2018 Genomic Sciences Program Annual PI Meeting
February 25-28, 2018

Sunday, February 25th

5:00-8:00 pm **Early Registration and poster setup**
Location: Lobby outside Fairfax Ballroom

Monday, February 26th

7:00-8:30 am **Registration**
Location: Lobby outside Fairfax Ballroom

7:00 - 8:30 **Breakfast** (on your own)

8:30 -9:00 **Welcome and Introduction to the Meeting**
Location: Fairfax Ballroom

8:30-8:40 **Sharlene Weatherwax -** Associate Director, DOE Office of Biological and Environmental Research (BER)
Opening Remarks

8:40 -8:50 **Todd Anderson -** Director, Biological Systems Science Division, BER, DOE
Meeting Introduction

8:50-9:00 **Kent Peters -** Program Manager, BER, DOE
Logistics

9:00 - 10:30 **Plenary Session: Bioenergy Research Centers: Moving into the next phase**
Location: Fairfax Ballroom
Moderator: Kent Peters

Session Description: The Bioenergy Research Center (BRC) Program enters its eleventh year with the launch of four BRCs. The directors will give an overview of research goals for the next 5 years.

Speakers:

9:00 - 9:20 **Tim Donohue -** University of Wisconsin
Great Lakes Bioenergy Research Center (GLBRC)

9:20 - 9:40 **Gerald Tuskan -** Oak Ridge National Laboratory
Center for Bioenergy Innovation (CBI)

9:40 – 10:00 **Evan DeLucia -** University of Illinois-Urbana-Champagne
Center for Advanced Biofuel and Bioproduct Innovation (CABBI)

10:00 – 10:20 **Jay Keasling -** Lawrence Berkeley National Laboratory
Joint BioEnergy Institute (JBEI)

10:30 - 11:00 **Break**

11:00 - 12:00 **Keynote Presentation: Katherine Yelick -** Lawrence Berkeley National Laboratory
HPC for Genomic Data at Scale

Location: Fairfax Ballroom
Moderator: Ramana Madupu

12:00 - 2:00 **Lunch** (on your own)

1:00 - 5:00 **KBase User Science Presentations**
Location: Potomac

Description of Session: Description of Session: KBase users and collaborators will speak about science accomplished with the system. Research covering assembly, annotation, comparative genomics, and modeling of microbes, fungi, plants and their communities will be presented, with examples ranging from single genome modeling to large scale community analysis. Speakers will discuss how KBase enabled their research and the dissemination of their data, analyses, and algorithms. Some speakers will describe their experiences adding analysis tools as KBase apps.

If planning to attend the session, please sign up at https://goo.gl/forms/BS3sas9RjyimAGAd2. This will inform the KBase team of your interest.

Single Genome Annotation

1:00 - 1:45 **Aindrila Mukhopadhyay -** Lawrence Berkeley National Laboratory
Querying the Genetic Potential of Bacterial Isolates from the Oak Ridge Site: Applications in Quorum Sensing, Plasmid Uptake and Mercury Resistance

Romy Chakraborty - Lawrence Berkeley National Laboratory
Discovering the genetic basis of a beneficial microbiome to improve crop productivity

Gyorgy Babnigg - Argonne National Laboratory
Identifying and Filling Gaps in the Biosynthesis Pathway for Indole-3-Acetic Acid in Pseudomonas Fluorescens

1:45 - 2:00 **Break**

2:00 – 2:45 **Microbiome analysis**

Hyun-Seob Song - Pacific Northwest National Laboratory
Analyzing Genomes, Constructing Community Metabolic Models, and Predicting Interactions Among Species within a Model Microbial Consortium

Chris Marshall - University of Pittsburgh
Analyzing Species Interactions in an Electrode-associated Microbiome System

Pam Weisenhorn - Argonne National Laboratory
Prediction of Auxotrophy from Genomic Data Reveals Functional

Delegation in a Variety of Microbiome Systems

2:45 – 3:00 **Break**

3:00 – 3:45 **Plants and PMI analysis**

Collin Timm - Johns Hopkins University
Metabolic Functions of Pseudomonas Fluorescens Strains from Populus Deltoides Depend on Rhizosphere or Endosphere Isolation Compartment

Crysten Blaby - Brookhaven National Laboratory
Trans-systems Analysis Identifies Conserved and Novel Mechanisms for Zinc-deficiency Acclimation in the Plant Lineage

Sunita Kumari – Cold Spring Harbor Laboratory
Abiotic Stress Induced Transcriptome Analysis of Poplar Roots Using KBase

3:45– 4:00 **Break**

4:00 – 4:30 **New apps in KBase**

Lin Wang - Pennsylvania State University
Integration of the OptStoic Pathway Design Approach into KBase

Janaka Edirisinghe - Argonne National Laboratory
Development and Validation of a New App for the Reconstruction of Genome-scale Metabolic Models for Fungal Genomes

4:30 - 5:00 Q&A

2:00 - 5:00 **Breakout Session A: Biosystems Design Awards 2017**
Location: Fairfax Ballroom A
Moderator: Pablo Rabinowicz

Session Description: The Biosystems Design element of the Genomic Science program aims to identify the fundamental biological principles that govern biological systems to enable computer-aided design and engineering of plants and microbes to address BER's mission in energy and the environment. In 2017, BER made twelve new Biosystems Design awards that will take multidisciplinary approaches to engineer plants and microbes for improved production of biofuels and bioproducts under changing environmental conditions. This session will introduce those new projects to the Genomic Science research community.

Speakers:

2:00 - 2:12 **Krishna Niyogi -** University of California, Berkeley
Systems analysis and engineering of biofuel production in *Chromochloris zofingiensis*, an emerging model green alga

2:12 - 2:24 **Michael Jewett -** Northwestern University
Establishing a clostridia foundry for biosystems design by integrating computational modeling, systems-level analyses, and cell-free engineering technologies

2:24 - 2:36 **Thomas Brutnell -** Donald Danforth Plant Science Center
Using systems approaches to improve photosynthesis and water use efficiency in sorghum

2:36 - 2:48 **Eduardo Blumwald -** University of California, Davis
SyPro poplar: Improving poplar biomass production under abiotic stress conditions: an integrated omics, bioinformatics, synthetic biology and genetic engineering approach

2:48 - 3:00 **Ryan Gill -** University of Colorado, Boulder
Design and engineering of synthetic control architectures

3:00 – 3:30 **Break**

3:30 – 3:42 **Gautam Dantas -** Washington University in St. Louis
Systems engineering of *Rhodococcus opacus* to enable production of drop-in fuels from lignocellulose

3:42 – 3:54 **Stephen Long -** University of Illinois, Urbana-Champaign
Building on success in systems design of high yielding low-input energycanes for marginal lands

3:54 – 4:06 **Matias Kirst -** University of Florida, Gainesville
Phylogenomic discovery and engineering of nitrogen fixation into the bioenergy woody crop poplar

4:06– 4:18 **Andrew Allen -** J. Craig Venter Institute, West Coast
Design, synthesis, and validation: genome scale optimization of energy flux through compartmentalized metabolic networks in a model photosynthetic eukaryotic microbe

4:18 – 4:30 **Huimin Zhao -** University of Illinois, Urbana-Champaign
Genome-scale design and engineering of non-model yeast organisms for production of biofuels and bioproducts

4:30 – 4:42 **Danny Schnell -** Michigan State University, East Lansing
A systems approach to increasing carbon flux to seed oil for biofuels and bioproducts production in *Camelina sativa*

4:42 - 4:54 **Robert Martienssen -** Cold Spring Harbor Laboratory
Biological Design of Lemnaceae aquatic plants for biodiesel production

4:54 - 5:00 Additional Q&A

2:00 - 5:00

Breakout Session B: Microbes Unite: Microbial Ecosystems across the Genomic Sciences Portfolio

Location: Fairfax Ballroom B
Moderator: Dawn Adin

Session Description: In our world, microorganisms are ubiquitous and they provide a diverse array of vital functions. Understanding how microbes “work” in their surroundings is a long-term, cross-cutting theme within the Genomic Sciences Program. The ability to recognize and eventually predict how microbial species’ respond to their environment is critical to understanding the potential impacts of a changing climate as well as for optimizing feedstock production. With the current advances in systems biology and genomics technologies, we are now starting to gain further insight into the role(s) microbes play within these extremely complex biological communities. This session will highlight projects spanning the portfolio that focus on the important role microbes play in in effective stewardship of our environment and in development of sustainable bioenergy landscapes

Speakers:

2:00 - 2:30 **Thomas Bruns -** University of California, Berkeley
Determination of the Roles of Pyrophilous Microbes in Breakdown and Sequestration of Pyrolyzed Forms of Soil Organic Matter

2:30 – 3:00 **Ashish Malik -** University of California, Irvine
Microbial trait distribution and decomposition response to drought: an in-situ litter study

3:00 – 3:30 **Break**

3:30 – 4:00 **Jessy Labbe -** Oak Ridge National Laboratory
The key fungal lineage of the Russulaceae: a new resource for untangling and linking beneficial plant-fungal associations and ecosystem functions

4:00– 4:30 **Sarah Evans -** Michigan State University
Plant and biogeochemical controls on the switchgrass microbiome: perspectives from a fine-scale time series

4:30 – 4:45 **Jennifer Pett-Ridge -** Lawrence Livermore National Laboratory
Microbes Persist: Systems Biology of the Soil Microbiome

4:45 – 5:00 **Patrick Chain -** Los Alamos National Laboratory
Exploring bacterial:fungal Interactions

5:00 – 5:15 **Janet Jansson -** Pacific Northwest National Laboratory
Deciphering the soil metaphenome

5:00 - 7:00 **Poster Session (odd numbered posters)**
Location: Tysons Ballroom

Tuesday, February 27th

7:00 - 8:30 **Breakfast** (on your own)

8:30 - 10:00 **Plenary Session: DOE User Facilities & Community Resources**
Location: Fairfax Ballroom
Moderator: Dan Drell

Session Description: Speakers will give overviews of the various DOE user facilities and resources.

Speakers:

8:30 – 8:50	**Nigel Mouncey** – Lawrence Berkeley National Laboratory, Joint Genome Institute (JGI) Beyond Bases: Integrative Genome Science at the JGI
8:50- 9:10	**Mary Lipton** – Pacific Northwest National Laboratory EMSL: Translating Genotype to Phenotype in Environmental Systems
9:10– 9:30	**Christine Chalk** – DOE Advanced Scientific Computing Research (ASCR) ASCR User Facilities & Community Resources
9:30 – 9:50	**Adam Arkin** – Lawrence Berkeley National Laboratory The KBase Platform for Dissemination of Tools and Analysis of Microbes, Plants and Their Communities: Examples from the users
9:50 – 10:10	**Ryan Tappero** – Brookhaven National Laboratory Imaging Resources for the Biological Community

10:10 - 10:30 **Break**

10:30- 12:00 **Plenary Session: A Portfolio Perspective: Diversity and Synergy in the Genomic Science Program**
Location: Fairfax Ballroom
Moderator: Cathy Ronning

Session Description: The Genomic Science Program supports systems biology and genomics-based research to advance BER's mission in energy and the environment, including carbon cycling, biogeochemical processes, and bioenergy feedstock development, with research topics spanning from microbes to plant-microbial ecosystems to plants. In this session, the breadth of the Genomic Sciences portfolio will be showcased by three projects that represent a cross-section of the GSP and highlight the diversity of research funded in the program – from microbes and microbial ecosystems to environmental and sustainability research to plant genomics. While these areas are distinct, together they provide an encompassing view of the many facets of bioenergy research.

Speakers:

10:30- 11:00	**Mary Firestone -** University of California, Berkeley Directing traffic in the rhizosphere: how phage and fauna shape the flow and fate of root carbon through microbial pathways

11:00 - 11:30 **Peggy Lemaux -** University of California, Berkeley
From Leaves to Roots to Microbes: How Sorghum Responds to Drought

11:30– 12:00 **Larry Smart -** Cornell University
Dissecting the genomic basis for triploid heterosis and disease resistance in willow hybrids

12:00 - 2:00 **Lunch** (on your own)

1:00 - 5:00

KBase Experience Hands-on Session

Location: Potomac
Maximum: 30 per hour. Advance registration required. Please sign up at https://goo.gl/forms/BS3sas9RjyimAGAd2.

Description of Session: This session will give you an opportunity to test the latest tools available in KBase in an interactive setting. Both new and returning KBase users will learn more about using KBase to facilitate their research.

Each hour will focus on a specific topic beginning with a 20-minute presentation followed by a 40-minute hands-on session during which individuals may try out the functionality on their own data. Members of the KBase team will be there to help you start using KBase on your laptop.

Topics:

1:00- 2:00	Introduction to KBase
2:00 - 3:00	Genome sequence assembly to metabolic modeling
3:30– 4:00	RNA-Seq analysis
4:00 – 5:00	How to integrate new applications into KBase using the SDK

2:00 - 5:00

Breakout Session C: Technologies to accelerating discovery

Location: Fairfax Ballroom A
Moderator: Kent Peters

Description of Session: Charles Darwin collected numerous biological samples and observations during his voyage on the HMS Beagle. Careful thought of his observations led to the theory of evolution. Today, DOE scientists advance our ability to collect data that is vastly more precise, complex and voluminous than in Darwin's time. This session will highlight technologies that not only increase our capacity to collect observations, but will lead the way to new insights and understandings of complex biological systems.

Speakers:

2:00 - 2:30 **Ian Blaby** – Brookhaven National Laboratory
HTP approaches to divine gene function

2:30 - 3:00 **Anup Singh** – Sandia National Laboratory
Microfluidic platforms for enabling synthetic biology

3:00 – 3:30 **Break**

3:30 – 4:00 **Sriram Kosuri** – University of California, Los Angeles
Multiplexed methods to explore sequence-function relationships

4:00 – 4:30 **Andrew Pawlowski** and **George Church** – Harvard University
Fluorescent In Situ Sequencing: Status and Directions

4:30 – 5:00 **Peter Weber** – Lawrence Livermore National Laboratory
Viral-microbial dynamics: pushing the limits of stable isotope probing and NanoSIMS

2:00 - 5:00

Breakout Session D: Computational Biology

Location: Fairfax Ballroom B
Moderator: Ramana Madupu

Description of Session: The Genomic Science program has made significant investments in basic research to obtain an understanding of relationships between molecular-scale functional biology and ecosystem-scale environmental processes. These fundamental genomic science activities are supported by ongoing efforts to combine molecular and genomic scale information and to develop integrated networks and computational models of system dynamics and behavior. Computational biology approaches to predictively model biological systems are therefore an essential part of systems biology research. This breakout will feature recent developments in computational biology methods for data analysis and modeling across the Genomic Science program portfolio.

Speakers:

2:00 - 2:30 **Christopher Voigt -** Massachusetts Institute of Technology
Genetic Circuit Design Automation: Applications in Industrial Production

2:30 - 3:00 **Ali Navid -** Lawrence Livermore National Laboratory
Investigation of biochemical interactions between phototrophic organisms and their surrounding microbiome

3:00 – 3:30 **Break**

3:30 – 4:00 **Kranthi Varala -** Purdue University
EvoNet: Genome-scale phylogenetic approaches to find molecular signatures of low-N and drought adaptations

4:00 – 4:30 **Deborah Weighill -** Oak Ridge National Laboratory
Integrated Networks and Pleiotropic Signatures: Unravelling Complex Gene-Phenotype Relationships in Poplar

4:30 – 5:00 **Eoin Brodie** – Lawrence Berkeley National Laboratory
Deciphering the functional traits of soil and subsurface microbes

2:00 - 5:00

Breakout Session E: USDA-DOE Plant Feedstock Genomics for Bioenergy

Location: Ash Grove Ballroom
Moderator: Cathy Ronning, DOE BER and Bill Goldner, USDA NIFA

Session Description: The joint USDA-DOE Plant Feedstocks Genomics for Bioenergy program supports fundamental genomics-based research leading to the development of improved and more sustainable plant feedstocks for the production of biofuels and biobased products. The session will include presentations by the 2015 awardees on their accomplishments in developing lignocellulosic feedstocks with improved disease resistance. The 2017 awardees will follow with a series of "speed talks" highlighting newly funded research spanning a variety of candidate feedstocks, including oilseeds.

2:00-2:10 **Cathy Ronning** and **Bill Goldner**
Introduction and Program Overview

2015 Awardees

2:10 - 2:40 **Hugo Cuevas -** USDA ARS Mayaguez PR
Genomic dissection of anthracnose resistant response in sorghum [*Sorghum bicolor* (L.) Moench]

2:40 - 3:10 **Peter Balint-Kurti -** North Carolina State University
The genetic basis of the MAMP response and its relationship to disease resistance in sorghum

3:10 - 3:30 **Break**

3:30 – 4:00 **George Newcombe -** University of Idaho
Characterizing the Defense Hierarchy of Populus trichocarpa and its Hybrids

2017 Awardees:

4:00 – 4:05 **Jared LeBoldus -** Oregon State University
Towards durable resistance to Septoria stem canker and leaf spot: A molecular understanding of resistance

4:05 – 4:10 **Andrew Groover -** US Forest Service (for **Luca Comai**, University of California, Davis)
Discovery and characterization of dosage-dependent disease resistance loci in biomass poplar

4:10 – 4:15 **Ed Eisenstein -** University of Maryland
Elucidating mechanisms of rust pathogenesis for engineering resistance in poplar

4:15 – 4:20 **David Lowry -** Michigan State University
Identification of adaptive fungal pathogen resistance loci in switchgrass

4:20 – 4:25 **Rebecca Bart -** Donald Danforth Plant Science Center
Optimizing tradeoffs implicit during bioenergy crop improvement: Understanding the effect of altered cell wall and sugar content on sorghum-associated pathogenic bacteria

4:25 – 4:30 **John Sedbrook -** Illinois State University
Advancing field pennycress as a new oilseed biofuels feedstock that does not require new land commitments

4:30-5:00 **Discussion and Adjourn**

5:00 - 7:00 **Poster Session (even numbered posters)**
Location: Tysons Ballroom

Wednesday, February 28th

7:00 - 9:00 **Breakfast** (on your own)

9:00- 10:20 **DOE 2017 Early Career Research Awards**
Location: Fairfax Ballroom
Moderator: Pablo Rabinowicz

Speakers:

9:00 - 9:20 **Kelly Wrighton -** Ohio State University
Genomes to ecosystem function: Targeting critical knowledge gaps in methanogenesis and translation to updated global biogeochemical models

9:20 - 9:40 **Neslihan Taş Baas -** Lawrence Berkeley National Laboratory
Awakening the sleeping giant: Multi-omics enabled quantification of the microbial controls on carbon cycling in permafrost ecosystems

9:40 – 10:00 **Nicholas Bouskill -** Lawrence Berkeley National Laboratory
Microbial environmental feedbacks and the evolution of soil organic matter

10:00 – 10:20 **David Weston -** Oak Ridge National Laboratory
Mutualism in the face of changing climatic conditions: Implications on a plant-microbiome system influencing peatland carbon and nitrogen cycling

10:20- 10:40 **BER workshop Report "Technologies for Characterizing Molecular and Cellular Systems Relevant to Bioenergy and Environment"**
Presenter: Elizabeth Wright
Introduction: Amy Swain

10:40- 12:00 **Plenary Session: BioImaging**
Location: Fairfax Ballroom
Moderator: Kent Peters

Description of Session: The Bioimaging Program's mission is to understand translation of genomic information into the mechanisms that power living cells, communities of cells, and whole organisms. The program's goal is to develop new imaging and measurement approaches to visualize the spatial and temporal relationships of key metabolic processes governing phenotypic expression in plants and microbes. This Bioimaging Breakout Session is intended to provide an outline of the program's current state and opportunity for potential collaborations between the two sister programs.

Speakers:

10:40- 11:00 **Jose Dinneny -** Carnegie Institute for Science
Seeing in the dark: visualizing root systems using luminescence reporters

11:00- 11:20 **Tuan Vo-Dinh -** Duke University
Molecular Sensing and Functional Imaging Genomic Targets in Plant

Systems

11:20 - 11:40 **Wayne Versaw -** Texas A&M University
Development of live imaging tools and methods to monitor phosphate allocation in plants with cellular and subcellular resolution

11:40 – 12:00 **Leslie Shor -** University of Connecticut
Resiliency “On”: linking bacterial gene expression and soil moisture retention using light-controlled genes at the pore scale

12:00 **Close-out and Adjournment**