A social–ecological framework for "micromanaging" microbial services

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Despite playing a central role in the regulation of ecosystem services, microorganisms are often neglected when evaluating feedbacks between social and ecological systems. A social–ecological framework is a tool for evaluating how social factors affect ecosystems through human actions and how ecological factors in turn affect social systems through ecosystem services. Here, we consider linkages and trade-offs between social and biophysical factors that arise when unique microbial attributes such as complexity, dispersal, and rapid evolution are integrated into a social–ecological framework. Using case studies from food production systems, wastewater treatment facilities, and synthetic biology, we show that unintended dis-services can arise when microbial information is limited or is ignored as a result of socioeconomic policies and practices. In contrast, when knowledge about microorganisms is integrated into a social–ecological framework, we can identify how to best maximize microbial services. New scientific tools used to characterize microbial traits, communities, and functions will enhance our ability to monitor microorganisms in diverse systems. However, communication and collaboration among stakeholders – including policy makers, landowners, resource managers, and scientists – are also needed to foster more effective "micromanagement" of microbial services.

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Environmental problems are intensifying and threatening biodiversity and sustainability worldwide. Scientific understanding is a necessary step toward addressing these problems, but natural science alone is insufficient for achieving desired outcomes that benefit humans and the environment. Human behavior strongly influences ecological and social outcomes; individual decisions and institutional systems affect how environmental problems are addressed. These social–ecological outcomes can relate to monetary (eg economic growth, human health) or non-monetary (eg human well-being, improved water quality) values. Social–ecological frameworks represent a promising approach for addressing the human dimension of environmental problems. Specifically, a social–ecological framework is a conceptual model used to examine complex interactions between people and ecological entities and processes. Social–ecological frameworks identify how social factors influence biodiversity, community structure, and ecosystem processes, as well as how ecological change affects social systems through ecosystem services (Figure 1). There is growing appreciation that the integration of social and natural sciences is essential for understanding environmental issues and managing ecosystem services (Grimm *et al.* 2000; Collins *et al.* 2011). To date, this approach has focused almost exclusively on macro-organisms (plants and animals). We argue that a social–ecological framework is also critical for managing microorganisms, including bacteria, fungi, archaea, and viruses.

In a nutshell:

- Social–ecological frameworks are effective for identifying complex relationships, exploring management options, and overcoming barriers toward meeting social and ecological goals
- Microorganisms are rarely considered in social–ecological frameworks, despite their important roles in human health, food production, and many other ecosystem services
- Microorganisms are small, are genetically and functionally diverse, and can rapidly evolve; these distinctive microbial features must be considered within social–ecological frameworks
- New techniques in microbiology can serve as social–ecological indicators for "next-generation" microbial management
- Implementing policies to support desired microbial services will enhance our ability to mitigate some of society's most pressing environmental concerns

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Integrating microbes into social–ecological frameworks

Although responsible for delivering a suite of ecosystem services and dis-services, microorganisms have not been adequately incorporated into social–ecological frameworks. Microorganisms are responsible for disease outbreaks that have shaped the course of human history through their negative impacts on humans, non-human animals, and crops. These "germs" may be the best-known microbial taxa. Despite justifiable public-health concerns about microbial pathogens, there are only

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slightly more than 1000 microbial taxa that are recognized as human pathogens (Taylor *et al.* 2001), a number that pales in comparison to the estimated ~1 × 10^4 microbial taxa that are typically found in a single gram of soil (Fierer and Lennon 2011). Non-pathogenic microorganisms provide services that are not only vital for human well-being but also costly when we are forced to rely on substitutes. For example, soil microorganisms are critical for food production, water purification, and nutrient cycling. Globally, the services generated from soil biota have been valued at $1.5–13 trillion per year (adjusted to 2014 markets: $1.9–16 trillion; van der Putten *et al.* 2004). Understanding the role of microorganisms in a community context shifts the focus from accounting for one "bad" microbe at a time to considering how microbial communities interact to maintain human and environmental health.

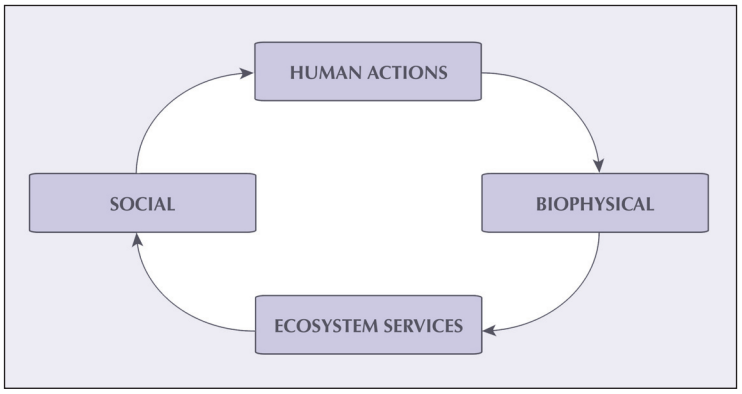

Figure 1. *Social–ecological framework relating social and biophysical templates through ecosystem services (modified from Collins* et al. *2011).*

Microorganisms possess distinctive properties that influence the management of microbial functions over broad spatial and temporal scales (Panel 1). For instance, many microbial taxa have the ability to reproduce quickly, disperse long distances, and persist in the environment for extended periods of time. In addition, as compared with other organisms, microorganisms are genetically, functionally, and physiologically diverse and thrive in a wide range of environments (Panel 1). Finally, they can evolve rapidly because of their large population sizes, fast growth rates, and capacity to exchange genes with distantly related individuals. Because of these attributes, microbes can influence social–ecological processes in unexpected ways that are not accounted for in existing models.

While managing microorganisms remains largely unexplored, advances in microbiology have improved our ability to effectively monitor and manage microbial communities associated with the human body, indoor spaces, agricultural habitats, and natural ecosystems (Panel 2). To do so, however, we need to monitor microbial traits that are informative, easy to measure, and responsive to human manipulation (Panel 2). New methods to characterize microorganisms, including isotopic analyses, advanced microscopy, high throughput sequencing, and other "omics" approaches, provide opportunities for integrating novel information about microorganisms into social–ecological frameworks (Panel 2). Examples of microbial traits to monitor include their ability to disperse long distances, initiate dormancy in response to stressful environmental conditions, and acquire resistance to a variety of antibiotics (Panel 2). Monitoring specific microbial populations and their ecological and

Panel 1. Unique features of microbes important for management

While applying a social–ecological framework can help us to better understand relationships between society and microorganisms, it is critical to give special attention to the scale, complexity, and evolutionary potential of microorganisms.

Scale. Both spatial and temporal scales need to be considered when managing microbes. The home range of microorganisms is difficult to measure and define but is shaped by a species' niche and its dispersal ability. It is generally assumed that microbes have the capacity to move long distances via passive dispersal (eg wind) or through associations with hosts. Nevertheless, humans have the ability to break down dispersal barriers of microorganisms, which can lead to "invisible invasions" (Litchman 2010). Microbial processes also have the potential to span large temporal scales. Owing to their rapid growth rates, it is assumed that microbial communities are "responsive" and have the capacity to recover rapidly from perturbations. However, many populations are slow-growing or dormant (Lennon and Jones 2011), which sets the stage for historical legacies associated with prior land-use or environmental impacts.

Complexity. Microbial communities are often hyper-diverse and are composed of interacting species that carry out interdependent processes. Therefore, when managing microbes, the focus cannot be on a single microbial species. Many microorganisms live in cooperative, multi-species consortia. As such, perturbations that affect one species will often have cascading effects on the metabolism of other species, along with the functioning and stability of the aggregate community. These types of interactions can lead to trade-offs between desirable services such as nutrient removal and undesirable microbial functions such as nutrient release.

Rapid evolution. Rarely considered in a social–ecological framework, evolution represents a major source of uncertainty when managing microorganisms. Due to their large population sizes and rapid growth rates, microorganisms have the capacity to evolve on social–ecological timescales. In addition, they can acquire new traits (eg virulence and antibiotic resistance) from distantly related species via lateral gene transfer. This makes it possible to synthetically modify microbes to enhance desired microbial functions; however, it can also lead to unexpected movement of traits that are economically or ecologically "undesirable". Although rapid evolution may be perceived as a potential risk or challenge for management, especially in agricultural and industrial contexts, it may be harnessed to improve microbial services (greater plant yields supported by nitrogen-fixing bacteria) and diminish negative impacts (reduced nutrient pollution).

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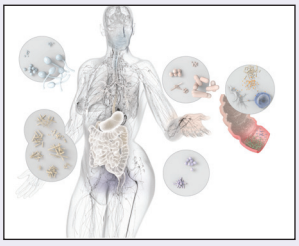
Panel 2. "Micromanaging" at a glance: microorganisms are being managed for desired social–ecological outcomes in various systems

Social–ecological scenario	*Example image*	*Role of microbial process*	*Microbial indicators*
(a) Built environment – Given that humans spend ~90% of their lives indoors, researchers are trying to manage microorganisms in these "ecosystems" through building design and air-handling systems (Kembel *et al.* 2012).	D O'Dell	More diverse microbial communities from outdoor air can reduce populations of human-dominated and potentially pathogenic microbial populations in indoor spaces.	• Composition and identity of human-dominated microbes and environmentally associated microbes • Microbial traits to be considered: capacity for dispersal, dormancy, and pathogenicity
(b) Human microbiome – The human gut microbiome is composed of microorganisms that carry out functions responsible for health and nutrition (Turnbaugh *et al.* 2009).	 © B Christie Design	The diversity of the gut microbiome is related to a range of metabolic processes that influence not only nutrition but also host immune responses (Kau *et al.* 2011).	• Community composition of the gut microbial community in human subjects with defined differences in physiological states (eg obesity, leanness measured using body mass index) • Microbial trait to be considered: indicator taxa (Mariat *et al.* 2009) with the capacity to extract energy from complex polysaccharides
(c) Hazardous waste sites – Hydrocarbon-degrading bacteria can substantially reduce petroleum concentrations in polluted marine waters (Yakimov *et al.* 2007).	© J Kurtz/ZUMA Press/Corbis	The management of oil-degrading bacteria can provide efficient, cost-saving pollution mitigation strategies.	• Abundance of oil-degrading bacteria • Shotgun metagenomic sequencing of environmental samples to assess potential for contaminant-degrading genes • Microbial trait to be considered: capacity to metabolize complex carbon needed for oil degradation
(d) Restored wetlands – Wetland restoration can ameliorate the negative impacts of nutrient runoff on water quality in agricultural landscapes.	M Ardón	Specialized groups of microorganisms (eg denitrifiers) are capable of diminishing the concentration of nutrients (eg NO_3^-) in the environment that lead to eutrophication of surface waters (Peralta *et al.* 2010).	• Abundance, composition, and structure of key microbial functional groups involved in nutrient mitigation • Microbial trait to be considered: capacity of microbial communities to process nutrients under various redox states
(e) Industrial cattle production – Antibiotics are commonly used in livestock production to treat illness, for prophylaxis and prevention of disease, and to increase animal growth rates.	K Steensma	Manipulating industrial livestock production and confined animal feeding operations for less reliance on antibiotic use would decrease the spread of antibiotic resistance genes and antibiotic-resistant pathogenic microbes in the environment (Gillings and Stokes 2012).	• Quantification of known antibiotic resistance genes • Microbial trait to be considered: capacity for antibiotic resistance and pathogenicity

evolutionary potential can lead to more effective management of microbial services.

Using a social–ecological framework to manage microbial services

Here, we develop an expanded social–ecological framework for managing microorganisms with the goal of maximizing desired social and ecological outcomes such as human health, economic growth, recreation, aesthetics, improved water quality, increased carbon storage, reduced greenhouse-gas emissions, and contaminant degradation (Figure 2). The framework explicitly connects social factors such as scientific knowledge, cultural values, and economic markets with environmental factors that can influence the structure and function of microbial communities. The direct link between human behavior and microbial communities is key to "micromanaging" for desired social and biophysical outcomes (Figure 2). Through their behaviors, humans manipulate the surrounding environment via changes in biophysical factors, which we define as abiotic and biotic variables that influence ecosystem structure and function. Changes in biophysical factors due to human actions (eg management) can directly influence microbial ecology and evolution. For example, land-use conversion from agriculture to restored wetlands causes shifts in the microbial community composition, which alter rates of microbial processes that affect nutrient cycling in the environment (Peralta *et al.* 2010). In turn, biophysical outcomes can affect social outcomes through ecosystem services and dis-services (Collins *et al.* 2011). For instance, incorporating

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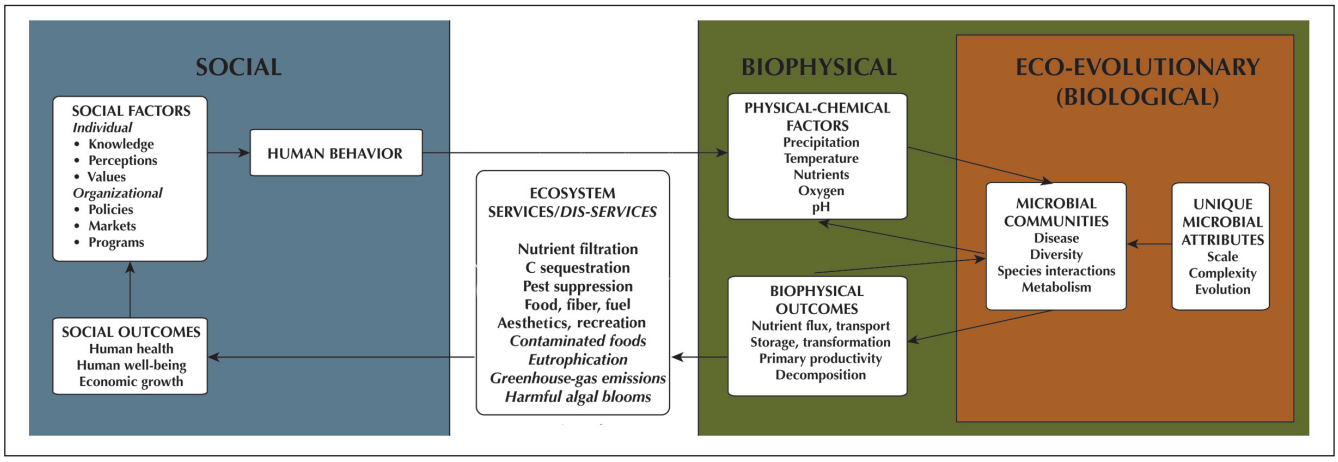

Figure 2. *Integration of microorganisms into a social–ecological framework while considering unique microbial properties. We use this framework to investigate relationships between social, biophysical, and eco-evolutionary microbial processes through ecosystem services and dis-services.*

stormwater structures and planting wetland vegetation can partially restore lost flood-control services in flood-prone residential areas. Our proposed framework can be used to identify how microorganisms respond to changes in environmental conditions affected by human behaviors. The management of microorganisms can result in desirable and undesirable impacts on human health and well-being, as well as on economic growth. A social–ecological framework can be used to better understand human–microbial relationships and to guide adaptive management of these complex systems. In the following section, we use case studies to explore how a social–ecological framework (Figure 2) can be applied to better understand our relationships with microbes, how to avoid microbial dis-services, and how to harness microbial processes to enhance ecosystem services.

Food production and human health

Managing microbes is critical for the maintenance and safety of our food production systems. It is estimated that contamination caused by *Escherichia coli* O157:H7 alone directly causes tens of thousands of food-borne illnesses in the US each year, resulting in economic costs totaling about $400 million, owing to medical expenses, premature deaths, and reductions in worker productivity (Frenzen *et al.* 2005). We may be able to reduce these negative impacts and costs to society by developing new food-management policies informed by the ecology and evolution of microorganisms.

The impacts and spread of some pathogenic bacteria are attributable to the unique evolutionary potential of microorganisms. Most variants of *E coli* are non-pathogenic to humans and animals. These bacteria are part of the normal mammalian gut community, but some of the management practices used in industrial food production have altered the gut environment and led to the evolution and outbreaks of disease-causing variants, such as *E coli* O157:H7. For example, shifts toward grain-based diets in industrial livestock systems promote faster animal growth; however, this type of diet also decreases the pH in cattle digestive systems, thereby selecting for *E coli* O157:H7, a more acid-resistant strain (Diez-Gonzalez *et al.* 1998). Furthermore, the expression of virulence factors in pathogenic *E coli* can be enhanced in stressful, low pH environments (Chung *et al.* 2006). In sum, the prevalence of pathogenic *E coli* O157:H7 in our food production systems involves evolutionary processes that have been exacerbated by activities aimed at maximizing agricultural production.

A given pathogen's proliferation and impacts in food production systems are also affected by its dispersal ability. Owing to their small size, microbes have the potential to be transported long distances via passive dispersal mechanisms. Nevertheless, some studies have shown that microorganisms are locally adapted and have restricted geographic ranges (Martiny *et al.* 2006). Agricultural management practices can greatly expand the distribution of pathogenic variants during post-harvest processing. Scientists have linked the increasing number of human illnesses from fresh produce to industrial processing (Beuchat 2002), and the majority of illnesses from salad greens have been traced to processed products. Two companies – each using large centralized processing facilities where greens harvested from many locations are mixed, washed, and packaged, thereby relaxing dispersal barriers for microorganisms – control 72% of processed salad production. In these facilities, localized contamination from a single source can affect thousands of bags of salad (Stuart and Worosz 2012). In 2006, *E coli* O157:H7 made media headlines due to an outbreak associated with processed, bagged spinach. The California leafy greens (spinach and lettuce) industry responded by attempting to reduce dispersal of the microbial pathogen by removing potential vectors, including wildlife. Despite evidence that less than 1% of wildlife carry *E coli* O157:H7, the leafy greens industry in California required farmers to use poison bait and traps to eliminate wildlife (Beretti

and Stuart 2008). Deliberate degradation of wildlife habitat (eg removal of vegetation) adjacent to farmland was also encouraged, which increased pollution in regional waterways due to loss of water filtration capacity and related services offered by vegetated riparian buffers (Beretti and Stuart 2008). Removal of wildlife in agricultural areas in California was recognized as one of the top 15 global threats to biodiversity conservation in 2012 (Sutherland *et al.* 2012). Ultimately, the decision to remove wildlife was an unsuccessful management strategy aimed at reducing microbial dispersal capacity, and thus food contamination risk, which resulted in negative ecological outcomes.

New policies and programs based on a better understanding of the relationships between microbes and production systems could reduce the incidence of associated food-related illnesses. Economic factors, including maximization of production per capital investment (machinery and facilities), support high-volume, centralized food production, but these systems will continue to pose challenges for the effective management of microbial services. In spite of evidence that centralized food production systems are more vulnerable to large-scale contamination, there are currently no US Food and Drug Administration regulations that encourage decentralization of processing plants. By integrating a social–ecological framework, we can clearly compare trade-offs between social and ecological outcomes (WebFigure 1). For instance, management strategies to minimize the prevalence of *E coli* O157:H7 might include increasing the gut pH of cattle by increasing the proportion of forage relative to grain in cattle diets, while the risks of cross-contamination could be reduced if post-harvest facilities minimized microbial dispersal by processing and monitoring smaller batches of produce. While economically efficient food production systems for leafy greens and other processed foods remain intact, consumers will be at risk of large-scale outbreaks of food-borne illness.

Managing biological wastewater treatment for complex waste streams

From ancient civilizations to modern industrialized societies, methods used to manage wastewater continue to influence human and environmental health. The passage of the US Clean Water Act in 1972 was a major milestone in water-quality improvement; the Act made it mandatory to process the biological contents of sewage to reduce contaminants in waterways. Given the limits to the global water supply, drinking-water source protection increasingly relies on microbially managed wastewater treatment. Here, we describe a situation where social–ecological interactions tend to yield net positive outcomes.

In wastewater treatment processes, environmental conditions are managed in ways that select for microorganisms that carry out desirable functions. The ability of some microbes to bioaccumulate and remove phosphorus (P) from the environment serves as the basis for a process known as enhanced biological P removal (EBPR). This bioengineering strategy can be harnessed by wastewater treatment facilities to improve water quality through microbially mediated removal of organic matter and nutrients from wastewater. EBPR facilities use batch reactors to cycle through anoxic and oxic conditions, thereby selecting for polyphosphate-accumulating organisms (PAOs), the major players in the bioaccumulation of phosphate. In sum, when PAO management is based on the ecophysiological principles of microbial metabolism, we can enhance nutrient removal in our waste streams to maximize water quality (WebFigure 1).

Recent advances in microbiology have allowed engineers to harness EBPR as an effective wastewater management strategy. Traditionally, environmental microbiologists have used enrichment and cultivation techniques to study microorganisms. However, these approaches greatly underestimate the abundance and diversity of microorganisms in EBPR communities. Culture-independent microbial techniques involving molecular methods and microscopy have greatly improved our understanding of the functional potential of PAOs in wastewater bioreactors. For example, genomic sequencing opened the door to subsequent transcriptomic (He and McMahon 2011) and proteomic (Wexler *et al.* 2009) analyses, which have yielded novel insight into the physiology and metabolism of "*Candidatus* Accumulibacter phosphatis", the dominant PAO in EBPR systems. By harnessing new microbial tools, it may also be possible to enhance nutrient removal capacity by supporting EBPR communities not only to remove P, but also to reduce nitrogen concentrations through the process of denitrification (Nielsen *et al.* 2012). Next-generation microbial methods may facilitate expansion from small-scale to large-scale wastewater plants by focusing on the complex metabolic differences among PAO strains and functions such as denitrification that may ultimately enhance nutrient removal capacity.

Ecological principles regarding the relationship between biodiversity and stability (Ives and Carpenter 2007) might help us better manage wastewater treatment plants. For example, microbial communities involved in EBPR are generally composed of fewer species than other microbial communities, which may make the former inherently susceptible to perturbations. Increasing supplies of antibiotics, hormones, pharmaceuticals, and nanoparticles in the wastewater may challenge the continued efficacy of these treatment facilities. To reduce the negative impacts of synthetic products on downstream aquatic ecosystems, bioreactors can be designed to capture or degrade these contaminants prior to effluent release. Biologically selecting for or seeding bioreactors with microorganisms capable of processing antibiotics, pharmaceuticals, and other "micropollutants" is also of interest to wastewater managers and other stakeholders (Dunlavey *et al.* 2010). However, trade-offs among traits

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involved in virus resistance, nutrient uptake, and tolerance to chemical stressors may lead to constraints on the desired multifunctionality of microbial communities. These ecological limitations are important for ensuring not only safe drinking water but also the sustainable use of natural resources, including P. Phosphorus removal from wastewater is becoming economically attractive due to limited P stocks, increased prices, and government regulation of nutrients in the environment (Elser and Bennett 2011). This classic example of managing biological wastewater treatment for social–ecological gain has provided opportunities to improve water purification and focus on resource recovery (eg for fertilizer pellets; WebFigure 1).

Can we micromanage synthetic microbiology?

Synthetic microbiology, a discipline focused on the design and application of new biological pathways, represents a case where social and eco-evolutionary outcomes are largely unknown (WebFigure 1). We argue that a social–ecological framework may help guide humans in designing organisms for positive social–ecological outcomes, such as efficient vaccine production, based on scientific information.

Decades ago, conventional genetic engineering modified organisms by introducing specific genes of known function from the genome of one taxon into that of another. A classic example involves the *cry* toxin genes produced by the bacterium *Bacillus thuringiensis* (*Bt*). The *cry* genes provide transgenic plants with insecticidal properties that improve pest control. However, the widespread introduction of *Bt* crops into agricultural landscapes led to an environmental trade-off: a decrease in insecticide application but increased numbers of toxin-resistant insects in the field (Pardo-Lopez *et al.* 2013).

More recently, synthetic microbiology has offered promising solutions to address complex environmental and human health issues. In contrast to the genetic engineering methods from a few decades ago, modern synthetic biology allows the construction of new genetic combinations not yet found in nature. Synthetic biology focuses on designing new biological pathways or organisms, or combining existing pathways in novel ways to supply various products (eg pharmaceuticals and sustainable fuel). Synthetic biology involves the manipulation of basic elements (eg promoters, transcriptional repressors) to create simple genetic devices or modules with desired functions (Purnick and Weiss 2009). More recent developments involve controlling the behavior of microbial populations through the engineering of interacting populations, making it feasible to sustainably produce fuel and pharmaceuticals. Specifically, some synthetic microbiologists are attempting to optimize the cooperative nature of microbial consortia by manipulating bacterial communications systems (Keller and Surette 2006).

Synthetic biology holds great promise for improving industrial production of pharmaceuticals involved in targeted cancer treatments, for generating sustainably produced fuels, and for assisting with hazardous waste cleanup. By manipulating metabolic machinery, synthetic microbiologists have been working toward producing cost-effective, stable supplies of medicines to meet global demands. For example, scientists have successfully developed an industrial-scale method of synthetically producing the anti-malaria drug artemisinin by exploiting the biochemistry of naturally occurring organic compounds like isoprenoids (Ro *et al.* 2006). It takes a long time to produce the necessary quantities of natural artemisinin from the woodworm plant (*Artemisia annua*). Combining and inserting genes and known pathways into yeast (*Saccharomyces cerevisiae*) can increase production of artemisinin and cut production costs 10-fold. However, there is a trade-off in terms of the negative economic impacts on growers of the wormwood plant, as natural artemisinin is replaced by faster and cheaper synthetic production. Synthetic artemisinin production is further challenged by the uncertainty involved in obtaining the financial support needed to distribute the drugs to developing countries (Peplow 2013). If we can improve dialogue among different stakeholders (eg growers, scientists, pharmaceutical companies), it may be possible to achieve positive outcomes from the industrial production of artemisinin, including a reduction in the negative social impacts.

By explicitly considering the ecology and evolution of microorganisms, scientists may be able to mitigate the negative impacts to both human health and the environment. For example, de novo protein engineering has the capability to build products where no known genetic template exists (Heinemann and Panke 2006), but it is not known how long such newly synthesized products will persist in the environment. There is some concern that synthetic organisms may outcompete native species if the former possess invasive properties allowing faster establishment and growth (Purnick and Weiss 2009). In an effort to reduce the risks associated with possible unintended or negative functions of synthetic organisms, scientists can design "fail-safe" switches to ensure that the engineered biochemical pathways operate as expected in specific environments (Purnick and Weiss 2009). However, the reliability of these synthetic designs is challenged by the strong selective pressure to lose engineered functions. Consideration should therefore be given to the ecological and evolutionary processes that will influence the performance of synthetic microorganisms and the persistence of their genetic information in the natural environment.

The synthetic biology community must openly engage with the public, and be honest about both the benefits and potential risks associated with this new technology. It will be important to extend scientific communication beyond disciplinary academic fields, to partner with policy makers, social scientists, and ethicists – and to suc-

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cessfully engage with the public and the popular press – in discussing possible outcomes. This is already happening in synthetic biology workshops and conferences, while synthetic biology centers are discussing topics ranging from ethics to safety with policy makers and the public (Purnick and Weiss 2009). Ways to regulate synthetic microorganisms in a social–ecological framework include transparency among stakeholders (including scientists, the public, and policy makers); third-party assessment of risks and benefits; and pre-market testing of synthetic products prior to public introduction (Macoubrie 2006). Because of the possible trade-offs and risks, a social–ecological framework will be valuable in guiding decisions and assessing outcomes associated with synthetically designed microorganisms (WebFigure 1).

Managing microorganisms under uncertainty

A social–ecological framework can be used to identify relationships that influence microbial services and disservices and guide adaptive management. Adaptive management is based on an iterative learning process whereby new information is incorporated to reshape management (Holling 1978). Adaptive management also stresses the importance of complexity, monitoring, feedback, learning, and stakeholder involvement in decision making (NRC 2004), and is particularly useful in cases where: (1) a system is dynamic and changing in response to environmental conditions and management interventions; (2) conditions are highly variable and unpredictable; (3) management interventions influence the system directly or indirectly; and (4) uncertainty regarding relationships and processes limits management actions (Williams and Brown 2014). Given the characteristic features of microbes (Panel 1), we anticipate that management of microbial services will require an adaptive strategy. As microbial-based social–ecological relationships change, decision makers will face complex situations and uncertainties that will demand the flexibility and iterative learning associated with adaptive management. Recent technological advances offer improved methods for monitoring microbial ecology at fine spatial and temporal scales and can provide useful data to inform adaptive management (Shade *et al.* 2009). Information gained from these advances will help guide a diverse range of decision makers who face uncertainties regarding microbial management.

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UC Cooperative Extension Area Orchard Systems Advisor

Kern & Kings Counties

University *of* California
Agriculture and Natural Resources

BACKGROUND: The University of California's Division of Agriculture and Natural Resources (UC ANR), a statewide program with local development and delivery, is seeking a Cooperative Extension Area Orchard Systems Advisor (CE Advisor) to conduct a multi-county-based extension, education, and applied research program. The main focus of this position is almonds in Kern and Kings Counties, and additional responsibilities will be focused on deciduous fruits (particularly cherries) and walnut production in Kern County.

NATURE AND PURPOSE: The CE Advisor will facilitate interactions and information exchange among campus-based academics, other Cooperative Extension advisors and specialists, and community stakeholders. The CE Advisor will conduct applied research to address issues identified through a thorough needs assessment. Educational effort will be carried out through a wide array of approaches to disseminate research-based information to solve local issues.

MAJOR RESPONSIBILITIES:

- Conduct and report regular needs assessments to identify priority issues or problems relevant to the local clientele groups being served
- Develop and implement effective UC ANR Cooperative Extension applied research and educational programs to address the identified priority needs of the clientele that are consistent with ANR's Strategic Vision and ANR initiatives (**http://ucanr.edu/files/906.pdf**)
  - ◊ Conduct applied research designed to monitor changes and solve locally relevant problems
  - ◊ Disseminate useful, science-based information to inform clientele, using extension methods that are responsive to clientele needs and appropriate for the audience and situation
  - ◊ Maintain and promote Cooperative Extension's credibility by providing science-based knowledge and skills independent of personal or parochial interests
  - ◊ Evaluate programs and report accomplishments, results, and potential or actual impacts to scientific and lay audiences
  - ◊ Develop collaborative teams with other UC ANR academics, including campus-based specialists, Agricultural Experiment Station faculty, Cooperative Extension advisors, and/or others, to address priority issues for UC ANR

EDUCATION AND EXPERIENCE: A minimum of a Master's Degree is required in disciplines such as horticulture or pomology, although other related advanced degrees such as viticulture, soil science, plant physiology, or a closely related field will be considered. Additional background or experience in the related commodities, water management, and/or plant mineral nutrition is desired. Excellent written, public speaking, and interpersonal communication skills are required. Some research or extension experience is highly desirable.

SALARY: Beginning salary will be in the Cooperative Extension Assistant Advisor Rank and commensurate with applicable experience and professional qualifications. For information regarding the Cooperative Extension Advisor salary scale, please refer to: **http://ucanr.edu/sites/anrstaff/files/187037.pdf.**

HOW TO APPLY: Please visit **http://ucanr.edu/Jobs/Jobs_990** to view the full job description and application instructions.
The application closing date is November 30, 2014.