The Genetic Resources Core Facility (GRCF) 2024 Symposium

2024 GRCF Symposium

Come to Learn, Engage, Network & Celebrate

April 25, 2024, 9:00 am - 2:45 pm, Turner Concourse

Featuring eleven talks, exhibit concourse, light food, and GRCF Flair!

Welcome to the Annual GRCF Symposium!

We extend our warmest welcome to all attendees joining us for this year's symposium! It's with great excitement that we gather once again to celebrate advancements in research and technology alongside esteemed speakers from the Johns Hopkins community and leaders in industry. We look forward to reconnecting and fostering collaborations that drive innovation forward.

Throughout the symposium, we invite you to attend our seminars and explore our information tables, where you can learn more about leading edge technologies and products and discover the GRCF's comprehensive service offerings. Whether you're seeking expertise, resources, or simply looking to network, our team is here to support your research journey.

Thank you for joining us as we come together to explore, learn, and inspire. Let's make this symposium an enriching experience for all!

The GRCF Team

AGENDA

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2024 GRCF SYMPOSIUM AGENDA

Start Time	End Time	Event	Room	Featuring	Title
9:00 AM	9:45 AM	Plenary Session	Tilghman Auditorium	Ava Hoffman	"Digging into genomics with BIODIGS at under-resourced institutions"
10:00 AM	10:45 AM	Breakout Session I	G-01	Illumina	Leveraging Illumina Sequencing with the NovaSeq X Plus
			G-03	New England BioLabs	DNA Methylation applications utilizing NEBNext EM-Seq and E5hmC-Seq
			West Room	JHU Sustainability	Fostering a Culture of Sustainability in the Lab
11:00 AM	12:00 PM	Keynote Address	Tilghman Auditorium	Alan F. Scott	"Sequencing Benny: The Biodiversity Crisis"
12:00 PM	1:00 PM	Lunch	Turner Concourse	1876 Distinction Caterer	Boxed Lunch
1:00 PM	1:45 PM	Breakout Session II	G-01	Oxford Nanopore	Nanopore Sequencing: What you're missing matters!
			G-03	Cytiva	Laboratory Filtration 101
			West Room	Thermo Fisher	New Innovations in Stem Cell Workflows: From Gene Editing to iPSC Cell Survival and Suspension Culture
2:00 PM	2:45 PM	Breakout Session III	G-01	QIAGEN	Harnessing digital PCR to investigate HIV-1 persistence in clinical samples
			G-03	Corning	Practical tips and tricks for generating 3D cell culture environments and scaling up 3D models
			West Room	Bio-Rad	Counting with Droplet Digital PCR — More Applications than Anyone Ever Dreamed Of

Plenary & Keynote

Digging into genomics with BIODIGS at under-resourced institutions, Ava Hoffman, Associate Biostatistics, JHU School of Public Health, Ph.D., 9 am -9:45 am, Tilghman Auditorium.

Abstract: Soil microbes play critical roles in human and environmental health, yet the vast majority of species remain uncharacterized and poorly understood. We have launched BioDIGS, a collaborative soil metagenome project, as part of the Genomic Data Science Community Network (GDSCN), a collective of >25 faculty members at Community Colleges, Historically Black Colleges and Universities, Hispanic Serving Institutions, and Tribal Colleges and Universities. Through BioDIGS, we have collected soil from >100 different environments across the US, performing short and long-read DNA sequencing. We further augment our dataset with >3000 public soil meta-genomes to present one of the most comprehensive studies of soil biodiversity ever attempted. Our results highlight significant associations between metagenome diversity and heavy metal content, especially lead and arsenic at certain urban sites. Finally, using long-read sequencing we have assembled complete genomes and high quality MAGs for over 100 novel species, as well as gigabases of novel gene sequences.

Sequencing Benny: The Biodiversity Crisis, Alan F. Scott, Ph.D., Associate Professor, JHU SOM, Emeritus Director & Founder, JHU Genetic Resources Core Facility., 11 am -12 pm, Tilghman Auditorium.

Abstract: The talk will discuss the biodiversity crisis, the genetics of endangered species,the role sequencing efforts are making in identifying and monitoring change and the current and likely future of the Earth's climate and what we can do as individuals to help transition to a sustainable planet.

Breakout Session I

Leveraging Illumina Sequencing with the NovaSeq X Plus, Bao Ho, Ph.D., Sequencing Specialist, 10 am - 10:45 am, MRB G-01.

Abstract: Illumina sequencing has become more accessible than ever with the arrival of the NovaSeq X Plus at the GRCF. Equipped with the industry'smost robust and sustainable chemistry, coupled with ultra-high aperture optics and most accurate secondary analysis, the instrument enableswhole genome, whole transcriptome, single cell and other high intensity sequencing applications with quality, efficiency, and affordability. Join us to learn more about how Illumina sequencing on the NovaSeq X Plus can advance your research further

DNA Methylation applications utilizing NEBNext EM-Seq and E5hmC-Seq, Jeanne Geskes, Field Applications Scientist, NGS, 10 am - 10:45 am, MRB G-03.

Abstract: Epigenetics is a broad study of different reversible genomic changes. DNA methylation is an epigenetic mechanism for the study of covalentchanges of cytosines, specifically 5-metylcytosine(5mC) and 5-hydroxymethylcytosine (5hmC). A wide range of biological processes areassociated with methylation of DNA. Deactivation of Chromosome X, genomic imprinting, stem cell differentiation, gene expression control andchromosomal stability are all associated with DNA methylation. We will discuss the next generation sequencing tools for studying DNAmethylation and discerning between 5mC and 5hmC and the data associated with its application for research.

Fostering a Culture of Sustainability in the Lab, Ryan Weeks,Ph.D., Sr. Sustainability Specialist, 10 am -10:45 am, West Room.

Abstract: The chemical, petrochemical, and healthcare industries are major contributors to global climate change, accounting for over 5.8% and 4.4% oftotal greenhouse gas emissions. The millions of labs in these industries produce life-changing breakthroughs, however, the environmentalimpact of their day-to-day research and operations is often left unconsidered. Given this impact and the need for climate action, scientists must begin incorporating sustainability within their day-to-day operations and fostering a culture of sustainability within the research community inorder to reduce their significant environmental impact. This presentation will explore some of the environmental and social impacts oflaboratories globally and within the Baltimore region. We will discuss behaviors that leaders, including the GRCF, are using to lessen theirimpact and how JHU scientists can apply these behaviors to their own research strategies. Additionally, students will hear about various opportunities to reduce their impact at JHU by making their labs more sustainable through JHU's Green Labs Initiatives.

Breakout Session II

Nanopore Sequencing: What you're missing matters!, Greg Gonye, Ph.D. - Regional Sequencing Specialist, 1 pm -1:45 pm, MRB G-01.

Abstract: The unique attributes of nanopore sequencing, such as the ability to sequence native DNA and RNA fragments of any length, fully address thelimitations of traditional sequencing by synthesis technologies. From assembling and closing genomes telomere to telomere, uncovering singlenucleotide mutations in full-length mRNA transcripts unique to tumor cells, this seminar will highlight how recent improvements in accuracy andyield have greatly expanded nanopore sequencing applications, resulting in new biological insights. Case studies will demonstrate howresearchers are applying the unique benefits of nanopore sequencing technology across the full spectrum of basic to clinical research.

Laboratory Filtration 101, Melissa Gammell, Laboratory Filtration Specialist, 1 pm -1:45 pm, MRB G-03.

Abstract: In this seminar you will learn more about the basics of laboratory filtration, why scientists perform filtration, the different types of filter media andsome important considerations to make when selecting filtration devices. We will also discuss some of the high-level applications andmarketplace opportunities for laboratory filtration.

New Innovations in Stem Cell Workflows: From Gene Editing to iPSC Cell Survival and Suspension Culture, Brett Strahin, Technical Specialist, Cell Biology, 1 pm -1:45 pm, West Room.

Abstract: Thermo Fisher has developed innovative protocols and reagents to enhance the efficiency of gene editing using CRISPR/Cas9 technology iniPSCs, allowing for precise modifications in the genome and limitation of off-target effects. Additionally, significant progress has been made forrepeatable 3D iPSC culture, expansion, and characterization, providing a more physiologically relevant and robust platform for studying iPSCbehavior and differentiation. These advancements in iPSC research contribute to the development of more efficient and reliable techniques forstudying disease mechanisms, drug screening, and regenerative medicine applications.

Breakout Session III

Harnessing digital PCR to investigate HIV-1 persistence in clinical samples, Francesco R Simonetti, MD, Ph.D., 2 pm -2:45 pm, MRB G-01.

Abstract: Even after decades of effective treatment, HIV infection cannot be cured due to a small pool of latently infected CD4+ T cells that persist due to proliferative and survival stimuli. The characterization of these cells is challenging due to their rarity (1:104-1:106) and the lack of markers that could distinguish cells carrying transcriptionally silent HIV genomes (proviruses) from uninfected cells. In this talk, we will present recent studies from our group in which we harnessed digital PCR to quantify and study HIV-i nfected cells. Due to the vastness of the human genome, the likelihood that two independent HIV i nfection events lead to the same integration site is infinitely small. Thus, if two cells share the same HIV-human, they must be the progeny of the same clone. We exploit proviral integration as a molecular barcode to tag HIV-infected clones. We use this approach to track clonal dynamics over time, determine infected cell phenotypes, and their antigen specificity by activation-induced markers. This approach can be also used by designing probe-based assays targeting small defects, unique to proviruses of interest, or the VDJ rearrangements of the infected CD4+ T cell clonotypes. Lastly, we will present a novel limiting-dilution approach to quantify HIV RNA molecules from individual cells, recently used to investigate latency reversal upon cell engagement with cognate antigens.

Practical tips and tricks for generating 3D cell culture environments and scaling up 3D models, Catherine Siler, Ph.D., Field Application Scientist Manager, 2 pm -2:45 pm, MRB G-03.

Abstract: When it comes to modeling human development and disease, traditional 2D cell culture models are often unable to capture complex biological properties observed in vivo. Animal models attempt to overcome these inadequacies but involve a significant investment of time and resources while not accurately capturing human development and disease states. Cellsgrown in 3D more closely mimic in vivo behavior in tissues and organs. These models are gaining increased importance for attaining in vivo-like conditions to study developmental cues and therapeutic possibilities This seminar will feature two sections: First, we will introduce commonly used approaches involving both scaffold and scaffold-free methods for generating 3D cell culture models Secondly, we will focus on organoid models, including methods for derivation, tips for growth and maintenance, and assay considerations.

Counting with Droplet Digital PCR — More Applications than Anyone Ever Dreamed Of, 2 pm -2:45 pm, West Room.

Abstract: More than 200 peer-reviewed publications have been published that leveraged the high performance, high throughput, and tremendousversatility of Bio-Rad's QX100/QX200 Droplet Digital PCR (ddPCR) Systems. The superior precision, sensitivity, and reproducibility that have made these systems the industry standard for digital PCR have produced new biological in-sights and advanced the use of digital PCR in many new areas of investigation. Among the applications reviewed in this webinar is the adoption of ddPCR for liquid biopsy in cancer therapy monitoring, assisting genome editing of stem cells for disease modeling and therapy, in vivo count monitoring of therapeutically engineeredimmune cells in HIV eradication strategies, and identification of under-recognized somatic mosaicisms.

Exhibitors

Hopkins Exhibitors

Genetic Resources Core Facility (GRCF)

- Cell Center
- Core Store
- DNA Services
- JHU BioBank

JHU Sustainability

Corporate Exhibitors

10X Genomics

BD BioSciences

BioLegend

Bio-Rad

Cell Signaling Technology

Corning Life Sciences

Cytiva

Integrated DNA Technologies (IDT)

Illumina, Inc.

New England BioLabs (NEB)

Oxford Nanopore Technologies

Promega Corporation

QIAGEN

Quality Biological Inc.

Thermo Fisher Scientific

Twist Bioscience

Registration | Exhibitor Expo | Sessions

Catering

Catering

MENS ROOM

MILES ROOM

East Room

LADIES ROOM

Genetic Resouces Core Facility

QIAGEN

Cell Signaling

New England BioLabs

Thermo Fisher

Cell Center & JHU BioBank

Core Store

DNA Services

Illumina

10X Genomics

Oxford Nanopore

Promega

Catering

Catering

BD Biosciences

Bio-Rad

Corning Life Sciences

Twist Biosciences

Quality Biological

IDT

KITCHEN

Tilghman Auditorium

Cytiva

JHU Sustainability

BioLegend

WEST ROOM

Register Here

Register Here

LADIES ROOM

MRB G-01

MRB G-03