



Greetings Colleagues,

IGS is located on the campus of the University of Maryland, Baltimore, the state's public health and law university, which includes seven professional schools. We are part of the School of Medicine, and at this season, our faculty roles become particularly visible as we cross the campus in caps and gowns hurrying to participate in graduation ceremonies and student celebrations. As we applaud their accomplishments, it's also a good time to reflect on the role IGS plays in educating the next generation of graduate and medical students.

Recent advances in next-generation sequencing and bioinformatics are transforming biomedical science research, and so, understanding the tools of genomics has become increasingly important for scientific, medical and interdisciplinary graduate studies. Soon after arriving at the School of Medicine, IGS faculty became involved in teaching and curriculum development in areas of genomics and bioinformatics within the Graduate Program in Life Sciences (GPILS). Dr. Scott Devine is the Track Leader of the Genome Biology track within the GPILS Molecular Medicine program. Dr. Devine and other IGS faculty have worked hard to develop a comprehensive curriculum to provide students with the background and critical skills needed for applied bioinformatics and genomics. Course

curriculum includes human, microbial and model system genomics, multi-omics applications, and programming for bioinformatics. The successful renewal of the NIH-supported T32 Training Program in Immunity and Infection, led by Dr. James Kaper, Professor and Chair of the Department of Microbiology and Immunology, includes a new Microbial Genomics track, led by Dr. Jacques Ravel, Professor and Associate Director, Genomics at IGS. The integration of human and microbial genomics in the educational curriculum is preparing our students to the future of medical practice and clinical research. Our state-of-the-art resources provide the students with extraordinary opportunities for hands-on exposure to cutting edge tools and mentoring from our faculty, who are leaders in their fields.

Erin Golembewski, PhD, Senior Associate Dean of the UMB Graduate School, shared this, "With its highly qualified faculty and state-of-the art research facilities, IGS has been a recruitment magnet for the best and brightest doctoral students. IGS resources have delivered cutting edge bioinformatics and genomics course work and research to graduate students."

Our educational efforts were rewarded this year, with the selection of IGS' own Dr. Lynn Schriml, Assistant Professor in Department of Epidemiology and Public Health (EPH) and the Division of Genomic Epidemiology and Clinical Outcomes, for the prestigious University of Maryland Medical School Teaching award. We are proud of this recognition of our efforts to contribute to UMB educational mission. (page 3)

IGS is not only training today's students, but future students! For the second time, Dr. Michelle Giglio, IGS Academic and Outreach Coordinator, and IGS faculty and staff, organized a genomics and bioinformatics STEM event as part of the enrichment program offered by the Center for Talented Youth (CTY), a non-profit organization that coordinates innovative educational opportunities to develop the talents of highly motivated young students. This event was again a major success and reached 70 young students from several states. (page 4)

Enrollment in the Genome Biology track and associated courses has increased in recent years, and it is very fulfilling to be helping students apply genomic approaches to biological questions. As the generation and analysis of big data continues to permeate all of the biomedical sciences, we envision a future where all UMB graduate and medical students will have the opportunity to learn how to navigate large databases to answer compelling questions on their quest to turn data into knowledge.

As always, I welcome your feedback,

Claire M. Fraser, PhD

Professor of Medicine and Microbiology and Immunology Director, Institute for Genome Sciences University of Maryland School of Medicine







Marcus Chibucos, PhD & Michelle Giglio, PhD Ontology & Biological Data Management

Drs. Marcus Chibucos (PI) and Michelle Giglio (co-I) have recently been awarded a \$1.4 million dollar three-year grant from the National Science Foundation (NSF) through the Advances in Bioinformatics program.

Dr. Chibucos specialized in the comparative genomics of plant pathogens prior to coming to IGS in 2008. In 2012, he joined the faculty as a Research Associate within the Department of Microbiology and Immunology. His research interests focus on genome annotation, comparative genomics and transcriptomics analysis of a wide range of animals and plant pathogens.

Dr. Giglio has worked for nearly 17 years in the area of prokaryotic genomics. She joined IGS in 2007 as an Assistant Professor and has worked on projects involving the Human Microbiome, microbial sequence analysis and ontology development. She is heavily involved in outreach and training activities.

This NSF award will fund the development and dissemination of the Evidence Ontology (EO). Researchers generate biological data from many diverse methods that range from laboratory experiments to computer-based analyses. These data serve as evidences that researchers use to make inferences and draw scientific conclusions. The process of biocuration seeks to capture these conclusions and the evidence that led to them in a standardized way, and makes this information readily accessible to the entire scientific community. An ontology is a controlled vocabulary of terms where each term is carefully defined and linked to other terms by precise relationships. The EO is a community standard for describing types of research evidence used to support scientific conclusions. The EO will be promoted through outreach, training and education efforts, including workshops and internships. Broader impact will include outreach efforts to local Baltimore area students focusing on teaching the importance of structuring information in a controlled way. Summer interns will engage in EO development and bioinformatics activities.



Rebecca Brotman, PhD, MPH New Grant on the Microbiome and Women's Health

Dr. Rebecca Brotman is an infectious diseases epidemiologist at IGS and an Assistant Professor in the Department of Epidemiology and Public Health at the SOM. Her research focus is on the human microbiome and women's health. She has developed a research career concentrated on elucidating the role of the vaginal microbiome in reducing susceptibility to urogenital infections.

There are approximately 20 million new sexually transmitted infections (STIs) detected in the US each year, which add \$16 billion in medical costs to the healthcare system. One approach to STI prevention that has not been fully explored is harnessing the protective features of the vaginal microbiome. It is thought that vaginal *Lactobacillus* spp. creates an acidic and hostile environment to pathogens but there may be variations in the levels of protection that various *Lactobacillus* spp. provide. Dr. Brotman developed a successful NIH RO1 research proposal that combines her previous epidemiological research work with metagenomic analysis of the vaginal microbiome. The study is a collaboration with Dr. Jacques Ravel, Associate Director for Genomics at IGS, Dr. Xin He, Assistant Professor of Biostatistics and Epidemiology at the University of Maryland College Park and Dr. Mark Klebanoff, Professor of Pediatrics at the Ohio State University College of Medicine.

In 2003, Dr. Brotman was part of a team analyzing the NIH Longitudinal Study of Vaginal Flora in which 3,620 women were followed over a one-year period, with quarterly clinical assessments. A total of 681 women were observed to acquire an incident *Chlamydia trachomatis*, *Neisseria gonorrhea*, or *Trichomonas vaginalis* genital infection. At that time, the samples were examined microscopically and by cultivation methods to determine the composition of the vaginal microbiota. Dr. Brotman's newly-awarded five-year RO1 aims to utilize powerful, high throughput sequencing approaches to look at the microbiome as a whole and elucidate the contribution of the vaginal microbiome in protecting against sexually transmitted pathogens.

Her study will employ complex genomic measurements of the vaginal microbiome composition, structure and function, and will also capture host immune status prior to infection. This multi-pronged approach, combined with a comprehensive behavioral dataset, may provide new insights into how these fragile ecosystems put women at risk or protect them from infection.

"With this extremely large longitudinal study of women, we will be able to quantify how the vaginal microbiome influence a woman's susceptibility to infection. Different communities of commensal bacteria are likely to differ in terms of their ability to defend the lower genital tract, and this new project will identify the protective and deleterious bacterial species and strains, along with providing data on how the vaginal microbiome functions," explained Dr. Brotman.

"We have the expectation that, in the future, we will be able to leverage the vaginal microbiome to improve women's health. Therapy in the form of personalized probiotics and prebiotics could be used to manage, modulate and restore the microbiota and ultimately prevent STIs. The data collected in this study will be used to develop novel interventions to protect women's reproductive health," said Dr. Jacques Ravel, Professor, Microbiology and Immunology, IGS at SOM.



Lynn Schriml, PhD

SOM Teaching Award - May 2015

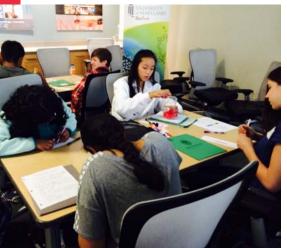
In addition to their research, IGS faculty are teaching professors within their School of Medicine departments. The University of Maryland School of Medicine (UMSOM) is one of the top academic medical schools in the U.S., and sharing their passion for genomics and bioinformatics is another way that IGS faculty impact the next generation of clinical researcher. In May 2015, Dr. Lynn M. Schriml, an Assistant Professor in Department of Epidemiology and Public Health (EPH) and Division of Genomic Epidemiology and Clinical Outcomes, received the prestigious Medical School Teaching award for her contribution to the UM SOM Epidemiology Small Group sessions.

At the EPH Commencement Celebration, Dr. El-Kamary, Associate Professor in the Department of Epidemiology and Public Health presented the award and expressed that Dr. Schriml is a tremendous asset to their department. She was one of the first faculty members to volunteer for this teaching activity and has made herself available for teaching sessions throughout the year. Dr. El-Kamary remarked that Dr. Schriml "is passionate about teaching and has great rapport with the students, who never fail to give her excellent evaluations year after year."

Kudo's to Dr. Schriml for her hard work!

STEM





CTY parents and youth at IGS

Hands-on **STEM**Genomics & Bioinformatics Activities:

the Center for Talented Youth at IGS

On Saturday April 18th, a beautiful spring day, a group of high school students and their parents came to the UM BioPark for a full schedule of hands-on science activities hosted by the Institute for Genome Sciences (IGS).

This genomics and bioinformatics event was part of the enrichment program offered by the Center for Talented Youth (CTY), a non-profit organization that coordinates innovative educational opportunities to develop the talents of highly motivated students. CTY programs are hosted by academic research centers, museums and other sites that are at the forefront of their respective fields. The April program was the second time that IGS organized this event in the past two years. IGS is one of the few U.S. research centers that periodically offers high school students a combined genomics and bioinformatics program. Registration filled quickly on the CTY's site and more than 70 parents and students came, not only from the metro Baltimore/DC region, but also from as far away as New York, New Jersey, and Northern Virginia.

Dr. Michelle Giglio, Assistant Professor in the Department of Medicine and the Academic and Outreach Coordinator for IGS, developed the content and activities for the event. The day started with a presentation from Dr. Giglio that reviewed the basics of DNA, genomes and 'omics sciences. Attendees then divided into groups and rotated through three different workshops. Dr. Giglio ran one of the workshops, while the other two were led by Drs. Emmanuel Mongodin and Joana Carneiro Da Silva, both Assistant Professors in the Department of Microbiology and Immunology, SOM IGS. They also helped to develop the curriculum for the workshop modules. Essential to the success of the day were the IGS faculty and staff who volunteered their time to assist in the event: Drs. Lynn Schriml, James Munro, Marcus Chibucos, and Lori McKay, Sarah Pick, Sean Daugherty, and Carrie McCracken.

The three activity workshops focused on areas where new research is changing the way we approach medicine and health care. They were: Microbiome Analysis, Comparative Genomics of Pathogens and Human Variation/Personalized Genomics. All attendees were able to attend all three workshops where they engaged in hands-on activities. Dr. Giglio and her colleagues were able to illustrate how both biology and computer skills are needed in genomic research. Several Baltimore families from a local charter school participated through a scholarship program. Dr. Giglio coordinated the scholarship program with Brian Sturdivant, who works closely with Baltimore City schools to promote interest in and access to science education.

"High schools are just beginning to include the basics of genomics and bioinformatics in their curriculums," explained Dr. Giglio, "so events like this help show students the true real-world impact of research like this on their lives and health."

The Center for Talented Youth (CTY) is operated through Johns Hopkins University and offers educational programs for the most advanced K-12 learners worldwide.



Featuring

Kathy O'Keefe,Director, Grants and Contracts

As members of a pre-eminent research institution, submitting grants and contracts is a priority for IGS faculty. Our faculty have a reputation for maintaining very high rates of grant submissions per individual faculty and also have above average success in getting their applications awarded. All of this keeps Kathy O'Keefe, Director, Contracts and Grants very busy. Her successful management of Pre-Award submissions and Post-Award reporting contributes to a robust and varied portfolio of IGS funded research projects.

In fiscal year 2014, IGS faculty submitted 71 grant proposals that amounted to nearly 78 million dollars requested in grant funding. In aggregate, IGS submissions to traditional federal sponsors and non-traditional industry and private foundations during the past seven years have exceeded 596 million dollars. Our funded awards for fiscal year 2014 generated a total of \$12,094,598 in extramural funds. Managing this large pool of proposals and awards is demanding on Kathy and her office.

Kathy's responsibilities span the entire life cycle of a grant. At the proposal stage, she works carefully with the principal investigators (PI) to understand the research mission, draft a detailed budget, and make sure that the PI is aware of all internal and program specific deadlines. Each submission has its own set of instructions and adherence to those details ensures a successful proposal outcome. In developing the budget, Kathy works closely with IGS faculty to carefully plan personnel effort, supplies, travel, sequencing and informatics costs in support of the proposed research. Once a grant is funded, Kathy works in concert with the PI and IGS finance office to manage post-award expenditures and reporting.

Due to the collaborative nature of genomics research, IGS faculty frequently have sub-awards on their proposals/awards or are sub-recipients on proposals/awards for other principal investigators and institutions. This is yet another layer that Kathy manages in a successful fashion.

In addition to working with IGS faculty and their collaborators, Kathy has developed strong communication ties with grant management officials at federal and private funding agencies such as the NIH and NSF. This allows her to work in conjunction with the primary investigators and their grant directors to navigate the many facets of grant management culminating in annual and final progress reports.

Kathy first began working with grants and contracts at the Sleep Disorders Center at Stanford University. She later became an institutional official in Stanford School of Medicine's Research Management Group. After working at Stanford for 11 years, and living her whole life in California, Kathy made the move to the east coast in order to work at The Institute for Genomic Research (TIGR) and the J. Craig Venter Institute (JCVI) before joining IGS.

Kathy feels the most rewarding part of her job is witnessing the progress of the scientific research. "We start with a proposal, receive an award and then I see the actual development of the science as it progresses through each stated specific aim. It's very gratifying," she says.

Kathy completed the NYC Marathon in November 2014, which was her fifth and final marathon. She now enjoys spending time on the tennis courts with her husband or chasing after their two dogs.



Staff Senate: Riham Keryakos

In spring 2015, Riham Keryakos, Office Manager, was nominated to serve on the Staff Senate, the first time that an IGS employee will be participating in this forum.

Started in 1994, the Staff Senate serves as an advisor and channel of communication to the President and the President's cabinet in the areas of policy and procedures which affect the quality of the staff's work life and their level of contribution to the strategic goals of the University. They also lead many University-wide community outreach activities. The Staff Senate consists of 20 staff members, 16 members from the exempt staff category and four members from the excluded non-exempt staff category. Each Senator serves a two-year term.

"Riham is very committed to exploring issues important to the University and IGS staff, and will be an excellent addition to the Staff Senate," said Dr. Jacques Ravel, Professor, Microbiology and Immunology, SOM, and Associate Director Genomics, IGS.



New Grant

Julie Dunning Hotopp, PhD

Dr. Julie Dunning Hotopp, PhD, Associate Professor, Microbiology & Immunology, received a three year grant from the National Science Foundation, which started June 1st and is titled the "Cloud-based Identification and Visualization of Lateral Gene Transfers in Genome Data."

Dr. Hotopp's early work on bacteria-animal lateral gene transfer (LGT) has revolutionized our understanding of the prevalence of these mutations in animal

genomes. Many of her findings are based on computational analyses she has developed to detect these mutations, which previously were not being measured. With this grant, she and her lab will be developing a virtual machine to enable all researchers to detect LGT in genome sequencing data.

All genomes accumulate mutations that are both beneficial and detrimental to the organism. The best understood mutations are those that involve alteration, insertion, or deletion of a single base pair. Numerous tools are available for identifying and validating such changes. Yet in many organisms, it is increasingly appreciated that large, even massive, insertions of DNA from other organisms can occur. These events are termed lateral gene transfer and have the potential to impact profoundly the organism, either in a detrimental or beneficial way. The Hotopp group will be developing a single tool to identify such lateral gene transfers from genome sequencing data, and to make this tool available to the research community in a user friendly format.

"Making the tools available to more scientists should increase our understanding of the occurrence and importance of such mutations in all organisms," said Dr. Hotopp. "You won't need to be experts in bioinformatics to use these tools."

In addition, her lab will develop YouTube whiteboard videos to educate the public about these mutations, genomics, and the tools developed in this proposal. The first of these videos can be found at: https://www.youtube.com/watch?v=PZG4qjVjJ70

Seminar Series

The IGS 2014 – 2015 seminar series concluded on May 28th with a dynamic presentation by Jonathan Zenilman, MD, the Chief of the Infectious Disease Division at Johns Hopkins Bayview Medical Center. His seminar titled -"The USPHS STD Studies in Guatemala- Ethics Gone Awry" - was a fitting conclusion to our interdisciplinary series. Dr. Zenilman discussed his involvement as a member of the Presidential Commission for the Study of Bioethical Issues, which was tasked by President Obama in 2010 to investigate the American John Cutler's deliberate inoculation of nearly 700 Guatemalans (prison inmates, mental patients and soldiers) between 1946 and 1948 with syphilis in what was thought to be an effort to test the effectiveness of penicillin. Cutler's never-published study documents were discovered after his death in his office at the University of Pittsburgh by Susan Reverby (Wellesley) in 2003, and led to the investigation.



Dr. Jonathan Zenilman, Johns Hopkins Bayview

Drs. Jacques Ravel and Vincent Bruno have co-chaired the seminar committee which has coordinated a full schedule of speakers based on recommendations from the faculty. "We have had a series of high profile speakers who have shared their most recent and cutting edge science with us." said Dr. Bruno. "This has been an excellent way to exchange ideas and has greatly improved our interdisciplinary approach to addressing important scientific questions."

Attendees have come from the various UMB professional schools, such as the Dental and Nursing Schools, as well as the UM School of Medicine and other local scientists from the Johns Hopkins University. The seminar series is on hiatus for the summer and will resume in the fall 2015. To be added to the invitation list, please contact Riham Keryakos (rkeryakos@som.umaryland.edu), who handles administration and promotion of the series.

Gut Microbes and Transplant Organs





Dr. Mongodin

Dr. Bromberg

Emmanuel Mongodin, PhD, Associate Professor, Microbiology and Immunology at the University of Maryland School of Medicine and IGS, and Jonathan Bromberg, MD, PhD, Associate Professor of Surgery, Microbiology and Immunology at SOM, have been examining whether certain gut bacteria can reduce the body's immune response to transplanted organs.

"The instestinal tract is our largest immune organ, and changes in the gut microbione (the microbes inhabiting our gut) can have major impact on our immune system" says Dr. Mongodin. Knowing this, he and Dr. Bromberg wondered whether manipulating the microbiome could affect organ transplant rejection. Organ rejection is a significant problem among transplant patients. Even in those who take immunosuppressive drugs, the immune system remains skeptical of the new organ; in a significant proportion of people, the transplanted organ becomes increasingly damaged from chronic immune response.

Drs. Bromberg and Mongodin's teams performed heart transplants in a group of mice whose gut microbiome was altered with

"Our understanding of the aetiology of complex diseases has...evolved with increased awareness that the human microbiota has an active and critical role in maintaining health and inducing disease... Findings from bioinformatic studies indicate that the microbiota and microbiome have multiple effects on the innate and adaptive immune systems, with effects on infection, autoimmune disease and cancer...."

Jonathan Bromberg and Emmanuel Mongodin, National Review Nephrology, 12 May 2015 microbes that are known to turn down the immune system, while another group was given a microbiome that would activate it. A third group did not receive any new bacteria. After a month, the researchers examined the transplanted hearts. Those in the first group – with the microbes that decreased immune activity – had much less heart damage than those in the other two groups.

"We are in the early stage of studying how genomic knowledge can impact how we proceed with transplantation," said Dr. Mongodin. He and Dr. Bromberg also plan to look at gut bacteria in humans, to see if they can find signature differences between anti-inflammatory and pro-inflammatory gut microbial ecosystems. "We are just starting to understand how the composition of microbiota can affect the immune system, and the implications of changes in the gut microbiota composition on organ failure," said Dr. Mongodin.



Latéy is pictured here with 2 students from the Prince George's County School District who were inspired by her comments.

IGS Graduate Student in the News:

Latéy Bradford — Promise Research Symposium and Congressional Blastoff STEM Forum

Latéy Bradford (Ravel Lab), a PhD Candidate within the GPILS Program in Molecular Microbiology and Immunology (as an MD/ PhD student) was selected to present a TED-style talk at a recent conference sponsored by the University System of Maryland PROMISE Alliance for Graduate Education at the University of College Park on February 13, 2015. Latéy gave an engaging overview of her dissertation topic: "The Dynamics in the Vaginal Ecosystem and Development of Vulvovaginal Candidiasis". She received an award for the best presentation in this category.

Latéy was invited by Congresswoman Donna F. Edwards (MD - 4th District) to participate in the Congresswoman's annual Blastoff STEM Forum on April 28, 2015. Latéy was asked to serve as a panelist in a discussion on strategies to encourage and support today's youth in their pursuit of STEM careers. Joining a distinguished panel where she was the only graduate student, Latéy spoke to middle school and high school students in the audience about the reasons she aspires to become a physician scientist. Because of her insightful comments and inspiring ideas she also gained the attention of non-profit leaders, government officials, and educators who were in attendance.



Owen White, PhD Receives Franklin Award for Open Access

at Bio-IT Conference in April 2015

Owen White, PhD, Professor of Epidemiology and Public Health and Associate Director of Informatics at IGS at the University of Maryland School of Medicine as well as Co-Director of the UM Center for Health-related Informatics and Bioimaging (CHIB), received the Benjamin Franklin Award for Open Access in the Life Sciences from Bioinformatics.org, also known as the Bioinformatics Organization on April 22 in Boston.

Dr. White has been dedicated to open source/open access throughout his scientific career. As a Principal Investigator with the Human Microbiome Project Data Analysis and Coordination Center (HMP DACC), he led the multi-year, multi-institutional aggregation and organization of data for the HMP and other large-scale data informatics projects. Dr. White received his award and delivered a laureate presentation at the **Bio-IT World Conference and Expo** on April 22 in Boston. The Benjamin Franklin Award for Open Access in the Life Sciences is a humanitarian/bioethics award presented annually by Bioinformatics.org to an individual who has promoted free and open access to the materials and methods used in the life sciences. Dr. White, the 14th recipient of the award, was selected from a pool of internationally recognized nominees.

A key challenge presented by large-scale genome sequencing is the effective display of uniform information to the scientific community. In addition to his work with the HMP DACC, Dr. White has also developed several web resources such as the Comprehensive Microbial Resource and Pathema containing annotation from microbial genomes, Gemina, a web-based system designed to identity infectious pathogens, Sybil, a web-based open source software package for comparative genomics. Dr. White has developed automated annotation systems for bacterial, eukaryotic and microbiome organisms as well as several bioinformatic training programs.



Personal Genomics & Law Enforcement: \
Congressional Panel

On March 19, 2015, Congresswoman Louise Slaughter and Senator Elizabeth Warren hosted a panel on genetics and law enforcement, and the challenges associated with genetic privacy in a press briefing held in Washington, DC. Participants on the panel included several experts in privacy laws, as well as Dr. Claire Fraser, who spoke about genomics-enabled studies of the microbial world. The Congressional briefing was organized by the Personal Genetics Education Project, Harvard Medical School.

"The value of genomics approaches derives from the speed at which evidence can be collected, and the enormous amount of this information that can be generated," said Dr. Fraser. "But we still need to develop a framework and standards for data interpretation that will achieve an even higher level of analytical value."





Interview with

Anup Mahurkar

The Informatics Resource Center (IRC) comprises of scientists, bioinformatics analysts, and software engineers who support genome-based research. There are two "cores" within the IRC—the Genome Informatics Core (GIC) and the High Performance Computing Core (HPCC). Anup Mahurkar, MIM, as Executive Director of Software Engineering and IT, and Director of the IRC, directs both cores. The IRC leadership includes pioneering researchers with many years of experience in the informatics field. On UMB campus, the IRC team is actively working with collaborators at several of the UMB schools. This work has led to a number of joint publications in high-profile journals.

Q&A WITH THE DIRECTOR OF THE [RC]

What s the difference between your two cores?

AM: Our High Performance Computing Core (HPCC), gives you access to a massive computational grid attached to high-performance storage. This core would be appealing to someone who needs to crunch large-scale data, big data. The Genome Informatics Core (GIC) provides genome analysis and software development for IGS and any UMB campus researchers. Our core services are used primarily by our Institute and UMB collaborators, as well as by any researchers who want a fee-for-service menu option. We work closely with the GRC (the Genomics Resource Center) to allow investigators a "one-stop shop" for sequencing and analysis.

What services do you provide?

The major services people use are genome annotation, microbiome annotation and analysis, functional genome and epigenome analysis. Investigators can order any or all of these services. A standard analysis can take from one week to three weeks to perform, depending on the number of samples requested.

Who do you work with and how do investigators find out about your services?

We work with anyone – researchers at UMB, other universities, federal agencies, as well as commercial enterprises. Many at UMB find out about us through their IGS collaborators or through their work with the GRC, our colleagues on the fifth floor at the UMB BioPark.

What s the capability of the HPCC?

The HPCC contains a computational grid with over 3,000 cores, and over 2.5 petabytes of storage capability. A petabyte (PB) is 10¹⁵ bytes of data, 1,000 terabytes (TB) or 1,000,000 gigabytes (GB). That's a lot of computing power and storage available to researchers at UMB! We are also continually evaluating our systems and upgrading.

What are some of the other capabilities of the GIC or IRC?

There are many IT experts in the IRC. A significant part of their work is web development and web hosting in support of grants awarded to our faculty and their collaborators. A particular focus for us is in building web resources where researchers can share multi-omic data and results with the wider research community. As an example, we supported the NIH funded Human Microbiome Project by successfully engineering a resource (HMP DACC) to distribute the large amount of data generated by this massive project. We also have a strong focus in the development of ontologies and controlled vocabularies that are used by large consortia for marking up the metadata using community supported and developed standards. Controlled vocabularies afford the ability to compare dataset generated at two different institutions and as such as are very important.



Luke Tallon & Dr. Lisa Sadzewicz



GRC hosts the PacBio Americas User Group Meeting on 6/17/15

GRC UPDATE

It's been a busy few months in the Genomics Resource Center (GRC). We have installed and validated our new HiSeq 4000 system, which is capable of generating 1.5 The of data every 3.5 days. That's enough to sequence 12 human genomes in one run! Initial results are promising and we are excited to roll this new platform into production. For more information, please see our blog. We have also taken delivery of a MiSeq Dx for clinical sequencing applications. Initially, using this platform, we will focus on two targeted gene panels, one cancer panel and one pharmacogenomics panel. Soon, we expect to expand through the addition of new panels and a HiSeq instrument for clinical exomes and whole genomes. Stay tuned!

On June 17, 2015, we hosted the annual Pacific Biosciences Americas User Group Meeting. The GRC is now a PacBio Certified Service Provider and we are pleased to continue hosting this meeting for the third consecutive year. Each year this meeting brings together PacBio users and researchers from around the Americas to learn about new and innovative ways to use this disruptive technology. It was a full day of exciting presentations and discussions. Check out the agenda here.

After our return from a busy and exciting American Society of Microbiology (ASM) Annual Meeting in New Orleans, where we showcased the GRC, we are looking forward to a number of new sequencing and analysis projects. Have a great summer and stay cool!

Q&A

WITH THE CO-DIRECTORS OF THE GRC

Can anyone use GRC services?

Yes! We offer our services and expertise to investigators worldwide for projects large and small. If you have a sequencing or analysis project, please contact us to learn more about how we can help you.

I ve heard PacBio is great for sequence ing microbial genomes, but what about larger genomes?

Long reads are a crucial part of *de novo* assembly of genomes of all size. We have sequenced a number of parasite, insect, plant, and animal genomes using PacBio SMRT sequencing alone and in combination with short-read Illumina data. The improvement over a short-read only approach is impressive. If your goal is to generate the most complete and accurate genome assembly possible, long read data is essential. Contact us!

Do you offer any support beyond sequencing and basic analysis?

We do! Unlike some sequencing centers, who bidyou adieu upon data delivery, our scientists and bidinformaticians in the GRC and the IRC will work with you to interpret your data, submit it to public archives if needed, and contribute to manuscript preparation.

PUBLICATION LIST
MARCH '15-JUNE '15

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