maes, C. M. Parry, S. Van Puyvelde, H. E. Webb, A. O. Afolayan, A. P. Alexander, S. Anandan, J. R. Andrews, P. M. Ashton, B. Basnyat, A. Bavdekar, Bogoch, II, J. D. Clemens, K. E. da Silva, A. De, J. de Ligt, P. L. Diaz Guevara, C. Dolecek, S. Dutta, M. M. Ehlers, L. Francois Watkins, D. O. Garrett, G. Godbole, M. A. Gordon, A. R. Greenhill, C. Griffin, M. Gupta, R. S. Hendriksen, R. S. Heyderman, Y. Hooda, J. C. Hormazabal, O. O. Ikhimiukor, J. Iqbal, J. J. Jacob, C. Jenkins, D. R. Jinka, J. John, G. Kang, A. Kanteh, A. Kapil, A. Karkey, S. Kariuki, R. A. Kingsley, R. M. Koshy, A. C. Lauer, M. M. Levine, R. K. Lingegowda, S. P. Luby, G. A. Mackenzie, T. Mashe, C. Msefula, A. Mutreja, G. Nagaraj, S. Nagaraj, S. Nair, T. K. Naseri, S. Nimarota-Brown, E. Njamkepo, I. N. Okeke, S. P. B. Perumal, A. J. Pollard, A. K. Pragasam, F. Qadri, F. N. Qamar, S. I. A. Rahman, S. D. Rambocus, D. A. Rasko, P. Ray, R. Robins-Browne, T. Rongsen-Chandola, J. P. Rutanga, S. K. Saha, S. Saha, K. Saigal, M. S. I. Sajib, J. C. Seidman, J. Shakya, V. Shamanna, J. Shastri, R. Shrestha, S. Sia, M. J. Sikorski, A. Singh, A. M. Smith, K. A. Tagg, D. Tamrakar, A. M. Tanmoy, M. Thomas, M. S. Thomas, R. Thomsen, N. R. Thomson, S. Tupua, K. Vaidya, M. Valcanis, B. Veeraraghavan, F. X. Weill, J. Wright, G. Dougan, S. Argimon, J. A. Keane, D. M. Aanensen, S. Baker, K. E. Holt and A. Global Typhoid Genomics Consortium Group (2023). **"Global diversity and antimicrobial resistance of typhoid fever pathogens: Insights from a meta-analysis of 13,000 *Salmonella Typhi* genomes."** Elife 12.

17. Chandler, C. E., C. E. Hofstaedter, T. H. Hazen, D. A. Rasko and R. K. Ernst (2023). **"Genomic and Functional Characterization of Longitudinal *Pseudomonas aeruginosa* Isolates from Young Patients with Cystic Fibrosis."** Microbiol Spectr 11(4): e0155623.

18. Devine, S. E. (2023). **"Emerging Opportunities to Study Mobile Element Insertions and Their Source Elements in an Expanding Universe of Sequenced Human Genomes."** Genes (Basel) 14(10).

19. Dorsey, S. G., E. Mocci, M. V. Lane and B. K. Krueger (2024). **"Rapid effects of valproic acid on the fetal brain transcriptome: Implications for brain development and autism."** Res Sq.

20. Doshi, T. L., S. G. Dorsey, W. Huang, M. A. Kane and M. Lim (2024). **"Proteomic Analysis to Identify Prospective Biomarkers of Treatment Outcome After Microvascular Decompression for Trigeminal Neuralgia: A Preliminary Study."** J Pain 25(3): 781-790.

21. Gabor, C. E., T. H. Hazen, B. C. Delaine-Elias, D. A. Rasko and E. M. Barry (2023). **"Genomic, transcriptomic, and phenotypic differences among archetype *Shigella flexneri* strains of serotypes 2a, 3a, and 6."** mSphere 8(6): e0040823.

22. Gavzy, S. J., A. Kensiski, Z. L. Lee, E. F. Mongodin, B. Ma and J. S. Bromberg (2023). **"*Bifidobacterium* mechanisms of immune modulation and tolerance."** Gut Microbes 15(2): 2291164.

23. Ghosh, S., C. P. Ahearn, C. R. Isabella, V. M. Marando, G. J. Dodge, H. Bartlett, R. L. McPherson, A. E. Dugan, S. Jain, L. Neznanova, H. Tettelin, R. Putnik, C. L. Grimes, S. Ruhl, L. L. Kiessling and B. Imperiali (2023). **"Human oral lectin ZG16B acts as a cell wall polysaccharide probe to decode host-microbe interactions with oral commensals."** Proc Natl Acad Sci U S A 120(22): e2216304120.

24. Gopalakrishna, K. P., G. H. Hillebrand, V. H. Bhavana, J. L. Elder, A. D'Mello, H. Tettelin and T. A. Hooven (2023). **"Group B *Streptococcus Cas9* variants provide insight into programmable gene repression and CRISPR-Cas transcriptional effects."** Commun Biol 6(1): 620.

25. Graf, K. T., H. Liu, S. G. Filler and V. M. Bruno (2023). **"Depletion of Extracellular Chemokines by *Aspergillus Melanin*."** mBio 14(3): e0019423.

PUBLICATIONS

26. Green, S. J., T. Torok, J. E. Allen, E. Eloe-Fadrosh, S. A. Jackson, S. C. Jiang, S. S. Levine, S. Levy, L. M. Schriml, W. K. Thomas, J. M. Wood and S. W. Tighe (2023). **"Metagenomic Methods for Addressing NASA's Planetary Protection Policy Requirements on Future Missions: A Workshop Report."** Astrobiology 23(8): 897-907.

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