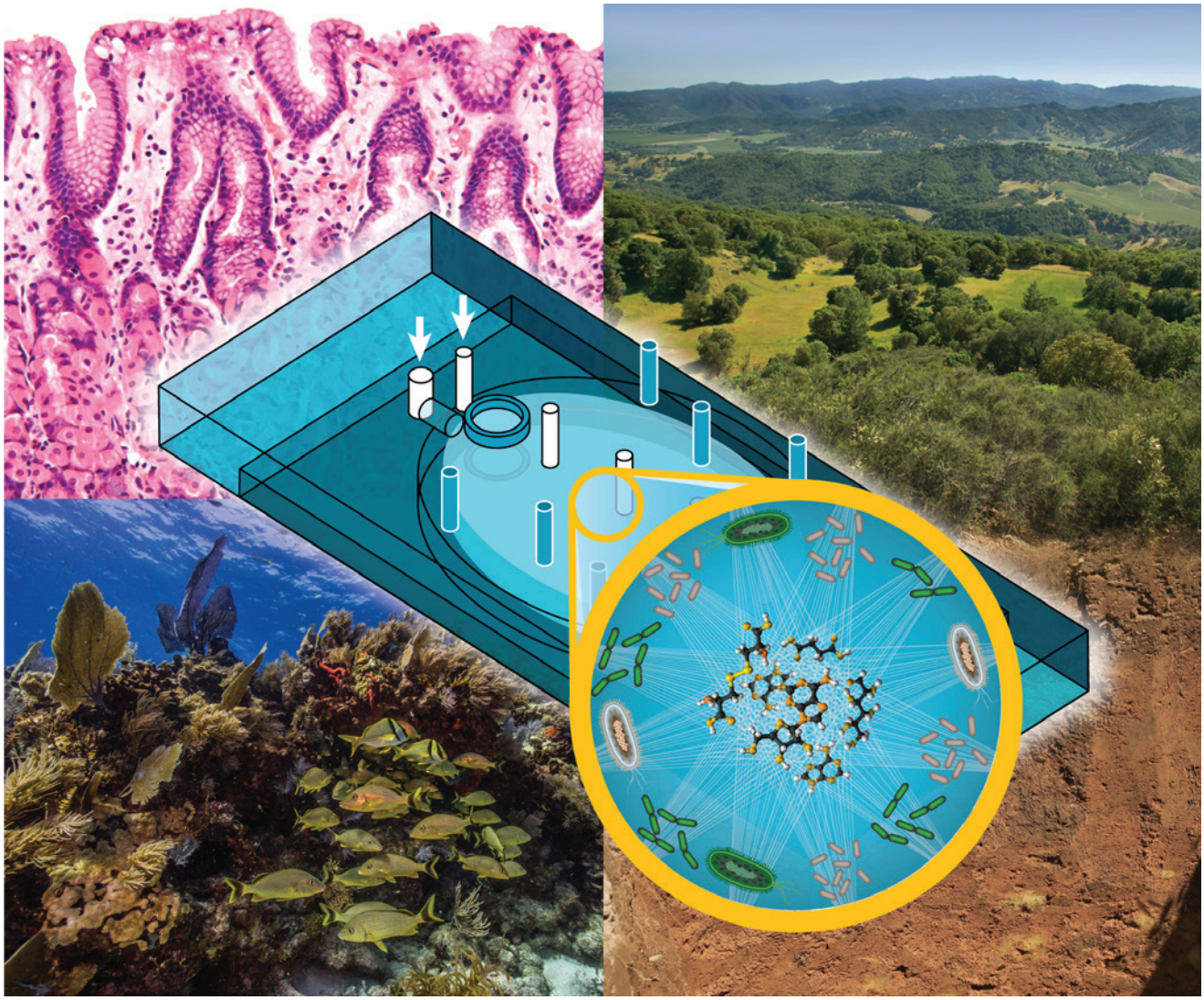
EcoFAB

# 2017 EcoFAB Summit: Model Ecosystems Linking Genome Biology to Ecosystem Processes



EcoFAB Workshop

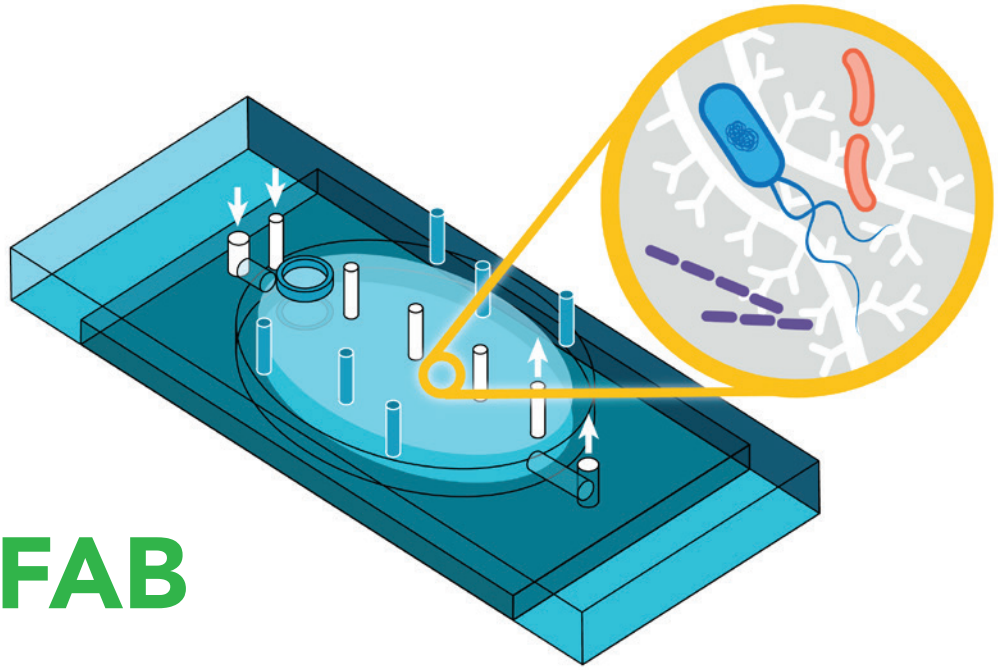
April 27–28th, 2017, Washington DC


## Co-Chairs

Trent Northen, Ph.D. LBNL
Karsten Zengler, Ph.D. UCSD
Kirsten Hofmockel, Ph.D. PNNL

## Organizer

Lawrence Berkeley National Laboratory
Trent Northen, Ph.D.
TRNorthen@lbl.gov



EcoFAB

## Executive Summary

The vital role microbiomes play in ecosystems is increasingly apparent, yet the diversity of these microbiomes and the complexity of their native habitats represent major challenges for the field. Understanding microbiomes in a functional context is further complicated by both the lack of standardized and reproducible experimental systems with which to study them, as well as the absence of standardized methods of data collection and analysis. Fabricated ecosystems, or EcoFABs, hold promise for replicating important microbial ecosystem processes, properties, and dynamics in reproducible laboratory environments. While accurately reproducing the full complexity of natural environments is unlikely, simplified systems will enable the discovery and testing of causal mechanisms underlying the structure and function of microbial systems (Fig. 1). EcoFABs consist of growth chambers populated with controlled microbiomes relevant to some aspect of the environment or a process of interest. These EcoFABs can be designed to accommodate imaging and systems biology approaches to assess microbiome dynamics. Through the development of specific, environment-optimized EcoFABs, scientists will: discover design principles that govern microbiome assembly and structure; understand the functions of genes, microbes, and metabolomes; and predict microbiome activities and the tipping points between health and disease. In addition to these scientific advances, the creation of standardized EcoFABs will bring together communities of scientists working on shared systems, enabling more effective knowledge transfer between researchers — just as model organisms and cell systems have done in molecular and cell biology. By expanding our understanding of the recruitment, assembly, structure, and functions of microbiomes, significant scientific and technical advances can be made in positively impacting biomedical and environmental sciences. Specifically, standardized model ecosystems will

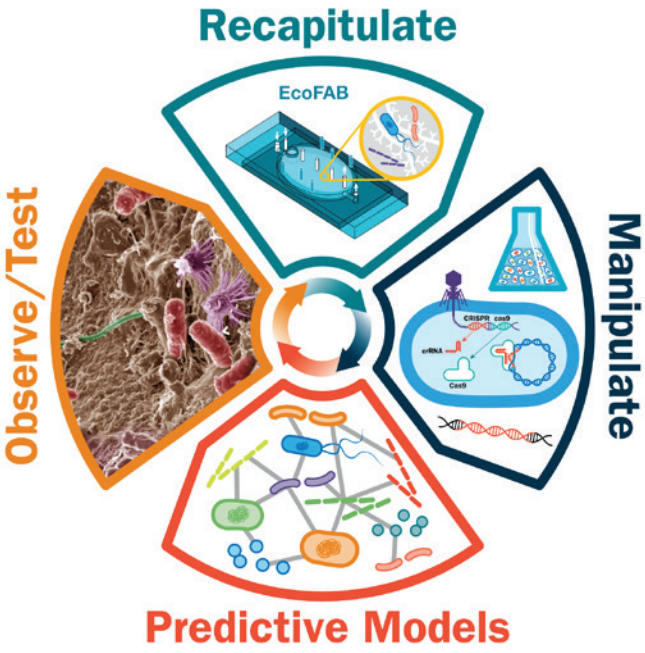



Figure 1. Process of constructing, using, and iteratively improving EcoFABs. Natural ecosystems are carefully observed to determine target processes for laboratory recapitulation. These are then constructed and manipulated to dissect causal mechanisms, which are captured in predictive models for testing in the natural ecosystems.

enable the greater scientific community to systematically control the complexity of microbiomes, which will lead towards mechanistic understandings of microbial processes that can be reproduced across experiments.

On April 2017, Lawrence Berkeley National Laboratory, along with Pacific Northwest National Laboratory and the University of California, San Diego, brought together 60 thought leaders in microbiome science and laboratory model microbiomes at the EcoFAB Summit to discuss challenges in microbiome research that could be addressed by deploying defined model microbiomes. The Summit was convened to identify common approaches to studying microbiomes, to develop a set of principles for building EcoFABs, and to identify challenges that could be addressed through broad adoption and use of EcoFABs. The assembled group discussed recent advances in developing laboratory ecosystems for studying microbiomes, the scientific and technical challenges in microbiome science that would be addressed by standardized EcoFABs, and opportunities to develop model EcoFABs for soil, plant, aquatic, and metazoan microbiomes.

**To that end, the group formulated a set of recommendations to advance EcoFAB development and adoption:**

1. **Organize communities of scientists to lead EcoFAB development.** A steering committee and working groups will be needed to develop and implement processes for scientific community engagement, development of data standards, principles for data sharing, and dissemination and adoption of EcoFABs.
2. **Establish common parameters for EcoFABs.** Each EcoFAB should have a defined microbiome, physical setup, protocols, and a suite of standardized assays associated with it. These parameters should align to established selection criteria and include tolerances to accommodate the variability inherent to natural systems. Prototyping of EcoFABs will be critical to outlining these parameters and understanding the variability of experimental systems.
3. **Validate EcoFABs to ensure efficacy for translation and application to broad scientific challenges.** EcoFABs should be tested for reproducibility across multiple labs and demonstrate the ability to accurately predict "real world" conditions.
4. **Establish data collection standards and data portal(s) for EcoFAB users.** The scientific community will need to define the minimum set of data to be collected in each experiment, including establishing metadata standards and the types of assays and analyses required to establish the validity of an EcoFAB. Further, the community will need to ensure access to information (including raw and analyzed data) through a common data portal (or portals).
5. **Develop a strategy for dissemination and adoption of EcoFABs.** A staged approach for dissemination and adoption should be undertaken. Prototype systems should focus on recapitulating a subset of key environmental variables and common parameters to then iterate and refine EcoFABs. Over time they should incorporate more complexity, leading to defined systems appropriate for addressing specific and ecologically relevant scientific challenges.

A few research communities have already begun to develop model systems that could be considered first-generation EcoFABs: A recent example is the 'minigut', a laboratory model of the human colon, that has been used successfully to study wall contractions and flow on bacterial populations (Fig. 2). Related systems have been developed to help understand microbiome composition, assembly, and causal effects on the host plant (Fig. 3). Prototype systems are just now being established for many other microbiomes. In addition, there are many promising technologies and study systems that can be immediately implemented within EcoFABs including transparent artificial soils, sensors, chemiluminescent microbes, and genetic variants of plants and microbes. Workshop participants agreed that, once developed, these and other EcoFABs will fill an important unmet need for defined and reproducible approaches for understanding microbiome processes and host interactions.

The EcoFAB Summit attendees developed a set of actions and priorities for EcoFAB adoption and dissemination. Further engagement with scientists at universities, national laboratories, and industry is needed to continue to develop, iterate, and refine the parameters for EcoFABs of interest. Additionally, the group felt that meeting with the Genome Standards Consortium and the National Institute of Standards and Technology would

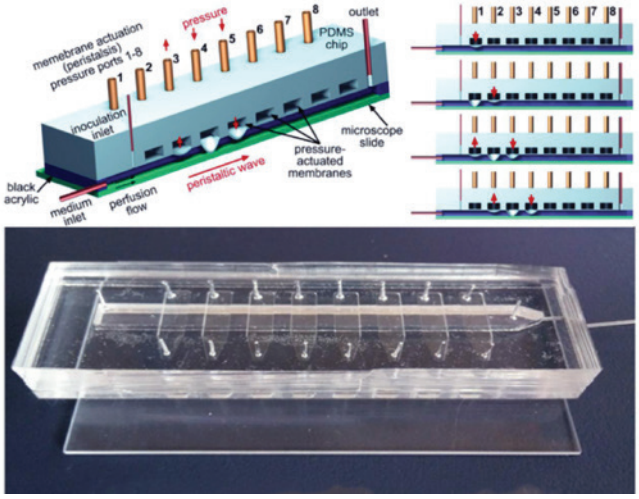



Figure 2. Minigut system designed to propagate a peristaltic wave found in the human colon. (Top Left) Design. (Top Right) Wave propagation through sequential valve actuation. (Bottom) Photo of the polydimethylsiloxane minigut device. Cremer et al, PNAS 2016, 113(41)

greatly inform efforts to establish standards for EcoFAB data collection and dissemination. Finally, the attendees agreed that significant insights would be gained from meeting with the members of the Microbiome Interagency Working Group impaneled by the National Science and Technology Council in order to understand the US government perspective on microbiome research and opportunities for EcoFABs to potentially address specific national-scale challenges.

EcoFABs hold great promise to advance our understanding of microbiomes that influence important biological processes. Further development of prototype systems, establishment of criteria for microbiome studies in EcoFABs (including standards and reference protocols), and iterative refinement of EcoFABs will be necessary to gain broad adoption across the scientific community. A multidisciplinary approach that integrates contributions from biologists, chemists, geologists, ecologists, physiologists, informaticists, computer scientists, and engineers will be critical to establish EcoFABs as functional and defined systems to dissect microbiomes.

## Introduction

In recent years, our understanding of microbiomes has grown dramatically as has our recognition of their importance to diverse systems from farms and soils to the human gut. However, one of the major challenges for developing a generalized understanding of microbiomes in these complex environments is the lack of controlled, reproducible, and standardized model systems with which to perturb and study them. Biological and biomedical research communities have long histories of using microbial, animal, and tissue culture model systems. Each of these models have known advantages and limitations, yet, together model systems have broadly advanced our understanding of biological systems. Yet, there are no agreed-upon model ecosystems for studying microbial communities and microbiomes (beyond the animal host itself). Consequently, nearly every researcher in the field is studying a different set of microbes in a different system. Moreover, comparisons across systems such as soil and aquatic environments or the human body are nearly impossible due to a lack of defined principles and standards for microbiome studies.

**EcoFABs stand to provide reproducible dynamics and steady states in benchtop microbial ecologies—systems with properties analogous to the stages of development of a model organisms.**

Microbiome science can build on the great tradition of model organisms, where communities of scientists agreed upon particular organisms (*Caenorhabditis elegans, Escherichia coli, Arabidopsis thaliana*, specific strains of inbred mice (e.g., BALB/c, C57/BL6), and many others) that their fields would focus on, building a unified set of resources. Model organisms have enabled, and continue to enable, thousands of scientists to focus on the same systems and reproduce each other's results, thereby having a transformative impact on science. Indeed, most of what we know about molecular biology was learned from studying widely-used and community-accepted model systems.

As scientists strive to study microbiomes, it is essential to develop common laboratory ecosystems enabling reproducible studies. Bringing together communities of scientists to design and model ecosystems has the potential to greatly advance microbiome science. Importantly, these systems should be designed to be disseminated between scientists, bringing together diverse expertise and approaches to study the same controlled ecosystems to greatly accelerate our understanding of microbial communities. EcoFABs will also enable use of genetic variants, imaging and multi-omic tools to facilitate discovery of causal mechanisms, which is currently extremely challenging in native ecosystems.

### Need for standardized laboratory microbiomes

Most approaches aimed at improving our understanding of microbiomes are focused on examination of extremely simple lab consortia or fully-complex natural communities. Consortia have the advantage that the constituent isolates can (in most cases) be characterized independently and even genetically manipulated to determine causal mechanisms. The degree to which consortia-based findings can be abstracted to natural communities is unclear. In contrast, natural communities (e.g. field or clinical studies) are so unconstrained that it is difficult to establish causation, requiring studies of wildly impractical proportion to adequately constrain the large number of experimental variables.

Advancing integrated efforts around model microbial communities is urgently needed to enable standardized screening and systems biology based prediction of microbial community activities within ecological frameworks. These efforts will greatly benefit from recent advances in metagenomics that now enable assembly of genomes for a large fraction of microbial communities ranging from the human microbiome to soil ecosystems. The integration of this information along with chemical analysis (e.g. metabolomics), imaging, and synthetic biology tools has the potential to rapidly advance causal mechanisms and develop generalizable principles describing microbiome recruitment, assembly, resilience, and activities. This will ultimately enable harnessing microbiomes to address critical environmental, energy and health challenges.

## Section 1: What is an EcoFAB?

Ecosystem fabrication is an approach to creating controlled microbial ecologies within a laboratory setting that enable discovery and dissection of environmental variables, activities, and interactions. A fabricated ecosystem, or EcoFAB, is comprised of a physical chamber, components to replicate an ecosystem of interest (e.g. soil, plants), the microbial communities to be tested, and any measurement technologies (e.g. sensors or sampling apparatus). This approach uses widely-accessible 3D printing technologies to fabricate controlled microbiome habitats that can be standardized and easily disseminated between labs.

As an illustrative example shown in Fig. 2, researchers at LBNL use 3D printing to create molds for casting the biocompatible polymer polydimethylsiloxane (PDMS) into the upper portion of a fluidics chamber. This is subsequently attached to a microscope slide, completing the chamber. This is then placed into a sterile container, providing a gnotobiotic system for studying microbial interactions. This chamber design includes a port for growing the model grass *Brachypodium distachyon*, tubing that allows sterile introduction and sampling of microbes and metabolites, and a lighting system.

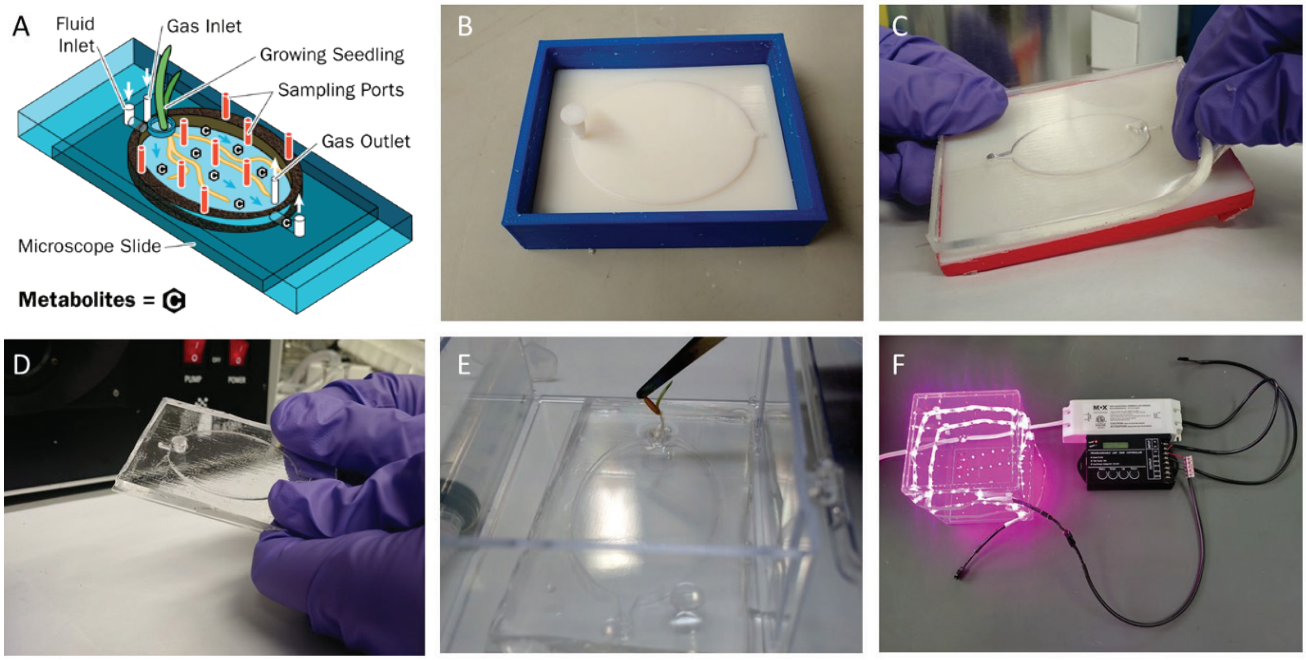



Figure 3. Plant-microbe EcoFAB. (A) Design (Top—side view and Bottom—top view). (B) 3D printed mold. (C) Upper chamber made from casting PDMS in the mold. (D) Sealing the upper chamber onto a microscope slide. (E) Inserting a germinated seed and microbes into the EcoFAB chamber. (F) Completed EcoFAB with controlled LED lighting system.

## Section 2: Challenges in Microbiome Science Relevant to EcoFABs

While each microbiome represents its unique challenge, several overarching themes in microbiome sciences have emerged that can be addressed by using EcoFABs.

1. **Defining ecological design principles for microbiome assembly, structure, interactions, and integrated activities.** The Summit participants identified that the development of multiple model microbiomes (e.g. associated to animal, plant, soil, or aquatic systems) with standardized methods, validation criteria, and data standards would enable development of unifying principles in microbiome science. EcoFABs could be utilized to identify variables that govern microbial community structure-function relationships and stochasticity in these relationships, including the effect of dormancy, persistent states, and phenotypic heterogeneity on the community composition and function. Identifying these relationships at various spatial and temporal scales will also provide insights into the role of key organisms on community assembly and structure. This will enable scientists to define the core microbiome, both on an organismal and functional level. It will also enable scientists to delineate functional redundancies or complementarities and understand interactions and exchanges that stabilize communities and govern activities and environmental responses. This knowledge will allow scientists to determine host and environmental factors, such as host products, and interactions drive selection (and genome evolution) within specific community-environmental contexts, ultimately enabling engineering strategies for microbiome control.
2. **Developing new technologies critically needed to study microbiome functions and interactions at relevant time and spatial scales:** Microbiome studies are often limited by an inability to obtain reproducible information with spatial and temporal (time-series) resolution. EcoFABs would address these challenges by managing complexity and adding a new benchmark for reproducibility in laboratory microbiome experiments. Specifically, EcoFABs will be used to control a given environment while providing access to spatial structure and dynamic processes. This will increase understanding of successional states and approaches to accelerate or slow successional processes.
3. **Advancing a foundational understanding of the ecological function of genes, microbes and metabolites:** Current microbiome research is limited by a lack of understanding across scales. At a molecular level we do not know the function of most proteins

(annotated as unknown or hypothetical), and thus cannot delineate novel metabolisms present in different microbiomes. At a cellular level we are presently unable to predict interactions of different microbes and lack knowledge about the phenotype to genotype relationship in a community context. At a community level, we do not know the environmental feedbacks and interactions that drive microbiome assembly, activities, and impacts. EcoFABs will enable new functional annotations of individual microbes, genomes, host and microbial genes, proteins and metabolites within specific ecological contexts. Additionally, EcoFABs may support the growth of organisms in co-cultures that have evaded isolation to enable analysis of their activities.

4. **Predicting the health and trajectories of microbiomes:** The lack of knowledge about function hampers present efforts to predict states of the microbiome and transitions between different states due to environmental (abiotic or biotic) perturbations. For example, it is currently challenging to forecast how genotypic variance (e.g. of the host) influence microbiome structure and function. Mapping possible and actual nutrient and energy flow through the microbiome and across trophic levels would be an important foundation upon which to build.
5. **Ability to engineer and manage microbiome activities:** The ability to design targeted interventions to manage microbiomes would be of great importance to improve plant, soil, water, human and animal health, e.g. advancing low-input crops, improving soil fertility, better wastewater treatment solutions, reducing diseases, etc. To achieve this, we need to define what constitutes a stable community and what community-level properties are inherently dynamic within defined boundaries. The underlying architecture of microbial interactions (microbe-microbe and microbe-host) will provide insight into what are the most effective levers to control microbiome composition and function, which could include abiotic factors, diet, host genetics, and plant association amongst others. This could, for example, provide new understanding of how pathogenic microbes disrupt this network for invasion. It will also allow use of synthetic biology tools to manage whole microbial populations within microbiomes, *in situ*. However, this capability will likely require innovations in genetic transformation approaches and the ability to control horizontal gene transfer between different species and populations.

## Section 3: Overarching EcoFAB design principles

EcoFABs enable standardization and control of the initial community structure, genetics and bulk environmental parameters. However, much of the diversity within microbiomes is thought to be neutral resulting in stochastic assembly and dynamics which could easily lead to irreproducibility. Therefore, it will be critical to develop systems that reproducibly display the same system dynamics and reproducible genotype-environment interactions. The goal of achieving stability across labs should guide the construction of basal culture conditions, including minimal microbiomes. This requirement could be relaxed in a "functional group paradigm" where microbes are defined in particular ecological or functional niches — such definitions may be use-case specific. We anticipate that the control of an *in vitro* device will be a reasonable place to start, however much more work will be needed to define standard microbiomes. Many microbial communities will not constitute useful laboratory models, just as most individual species are not genetic model organisms. Intelligently selecting small subsets of useful systems guided by the following design principles will be an important step toward realizing the potential of the technology.

## EcoFAB design principles

1. **Keep it simple:** Base EcoFABs and minimal analyses should be as simple and inexpensive as possible to enable widespread adoption, large numbers of replicates, and integrated studies across labs, recognizing that some studies will require specialized EcoFABs
2. **Design for extensibility:** Enable extensions to address the needs of large groups of researchers from diverse fields
3. **Standardize system dynamics:** EcoFABs should be standardized to 'boot-up' and display reproducible dynamics
4. **Accurately recapitulate important aspects of natural systems:** EcoFABs should capture key natural processes
5. **Enable mechanistic studies:** Genetically tractable organisms should be used when possible to enable mechanistic insight at the molecular level
6. **Embrace complexity:** Allow experimentation from minimal to complex microbiomes and habitats
7. **Build in simple analytics and sensors:** Enable debugging, comparison, and standardization by including inexpensive sensors and analytical measures
8. **Space and time are important:** Move towards manipulation, imaging, and analysis spanning relevant scales from individual microbes to whole communities over time
9. **Future proof data:** Data standards, analytical approaches, system tolerances, and modeling approaches must be considered upfront to enable future cross-EcoFAB meta-analyses. When possible, data should also be preserved in its original, raw form to enable future analyses.
10. **Give it away.** To maximize impact and usefulness, the EcoFAB resources should be freely accessible to the greater scientific community. This means that the base-level capabilities will need to be common to most research groups and that we will embrace a culture of sharing and inter-lab cooperation. Open access experimental design and standardized reporting methods will also aid the overall inclusiveness of the EcoFAB movement.

# Section 4: Recommendations

Given the challenges common among all microbiome sciences, the workshop resulted in a set of recommendations on how EcoFABs would benefit microbiome research at large. If implemented, these recommendations would significantly advance microbiome science by building data standards, advance data sharing and analysis, and allow interpretation of results in the context of robust and validated protocols.

1. **Community organization:** Effective advancement of laboratory microbiomes will require a group responsible for developing and implementing data standards, data sharing, and EcoFAB dissemination and adoption.
   a. **Steering committee:**
      i. Defines criteria for design, dissemination, and data standards
      ii. Promotes efforts to agencies, societies, committees, and the larger microbiome community
      iii. Prepares annual white paper(s) identifying key challenges
   b. **Working groups:** topical and ideally regional groups focused on specific systems. Primary focus is on development of widely applicable designs and coordination of ring-trials
      i. Animal microbiomes
      ii. Plant microbiomes
      iii. Soil microbiomes
      iv. Aquatic microbiomes

2. **Validation of initial EcoFABs:** EcoFABs will need to be validated across a set of defined parameters and across multiple laboratories.
    a. Criteria for building and validating EcoFABs: Uniform trajectory of a fixed-composition and distributable initial culture as assessed using a ring experiment.
    b. Demonstration of accurate 'field' predictions based on EcoFAB discoveries

3. **Tiered approach for demonstration, dissemination and adoption**
    a. Initial development and demonstration will likely be driven by research teams focused on specific scientific questions. Adoption of EcoFABs by the wider scientific community will rely on validation (above) and ease of integration into existing research programs. Minimal systems with defined scientific and technical parameters will likely be easier to deploy and hence be adopted earlier.
    b. In addition to validation, adoption of minimal systems across a wide group of scientists will be necessary to refine EcoFAB design principles and demonstrate their utility.
    c. Adoption of a few, robust, and highly complex EcoFABS as model systems is a long-term goal, dependent upon validation of simpler EcoFABs, proven acceptance of increasingly complex systems across research groups, and ability to derive insights not currently apparent with existing study systems.

4. **Common protocols, designs, and microbes:** Standard operating procedures (SOPs) need to be developed to ensure reproducible results. These SOPs will define inoculum, physical setup, culture conditions, and provide acceptable dynamic ranges of experimental parameters including tolerances for genetic, epigenetic, metabolic, community stability, etc. These will be made available online and possibly as a special issue focused synthetic experimental environments.

5. **Data collection standards coupled with central portal:** Data, designs, protocols must be standardized to the extent that ideally EcoFABs will have embedded analytical devices to enable a baseline for comparison. The resulting data should be made accessible through a common data portal to enable rapid empirical advances and large-scale meta-analysis.

# Conclusion and Next Steps

## Conclusions

EcoFABs are model environmental systems that are easy to maintain and manipulate, allowing reproducible communities to be experimentally manipulated and studied by the broad scientific community. Development of reproducible standardized laboratory ecosystems that are widely accepted, along with common protocols and data standards, will enable researchers to build on each other's work, test predictions, identify governing mechanisms, and build predictive models. EcoFAB will enable microbiome science to rapidly advance from observational, correlative studies to reproducible mechanistic investigations that identify causative agencies. Comparison of findings and mechanisms across diverse EcoFAB model systems will enable the development of general principles that are applicable across microbiomes, and ultimately validated in studies of natural systems. Advancing this vision will require effective community organization and participation to prioritize widely applicable EcoFABs, set design and reporting standards, and establish venues for exchanging findings and ideas that advance microbiome science.

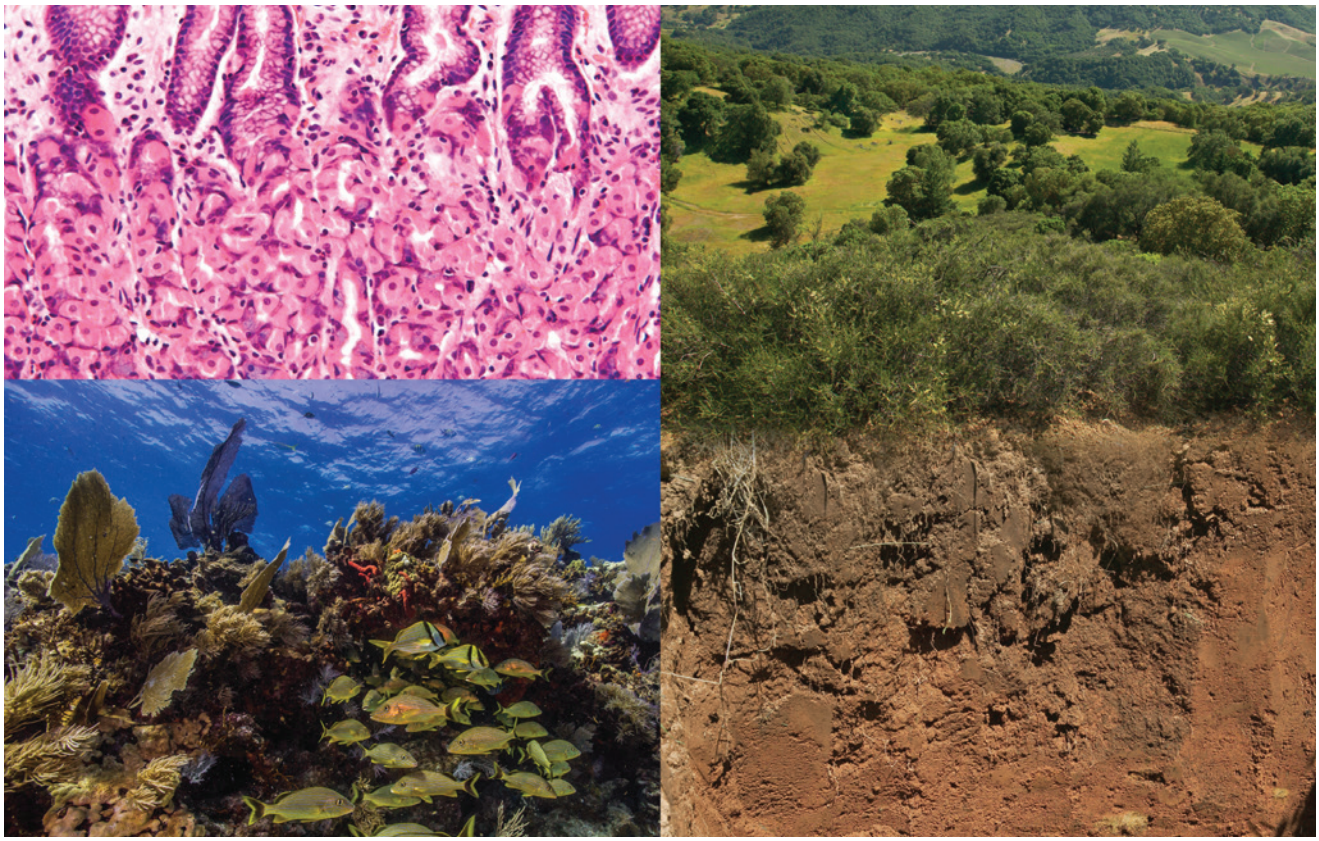
## Next steps

EcoFAB Summit participants discussed a series of next steps aimed at gathering more input from the scientific community and developing initial EcoFABs for validation. These next steps include:

- **Form steering committee and working groups**
- **Perform the first ring-trial for prototype plant-microbe EcoFAB design**
- **Engage the scientific community through a listening tour and workshops**
- **Present EcoFAB concept to stakeholders for further discussion**
    - **Genome Standards Consortium**
    - **Microbiome Interagency Working Group**
    - **EcoFAB session at 2018 AAAS annual meeting**

# Appendix 1: Ecosystem Specific Challenges

| Challenge | Soil | Plant | Animal | Aquatic |
|---|---|---|---|---|
| Endophytes | | | | |
| Lumenal interactions | | | | |
| Immune system interactions | | | | |
| Mineral surfaces | | | | |
| Wet dry cycles | | | | |
| Require illumination | | | | |
| Realistic flow is critical | | | | |
| Contributions of fungi | | | | |
| pH and redox gradients | | | | |
| Pore space | | | | |
| Inputs from plant biomass | | | | |
| Viscosity and diffusion restriction | | | | |



# Appendix 2: Workshop Attendees

Public attendees only

| First Name | Last Name | Institution | Title |
|---|---|---|---|
| Nitin | Baliga | Institute for Systems Biology | Senior Vice President and Director |
| Scott | Behie | Berkeley | Postdoctoral Fellow |
| Hans | Bernstein* | Pacific Northwest National Laboratory | Senior Research Scientist |
| Eoin | Brodie | Lawrence Berkeley National Lab | Deputy Director |
| James | Brown* | University of Birmingham, UK | Professor and Chair of Environmental Bioinformatics |
| David | Butler | National Academies of Sciences, Engineering, and Medicine | Scholar, Health and Medicine Division |
| Romy | Chakraborty | LBNL | Scientist, Department Head |
| Katy | Christiansen | Lawrence Berkeley National Laboratory | Strategic Program Coordinator |
| Timothy | Conner | USDA/National Institute for Food and Ag | Division Director |
| Otto | Cordero* | MIT | Professor |
| Matthew | DiLeo | Novozymes | Group Leader |

| First Name | Last Name | Institution | Title |
|---|---|---|---|
| José | Dinneny | Carnegie Institution for Science, Department of Plant Biology | Principal Investigator |
| James | Dobrowolski | USDA National Institute of Food and Agriculture | National Program Leader for Water |
| Emiley | Eloe-Fadrosh | DOE Joint Genome Institute | Metagenome Program Lead |
| Sheri | Floge* | The Ohio State University | Postdoctoral Fellow |
| Samuel | Forry | NIST | Principal Investigator |
| Carolin | Frank | UC Merced | Professor |
| Justin | Gallivan | DARPA | Program Manager |
| Manuel | Garavito | Wisconsin Institute for Discovery | Postdoctoral associate |
| N. Louise | Glass | Lawrence Berkeley National Laboratory | Director, Environmental Genomics and Systems Biology |
| Christopher | Henry* | Argonne National Laboratory | Computational Biologist |
| Matthias | Hess | UC Davis | Assistant Professor |
| Kirsten | Hofmockel | PNNL | Lead Scientist for Integrative Research |
| Terry | Hwa | UC San Diego | Professor |
| Scott | Jackson | NIST | Group Leader |
| Christer | Jansson* | PNNL | Director of Plant Sciences |
| Angela | Kent* | University of Illinois at Urbana-Champaign | Associate Professor |
| Rob | Knight | University of California, San Diego | Professor |
| Robert | Kokoska | US Army Research Office | Microbiology Program Manager |
| Steve | Lindemann* | Purdue University | Assistant Professor |
| Edward | Mandell | DARPA/Booz Allen Hamilton | BTO Tech SETA |
| Costas | Maranas | Penn State | Professor |
| Neo | Martinez | University of Arizona | Associate Professor of Ecology and Evolutionary Biology |
| Sandrine | Miller-Montgomery | UC San Diego | Executive Director, Center for Microbiome Innovation |
| Trent | Northen | Lawrence Berkeley National Laboratory | Staff Scientist |
| Andrea | Ottesen | CFSAN FDA | Research Microbiologist |

| First Name | Last Name | Institution | Title |
|---|---|---|---|
| Dale | Pelletier | Oak Ridge National Laboratory | Staff Scientist |
| Jennifer | Pett-Ridge | LLNL | Deputy Group Lead, SFA lead |
| Lita | Proctor | NIH | Program director, Human Microbiome Project |
| Brad | Ringeisen | DARPA Biological Technologies Office (BTO) | Deputy Director, DARPA/ BTO |
| Elizabeth | Shank* | University of North Carolina at Chapel Hill | Assistant Professor |
| James | Tiedje | Michigan State University | Professor |
| Lisa | Tiemann | Michigan State University | Assistant professor |
| Michael | Udvardi | The Samuel Roberts Noble Foundation | Director |
| Ophelia | Venturelli | University of Wisconsin-Madison | Assistant Professor |
| John | Vogel | JGI | Staff Scientist |
| Marc | von Keitz | ARPA-E | Program Director |
| Gary | Vora | Naval Research Laboratory | Deputy Laboratory Head, Code 6910 |
| Matthew | Wallenstein | Colorado State University | Associate Professor |
| Yasuo | Yoshikuni | DOE Joint Genome Institute | Head, DNA Synthesis Science Program |
| Karsten | Zengler | UC San Diego | Associate Professor |

*Breakout/writing lead

**Other contributors:** Jeff Dangl, University of North Carolina at Chapel Hill

Special thanks to Katy Christiansen

# Appendix 3: Workshop Agenda


### 2017 EcoFAB Summit

Developing a community strategy to advance standardized model ecosystems
Washington Marriott Wardman Park, Washington DC
April 27th to mid-day April 28th

### Organizers

Trent Northen, Lawrence Berkeley National Laboratory
Karsten Zengler, University California, San Diego
Kirsten Hofmockel, Pacific Northwest National Laboratory

## Day 1 Agenda: April 27th

9–9:15 am **Goals for the Summit**
Trent Northen, Karsten Zengler, Kirsten Hofmockel

9:15–9:30 am **Discussion of goals**

9:30–11:30 am **Session I:** *Grand challenges in microbiome research.*
Kirsten Hofmockel, Pacific Northwest National Laboratory

9:30–10:15 am **Plenary Talk:** *The opportunities and challenges of metagenomics studies of ecosystems.*
Jill Banfield, University of California, Berkeley

10:15–10:35 am *Envisioning the next genre of microbiome research*. James Tiedje, Michigan State University

10:35–10:50 am Break

---

10:50–11:10 am *Sequencing until the cows come home: What else besides sequence data do we need to understand the microbiomes of animal systems?* Matthias Hess, University of California, Davis

11:10–11:30 am *Systems biology of collapse, resilience, and drug tolerance in microbe*.
Nitin Baliga, Institute for Systems Biology

11:30–11:45 am Session I Discussion: *Decide on 10 largest challenges facing microbiome research*

11:45–1 pm **Roundtable Discussion: Grand Challenges** (working lunch)

1–2 pm **Decide on top 10 challenges that could be addressed using model ecosystems**

2–4 pm **Session II:** *Enabling technologies and computational models*.
Karsten Zengler, University of California, San Diego

2–2:45 pm **Plenary Talk:** *Overcoming technical challenges in microbiome research, from ecosystem to bench to model system*. Rob Knight, University of California, San Diego

2:45–3:05 pm *Uncovering microbial and viral diversity at ecosystem scales*.
Emiley Eloe-Fadrosh, Lawrence Berkeley National Laboratory

3:05–3:25 pm *Chemical and physical communication in the soil microbiome*.
Beth Shank, University of North Carolina at Chapel Hill

3:25–3:45 pm *Challenges and opportunities in modeling metabolism in communities*.
Costas Maranas, Pennsylvania State University

3:45–4 pm **Session II Discussion**

4–4:15 pm Break

---

4:15–5:15 pm **Decide top 10 technologies that should be developed within EcoFABs to address grand challenges**

5:15–5:30 pm **Introduce goals for next day**

## Day 2 Agenda: April 28th

8:30–10:10 am **Session III:** *Early successes using model microbiomes*.
Trent Northen, Lawrence Berkeley National Laboratory

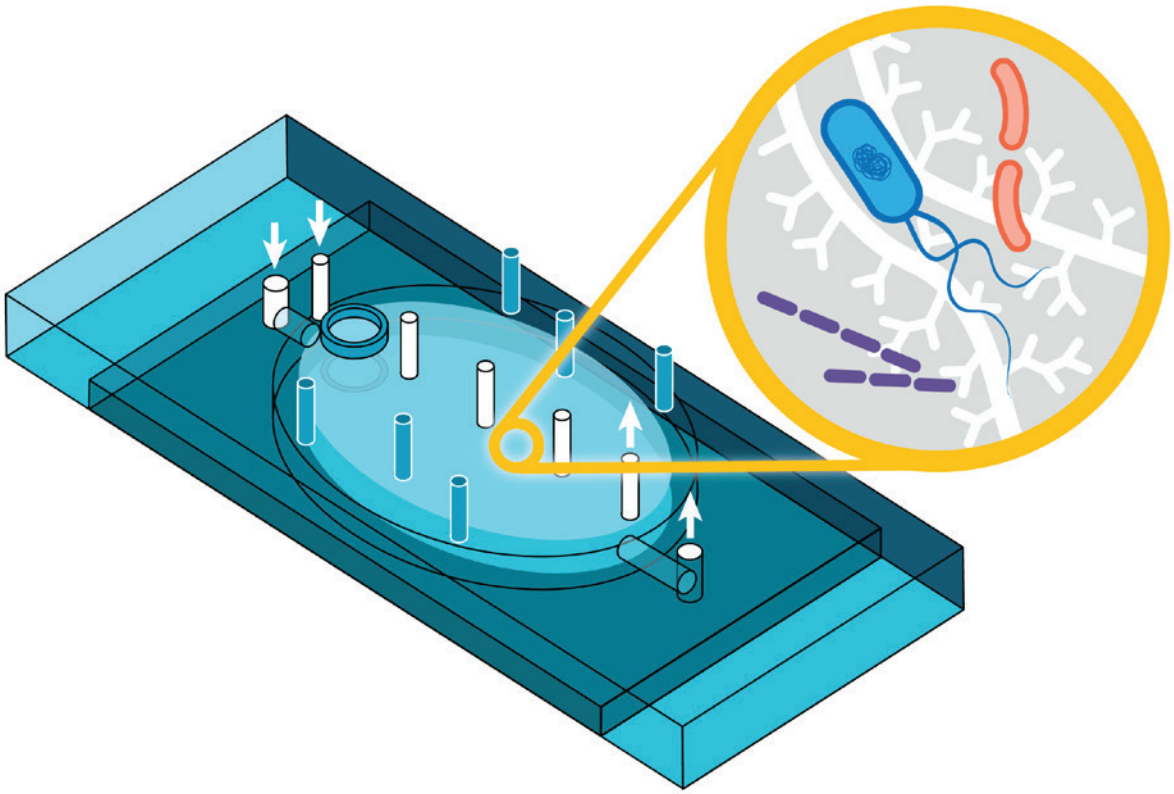
8:30–9:15 am **Plenary Talk:** *Understanding the Bacteroidetes-Firmicute ratio in human gut*.
Terry Hwa, University of California, San Diego.

9:15–9:35 am *A model system to study microbe-mediated plant growth promotion in the grasses*.
John Vogel, Lawrence Berkeley National Laboratory

9:35–9:55 am *Using stable isotopes to deconstruct the players and processes of root-microbe-mineral interactions*.
Jennifer Pett-Ridge, Lawrence Livermore National Laboratory

9:55–10:10 am **Session III Discussion**

| | |
|---|---|
| 10:10–10:30 am | Break |
| 10:30–10:40 am | *Assignments for breakouts: determine the top priorities for advancing two model plant EcoFABs, one animal EcoFAB, and one soil EcoFAB.*<br>Trent Northen, Kirsten Hofmockel, Karsten Zengler |
| 10:40–12 pm | **Breakouts** |
| 12–1 pm | **Breakout results** (working lunch) |
| 1–1:30 pm | **Group input and revision of priorities for model EcoFABs** |
| 1:30–2 pm | **Program manager talks on agency strategies relevant to model laboratory ecosystems and microbiome research** (5 minutes each) |
| 2–2:30 pm | **Summary of next steps** |
| 2:30 pm | Close |

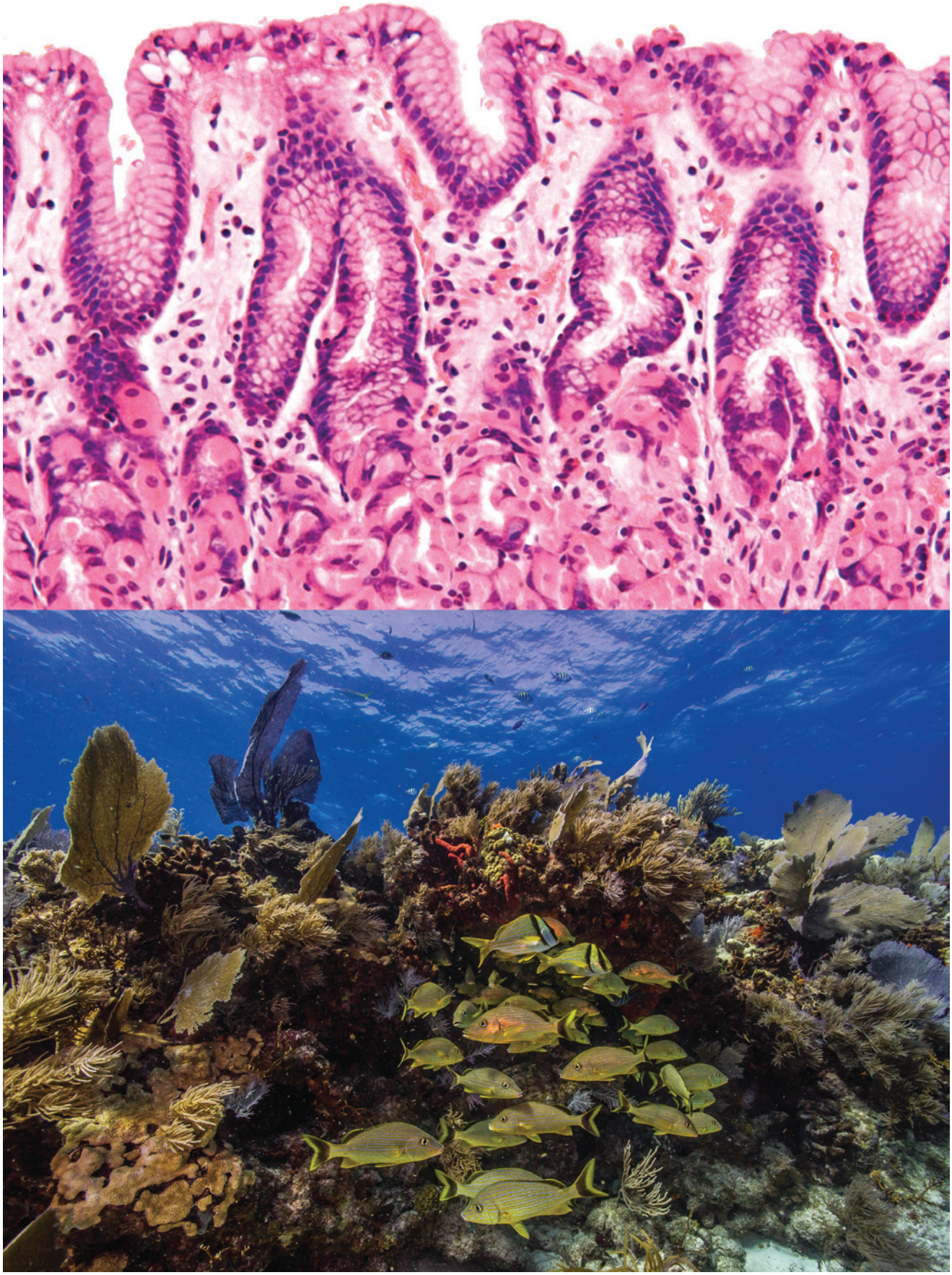


**Photography Credit**

Gastric mucosa: Copyright © 2011 Michael Bonert

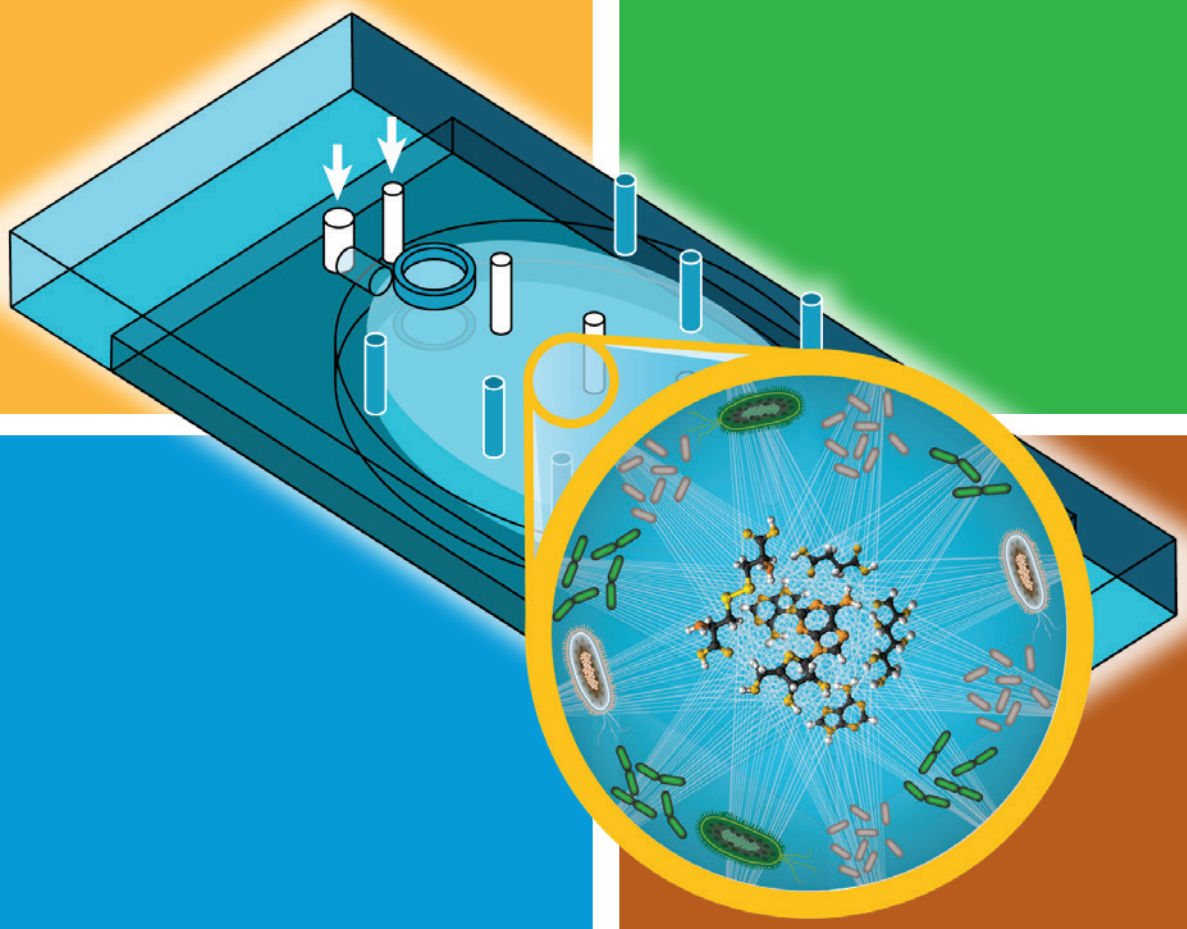
Biscayne coral reefs III: NPS image by Shaun Wolfe

Plant landscape and soil photographs: © 2010 The Regents of the University of California, through the Lawrence Berkeley National Laboratory



Animal microbiomes

Plant microbiomes



Aquatic microbiomes

Soil microbiomes

18-BS-4453