



U.S. DEPARTMENT OF  
**ENERGY**

Office of  
Science

## **Biological and Environmental Research Program**

Biological Systems Science Division

2024 Agenda

# **Genomic Science Program and Enabling Capabilities and Resources**

## **Principal Investigator Meetings**

April 2-4, 2024

Bethesda, MD

### **Meeting Organizers**

Kari Perez

Vijay Sharma

Paul Sammak

Ramana Madupu

# Welcome

As a major supporter of basic genome-enabled research, BER's Biological Systems Science Division (BSSD) fosters scientific discovery by combining fundamental biological research across disciplines with enabling capabilities and world-class user facilities. BSSD's overarching goal is to provide the necessary fundamental science to understand, predict, manipulate, and design biological systems that underpin innovations for bioenergy and bioproduct production and enhance our understanding of natural, DOE-relevant environmental processes ([BSSD Strategic Plan](#)).

This year, the principal investigator meetings for BSSD's Genomic Science Program (GSP) and Enabling Capabilities and Resources (ECR) feature joint sessions leading to a better integration and understanding of the larger BSSD mission. The Computational Biology, User Facilities, and Biomolecular Characterization and Imaging Science portfolios are included in the ECR meeting. GSP objectives continue to provide systems-level understanding of plants, microbes, and their communities through the program's Bioenergy, Biosystems Design, and Environmental Microbiome Research portfolios.

To accelerate the bioeconomy, BSSD pursues innovative science underpinning advances in sustainable biofuels and bioproducts; the design, modification, and optimization of plants and microbes for beneficial purposes; and the development of next-generation technologies and computational resources for systems biology research.

---

**Click titles below to navigate to each session** (*All times Eastern*)

## TUESDAY, APRIL 2

- *Opening Session*
- *Joint Keynote Presentation*
- *Joint Plenary Session 1: GSP Early Career Research Program Awardees*
- *Joint Plenary Session 2: Multidisciplinary Science Enabled by Facility Collaboration*
- *Poster Session 1*
- *KBase Tutorials and Workshop*
- *GSP Breakout Session 1: Sustainable Feedstock Development for Bioenergy*
- *GSP Breakout Session 2: Advancing the U.S. Bioeconomy by Designing and Engineering Microbiological Systems*
- *ECR Breakout Session 1: Quantum Imaging and Sensing*
- *Joint Plenary Session 3: Phenomics and Function*

## WEDNESDAY, APRIL 3

- *Joint Plenary Session 4: Bioenergy Research Centers*
- *GSP-Led Key Note Presentation*
- *Poster Session 2*
- *Joint Plenary Session 5: BER Data Science and Infrastructure*
- *GSP Breakout Session 3: Environmental Microbiology*
- *GSP Breakout Session 4: Plant Gene Function*
- *ECR Breakout Session 2: KBase Science Session: Data Integration to Support (or Refute) Predictions*

## THURSDAY, APRIL 4

- *GSP Breakout Session 5: Systems Biology of Bioenergy-Relevant Microbes*
- *ECR Breakout Session 3: Bioimaging Academic and National Laboratories*
- *KBase Tutorials and Workshop*
- *GSP Breakout Session 6: DOE Office of Science New Initiatives – Focus on ACCELERATE and BRaVE*
- *ECR Breakout Session 4: Program Discussion Among ECR Principal Investigators*

**NOTE:** All times Eastern

## TUESDAY, APRIL 2

Room A-D

### Opening Session

---

**8:00 a.m. Coffee and Snacks**

**8:30 a.m. Welcome and Logistics**

**Speakers:** Kari Perez, Program Manager, Biological Systems Science Division; Vijay Sharma, Program Manager, Biological Systems Science Division; and Tracey Vieser, Oak Ridge Institute for Science and Education

**8:35 a.m. Opening Remarks**

**Speaker:** Dorothy Koch, Associate Director, Biological and Environmental Research Program

**8:40 a.m. Meeting Introduction**

**Speaker:** Todd Anderson, Director, Biological Systems Science Division

### ECR-Led Keynote Presentation

---

Room A-D

**9:00 a.m. How Generative AI Can Impact Biological Research**

**Speaker:** Rick Stevens, Associate Laboratory Director for Computing, Argonne National Laboratory

Dr. Stevens will discuss the variety of approaches groups are taking to build domain-specific foundation models for biological problems (e.g., protein design and single-cell analysis), current results of these efforts, and future directions. He will also discuss the use of general purpose large-language models (LLMs) in biological use cases, including the automated analysis of tens of thousands of scientific papers; methods for high-throughput knowledge extraction, distillation, and synthesis; and how frontier AI systems can be used to explore the landscape of biological hypotheses and drive experimental design.

## ***Joint Plenary Session 1***

**Room A-D**

**10:00 a.m. Genomic Science Early Career Research Program Awardees**

**Moderator:** Pablo Rabinowicz

The 2023 Office of Science Early Career Research Program awardees from BER's Biological Systems Science Division will present their new projects.

**10:00–10:20 a.m. Elucidation and Validation of Genes Associated with Biological Nitrification Inhibition in *Populus***

**PI:** John Cahill, Oak Ridge National Laboratory

**10:20–10:40 a.m. Engineering Continuous Trait Variation in Bioenergy Feedstocks to Optimize Growth on Marginal Lands**

**PI:** Jennifer Brophy, Stanford University

**10:40 a.m. Break**

## ***Joint Plenary Session 2***

**Room A-D**

**10:55 a.m. Multidisciplinary Science Enabled by Facility Collaboration**

**Moderators:** Ramana Madupu and Amy Swain

Great breakthrough opportunities happen at the intersection of multidisciplinary science when experts from different domains come together to tackle grand challenges central to BER mission science. Multiple analytical approaches and techniques must be brought to bear on these complex problems. This session will highlight a breadth of BER science that has been made possible through access to advanced capabilities beyond those available at many institutions. DOE provides access to such capabilities through national scientific user facilities and computational resources. BER's facilities and user resources engage collaboratively to assist researchers in using complementary capabilities at multiple facilities. Facility experts can train users and help design experiments, take measurements, and, in some cases, help interpret user data. These facilities provide users with free access to the capabilities through proposal processes.

**10:55–11:00 a.m. Introduction**

**11:00–11:18 a.m. Opportunities for Team Science Enabled by Integrated User Facilities**

**Speaker:** Yasuo Yoshikuni, Joint Genome Institute (JGI), Lawrence Berkeley National Laboratory

**11:18–11:36 a.m. TerraForms User Program—Capability Development, User Science, Collaborations and Deployment**

**Speaker:** Arunima Bhattacharjee, Environmental Molecular Sciences Laboratory (EMSL), Pacific Northwest National Laboratory



- 11:36–11:54 a.m. From Roots to Atmosphere: Utilizing DOE Facilities to Track Drought’s Carbon Impact on Ecosystem Processes**  
*Speaker:* Malak Tfaily, University of Arizona
- 11:54 a.m.–12:12 p.m. Utilizing Metaomic and Chemical Imaging Approaches to Explore the Dynamics of Nutrient Exchange and Environmental Adaptation Mediated by Plant-Fungal Symbiosis**  
*Speaker:* Hui-ling (Sunny) Liao, University of Florida
- 12:12–12:30 p.m. A Single Consortium View of Syntrophic Methane Oxidation by Environmental Archaea and Bacteria**  
*Speaker:* Victoria Orphan, California Institute of Technology

### Poster Session 1 (Room E-H) and Lunch (Foyer)

12:30 p.m.

### KBase Tutorials and Workshop

White Oak (A and B)

12:30 p.m. **KBase Workshops (Registration required)**  
Ramana Madupu and Elisha Wood-Charlson

12:30-1:30 p.m. **Microbial Annotation**  
*Speakers:* Hyun-Seob Song, Bill Nelson, Jason McDermott, Patrik D’haeseleer, Chris Henry

With the goal of improving the overall accuracy and precision of microbial annotations, developers from several Science Focus Areas (SFAs) teamed up with KBase to update ModelSEED tools for building improved metabolic models in KBase. In this workshop, participants will use KBase to build models from multiple input annotation sources, leveraging tools co-developed with the  $\mu$ Biospheres SFA at Lawrence Livermore National Laboratory. The workshop will also cover the new Snekmer annotation tool developed by the Persistence Control SFA at Pacific Northwest National Laboratory (PNNL) and demonstrate tools for using models derived from annotations to simulate phenotype data [based on experimental isolate phenotype data in KBase contributed by the Plant-Microbe Interfaces SFA at Oak Ridge National Laboratory and the Ecosystems and Networks Integrated with Genes and Molecular Assemblies (ENIGMA) SFA at Lawrence Berkeley National Laboratory]. Finally, the workshop will demonstrate the OMEGGA tool developed by the PNNL Soil Microbiome SFA to enable the fitting of metabolic models to phenotype data to propose novel annotations.

**Registration required:** This session will be hybrid, with space for ~30 people in person. Please register via Zoom.

**Registration link:**

[https://lbln.zoom.us/meeting/register/tJEodu2srDwtHdTbG14D4fYP\\_opWmWMa99RL](https://lbln.zoom.us/meeting/register/tJEodu2srDwtHdTbG14D4fYP_opWmWMa99RL)

**1:30-2:30 p.m. Long-Read Isolate Sequencing and Analysis**

**Speakers:** Lauren Lui, Ben Allen, Elisha Wood-Charlson

In early December 2023, ENIGMA and KBase partnered to deliver a Long-read Isolate Sequencing and Assembly (LISA) workshop (<https://sites.google.com/lbl.gov/lisa-workshop>). This session will walk through the LISA workshop structure and outline the wet lab and computational procedures used to generate and analyze long-read isolate sequence data. KBase speakers will also emphasize the ease and importance of sharing data among the BER research community while still giving credit to users for their contributions. If interested in long-read sequencing and how to generate data that are comparable across BER-relevant research, join KBase for this interactive walk-through on how to do long-read sequencing, analysis, and publishing.

**Registration required:** This session will be hybrid, with space for ~30 people in person. Please register via Zoom.

**Registration link:**

<https://lbl.zoom.us/meeting/register/tjltcuugrTkjGNzL7D-CXMMTJAioxxcvoHm->

**KBase 1-on-1 Consultation and Help (by appointment)**

KBase staff would love to meet with you (in person or virtually) to discuss collaboration ideas, expand your knowledge of the platform, or help with any issues or concerns. Please pick a time that is convenient for you, and we will do our best to accommodate. We may ask to reschedule, pending conflicts with the conference agenda.

**Schedule with us at:**

<https://doodle.com/bp/elisha3/chat-with-kbase-1-1>

## ***GSP Breakout Sessions***

---

**2:30-5:00 p.m. GENOMIC SCIENCE PROGRAM BREAKOUT SESSION 1:  
SUSTAINABLE FEEDSTOCK DEVELOPMENT FOR BIOENERGY**

**White Oak A and B**

**Moderator:** Kari Perez

Plants respond to environmental change through complex networks, many involving interactions with the surrounding microbiome, that can influence plant growth, development, and metabolism. Systems biology and omics technologies together with computational approaches are allowing researchers to map these complex networks, enabling a predictive understanding of their performance. Systems Biology Research to Advance Sustainable Bioenergy Crop Development awardees are applying these tools to examine the ecological impacts of fully sustainable, bioenergy crop production. This session will highlight progress in understanding how candidate biofuel/bioproductions plants interact with environmental factors to affect long-term plant feedstock performance.

- 2:30-2:35 p.m.**      **Introduction**  
*Speaker:* Kari Perez
- 2:35-2:55 p.m.**      **EndoPopulus: Elucidation of the Roles of Diazotrophic Endophyte Communities in Promoting Productivity and Resilience of *Populus* Through Systems Biology Approaches**  
*Speaker:* Sharon Doty, University of Washington, Seattle
- 2:55-3:15 p.m.**      **A Systems Understanding of Nitrogen-Fixation on the Aerial Roots of Sorghum (*Sorghum bicolor*)**  
*Speaker:* Jean-Michel Ané, University of Wisconsin, Madison
- Flash Talk:** Investigating Mucilage Production on Aerial Roots of Sorghum (*Sorghum bicolor*) Through Single-Cell Analysis  
*Speaker:* Rafael Espejel Venado, University of Wisconsin, Madison
- 3:15-3:35 p.m.**      **Integration of Experimental and Modeling Approaches to Understand, Predict, and Modulate Rhizosphere Processes for Improved Bioenergy Crop Productivity**  
*Speaker:* Karsten Zengler, University of California, San Diego
- Flash Talk:** Unraveling Metabolic Interactions Within a Rhizosphere Microbial Community  
*Speaker:* Manish Kumar, University of California, San Diego
- 3:35-3:55 p.m.**      **Systems Analysis of the Beneficial Associations of Sorghum with Arbuscular Mycorrhizal Fungi Studied with Genetics, Genomics, Imaging, and Microbiomics**  
*Speaker:* Jeffrey Bennetzen, University of Georgia, Athens
- 3:55-4:15 p.m.**      **Testing Predictions of Plant-Microbe-Environment Interactions to Optimize Climate Adaptation and Improve Sustainability in Switchgrass**  
*Speaker:* Tom Juenger, University of Texas, Austin
- 4:15-4:35 p.m.**      **Exploring Natural Variation of *Camelina* and Its Associated Microbiomes to Improve Nitrogen Use Efficiency and Oil-seed Yield**  
*Speaker:* Chaofu Lu, Montana State University, Bozeman
- Flash Talk:** Nutrient Availability and Nitrogen Remobilization Efficiency Influence Seed Yield in *Camelina*  
*Speaker:* Demian Dlakic, Montana State University, Bozeman



**4:35-4:55 p.m.**      **Interrogating Pennycress Natural and Induced Variation to Improve Abiotic Stress Tolerance and Oilseed Bioenergy Crop Resilience**

*Speaker:* John Sedbrook, Illinois State University

**Flash Talk:** 739 Genomes Reveal Natural Variation and Adaptation History in Pennycress

*Speaker:* Xing Wu, Illinois State University

**2:30-5:00 p.m. GENOMIC SCIENCE PROGRAM BREAKOUT SESSION 2:  
ADVANCING THE U.S. BIOECONOMY BY DESIGNING AND ENGINEERING  
MICROBIOLOGICAL SYSTEMS**

**Room A-C**

*Moderator:* Pablo Rabinowicz

Scientists have designed and engineered biological systems for multiple biotechnological applications thanks to the advent of sophisticated technologies such as genome editing and artificial intelligence. Nonetheless, new discoveries and innovations will continue to expand the potential of engineering biology to develop novel renewable products and materials to advance the U.S. bioeconomy while protecting the environment. The Genomic Science Program (GSP) is committed to contribute to this endeavor by supporting safe and secure genome engineering research and technology development. This session will showcase the breadth of the Biosystems Design portfolio and how it crosscuts with other GSP elements.

**2:30-2:50 p.m.**      **IMAGINE BioSecurity: Secure Biosystems Design to Advance the Bioeconomy**

*Speaker:* Michael Guarnieri, National Renewable Energy Laboratory

**2:50-3:10 p.m.**      **Engineering Gene Overlaps to Enhance Stability and Containment**

*Speaker:* Yongqin Jiao, Lawrence Livermore National Laboratory

**3:10-3:30 p.m.**      **Engineering Biology to Produce Chemicals with Multi-Gene CRISPRa/i Programs**

*Speaker:* James Carothers, University of Washington, Seattle

**3:30-3:50 p.m.**      **Systems Metabolic Engineering in *Novosphingobium aromaticivorans* for Lignin Valorization**

*Speaker:* Josh Michener, Oak Ridge National Laboratory

**3:50-4:00 p.m.**      **Break**



- 4:00-4:20 p.m.      **Manipulating *Auxenochlorella protothecoides*: Markers and Reporters, Tunable Dicistronic mRNAs, and Successful Trait Engineering**  
*Speaker:* Sabeeha Merchant, University of California, Berkeley
- 4:20-4:40 p.m.      **Engineering Genetic Firewalls for Biocontained Microbial Systems**  
*Speaker:* Akos Nyerges, Harvard Medical School  
*PI:* George Church
- 4:40-5:00 p.m.      **Integrating Cell-Free Systems and Genome Engineering to Accelerate Biosystems Design for Carbon-Negative Biomanufacturing**  
*Speaker:* Farren Isaacs, Yale University  
*PI:* Michael Jewett

### ECR Breakout Session

---

2:30–5:00 p.m. **ENABLING CAPABILITIES AND RESOURCES BREAKOUT SESSION 1:  
 QUANTUM IMAGING AND SENSING**

**Room D**

*Organizer:* Paul Sammak

*Moderator:* James Werner, Los Alamos National Laboratory

Fundamental quantum science-enabled research on imaging probes, detectors, and sensors overcome current challenges related to suboptimal stability and photo-bleaching, enabling prolonged imaging studies. For example, quantum-entangled pairs of single-photon-emitting probes can potentially offer an advantage over conventional methods by enhancing spatial and temporal resolution, measurement speed, long-term sample stability, or bioimaging technology sensitivity.

- 2:30-2:40 p.m.      **Introduction**  
*Speaker:* James Werner
- 2:40-3:00 p.m.      **Biological Imaging Using Entangled Photons**  
*Speaker:* Theodore Goodson, University of Michigan
- 3:00-3:20 p.m.      **Non-Destructive, Three-Dimensional Imaging of Processes in the Rhizosphere Utilizing High Energy Photons**  
*Speaker:* Shiva Abbaszadeh, University of California, Santa Cruz
- 3:20-3:40 p.m.      **A Quantum Enhanced X-Ray Microscope**  
*Speaker:* Justin Goodrich  
*PI:* Sean McSweeney, Brookhaven National Laboratory

- 3:40-4:00 p.m.**      **Non-Invasive Imaging of Nitrogen Assimilation in the Rhizosphere via Quantum-Entangled Hyperpolarized Spin States**  
*Speaker:* Thomas Theis, North Carolina State University
- 4:00-4:20 p.m.**      **Quantum Ghost Imaging of Water Content and Plant Health with Entangled Photon Pairs**  
*Speaker:* James Werner, Los Alamos National Laboratory
- 4:20-4:40 p.m.**      **The 3DQ Microscope: A Novel System Using Entangled Photons to Generate Volumetric Fluorescence and Scattering Images for Bioenergy Applications**  
*Speaker:* Audrey Eshun, Lawrence Livermore National Laboratory  
*PI:* Ted Laurence
- 4:40-5:00 p.m.**      **Probing Photoreception with New Quantum-Enabled Imaging**  
*Speaker:* James Evans, Pacific Northwest National Laboratory
- 5:00 p.m.**              **Break**

### Joint Plenary Session 3

Room D

- 5:10 p.m.**      **Phenomics and Function**  
*Moderators:* Paul Sammak, Shing Kwok, Kari Perez

How organisms and their communities respond to their changing environment requires a detailed understanding of both the genetic makeup of these organisms and the phenotypes they display in their environments. Phenotyping of organisms (or phenomics), either as individuals or populations, involves measurable traits, which can be physical, chemical, or biological. Parallel, detailed measurements of system stimuli, mechanisms, and responses promote an integrated understanding of biosystem function. Stimuli include environmental and genetic changes; mechanisms include transcripts, signaling pathways, and biomolecular interactions; and responses include physical and chemical characteristics. Evaluating input parameters and the resulting phenotypic states provides a stimulus-response framework for understanding biosystem function. Speakers in this session will describe their work measuring traits of interest at different scales, from single cells to a whole plant's interaction with its environment.

- 5:10-5:15 p.m.**      **Introduction**  
*Speaker:* Paul Sammak

- 5:15–5:40 p.m.      **Building a Genome-Wide Atlas of Cell Morphology**  
*Speaker:* James (JT) Neal, Broad Institute
- 5:40-6:00 p.m.      **Measuring the Molecules of Life: Why It Is So Important, and Why We're Not Very Good at It**  
*Speaker:* Thomas Metz, Pacific Northwest National Laboratory
- 6:00 -6:20 p.m.      **Understanding Plant/Environmental Interactions Using Single-Cell Approaches**  
*Speaker:* Benjamin Cole, Lawrence Berkeley National Laboratory
- 6:20-6:40 p.m.      **AI for Image-Based Plant and Microbial Phenotyping**  
*Speaker:* John Lagergren, Oak Ridge National Laboratory

## WEDNESDAY, APRIL 3

### *Joint Plenary Session 4*

**Room A-D**

- 8:30 a.m.      **Bioenergy Research Centers**  
*Moderator:* Shing Kwok

The path to generate sustainable bioproducts and biofuels from lignocellulosic bioenergy feedstock requires many different biological and chemical technologies. The Bioenergy Research Centers (BRCs) use integrated approaches to address the technological challenges underpinning bioproducts and biofuels production. In this plenary session, the BRCs will describe their recent research updates on synthetic biology efforts toward development of biofuels and bioproducts. Each center will describe recent progress on the development and use of synthetic biology tools in plants or microbes to engineer desired traits for optimal biofuels and bioproducts synthesis.

- 8:30-9:00 a.m.      **Center for Advanced Bioenergy and Bioproducts Innovation (CABBI)**  
**Synthetic Biology-Enabled Biomass Feedstock Improvement: Tool Development and Applications**  
*Speaker:* Edgar Cahoon, University of Nebraska, Lincoln
- 9:00-9:30 a.m.      **Center for Bioenergy Innovation (CBI)**  
**Multigene Engineering for Trait Stacking in Poplar**  
*Speaker:* Xiaohan Yang, Oak Ridge National Laboratory



- 9:30-10:00 a.m.      **Joint BioEnergy Institute (JBEI)**  
**Biodesign for Fuels and Chemicals Production in Microbes**  
*Speaker:* Aindrila Mukhopadhyay, Lawrence Berkeley National Laboratory
- 10:00-10:30 a.m.      **Great Lakes Bioenergy Research Center (GLBRC)**  
**Genetic Tools for Lignocellulosic Biofuel Production in *Zymomonas* and Beyond**  
*Speaker:* Michaela TerAvest, Michigan State University
- 10:30 a.m.              **Break**

### GSP-Led Keynote Presentation

**Room A-D**

- 10:45 a.m.      **Breeding for Future Climates: Retrospective Breeding, Plasticity, Genetic Trade-Offs, and Ideotype Breeding 2.0**  
*Speaker:* Patrick Schnable, Iowa State University

Dr. Schnable is a distinguished professor at Iowa State University (ISU) where he holds an endowed chair in genetics and is an endowed scholar in agricultural entrepreneurship. Schnable directs ISU's Plant Sciences Institute that is fostering collaborations among plant scientists, engineers, and computational scientists. His interdisciplinary research program has developed and/or deployed significant genomic tools and resources. He is the co-lead of the Genomes to Fields Initiative, which develops approaches to understand gene function across environments to enable the accurate prediction of corn plant phenotypes.

### Poster Session 2 (Room E-H) and Lunch (Foyer)

11:45 a.m.-1:45 p.m.

#### **OTHER ACTIVITIES**

12:15-1:45 p.m. **National Microbiome Data Collaborative Town Hall**

**White Oak (A and B)**

**Connecting Data, People, and Ideas with the National Microbiome Data Collaborative (Registration Required)**

The National Microbiome Data Collaborative (NMDC) supports researchers to create, use, and reuse microbiome data through a collaborative data ecosystem. NMDC tackles infrastructure challenges in microbiome data science with a focus on cultivating a scientific culture of data sharing and open science. This town hall highlights how a

collaborative data ecosystem advances microbiome research, describes the efforts of emerging leaders who are championing data stewardship across diverse microbiome research communities, and showcases the NMDC Field Notes mobile app that streamlines real-time collection of standardized metadata and field measurements.

**Registration link:**

<https://lbnl.zoom.us/meeting/register/tjUkceygpzgtHdKr7baPWMNePAkMeSC-ia2W>

- 12:15-12:20 p.m. Welcome and Overview**  
*Speaker:* Emiley Eloie-Fadrosh, NMDC
- 12:20-12:35 p.m. Charting the Unknown: Leveraging NMDC EDGE to Illuminate Puerto Rico's Ecological Diversity**  
Josué Rodríguez-Ramos, Pacific Northwest National Laboratory
- 12:35-12:50 p.m. Bacterial-Fungal Interactions in Plant Root Microbiomes Driving Soil C Sequestration**  
*Speaker:* Buck Hanson, Los Alamos National Laboratory
- 12:50-1:05 p.m. Microbial Controls on Biogeochemical Cycles in Arctic Soils and Permafrost**  
*Speaker:* Neslihan Tas, Lawrence Berkeley National Laboratory
- 1:05-1:35 p.m. Updates: Preview of NMDC Field Notes, a Mobile App for Real-Time Collection of Standardized Metadata and Field Measurements**  
NMDC Team
- Open Discussion**

---

***Joint Plenary Session 5***

**Room D**

**1:45-3:30 p.m. BER Data Science and Infrastructure**

*Moderator:* Ramana Madupu

BER-supported national scientific user facilities and experimental and observational facilities create high-quality, large-scale scientific data collections. These data structures require interoperability to enable BER scientists to leverage integrated analyses of these various data types for deeper understanding of system processes and knowledge discovery. This session will highlight efforts within BER to integrate computational and data science platforms and to develop interoperability of data, tools, and supporting information that span biological and environmental sciences. Presentations will include efforts to develop data compatibility, metadata standards, new software workflows, and tools for data transfer services to accelerate scientific discovery through the convergence of experimental and simulation data.

- 1:45–2:00 p.m.**      **A Unified Data Infrastructure for BER**  
*Speaker:* Kerstin Kleese van Dam,  
 Brookhaven National Laboratory
- 2:00–2:15 p.m.**      **Advancing Microbiome Research with the  
 National Microbiome Data Collaborative**  
*Speaker:* Lee Ann McCue, Pacific Northwest National Laboratory
- 2:15–2:30 p.m.**      **Partnerships to Improve FAIRness**  
*Speaker:* Kjersten Fagnan, Joint Genome Institute
- 2:30–2:45 p.m.**      **Coping with Data: Towards Community-Driven Data  
 Representation and Organization to Drive Biological  
 Data Science**  
*Speaker:* Adam Arkin, Lawrence Berkeley National Laboratory
- 2:45–3:00 p.m.**      **Microbiome Data Science: From the Earth Microbiome  
 to the Global Viromes**  
*Speaker:* Nikos Kyrpides, Joint Genome Institute
- 3:00–3:15 p.m.**      **The Landscape of Data Infrastructure from the National  
 Virtual Biosecurity for Bioenergy Crops Center Perspective**  
*Speaker:* Shantenu Jha, Brookhaven National Laboratory
- 3:15–3:30 p.m.**      **Panel Discussion: Challenges of Data Integration  
 Across BER Data Systems**  
*Moderator:* Lee Ann McCue  
*Panelists:* Kerstin Kleese van Dam, Shantenu Jha, Adam Arkin,  
 Nikos Kyrpides , Kjersten Fagnan
- 3:30 p.m.**      **Break**

### GSP Breakout Sessions

---

**3:45 p.m**      **GENOMIC SCIENCE PROGRAM BREAKOUT SESSION 3:  
 ENVIRONMENTAL MICROBIOLOGY**

**Room A-C**

*Moderator:* Boris Wawrik

Environmental microbiomes consist of interconnected and dynamic populations of microbes with high phyletic and genomic diversity. Networks of microbial interactions shape and condition the environment in ways that profoundly affect the physical world. This session highlights BER's support for studies that leverage integrated, multidisciplinary research to assess microbial cycling of elements in the environment and will seek to explore future trends and challenges in environmental microbiome research.



- 3:45–4:10 p.m.**      **Viral Infection Across Diverse Virocells and Conditions**  
*Speaker:* Cristina Howard-Varona, Ohio State University
- 4:10–4:35 p.m.**      **Microscale Metabolic Exchange Between Bacteria and Microalgae in Photosynthetic Biofuel Production Systems**  
*Speaker:* Xavier Mayali, Lawrence Livermore National Laboratory
- 4:35–5:00 p.m.**      **Unraveling the Traits that Enable Microbes to Thrive Post-Fire**  
*Speaker:* Sydney Glassman, University of California, Riverside
- 5:00–5:25 p.m.**      ***Sphagnum* Microbiomes as an Indicator of Major Ecosystem Change**  
*Speaker:* Caitlin Petro, Georgia Institute of Technology
- 5:25–5:50 p.m.**      **Development of Tools and Techniques to Investigate the Impacts of Bacterial-Fungal Interactions in Desert Soils and Beyond**  
*Speaker:* Aaron Jon Robinson, Los Alamos National Laboratory
- 5:50–6:15 p.m.**      **Methane Oxidation Mitigates Growing Emissions in an Arctic Landscape: Aerobic versus Anaerobic Consumption, Communities, and Controls**  
*Speaker:* Ruth Varner, University of New Hampshire

**3:45 p.m.**      **GENOMIC SCIENCE PROGRAM BREAKOUT SESSION 4:  
PLANT GENE FUNCTION**

**Room D**

**Moderator:** Vijay Sharma

Plant research faces unique challenges in biological and genetic diversity, such as teasing out the frequent segmental and whole-genome duplications that often result in large gene families and subfunctionalization of their member genes. These plant genome features add layers of complexity to the already intricate nature of eukaryotic gene expression and regulatory networks. This session highlights BER's support for studies to address the challenges and opportunities in associating gene(s) to function (i.e., genotype to phenotype) in plant systems.

- 3:45–3:50 p.m.**      **Introduction:** Vijay Sharma
- 3:50–4:00 p.m.**      **Specificity Among So Much Promiscuity in BAHD Acyltransferases from Energy Poplar**  
*Speaker:* Brian Fox, University of Wisconsin, Madison

- 4:05–4:15 p.m.**      **Winter Transcriptome Regulation in Wood-Forming Tissues of *Populus***  
*Speaker:* CJ Tsai, University of Georgia, Athens
- 4:20–4:30 p.m.**      **Functional Analysis of Genes Encoding Ubiquitin Proteasome System Components Affecting Poplar Wood Traits**  
*Speaker:* Andrew Groover, USDA Forest Service, Northern Research Station, University of Vermont
- 4:35–4:45 p.m.**      **CRISPR Activation of Poplar TOR Genes Improves Nitrogen Use Efficiency and Indicates Possible Functional Divergence**  
*Speaker:* Gary Coleman, University of Maryland, College Park
- 4:50–5:00 p.m.**      **Single-Cell Dissection of Gene Function in Cellular Lineages of Developing Biomass in *Populus* and Sorghum**  
*Speaker:* Matias Kirst, University of Florida, Gainesville
- 5:05–5:15 p.m.**      **Population Genetics and Comparative Genomics to Detect Genes Under Selection in Response to N Availability**  
*Speaker:* Jinliang Yang, University of Nebraska-Lincoln
- 5:20–5:30 p.m.**      **Investigating the Molecular Networks that Lead to a Loss of Photosynthetic Efficiency in Shaded Leaves of Energy Sorghum**  
*Speaker:* Laurie Leonelli, University of Illinois Urbana–Champaign
- 5:35–5:45 p.m.**      **Integrating Molecular Genetics and Precision Phenotyping to Elucidate the Genetic Basis for Drought Resilience in Sorghum**  
*Speaker:* Andrea Eveland, Donald Danforth Plant Science Center
- 5:50–6:00 p.m.**      **Functional Characterization of Plant Glycosyltransferases to Enable Predictive Biology**  
*Speaker:* Breeanna Urbanowicz, University of Georgia, Athens
- 6:05–6:15 p.m.**      **Deciphering Stress-Resilient Growth in *Brassicaceae* Models: A Comparative Genomics Analyses of Adaptations to Extreme Environments**  
*Speaker:* Maheshi Dassanayake, Louisiana State University

## ECR Breakout Session

---

**3:45 p.m.      ENABLING CAPABILITIES AND RESOURCES BREAKOUT SESSION 2:  
KBASE SCIENCE SESSION: DATA INTEGRATION TO SUPPORT  
(OR REFUTE) PREDICTIONS**

**White Oak A and B**

**Moderator:** Ramana Madupu

Much of biological science knowledge is based on prediction—algorithmic assessment of taxonomy and function determined by parameters based on current knowledge. But how certain are we that those parameters are accurate across the tree of life, ecosystems, and time? By exploring and integrating multiple lines of evidence (e.g., multiomics data, experimental validation, mechanistic modeling, and machine learning), we can build a story that supports or refutes our predictions. This session will feature examples of research questions and tools that integrate data to build trust in our assertion of the world around us.

**3:45 p.m.      Welcome: Why Bother with Data Integration,  
and Why Does My Data Matter?**

**3:50 p.m.      Measuring Microbial Phenotypes for Improving  
Genome-Based Predictions**

**Speaker:** Dale Pelletier, Oak Ridge National Laboratory

**4:05 p.m.      Knowledge Extraction from Literature**

**Speaker:** Shinjae Yoo, Brookhaven National Laboratory

**4:20 p.m.      Break**

**4:30 p.m.      Predicting Protein Function Using Structure and Sequence  
Similarity in KBase**

**Speaker:** Chris Henry, Argonne National Laboratory

**4:45 p.m.      Integrating Data to Predict Functions for Gaps  
in Metabolic Models**

**Speaker:** Bill Nelson, Pacific Northwest National Laboratory

**5:00 p.m.      Leveraging LLMs to Synthesize and Develop New Questions**

**Speaker:** Paramvir Dehal, Lawrence Berkeley  
National Laboratory

**5:15 p.m.      Getting Credit for Contributions in a Big Data World**

**Speaker:** Elisha Wood-Charlson, Lawrence Berkeley  
National Laboratory

**5:30 p.m.      Adjourn**



## THURSDAY, APRIL 4

### *GSP Breakout Sessions*

---

**8:30-11:00 a.m. GENOMIC SCIENCE PROGRAM BREAKOUT SESSION 5:  
SYSTEMS BIOLOGY OF BIOENERGY-RELEVANT MICROBES**

**Room A-C**

**Moderator:** Dawn Adin

The Genomic Science program supports research aimed at understanding the fundamental properties of bioenergy-relevant organisms at the genomic scale and aims to have researchers translate that gained knowledge to enhance the production capabilities of microbes for sustainable bioenergy. The portfolio supports projects spanning a diverse range of organisms and approaches to understand and harness the biosynthetic processing power of the microbial world. This session will provide opportunities for different projects in the portfolio to share their current research.

**8:30–8:55 a.m. Improving Bioprocess Robustness by Cellular  
Noise Engineering**

**Speaker:** Georgios Daletos, Massachusetts Institute of Technology

**8:55–9:20 a.m. Cell-Free Systems Biology: Characterizing Pyruvate  
Metabolism of *Clostridium thermocellum* with a  
Three-Enzyme Cascade Reaction**

**Speaker:** Daniel Olson, Dartmouth College

**9:20–9:45 a.m. An Integrated Genetic Approach to Address the Question  
of What Genes Made Fungi Uniquely Wood Decomposers**

**Speaker:** Jiwei Zhang, University of Minnesota, Twin Cities

**9:45–10:10 a.m. Novel Systems Approach for Rational Engineering of  
Robust Microbial Metabolic Pathways**

**Speaker:** Laura Jarboe, Iowa State University

**10:10–10:35 a.m. Optogenetic Control of Microbial Consortia for Biofuel and  
Chemical Production**

**Speaker:** José Avalos, Princeton University

**10:35–11:00 a.m. Reaction Network in the Metabolism of Lignin-Derived  
Aromatic Carbons in Soil *Pseudomonas* Species**

**Speaker:** Ludmilla Aristilde, Northwestern University

## ECR Breakout Sessions

---

### 8:30-11:00 a.m. **ENABLING CAPABILITIES AND RESOURCES BREAKOUT SESSION 3: BIOIMAGING ACADEMIC AND NATIONAL LABORATORIES**

#### **Room D**

**Organizer:** Paul Sammak

**Moderator:** Shiva Abbaszadeh

BSSD supports research that focuses on creating new bioimaging instrumentation capabilities. These tools are intended for imaging biological processes within and among cells in living plants and microorganisms. Multimodal imaging capabilities are featured prominently, enabling selective and deeper penetration to nondestructively resolve cellular structures.

**8:30–8:40 a.m. Introduction**

**Speaker:** Shiva Abbaszadeh

**8:40–9:00 a.m. Integrative Imaging of Plant Roots During Symbiosis with Mycorrhizal Fungi**

**Speaker:** Andreas Vasdekis, University of Idaho

**9:00–9:20 a.m. Ultra-Sensitive High-Resolution Label-Free Nonlinear Optical Microscopy for Imaging Plant-Microbe Interactions *In Vivo***

**Speaker:** Na Ji, University of California, Berkeley

**9:20–9:40 a.m. Deep Chemical Imaging of the Rhizosphere**

**Speaker:** Marcus Cicerone, Georgia Institute of Technology

**9:40–10:00 a.m. Development of High-Throughput Light-Sheet Fluorescence Lifetime Microscopy for 3D Functional Imaging of Metabolic Pathways in Plants and Microorganisms**

**Speaker:** Adam Bowman, Stanford University

**PI:** Mark Kasevich

**10:00–10:20 a.m. Novel *In Vivo* Visualization of Bioenergy Metabolic and Cellular Phenotypes in Living Woody Tissues**

**Speaker:** Andrew Groover, USDA Forest Service, Northern Research Station

**PI:** Leslie Sieburth, University of Utah

**10:20–10:40 a.m. Novel Multimodal Chemical Nano-Imaging Approach to Visualize and Identify Small Biomolecules Exchanged in Microbial Communities**

**Speaker:** Scott Lea, Pacific Northwest National Laboratory

**10:40–11:00 a.m. Optical and X-Ray Multimodal-Hybrid Microscope Systems for Imaging of Plant-Pathogen Interactions**  
**Speaker:** Soichi Wakatsuki, SLAC National Accelerator Laboratory

## ***KBase Tutorials and Workshops***

**White Oak (A and B)**

**8:30-10:30 a.m. KBase Workshops (Registration required)**

Ramana Madupu and Elisha Wood-Charlson

**8:30-9:30 a.m. Microbial Community Modeling — KBase and Oak Ridge National Laboratory's Plant-Microbe Interfaces SFA**

**Speakers:** Priya Ranjan, Ulas Karaoz, Gianna Marschmann, Chris Henry

This session will demonstrate new workflows envisioned for analyzing microbial communities in KBase using tools currently under development. We will demonstrate how to build community metabolic models and highlight new tools for performing community-level flux balance analysis with examples of successful analyses of species interactions from multiple microbiome systems. We also will demonstrate the ComScores tool being co-developed with the Plant-Microbe Interfaces SFA for predicting likely pairwise interactions among all the genomes in an input set. Also featured will be new apps that enable seamless prediction of ecophysiological traits of bacteria and archaea from KBase genomes (microTrait) and their representation in a coherent dynamic energy budget-based, trait-based modeling framework (DEBmicroTrait).

**Registration required:** This session will be hybrid, with space for ~30 people in person. Please register via Zoom.

**Registration link:**

[https://lbnl.zoom.us/meeting/register/tjUocuihqjwoGtQqVd117fQmJlAuLL\\_fDul](https://lbnl.zoom.us/meeting/register/tjUocuihqjwoGtQqVd117fQmJlAuLL_fDul)

**9:30-10:30 a.m. Quantitative Stable Isotope Probing — KBase and Lawrence Livermore National Laboratory's Microbes Persist SFA**

**Speakers:** Jeff Kimbrel, Kathleen Beilsmith, Elisha Wood-Charlson

The ability to conduct quantitative stable isotope probing (qSIP) has become more accessible to the BER community through the efforts of Lawrence Livermore National Laboratory's Microbes Persist SFA to streamline and share qSIP data analysis steps in KBase. This workshop will demonstrate how the SFA and KBase teams are envisioning the upload and validation of sample and qSIP fraction tables as well as subsequent qSIP analysis and comparison features in KBase. If you already do qSIP or are thinking about including qSIP in your future research plans, please join this workshop and give us feedback on the integration and user experience of these features.

**Registration required:** This session will be hybrid, with space for ~30 people in person. Please register via Zoom.

**Registration link:**

<https://lbnl.zoom.us/meeting/register/tjYocQggT8tGdfoKJZBeE9vkVmlknHrVNsX#/registration>



11:00 a.m. Break

## ***GSP Breakout Session***

---

11:15 a.m.-  
12:30 p.m. **GENOMIC SCIENCE PROGRAM BREAKOUT SESSION 6:  
DOE OFFICE OF SCIENCE NEW INITIATIVES – FOCUS ON ACCELERATE AND BRaVE**

### **Room A-C**

**Moderators:** Resham Kulkarni, Pablo Rabinowicz, Dawn Adin

The DOE Office of Science (SC) launched several initiatives in fiscal years 2022 and 2023. These collaborative efforts across different SC research programs include Accelerate Innovations in Emerging Technologies (ACCELERATE); Biopreparedness Research Virtual Environment (BRaVE); Energy Earthshots Research Centers (EERCs); Science Foundations for Energy Earthshots; Reaching a New Energy Sciences Workforce (RENEW); and Funding for Accelerated, Inclusive Research (FAIR). This session will provide a brief overview of these new initiatives followed by presentations from BSSD-supported ACCELERATE and BRaVE projects. ACCELERATE projects conduct basic research to facilitate the transition from discovery to commercialization of new technologies that will form the basis of future industries, and BRaVE projects aim to support national biopreparedness and response capabilities that can be advanced with DOE's unique capabilities.

**11:15–11:20 a.m. Overview of New Initiatives**

**Speaker:** Dawn Adin

**11:20–11:30 a.m. The Science of Scale-Up: Understanding and Predicting Microbial Behavior in Microenvironments Derived from Large-Scale Bioreactors**

**Speaker:** Davinia Salvachua, National Renewable Energy Laboratory

**11:30–11:45 a.m. Developing a National Virtual Biosecurity for Bioenergy Crops Center**

**Speaker:** Martin Schoonen, Brookhaven National Laboratory

**11:45–11:55 a.m. Decoding Host-Pathogen Dynamics with 4D (Epi)Genomics**

**Speakers:** Shawn Starkenburg and Christina Steadman, Los Alamos National Laboratory

**11:55 a.m.–12:05 p.m. Enhancing Biopreparedness Through a Model System to Understand the Molecular Mechanisms that Lead to Pathogenesis and Disease Transmission**

**Speaker:** Margaret Cheung, Pacific Northwest National Laboratory

- 12:05–12:15 p.m.**    **Phage Foundry: A High-Throughput Platform for Rapid Design and Development of Countermeasures to Combat Emerging Drug-Resistant Pathogens**  
*Speaker:* Vivek Mutalik, Lawrence Berkeley National Laboratory
- 12:15–12:25 p.m.**    **Unlocking the Molecular Basis of Plant-Pathogen Interactions to Create Resilient Bioenergy Crops**  
*Speaker:* Qun Liu, Brookhaven National Laboratory

## ECR Breakout Session

Room D

**11:15 a.m.**    **ENABLING CAPABILITIES AND RESOURCES BREAKOUT SESSION 4:  
PROGRAM DISCUSSION AMONG ECR PRINCIPAL INVESTIGATORS: OBSTACLES  
AND OPPORTUNITIES**

*Moderators:* Na Ji, University of California, Berkeley; Christopher Henry, Argonne National Laboratory; and Hugh O'Neill, Oak Ridge National Laboratory

In a roundtable discussion attendees will identify scientific opportunities for ECR principal investigators that support bioenergy and environmental research within BER and identify key biological questions and novel methods for exploring bioenergy and environmental research.

**12:30 p.m.**    **Adjourn**