

# UNDERSTANDING OUR MICROBIAL PLANET

THE NEW SCIENCE OF METAGENOMICS



NATIONAL ACADEMY OF SCIENCES   NATIONAL ACADEMY OF ENGINEERING   INSTITUTE OF MEDICINE   NATIONAL RESEARCH COUNCIL

**THE NATIONAL ACADEMIES**

*Advisers to the Nation on Science, Engineering, and Medicine*

**MICROBIAL COMMUNITIES** support all life on Earth; *metagenomics* is a revolutionary new approach to understanding the characteristics of our microbial world. This new science opens doors to a tremendous amount of scientific exploration and can help address some of the most complex medical, environmental, agricultural, and economic challenges of today's world.

## A NEW TOOL FOR SCIENTIFIC EXPLORATION...

**MEDICINE:** Examining how the microbial communities that normally inhabit our bodies affect human health can lead to new strategies for diagnosing, treating, and possibly preventing diseases.

**LIFE SCIENCES:** Deciphering how microbial communities function can partially answer fundamental questions about microbial, plant, and animal biology and greatly enhance our understanding of ecology and evolution.

**EARTH SCIENCES:** Exploring how microbial communities in the soil and in the ocean affect atmospheric balances and environmental conditions can help us understand, predict, and potentially address global changes.

## HELPING ADDRESS THE CHALLENGES OF TODAY'S WORLD...

**ALTERNATIVE ENERGY:** Harnessing the power of microbial communities may lead to more sustainable and environmentally friendly biologically-based energy sources.

**ENVIRONMENTAL REMEDIATION:** Developing microbe-based tools for monitoring environmental damage and cleaning up oil spills, groundwater, sewage, nuclear waste, and other hazards may help restore healthy ecosystems.

**BIOTECHNOLOGY:** Taking advantage of the diverse abilities of microbial communities may lead to the development of beneficial industrial, food, and health products.

**AGRICULTURE:** Gaining a better understanding of the beneficial microbes living in, on, and around domestic plants and animals can contribute to improved methods for detecting diseases in crops, livestock, and food products and can facilitate the development of farming practices that take advantage of the natural alliances among microbes and plants and animals.

**BIODEFENSE AND MICROBIAL FORENSICS:** Studying the DNA and biochemical fingerprints of microbial communities helps specialists monitor known and potential pathogens, create more effective vaccines and treatments against potential bioterror agents, and reconstruct events in which microbes have played a role.



# CONTENTS

TRILLIONS OF FRIENDS...MICROBES MAKE HUMAN LIFE POSSIBLE	3
WINDOW TO THE MICROBIAL UNIVERSE: THE NEW SCIENCE OF METAGENOMICS	5
What Is Metagenomics?	
How Does Metagenomics Work?	
APPLICATIONS: WHAT METAGENOMICS CAN DO	9
The World Within: Learning from the Microbial Inhabitants of the Human Body	
Global Impacts: The Role of Microbes in Maintaining Atmospheric Balances	
Bioenergy: Harnessing Microbial Power	
Smart Farming: How Microbes Help Our Crops	
Cleaning Up: Remediation of Environmental Contamination	
GETTING THE MOST OUT OF NEW SCIENTIFIC ADVANCES	16
SUMMARY	19





# TRILLIONS OF FRIENDS ... MICROBES MAKE HUMAN LIFE POSSIBLE

**M**ore than three billion years ago, organisms too small to be seen began a process that ultimately would enable the evolution of all complex life on Earth. At that time, Earth was very different from what it is today. All life was confined to single-celled microscopic organisms (*microbes*) that lived in the oceans; there were no animals or plants. Carbon dioxide and methane concentrations were very high, and oxygen was virtually absent. For most of the life on the planet, oxygen was poison. Some of Earth's early microbes began harvesting energy from the sun through photosynthesis, however, and eventually became capable of splitting water molecules, which released oxygen as a by-product. Bubble by bubble, these tiny organisms began gradually filling the atmosphere with oxygen. By approximately 650 million years ago, the atmosphere contained enough oxygen to sustain complex, multicellular life as we know it today.

Although those larger life forms tend to attract the most attention, microbes are by far the most abundant and diverse form of life and have remained the engine behind all life on Earth, maintaining the atmospheric and chemical conditions necessary for the survival of all larger life forms. In fact, all multicellular forms of life are themselves inhabited by microbes. These tiny beings make our world habitable; human beings are but guests in their universe.

Humans are inextricably linked with the microbial communities that surround and support us. Many basic bodily processes depend on the trillions of microbes that colonize the



*What we can learn from the microbes that sustain our planet and our bodies stretches the limits of imagination.*



human body beginning shortly after birth. The vast majority of the microbes that live in our bodies are not harmful—many, in fact, provide such essential functions as helping us digest food, break down toxins, and fight off other, disease-causing microbes.

What we can learn from the microbes that sustain our planet and our bodies stretches the limits of imagination. New scientific advances have enabled the scientific community to uncover even further the possibilities that lie within microbial communities. This booklet describes *metagenomics*, an emerging field that will revolutionize our understanding of the microbial world and could lead to practical applications in areas including medicine, energy, agriculture, biotechnology, and many others.

# WINDOW TO THE MICROBIAL UNIVERSE: THE NEW SCIENCE OF METAGENOMICS

When Antony van Leeuwenhoek peered into his primitive 17th-century microscope and discovered the single-celled organisms now called microbes, he sparked a wave of scientific exploration of the infinitely complex microbial world that would inspire scientists for hundreds of years to come. Over the centuries, scientists engaged in the study of microscopic organisms—called *microbiology*—devised ever more powerful ways of observing and understanding microbes. The new science of metagenomics represents a quantum leap forward in microbiology analogous to the revolutionary new view offered by that first microscope, and it provides new insights into a previously inaccessible living universe.

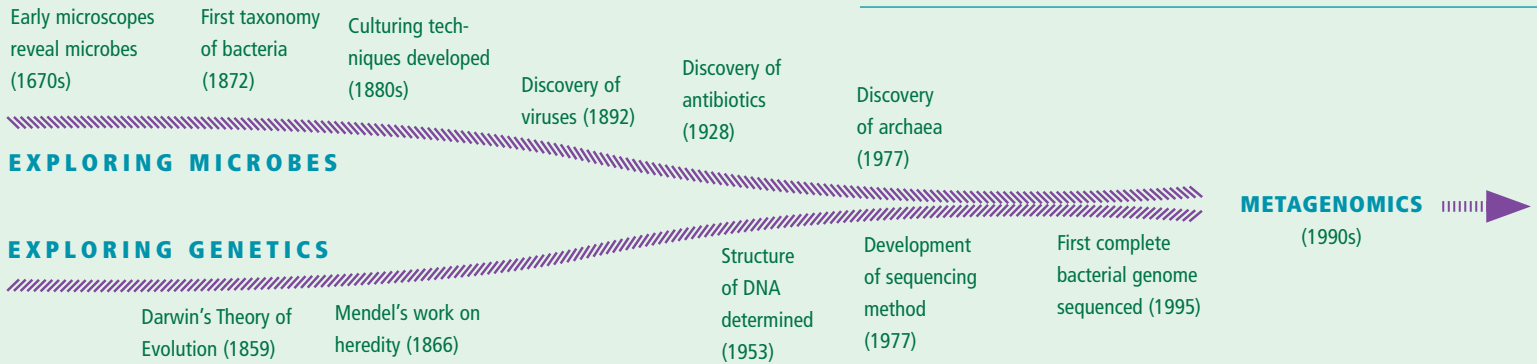
## WHAT IS METAGENOMICS?

Metagenomics is an emerging field in which the power of genomic analysis (the analysis of all the DNA in an organism) is applied to entire communities of microbes, bypassing the need to isolate and culture individual microbial species. In Greek, *meta* means “transcendent.” In its approach and methods, metagenomics transcends individual genes and genomes, enabling scientists to study all of the genomes in a community as a whole.

The tools of classical genomics and microbiology largely rely on isolating individual microbial species in pure cultures—that is, cultures containing only microbes of a particular



## NOTABLE MOMENTS IN MICROBIOLOGY



Since the discovery of microbial cells in the 17th century, scientific advancements have opened many new windows to the microbial world. Culturing microbes in the laboratory enabled scientists to explore a limited number of microbial species, and microbiology has enabled major medical advances such as the development of vaccines and antibiotics. Scientists began to understand DNA and the genetic mechanisms that drive living beings

and evolution, and the field of genomics, which emerged in the 1980s and '90s, enabled scientists to identify all of the genes in an organism and to study those genes either as an entire system or as isolated parts. The new field of metagenomics draws from and transcends the advances that have been made in microbiology, genomics, and other fields, opening up a multitude of new ways to explore the microbial world.

species. This means that the vast majority of the microbial world has been inaccessible to science because merely a minuscule fraction—most scientists estimate less than 1%—of the estimated millions of microbial species on Earth can be cultured. By allowing scientists to access a community's genome without relying on pure cultures, metagenomics transcends the limitations of classical genomics and microbiology.

Of course, metagenomics does not displace the need to study the genetic makeup of individual species or small groups of microbes using the techniques of classical genomics and microbiology. However, in the coming decades, the approaches of metagenomics will likely merge with the approaches of those classical branches of science, greatly increasing the potency of our understanding of the microbial world.

*Metagenomics transcends individual genes and genomes, enabling scientists to study the entire genetic makeup of a community as a whole. It is the science of microbial communities.*



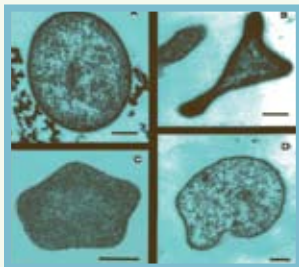
## HOW DOES METAGENOMICS WORK?

Metagenomics includes a wide variety of novel techniques and approaches, and it is likely that other new methods will arise as the field progresses. Currently, many metagenomics studies take the same first step: Researchers retrieve a sample from a particular environment (such as soil, seawater, or the human mouth) and do a mass extraction of the DNA from all the microbes in the sample. Increasingly, scientists are also extracting protein or RNA from the microbes in a sample. Most metagenomics projects currently focus on the microbes found in the sampled environment that have smaller amounts of DNA, such as bacteria and microbes known as archaea, which were identified as a major division of organisms in 1977 and can live in extreme environments like deep sea vents, as well as a variety of other habitats (see box 1).

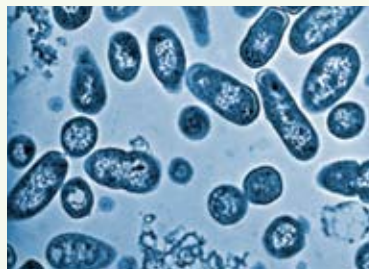
Typically, once the DNA is extracted from a sample, laboratory bacteria are induced to take up and replicate the DNA, thus creating a “library” that contains pieces of the genomes of all the microbes in the sample. (New sequencing technologies, however, facilitate sequencing DNA directly from a sample, which streamlines the process by bypassing the creation of a library.) A metagenomic library is not organized into neat volumes, however, each containing the genome of one species; instead, this library consists of millions of random fragments of DNA from all the microbes in the sampled community.

**BOX 1.** *Microbes* are living organisms too small to see—generally smaller than about 0.2 mm. The term includes Bacteria, Archaea, viruses, and small Eukaryotes. Currently, most metagenomics projects exclude eukaryotes

because their genomes contain so much DNA that their genes would overwhelm a metagenomic analysis, but eukaryotes will likely be included in the future as the field develops new techniques.



Archaea. (Image from NOAA)



Bacteria. (Image from Pacific Northwest National Laboratory)



Eukaryote. (Image from Nils Kroeger, Georgia Institute of Technology)

## THE METAGENOMICS PROCESS



Extract all DNA from  
microbial community in  
sampled environment

### DETERMINE WHAT THE GENES ARE (Sequence-based metagenomics)

- Identify genes and metabolic pathways
- Compare to other communities
- and more...

### DETERMINE WHAT THE GENES DO (Function-based metagenomics)

- Screen to identify functions of interest, such as vitamin or antibiotic production
- Find the genes that code for functions of interest
- and more...

What scientists do with a library of genomes, or *metagenome*, depends on what they want to find out. In **sequence-based metagenomics**, researchers focus on finding the entire *genetic sequence*—the pattern of the four different nucleotide bases (A, C, G, and T) in the DNA strands—found in a sample. The sequence can then be analyzed in many different ways. For example, researchers can use a community's sequence to determine the complete genome of an individual microbial species. Or, researchers might use the sequence to analyze the genome of the community as a whole, which can offer insights about population ecology and evolution.

**Function-based metagenomics** explores the products that microbes in a community can produce. In function-based metagenomics, researchers screen metagenomic libraries for various functions, such as vitamin or antibiotic production. Through this method, scientists can identify functions that are unknown in the limited number of microbes that can be grown in a laboratory. New antibiotics have already been discovered using this approach. Another approach to function-based metagenomics, made possible by recent technological advances, enables scientists to directly extract and identify novel proteins and metabolites (the products of cellular processes) from a microbial community.

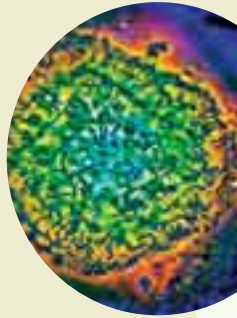


# APPLICATIONS: WHAT METAGENOMICS CAN DO

**T**he possibilities this new field offers are mind-boggling. Deciphering the enormous array of processes and interactions that characterize microbial communities on Earth can lead to advances in human health, improved understanding of large-scale climatic and atmospheric changes, methods for growing stronger and more nutritious crops, new approaches to cleaning up environmental contamination, and new sources of renewable energy. These are just a few examples of the many potential practical applications of metagenomics.

## THE WORLD WITHIN: LEARNING FROM THE MICROBIAL INHABITANTS OF THE HUMAN BODY

Humans always lived in a world dominated by microbes, and close relationships between microbes and humans are an ancient theme. The microbes that reside on and in the adult human body outnumber human cells by an estimated tenfold. (Nevertheless, human cells still make up the bulk of our weight because resident microbes are much smaller than human cells and collectively weigh only about two pounds.) The genomes of the microbial communities living on and within the human body (the *human microbiome*) contain many more genes than the human genome. Studying the human microbiome may lead to valuable new tools and guidelines in human and animal nutrition, drug discovery, and preventative medicine. Such study may also greatly expand the depth of our understanding of complex diseases including obesity, cancer, and certain immune disorders, such as asthma.



Bacteria in human saliva. Trillions of bacteria make up the normal microbial community found in and on the human body. (Image from Michael Abbey)

## GUT MICROBES AND OBESITY

Metagenomics studies can help researchers learn about common diseases like obesity. Recently, metagenomics was used to compare the genes in the microbial communities in the guts of obese mice with their leaner relatives. The results suggested that obesity is associated with a shift in the proportions of the two major groups of gut bacteria. When researchers transplanted gut microbial communities harvested from both obese and lean animals into lean germ-free mice, those that received gut microbes from the obese mice gained more fat. The take home lesson: the caloric value of the food we eat may vary depending upon the composition of a person's gut microbes. Differences in our gut microbial communities may be one of many factors that affect predisposition to obesity.



*Bacteria are nature's master chemists; a nearly endless variety of powerful compounds can be derived from microbial communities.*

The vast majority of our microbial partners live in the intestine. These 10 to 100 trillion microorganisms perform functions such as extracting nutrients and calories from otherwise indigestible components of our diets and making essential vitamins and amino acids. Some gut bacteria also help detoxify potentially harmful chemicals contained in what we eat. Some of the microbes living in and on the human body play a critical role in defending us against pathogens. This mutually beneficial relationship helps protect us from getting diseases while giving the microbes a place to live. Using metagenomics to gain a deeper understanding of the microbial communities in and on the human body could be immensely valuable in our understanding of both beneficial and harmful microbes and may lead to more effective ways to diagnose, treat, and possibly prevent disease.

The microbial world also offers a stunning array of biologically-active chemicals that bacteria have evolved through communicating with and competing against each other over billions of years. Bacteria are nature's master chemists; a nearly endless variety of powerful compounds can be derived from microbial communities. Hundreds of drugs available today were derived from compounds scientists originally found in microbes. Using metagenomics to study microbial communities may help us identify many more new compounds that will promote the health of humans, animals, and plants throughout the 21st century.





## GLOBAL IMPACTS: THE ROLE OF MICROBES IN MAINTAINING ATMOSPHERIC BALANCES

It may seem surprising to learn that bacteria are responsible for about half the photosynthesis on Earth. Most photosynthetic bacteria can be found freely swimming in the oceans that cover 70% of the Earth's surface. These bacteria affect key chemical balances in the Earth's atmosphere and play a crucial role in maintaining the habitability of the entire planet.

One of the most important ways photosynthetic bacteria affect life on Earth is through their role in the global carbon cycle. Carbon is the most abundant element in living things, including humans (excluding the hydrogen and oxygen in the water that makes up the bulk of our weight). However, most of the carbon on Earth is in the form of carbon dioxide ( $\text{CO}_2$ ), which cannot be used by animals and most bacteria. Through photosynthesis, plants and certain bacteria “fix” carbon from the atmosphere, turning it into a form that is useable to many more life forms (and releasing oxygen). Through the process of fixing carbon, photosynthetic bacteria remove  $\text{CO}_2$ —which is a major greenhouse gas—from the atmosphere. In this way, photosynthetic bacteria mitigate some of the effects of the release of  $\text{CO}_2$  and other greenhouse gases from human activities that most scientists believe is responsible for global warming.

To achieve complex chemical transformations, no single microbe can do it alone; it takes a community. Many microbial communities, including those involved in the generation and consumption of greenhouse gases, function through a “bucket brigade” system, in which each microbe performs its own individual task, with its end product becoming the starting fuel for its neighbor. Through metagenomics, scientists can examine the genetic bases behind these complex bucket brigades and explore how genes from various organisms influence each other's activities.

*To achieve complex chemical transformations, no single microbe can do it alone; it takes a community.*



Photosynthetic bacteria living in the sea have a major impact on the Earth's atmospheric balances. (Image from NASA)

Metagenomics can help scientists gain insights into the mechanisms behind changes of energy and matter in the sea, the composition of Earth's atmosphere, and global climate.

## BIOENERGY: HARNESSING MICROBIAL POWER

There is a growing awareness that the world's reliance on energy from nonrenewable fossil fuels is not sustainable. It is projected that U.S. energy demand will increase by more than

*The process that converts the cellulose from agricultural waste into usable ethanol (grain alcohol) depends on one essential ingredient: microbial communities.*

50% by 2025, and our dependence on fossil fuels puts us at risk of disturbances in energy supply due to changing political climates and international relations. Additionally, the greenhouse gas emissions that result from burning fossil fuels are widely believed to be a primary cause of global warming. All of these factors

make finding renewable, environmentally friendly fuels a major priority for America—and the world.

One emerging energy source is ethanol (grain alcohol)—a high-octane biofuel derived from corn, sugarcane, or other agricultural sources. *Cellulosic ethanol* is made from the cellulose found in such common agricultural wastes as corn fiber, corn stalks, wheat straw, and other biomass like switchgrass and miscanthus. But the process that converts the cellulose from agricultural waste into usable ethanol depends on one essential ingredient: microbial communities. First, several types of microorganisms must work in concert to transform the cellulose from agricultural wastes into sugars. Then, the sugars are fermented—also by microbes—to produce ethanol.





Still other microbes produce a variety of potential energy sources including hydrogen, methane, butanol, and even electric current. By carefully manipulating the availability of nutrients and other environmental conditions, scientists are working to develop ways to capture and store the useful by-products of such microbes. But much more needs to be known about how these microbial communities function before we can control and channel the energy sources they produce. Metagenomics offers an important means of achieving this knowledge and should be considered a part of America's strategic approach to addressing present and future needs for renewable energy sources.

## SMART FARMING: HOW MICROBES HELP OUR CROPS

One of the most valuable but least understood mysteries of farming is the "suppressive soil" phenomenon. In suppressive soils, plants stay healthy even when disease-causing organisms are present in high densities. If this soil is sterilized, killing helpful and harmful microbes alike, plants can become sick and die once the pathogens find their way back into the soil. Scientists speculate that microbes living in the suppressive soil actually protect plants from diseases—and if these microbes disappear, plants are far more susceptible to infection. Despite decades of research, scientists have only been able to pinpoint the microbes responsible for suppressing disease in a few locations. Scientists believe that a complex microbial community is responsible for suppressing disease, because no single microbial species can do it alone. The activities of suppressive soil communities are enormously beneficial to agriculture.

The microbial communities on and around plants are also critical to manufacturing the nutrients that plants need in order to grow. Certain bacteria convert atmospheric nitrogen into ammonia, a form that is readily usable by plants and animals. Other soil microbes recycle nutrients from decaying plants and animals, while still others convert elements, such as iron and manganese, to forms that can be used for plant nutrition. Once again, it takes a community to perform these critical biotransformations. For example, no one microbe is capable of converting ammonia to nitrate, yet teams of microbes do this very efficiently.



Starter microbes are added to a bioreactor to convert agricultural material into ethanol. (Image from USDA; photo by Keith Weller)



Complex microbial communities living in soil provide essential nutrients and help protect plants from diseases.



Metagenomics can facilitate the development of farming practices that take advantage of the natural alliances among microbes and plants and animals. (Image from James Tiedje)

While scientists have been able to glimpse the complex microbial communities that help keep crops healthy and productive, much about those communities remains mysterious. Metagenomics offers a unique opportunity to explore how microbial communities interact with crops and may eventually lead to ways to harness the power of soil microbial communities to produce healthier and more robust crops.

## CLEANING UP: REMEDIATION OF ENVIRONMENTAL CONTAMINATION

Microbial communities are crucial participants in cleaning up an astounding variety of both natural and human-made hazardous substances; they transform potentially deadly chemicals into forms that are benign both to people and to the environment. Some microbes consume methane gas—a major greenhouse gas—which seeps from landfills and swamps. Other microbes degrade the waste in sewage water at water treatment facilities. Communities of marine bacteria, similar to the soil microbes that degrade gasoline leaks on land, can help clean up oil spills in the Earth's oceans.

While we know that microbial communities are immensely useful in degrading waste and hazardous spills, our understanding of the processes involved—and how to channel

*Microbial communities transform many potentially deadly chemicals into forms that are benign both to people and to the environment.*



those processes to manage the fast-growing array of chemicals humans put into the environment—is as yet limited. Metagenomic analysis may help us identify the particular community members and functions needed to achieve the full chemical transformations that will keep our planet livable.

Marine microbes can help to degrade hazardous oil spills in the ocean. (Image from NOAA HAZMAT)



## KEEPING GROUNDWATER DRINKABLE

Just about every gas station in the United States has three or more underground storage tanks from which it dispenses gasoline. The sad truth about these tanks is that many of them are either currently leaking or will leak at some time in the future, releasing gasoline into the soil, where it has the potential to contaminate groundwater. Given the ubiquity and magnitude of the gasoline leaks—coupled with the fact that 50% of the U.S. population relies on groundwater as a source of drinking water—one must wonder how we are not all drinking water contaminated with gasoline!

The answer is that we are often protected by the vastly adaptable microbial community found in the soil. As gasoline is released into the ground, relatively dormant members of the soil microbial community are triggered to become active and degrade the harmful chemicals in gasoline. Because gasoline is composed of hundreds of chemicals, it takes a variety of microbes working together to degrade them all. For example, when some types of bacteria cause a depletion of oxygen in the groundwater near a gasoline spill, other types of bacteria that can use nitrate for energy begin biodegrading the gasoline. Bacteria that use iron, manganese, and sulfate follow. These community members work together in a pattern triggered by the movement of the leaking gasoline until the contaminants have been transformed into harmless carbon dioxide and water.

Microbes can break down gasoline leaking from underground storage tanks at gas stations.



# GETTING THE MOST OUT OF NEW SCIENTIFIC ADVANCES

Making full use of the powerful new tools provided by metagenomics and other new scientific advances is not without its challenges. The 2007 National Research Council report *The New Science of Metagenomics: Revealing the Secrets of Our Microbial Planet* addresses the challenges and opportunities metagenomics holds for the future of microbiology. The report describes a number of technological, methodological, and computational advances that are needed before metagenomics can reach its full potential.

**CHALLENGES TO METAGENOMICS METHODS.** There is an enormous amount of work to be done establishing the foundations, defining standard practices, and building the framework to support the field. Many stages of a metagenomics project remain challenging:

- Getting a good sample from an environment is an essential, but difficult, step. Scientists must determine the best way to sample an environment, how many times samples should be taken, and whether a sample is representative of the environment.
- Better DNA extraction techniques are needed. Detecting the rare members of a microbial community is a challenge, but it can be very important if a small number of microbes play a critical role in the community. Improved DNA extraction techniques could help ensure that a metagenomic library adequately represents the entire community's genome and has little or no contamination.
- Extending the analyses beyond the DNA sequence to study the proteins and metabolites (the products of cellular processes) generated by a community will be critical for understanding how a given microbial community operates and interacts with its habitat.



**DATA MANAGEMENT AND BIOINFORMATICS NEEDS.** Metagenomics projects generate enormous amounts of data, and effective data management systems will be essential for advancing the field. New databases with the following characteristics are needed:

- Data generated from metagenomics projects should be stored in databases that are freely accessible to all.
- Metagenomics databases should use common standards. Not only sequence data but also information on sampling methods, sample treatments, and sampled habitats should be recorded.
- Databases should include specialized tools that enable different scientists to analyze the data in different ways. This will ensure that data stored in the databases will be of increasing, rather than diminishing, value as technology advances.



**ORGANIZATIONAL AND INSTITUTIONAL FRAMEWORKS.** Metagenomics will benefit from the involvement of experts from a broad range of fields; included among these should be chemistry, genetics, microbiology, biochemistry, pathology, ecology, evolution, soil and atmospheric sciences, geology, oceanography, statistics, computer sciences, database development, mathematics, engineering, and others. Universities will need to rapidly evolve their educational, administrative, and mentoring structures to facilitate interdisciplinary collaboration to help metagenomics reach its full potential.

Because of the broad scope of metagenomics, this new field is of potential value in fulfilling the missions of several federal agencies, including the National Science Foundation, the National Institutes of Health, the Department of Energy, state agencies, and others.

Communication and coordination across the relevant agencies would be extremely useful in advancing the field.

**ESTABLISHING A "GLOBAL METAGENOMICS INITIATIVE."** *The New Science of Metagenomics: Revealing the Secrets of Our Microbial Planet* recommends that a Global Metagenomics Initiative be established in the United States that would include a small number of large-scale, comprehensive projects, a larger number of medium-sized projects, and many small-scale projects.

- Large-scale projects will each explore a microbial community in great depth, analyzing a habitat with attention to potential for discovery, variation, commonalities, and detailed investigation. Possible candidate communities include:
  - a community in a natural environment (such as seawater or soil),
  - a host-associated community (such as the microbes in the human gut or mouth), and
  - a "managed" environment community (such as a sewage treatment facility or bioremediation site).



- Medium-sized projects will encompass the greater diversity of microbial habitat types. Such projects should include a multidisciplinary approach to the study of microbial communities.
- Small-scale projects will be initiated by individual scientists to examine a slice of a community, a particular function in multiple communities, or a specific technical advance.

# SUMMARY

**H**umans might conceivably survive in a world lacking other large life forms, but without microbes all complex plants and animals—including ourselves—would likely die. It is microbes that convert key elements of life—such as carbon, nitrogen, and sulfur—into forms accessible to all other living things. Traditional microbiological approaches have already shown how useful microbes can be; the new approach of metagenomics will greatly expand our ability to discover and benefit from the incredible capabilities of the microbial world.

Metagenomics provides a new lens for viewing the microbial world that has the potential to revolutionize understanding of the entire living world. In metagenomics, the power of genomic analysis is applied to entire communities of microbes, bypassing the need to isolate and culture individual microbial species. This new approach will bring to light the many abilities of the microbial communities that drive Earth's energy and nutrient cycles and support the health of its inhabitants. Metagenomics will vastly enhance our knowledge of microbial communities and can lead to major advancements in many areas, including human health, agriculture, energy production, and environmental remediation.

---

*Without microbes all complex plants and animals—  
including ourselves—would likely die.*

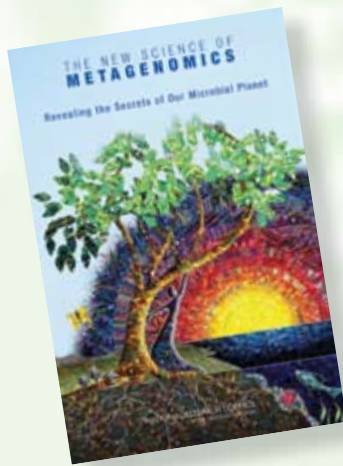
---





## ABOUT THE NATIONAL ACADEMIES

The National Academies—the National Academy of Sciences, National Academy of Engineering, Institute of Medicine, and the National Research Council—provide a public service by working outside the framework of government to ensure independent advice on matters of science, technology, and medicine. They enlist committees of the nation's top scientists, engineers, and other experts—all of whom volunteer their time to study specific concerns. The results of these deliberations are authoritative, peer-reviewed reports that have inspired some of the nation's most significant efforts to improve the health, education, and welfare of the population.



This booklet was derived from the National Research Council report *The New Science of Metagenomics: Revealing the Secrets of Our Microbial Planet* (2007) by the Committee on Metagenomics: Challenges and Functional Applications. [http://books.nap.edu/catalog.php?record\\_id=11902](http://books.nap.edu/catalog.php?record_id=11902)

## COMMITTEE ON METAGENOMICS: CHALLENGES AND FUNCTIONAL APPLICATIONS

**Jo Handelsman** (Co-chair), University of Wisconsin-Madison; **James M. Tiedje** (Co-chair), Michigan State University; **Lisa Alvarez-Cohen**, University of California, Berkeley; **Michael Ashburner**, University of Cambridge; **Isaac K. O. Cann**, University of Illinois, Urbana-Champaign; **Edward F. DeLong**, Massachusetts Institute of Technology; **W. Ford Doolittle**, Dalhousie University; **Claire M. Fraser-Liggett**, The Institute for Genomic Research; **Adam Godzik**, The Burnham Institute; **Jeffrey I. Gordon**, Washington University School of Medicine; **Margaret Riley**, University of Massachusetts, Amherst; **Molly B. Schmid**, Keck Graduate Institute; **Ann H. Reid** (Study Director), National Research Council.


Reports from the National Academies are available from the National Academies Press, 500 Fifth Street, NW, Washington, DC 20001; 800-624-6242; <http://www.nap.edu>. Reports are available online in a fully searchable format.

This booklet and related materials are available at <http://dels.nas.edu/metagenomics>.

This publication was written by Anne Jurkowski and Ann Reid and was designed by Van Nguyen. Cover art by Nicolle Rager Fuller ([www.sayo-art.com](http://www.sayo-art.com)); page 3 watermark image from U.S. Department of Energy; page 17 photo by Jeff Miller, University of Wisconsin-Madison.

Copyright 2007 by the National Academy of Sciences. All rights reserved.





**H**umankind has benefited enormously from the study of microbes since their discovery in the 17th century. However, such benefits have come from the study of just a miniscule fraction of the millions of species of microbes in the environment. In addition, scientists are realizing the importance of studying the collective properties of communities of microbes, which perform complex tasks essential to the health of human beings and our planet. The emerging field of metagenomics opens the door to exploring the vast array of microbes unstudied to date and to investigating entire microbial communities. Through a deeper understanding of the microbes that sustain life on Earth, the metagenomics approach offers the promise of an incredible array of new benefits.

## **THE NATIONAL ACADEMIES**

*Advisers to the Nation on Science, Engineering, and Medicine*

The nation turns to the National Academies—National Academy of Sciences, National Academy of Engineering, Institute of Medicine, and National Research Council for independent, objective advice on issues that affect people's lives worldwide.

[www.national-academies.org](http://www.national-academies.org)