CARL R. WOESE INSTITUTE FOR GENOMIC BIOLOGY

BUILDING CONNECTIONS. SHAPING DISCOVERIES.
2015 ANNUAL REPORT

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GENE E. ROBINSON

Director of the IGB. Swanlund Chair Professor of Entomology. Unites campus efforts related to genomic research and technology.

Director's Message

GENE E. ROBINSON

In biology, there is a concept that appears again and again: the close relationship between structure and function. This link is readily apparent when considering enzymes, specialized proteins that catalyze reactions within the cell.

Enzyme structures include pockets and folds that catch and hold reactants. These features enable their function of greatly reducing the time needed for the different chemical players to find each other and begin to interact—an apt metaphor for the ethos of the Carl R. Woese Institute for Genomic Biology (IGB).

In this year's annual report, we have used the IGB's structure, the physical character of the Institute and the everyday lives of the researchers and staff who inhabit it, to give a better

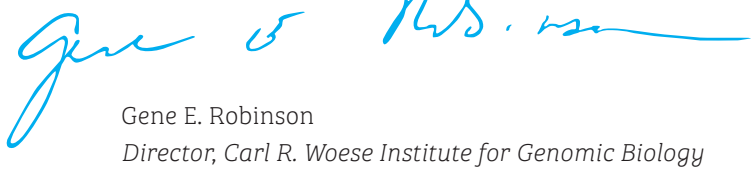
sense of its function, our activities and accomplishments. As this virtual tour of the building progresses, accompanied by stories of our new discoveries and achievements in the past year, we hope it will become clear that interdisciplinarity and cooperativity in research are not just abstractions here; our institute has been designed from the ground up to promote and support the interpersonal connections that make our work possible.

The IGB is more than an assemblage of offices and laboratories. It is a place for visitors from our campus, our community and beyond to converge and converse. In the past year, we have welcomed visitors to help us celebrate the scientific legacy of Carl Woese, the discoverer of third domain of life for whom our Institute is named. We also hosted events that introduced middle school girls to plant science and microscopy; sparked discussion on the complex roles of genomic technologies in Native American Heritage; and explored the connections between genomic research and the work of judges, lawyers and other professional groups.

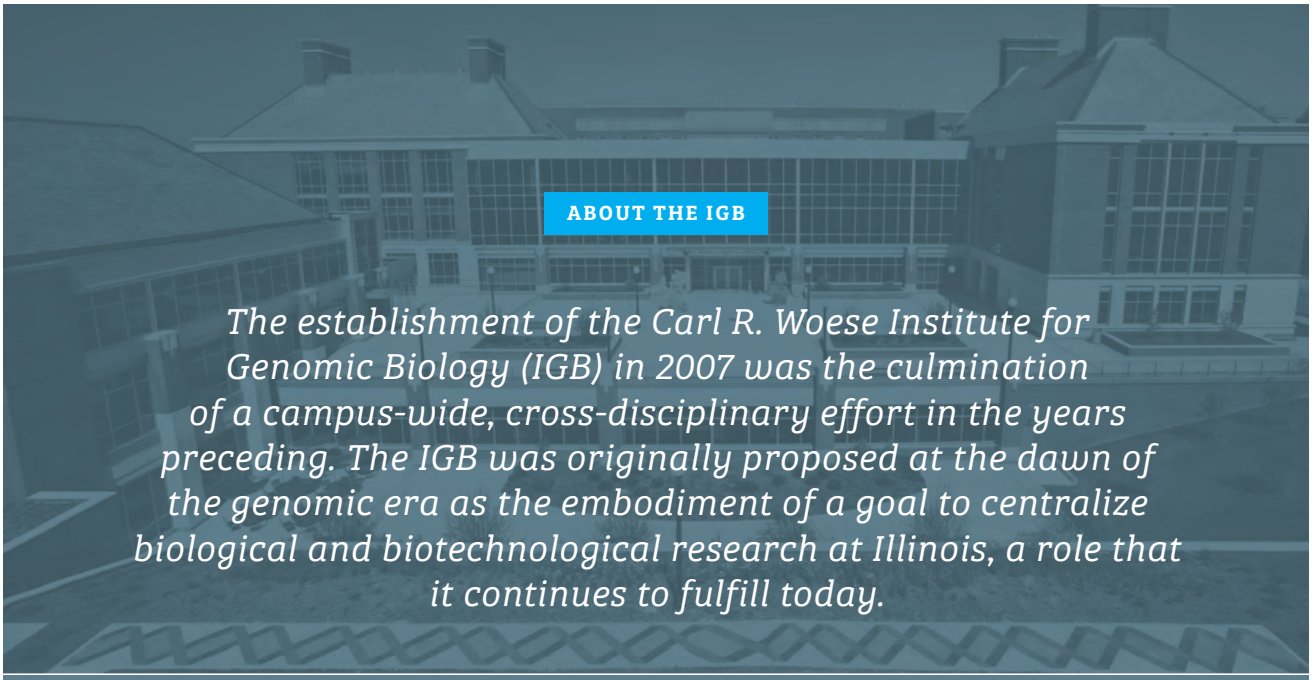
These connections to scientific and societal communities strengthen and are strengthened by the quality of the research conducted here. This year, we achieved numerous research breakthroughs in the areas of health, technological innovation, and human interactions with the environment. Often, genomic research transcends even these broad categories, as with the development of a drug delivery device inspired by glacial moraines, the design of bioenergy crops that remain productive over a broader range of climates, or the discovery of new details of human ecological history revealed by ancient microbial activity in aqueducts.

When the plan for the IGB was first proposed, campus leaders envisioned an institute whose existence would unify the many different groups at Illinois whose work intersected with the then-nascent field of genomics. Those who helped design the building that houses the Institute today worked to create a physical space that would make it easy for its members to form collaborations.

When the plan for the IGB was first proposed, campus leaders envisioned an institute whose existence would unify the many different groups at Illinois whose work intersected with the then-nascent field of genomics. Those who helped design the building that houses the Institute today worked to create a physical space that would make it easy for its members to form collaborations. Yet like the organisms we study, this vision of the IGB is not static; we continue to evolve, adapting to new opportunities as they arise. Thank you for taking the time to explore what we've become so far.



Gene E. Robinson
Director, Carl R. Woese Institute for Genomic Biology



ABOUT THE IGB

The establishment of the Carl R. Woese Institute for Genomic Biology (IGB) in 2007 was the culmination of a campus-wide, cross-disciplinary effort in the years preceding. The IGB was originally proposed at the dawn of the genomic era as the embodiment of a goal to centralize biological and biotechnological research at Illinois, a role that it continues to fulfill today.

A HOME FOR GENOMICS IN THE HEART OF CAMPUS

Because IGB members are drawn from many schools and departments, including biology, chemistry, physics, engineering, sociology, and business, the Institute's central and accessible location is crucial. The building's position in the heart of campus allows faculty and affiliate members to remain an integral part of their home departments while also pursuing collaborative projects in thematic research groups at the IGB.

SPACES FOR SYNTHESIS

Each IGB research theme is housed within one of the building's open laboratory spaces. These facilities promote interaction and flexibility, two precepts of the themes themselves. Research themes create synergy among groups of scientists from many different disciplines to tackle grand challenges related to health and wellbeing, technological development, environmental resources and conservation by engaging in fundamental and applied research. Each theme is reviewed every five years to ensure that its work capitalizes on advances in knowledge and technology, and anyone may propose a new theme.

A MEETING PLACE FOR SCIENCE AND SOCIETY

Genomic science has the power to shape and improve many aspects of our lives. The structure of the IGB includes classrooms, a teaching laboratory, and space for public gatherings of all kinds, reflecting the Institute's commitment to an open dialogue between scientific research and our global community. Through innovative outreach and education programs, the IGB invites people of all ages to learn about and participate in genomic research.

THE MISSION OF THE IGB IS TO ADVANCE LIFE SCIENCE RESEARCH AT THE UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN AND TO STIMULATE BIO-ECONOMIC DEVELOPMENT IN THE STATE OF ILLINOIS.

IGB themes, partnerships and facilities

This cutaway view of the IGB's Gatehouse and Research Buildings shows the research themes, partnerships, initiatives, and facilities that make us who we are. We will revisit this view throughout the report to mark our progress as we explore the Institute together.

RESEARCH BUILDING

BIOCOMPLEXITY (BCXT)

Explores the origin of life and the behavior of biological systems.

GATEHOUSE BUILDING

OUTREACH

Promotes open dialogue between genomic research and society.

GENE NETWORKS IN NEURAL & DEVELOPMENTAL PLASTICITY (GNDP)

Investigates the effects of gene regulatory network structure and function on biological diversity.

ADMINISTRATIVE SUPPORT

Facilitates and communicates progress in genomic research.

GENOMIC ECOLOGY OF GLOBAL CHANGE (GEGC)

Studies the intersection of plant genomics and global climate change.

CONCOURSE LEVEL

CORE FACILITIES

Provides cutting-edge microscopy and analytical equipment for genomic research.

FUNDAMENTAL RESEARCH

Expands the horizons of human knowledge, revealing new realms of scientic possibility in every area.

COMPUTING GENOMES FOR REPRODUCTIVE HEALTH (CGRH)

Examines the interplay among genetic and environmental factors that influence disorders of reproduction.

MINING MICROBIAL GENOMES (MMG)

Discovers small molecules that might provide new medical solutions.

REGENERATIVE BIOLOGY & TISSUE ENGINEERING (RBTE)

Studies the replacement or regeneration of tissues and organs.

BIOSYSTEMS DESIGN (BSD)

Applies engineering principles to real and artificial biological systems.

ENERGY BIOSCIENCES INSTITUTE (EBI)

Addresses the global energy challenge through a unique public-private collaboration, originally funded by a 10-year, $500 million grant from BP. The partnership includes the University of California, Berkeley; the University of Illinois at Urbana-Champaign; the Lawrence Berkeley National Laboratory; and BP.

CELLULAR DECISION MAKING IN CANCER (CDMC)

Works to better understand how cancer alters the inner workings of cells.

CENTER FOR NUTRITION, LEARNING, AND MEMORY (CNLM)

Determines the impacts of nutrition on learning and memory in the human brain. In addition to the IGB, the Center partners with Abbott Nutrition and the Beckman Institute for Advanced Science and Technology.

COMPGEN INITIATIVE

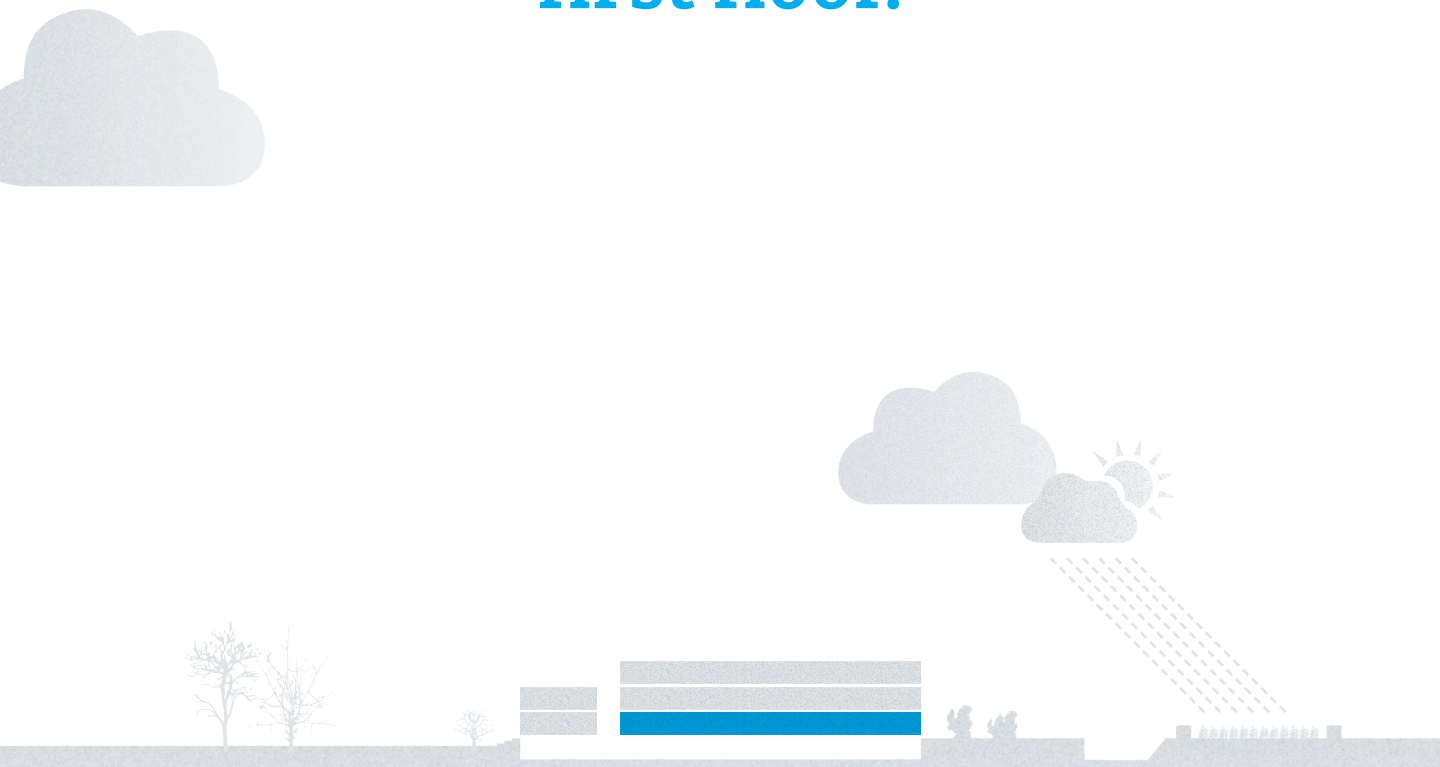
Combines principles of genomics with large-scale computing approaches to create technologies that facilitate interdisciplinary research in Big Data.

ENVIRONMENT		At IGB, we explore how genomes construct ecosystems and feed and fuel our world.
TECHNOLOGY		At IGB, we build tools that will help construct a better world.
HEALTH		At IGB, we uncover connections between genomes and wellbeing.
FUNDAMENTAL RESEARCH		At IGB, we expand the horizons of human knowledge.
CORE FACILITIES		At IGB, we innovate techniques to discover new microscopic worlds.
OUTREACH		At IGB, we engage with the public.
ADMINISTRATIVE SUPPORT		At IGB, we create new opportunities to pursue knowledge.

Welcome to the IGB.
Our Institute is a nexus for more than 130 faculty members and affiliates from over 30 different departments and units across campus. Here, they join hundreds of postdoctoral fellows, technicians, students, and staff to perform path-breaking research in genomics. Step inside and see how the work we do today will reshape the world of tomorrow.

Enter the IGB Research Building.

Let's start on the first floor.



Our global environment includes the totality of living and non-living things that make up the world we live in. Work in our Institute advances understanding of how factors such as the changing global climate and human activities have and will continue to impact the environment, ecosystems, and individual species. Research in this area also focuses on the development of sustainable food and biofuel sources, environmental resources we cannot live without.

ABOUT THE FIRST LEVEL, RESEARCH BUILDING

40,277 SQ. FT.	105 OFFICE SPACES	2 THEMATIC LAB MODULES	1 AWARD WALL

Gutgsell Endowed Professor of Plant Biology and Crop Sciences. Member of the Genomic Ecology of Global Change research theme and the Energy Biosciences Institute; affiliate of the Biosystems Design research theme. Directs multiple research efforts to develop more robust and efficient food and energy crops.

STEPHEN LONG

Assistant Professor of Plant Biology. Affiliate of the Genomic Ecology of Global Change research theme. Studies the interplay of molecular responses to environmental change in plants.

AMY MARSHALL-COLON

At a table in the IGB's Array Cafe, one of her favorite meeting spots, Amy Marshall-Colon (GEGC) leans forward to examine a dynamic portrait of a plant's germination and growth—a portrait painted in numbers rather than words.

Marshall-Colon, a young and energetic assistant professor of plant biology, is contemplating the details of a plant *in silico*: a sophisticated computer modeling platform that accounts for everything from the molecular-level availability of nutrients to the shading effects of a plant's neighbors in the field. Marshall-Colon, fellow plant biologists Stephen Long (BSD/EBI/GEGC) and James O'Dwyer (BCXT), and chemical and biomolecular engineer Diwakar Shukla are designing Plants *in Silico* to aid crop scientists, ecologists, and engineers in understanding how global climate change impacts a plant's biological systems (page 12).

STUTI SHRIVASTAVA

PhD candidate in the Department of Plant Biology. Works with Amy Marshall-Colon and collaborators to mathematically model plant response to environmental change.

The walk Marshall-Colon and her graduate student, Stuti Shrivastava, took this afternoon from the Department of Plant Biology in the Edward R. Madigan Laboratory building to this shared space in the IGB is a bit like the journey she's taken in her career so far. Rooted by her strong background in environmental science and agronomy, motivated by her passion for preserving the natural world, Marshall-Colon has branched out into new areas: transcriptomics, computational modeling, big data. The collaborations she has built since arriving in Illinois are represented in the open laboratory spaces above her.

"Collaborations are key to the success of systems biology research, because no one individual or even one lab can be expert in all areas of molecular biology," says Marshall-Colon. "The open space and dynamic nature of the IGB themes promotes collaborations that are productive and transformative."

Photosynthesis hack needed to feed the world by 2050

go.igb.illinois.edu/Photosynthesis2050

Using high-performance computing and genetic engineering to boost the photosynthetic efficiency of plants offers the best hope of increasing crop yields enough to feed a planet expected to have 9.5 billion people on it by 2050, researchers reported in the journal *Cell*. "If we have a success today, it won't appear in farmers' fields for 15 years at the very earliest," said Gutgsell Endowed Professor of Plant Biology and Crop Sciences Stephen Long (BSD/EBI/GEGC), who wrote the report with plant biologist Amy Marshall-Colon (GEGC) and Xin-Guang Zhu, a collaborator at the CAS-MPG Partner Institute of Computational Biology in Shanghai. "We have to be doing today what we may need in 30 years."

"We now know every step in the processes that drive photosynthesis in C3 crop plants such as soybeans and C4 plants such as maize," Long said.

"We have unprecedented computational resources that allow us to model every stage of photosynthesis and determine where the bottlenecks are, and advances

in genetic engineering will help us augment or circumvent those steps that impede efficiency."

Long and his colleagues are developing a sophisticated virtual plant based on computational modeling of the many factors that impact photosynthesis to help identify promising research approaches. Funding for this work was provided by the Bill & Melinda Gates Foundation, the USDA, the NSF and the Chinese Academy of Sciences.

Increase crop productivity by making crop plants more efficient and better neighbors

go.igb.illinois.edu/EfficientCrops

How can we meet the accelerating food needs of the world's population without increasing the amount of land used for farming? An article published in the *Proceedings of the National Academy of Sciences* emphasized the need to increase the global food supply. The authors created a roadmap for research to increase plant productivity by making plants better neighbors and borrowing molecular tricks from other species to make their use of light and carbon more efficient.

Robert Emerson Professor of Plant Biology Donald Ort (BSD/GEGC Theme Leader) was the lead author on the article, which was based on the outcomes of a 2013 workshop held at the Banbury Center at the Cold Spring Harbor Laboratory. The conference brought together plant biologists, who proposed potential targets for improvement in the photosynthetic process, with experts in synthetic biology and computational modeling who provided input on the molecular tools and refinements needed to achieve those improvements.

Ort and coauthors suggested multiple molecular strategies to realize increased photosynthetic efficiency. These included inserting the photosystem of a photosynthetic bacterium that captures infrared wavelengths, decreasing the amount of pigment in upper leaves to allow a more even distribution of light to all levels of the plant canopy, and developing crops with "smart canopies" that respond adaptively to changing light levels.

The workshop that gave rise to the review, "Redesigning Photosynthesis—Identifying Opportunities and Novel Ideas," was held May 13–16, 2013. The workshop was co-organized by Sabeeha Merchant, a professor of biochemistry and a

Left page | *Members of the GEGC research theme prepare for a busy field season by planting experimental crops.*

Left | *Robert Emerson Professor of Plant Biology Donald Ort coauthored a paper on the need to revolutionize the photosynthetic efficiency of crop plants.*

Right

Plant biology professor Ray Ming and colleagues discovered that papaya cultivation 4,000 years ago likely led to the evolution of hermaphrodite plants.

member of the Molecular Biology Institute at the University of California, Los Angeles. Twenty-three other coauthors attended from around the world, including Illinois plant biologist Stephen Long (BSD/GEGC).

Cultivated papaya genome sequence reveals ancient Mayan origins

go.igb.illinois.edu/Papaya

During each planting season, papaya farmers must make a gamble on the seeds they sow: how many will grow into plants with edible fruits? This productivity depends on the sex of each plant. A recent study of papaya genome sequence, reported in *Genome Research*, has brought researchers a step closer to identifying the genes involved and to understanding the ancient domestication that made cultivation possible.

Papaya plants are either male, female or hermaphrodite, and only the hermaphrodite plants produce marketable fruit. The research team, led by plant biology professor Ray Ming (EBI/GEGC), found that variation in one particular region of the papaya's male sex chromosome distinguished between male and hermaphrodite plants. The NSF supported this research.

"This research will one day lead to the development of a papaya that produces only hermaphrodite offspring, an advance that will enhance papaya root and canopy development while radically cutting papaya growers' production costs and their use of fertilizers and water," said Ming.

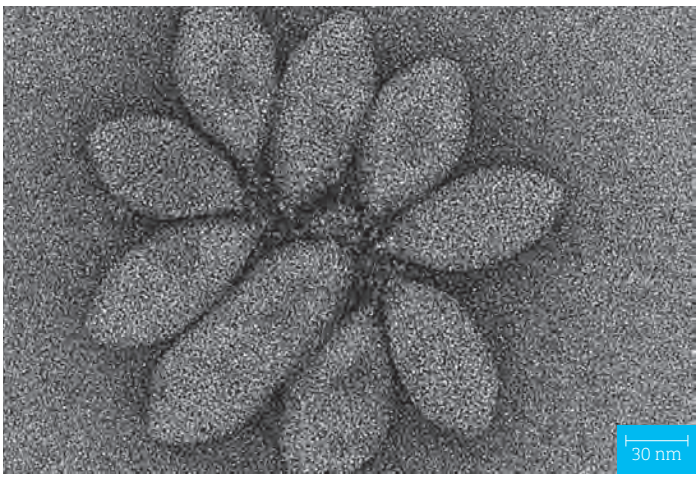
The study also found less than half of one percent difference between the male and hermaphrodite sequences, suggesting that the evolutionary event that caused them to diverge occurred in the not-too-distant past. Ming and his colleagues hypothesized that hermaphrodite papaya plants first appeared about 4,000 years ago, corresponding with the rise of the Maya civilization in Mesoamerica and suggesting that they arose as a result of domestication efforts by the Maya peoples.

Microbes scared to death by virus presence

go.igb.illinois.edu/DormantMicrobes

Microbes, like other organisms, can be infected by viruses. It's unsurprising that these viral infections sometimes kill microbes. What's unexpected is a recently discovered strategy some microbes use to protect themselves: they play dead, hoping the virus will move on.

"The microbe is hedging its bet," said microbiologist Rachel Whitaker (BCXT), lead author on the related article



Left | *Transmission Electron Micrograph (TEM) of viruses isolated from the Kamchatka Peninsula in Russia.*

published in mBio. *"If they go dormant, they might die, but we think this must be better than getting infected and passing it on."*

The microbes examined by Whitaker's lab, called *Sulfolobus islandicus*, will go dormant in the presence of just a few viruses. Even inactivated virus particles that cannot actually infect a host could still cause dormancy in the microbes—and if the dormant period lasted more than a day or two, the microbes died.

"People thought these inactivated viruses were just an accident, that they were just mispackaged," Whitaker said. "Now we know they are being sensed by the host so they are having an effect. People are starting to think that it is adaptive for the virus to produce inactivated virus particles." The study, which was supported by the NSF, has provided a more nuanced view of the ecological battles within microbiomes.

First report of a new crop virus in North America

go.igb.illinois.edu/CropVirus

The ailing switchgrass exhibited mosaic symptoms characteristic of a viral infection—splotchy, discolored leaves—yet tested negative for known infections. Extensive DNA sequencing revealed the plants were infected with a new species of virus, the first of its kind found in North America.

The virus, tentatively named switchgrass mosaic-associated virus 1 (SgMaV-1), was identified in an *Archives of Virology* article as a mastrevirus. Other members of the mastrevirus genus, a group of DNA viruses, are known to be responsible for decimating yields in staple food crops (including corn, wheat and sugarcane) throughout Africa, Europe, Asia, and Australia.

"My fear is that this virus is in corn and wheat, and we are not even aware of it," said first author Bright Agindotan (EBI), who recently moved from a postdoctoral position at the IGB to a faculty position at Montana State University. Associate Professor of Crop Sciences Carl Bradley and Assistant Professor of Crop Sciences Leslie Domier were coauthors on the study.

Additional research will be needed to determine infectivity, host range, pathogenicity, epidemiology, and vector transmission of SgMaV-1. The work that led to the discovery of the virus was supported by the EBI.

Genomic traces in monkey droppings provide a more detailed picture of feeding behavior

go.igb.illinois.edu/MonkeyDroppings

In South American rainforests, researchers

can tell one saddle-back tamarin from another, but it is difficult to track details of each squirrel-sized monkey's behavior—for example, what they are putting in their mouths. A recent study solved this problem by relying on droppings to find out what bugs and other invertebrates the monkeys munch on.

Using high-throughput sequencing, Associate Professor of Anthropology Ripan Malhi (CGRH/RBTE), graduate student Elizabeth Mallott, and Professor Emeritus of Anthropology Paul Garber found that 20 tamarins from five social groups in northern Bolivia consumed invertebrates from 11 orders, 15 families and 12 genera over a three-week period. The study was supported by the University of Illinois.

"This is really exciting; it is the first time that we have been able to get detailed data like this," said Mallott, a doctoral candidate in the Department of Anthropology.

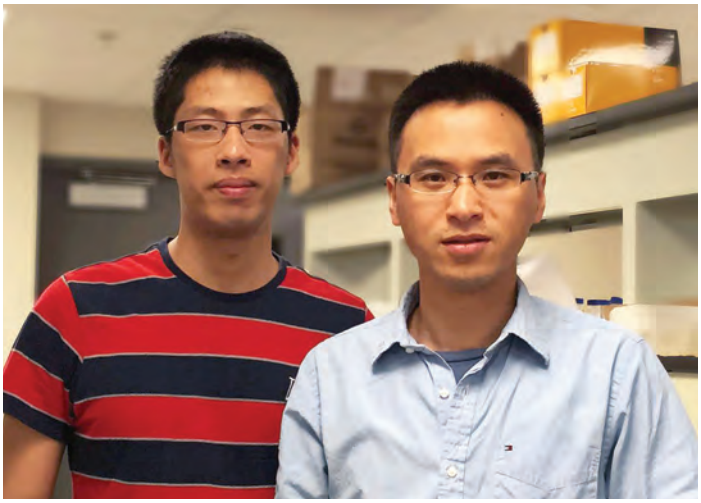
"Their hand goes into a tree hole, and we don't know what they are coming out with. It is nice to finally be able to report the amount of diversity of what goes into their mouth. We wouldn't be able to do it without these molecular methods," said Mallott.

The combination of behavioral observation, ecological sampling, and high-throughput sequencing will give researchers insight into the tamarins' foraging strategies and prey preferences. To follow up this study, which was published in the *American Journal of Physical Anthropology*, the researchers also plan to work on quantitatively identifying the invertebrates in the tamarin diet.

Exploring the secrets of fermentation hints at pathways to new biofuels

go.igb.illinois.edu/BiofuelFermentation

It takes millions of years for sugars and other carbon sources to be converted into the petroleum we use for fuel. In contrast, *Clostridium* bacteria can convert carbon sources into a promising potential biofuel, butanol, in just hours. A team of researchers led by Assistant



Left page, top — *Emeritus Professor of Anthropology Paul Garber, anthropology doctoral candidate Elizabeth Mallott, and Associate Professor of Anthropology Ripan Malhi.*

Left page, bottom — *Weddell's saddleback tamarins (*Saguinus weddelli*) at a field site in the Pando Region of northern Bolivia.*

Left — *Bioengineering graduate student Chen Liao (left), first author of the PNAS article, in the lab with Assistant Professor of Bioengineering Ting Lu.*

Professor of Bioengineering Ting Lu (BCXT/BSD) has now elucidated the complex interplay of biochemical reactions, gene regulation, and environmental cues that make this type of naturally occurring fermentation possible, providing new insights for advanced biofuel development.

*"*Clostridium *is very much like a factory during fermentation which converts carbon sources into renewable, advanced biofuels that can be directly used to fuel your cars," explained Lu.*

"This work advances our fundamental understanding of the complex, system-level process of clostridial acetone-butanol-ethanol fermentation."

The work was funded by the University of Illinois and the Council of Higher Education of Turkey, and published in the *Proceedings of the National Academy of Sciences.* Associate Professor of Food Microbiology Yong-Su Jin (BSD/EBI) also contributed to the study.

Evolutionary trees reveal patterns of microbial diversification

go.igb.illinois.edu/DiverseMicrobes

While teaching a class on statistical methods in physics, plant biologist James O'Dwyer (BCXT) realized that the technique he was presenting could be used in his own work to understand how microbes evolve over time. The results, published in the *Proceedings of the National Academy of Sciences*, revealed microbial family trees with distinct evolutionary patterns that may one day help us understand how harmful microbes evolve.

"The species concept is difficult for microbes," said O'Dwyer. Microbes typically reproduce asexually; this makes it difficult to use the traditional biological concept of species, which defines species as organisms that can interbreed. Ecologists and microbiologists have often lumped microbes with similar DNA sequences together as effective, "operational" taxonomic (classification) units.

O'Dwyer and co-authors Steven Kembel at the Université du Québec à Montréal and Thomas Sharpton at Oregon State University have sorted these sequence data into a new kind of family tree that displays sudden bursts of diversification.

Cold tolerant sugarcane could be grown on an additional 23 million acres of marginal land in the Southeastern U.S., replacing 28% of the fossil fuels currently imported from outside the U.S.

Right

"[These models] provide us with an echo of real ecological processes, like adaptive radiations, when an organism rapidly diversifies due to a change in environment or to fill a new niche," O'Dwyer said. "And these bursts are there throughout these phylogenetic trees, deep within their history."

Chill-tolerant hybrid sugarcane not only survives low temperatures—it thrives

go.igb.illinois.edu/Miscane

U.S. farmers have long hoped to extend sugarcane's growing range northward from the Gulf coast, substantially increasing the land available for sugar and biofuels. Several hybrid canes developed in the 1980s have proved hardy in cooler climes, surviving overwinter as far north as Booneville, Arkansas. But until now, no one had tested whether these "miscanes," as they are called, actually photosynthesize—and thus continue to grow—when the temperature dips.

Researchers now report that two miscanes (the offspring of crosses between sugarcane and a hardy, cold-tolerant grass, *Miscanthus*) perform as well as the grass species *Miscanthus x giganteus* at temperatures as low as 10 degrees Celsius (50 °F). Although the rate of photosynthesis drops in the miscanes at these temperatures, it doesn't stall out altogether as it does in sugarcane.

Modeling studies suggest that extending sugarcane's growing season by 30 days, which this improved cold tolerance could achieve, can boost sugarcane yield by as much as 25 percent in the U.S., said postdoctoral researcher Katarzyna (Kasia) Glowacka.

Lead author Professor of Crop Sciences Erik Sacks (EBI) emphasized that these results also indicate that miscanes could be grown for sugar or as a productive biofuels crop on the least productive land in the American South.

This research is part of the PETROSS (Plants Engineered to Replace Oil with Sugarcane and Sweet Sorghum) project, which is funded through the DOE Advanced Research Projects Agency-Energy (ARPA-E). Collaborators on the study included Gutgsell Endowed Professor of Crop Sciences and Plant Biology Stephen Long (BSD/EBI/GEGC) and USDA-ARS scientists in Canal Point, Florida.

Ground-level ozone reduces maize and soybean yields

go.igb.illinois.edu/Ozone

Despite government regulations, ground-level ozone, an odorless gas that forms as polluting nitrogen oxides are exposed to sunlight, continues to threaten crop quality and yield. In a new study, researchers quantified this loss from historical yield data for the first time. They showed that over the last 30 years, ozone emissions have reduced soybean and corn yields by five percent and ten percent respectively.

Postdoctoral fellow Justin McGrath (MMG) led the study with Gutgsell Endowed Professor of Crop Sciences and Plant Biology Stephen Long (BSD/EBI/GEGC) and USDA-ARS scientist Elizabeth Ainsworth (GEGC). Their research was supported by the NSF and University of Illinois, and findings were reported in the *Proceedings of the National Academy of Sciences.*

The researchers analyzed historical crop yields and climate and ozone data from 1980 to 2011 across the continental U.S., focusing on corn and soybeans. They found that higher levels of ground-level ozone were associated with reduced yields of both crops.

"Laboratory studies had suggested that soybean was vulnerable to ozone, but the ten percent yield loss in corn is a surprise and very significant," Ainsworth said.

The researchers calculated an annual loss of just over $9 billion nationwide between the two crops due to ozone damage. Emissions regulations have had a positive effect on reducing ozone-related damage to crop plants, but may need to be upgraded to reduce crop damage and ease the resulting financial burden on growers, Long said.

Fire ants traveled the world as stowaways

go.igb.illinois.edu/FireAnts

Spanish ships spread tropical fire ants around the globe in the 16th century, according to new research about one of the first worldwide invasive species.

"A lot of these ships, particularly if they were going somewhere to pick up commerce, would fill their ballast with soil and then they would dump the soil out in a new port and replace it with cargo," said entomologist Andrew Suarez (GDNP).

"They were unknowingly moving huge numbers of organisms in the ballast soil."

The researchers traced the ants' history by sequencing the genomes of modern tropical fire ants and looking at how much variation existed in populations from different geographical regions. Their results showed that ants outside the Americas were most genetically similar to ants from southwestern

Below | *USDA-ARS scientist Elizabeth Ainsworth examines experimental maize crops.*

Left | *William and Janet Lycan Professor of Chemistry Zan Luthey-Schulten.*

Right | *Spanish galleons used soil as ballast while traveling from Acapulco, Mexico, to Manila, Philippines, in the 16th century. That soil likely held tropical fire ants.*

Mexico, suggesting Mexico was the main source of the invasion. Decreasing diversity in populations further from the new world is consistent with small numbers of ants migrating to establish new populations. The timing of the genetic changes overlapped with the Spanish trade conquest.

The study was funded by the NSF and USDA and published in *Molecular Ecology*.

From the depths of a microscopic world, spontaneous cooperation

go.igb.illinois.edu/SpontaneousCooperation

Maybe it's not such a dog-eat-dog world after all. Computer simulations of group behavior enabled a group of Illinois researchers to uncover an unexpectedly cooperative dynamic: the spontaneous emergence of resource sharing. Who were the members of this digital collective? *Escherichia coli*, rod-shaped bacteria found in the digestive systems of humans and other animals.

The finding, initially predicted by mathematical models and then confirmed through empirical testing, was reported in *BMC Systems Biology*. William and Janet Lycan Professor of Chemistry Zan Luthey-Schulten (BCXT), graduate student John Cole, and colleagues have worked for several years on computer simulations of bacterial growth.

Modeling situations with uneven distributions of resources revealed something unexpected and novel, yet intuitive. The model predicted that the bacteria would spontaneously cooperate to maximize growth. "As soon as I saw it, I thought, it makes perfect sense," said Cole. "It has to be going on at some level, and I'm sure it's testable."

To test the model's predictions, Luthey-Schulten, Cole and colleagues grew and monitored bacterial colonies in the lab in conditions that matched those they had simulated. In real colonies, as in the simulated ones, cooperative task specialization emerged quickly even among genetically identical or near-identical cells. The authors hope that the model can be adapted to reveal new insights into the behavior of other groups of cells, including cancer-causing tumors.

This work was supported by the DOE, NIH, the Edelheit Foundation, and the Center for the Physics of Living Cells, which is funded by NSF. Support from NSF also provided computer time.

AWARDS

EVAN DELUCIA was named a fellow of the Ecological Society of America, which honors members who have made outstanding contributions to a wide range of fields served by the society, including those that advance or apply ecological knowledge in academics, government, and nonprofit organizations as well as the broader society.	*Professor of Plant Biology (EBI/GEGC)*
WEN-TSO LIU was appointed the Arthur C. Nauman Endowed Professor in the Department of Civil and Environmental Engineering.	*Professor of Civil and Environmental Engineering (BCXT/EBI)*
STEPHEN LONG was named by Thomson Reuters as a Highly Cited Researcher for 2015.	*Gutgsell Endowed Professor in the departments of crop sciences and plant biology (BSD/EBI/GEGC)*
DONALD ORT was named to the Agricultural Research Service Science Hall of Fame for his major impact on agricultural research and for his outstanding accomplishments within the agricultural research community. He was also named by Thomson Reuters as a Highly Cited Researcher for 2015.	*Robert Emerson Professor of Plant Biology (BSD/GEGC Theme Leader)*
VIJAY SINGH was named a University Scholar, a program created to recognize the university's most talented teachers, scholars and researchers. He also received the American Association of Cereal Chemists International Excellence in Teaching Award from the College of Agricultural, Consumer and Environmental Sciences.	*Professor of Agricultural and Biological Engineering (GEGC)*
BERKLEY WALKER received an Alexander von Humboldt Fellowship to conduct independent research with a host lab in Düsseldorf, Germany for two years.	*Postdoc, USDA-ARS, Ort Lab*
BRYAN WHITE was elected to Fellowship in the American Academy of Microbiology. The Academy, an honorific leadership group within the American Society for Microbiology, recognizes excellence, originality, and leadership in the microbiological sciences.	*Professor of Animal Sciences and Director of the Mayo Clinic/ University of Illinois Strategic Alliance for Technology-Based Healthcare (BCXT/ CGRH)*

Let's keep exploring the Research Building.

Head up to the second floor.

New technologies launched the genomic era. Now, progress in genomic research depends on further innovations in the tools that allow us to probe, manipulate, and analyze biological molecules. Whether focused on software or hardware, biomaterials or microfluidics, DNA editors or molecular motors, our technological research pushes the boundaries of the physically possible and paves the way for future discovery.

ABOUT THE SECOND LEVEL, RESEARCH BUILDING

	38,103 SQ. FT.	111 OFFICE SPACES	2 THEMATIC LAB MODULES
SCI-FI DVD RENTAL ARTWORK		HIGH-THROUGHPUT ROBOT	


F5
Thermo
SCIENTIFIC

YONG-SU JIN

Associate Professor of Food Science and Human Nutrition. Member of the Biosystems Design research theme and the Energy Biosciences Institute. Develops tools for more efficient metabolic engineering in yeast, and uses those tools to develop improved yeast strains for multiple applications.

At first glance into the window-lined IGB conference room, there are many obvious differences between the vigorous late-afternoon conversation to which Ting Lu (BCXT/BSD) is contributing and the communities of microbes that he thinks about every day—and yet to the whimsical mind, there is one similarity: unexpected cooperation within a diverse group.

Lu, an assistant professor of bioengineering, is meeting with Associate Professor of Chemical and Biomolecular Engineering Christopher Rao (BSD/EBI/RBTE) and Associate Professor of Food Science and Human Nutrition Yong-Su Jin (BSD/EBI). Despite their

CHRIS RAO

Associate Professor of Chemical and Biomolecular Engineering. Member of the Biosystems Design research theme and the Energy Biosciences Institute, and an affiliate of the Regenerative Biology and Tissue Engineering research theme. Investigates how individual cells process information and perform decision-making functions, and engineers bacteria for the production of biofuels.

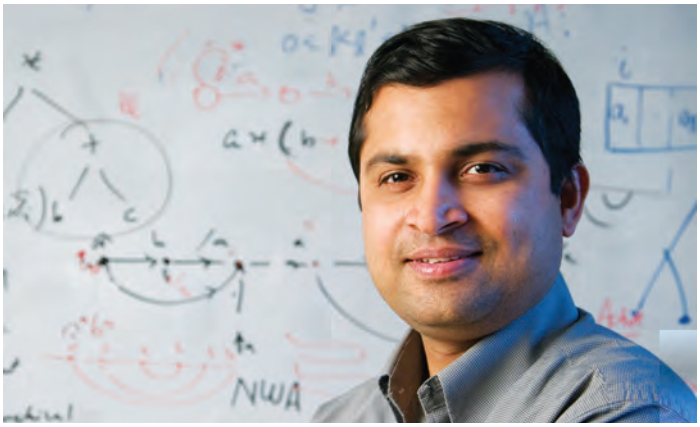
TING LU

Assistant Professor of Bioengineering. Member of the Biosystems Design research theme and affiliate of the Biocomplexity research theme. Analyzes and constructs bacterial gene regulatory circuits to improve our understanding and application of beneficial microbial functions.

disparate backgrounds, or perhaps in part because of them, the three meet weekly to discuss their work, exchange advice or share enthusiasm, and most of all to enjoy the fresh view and creative thinking that emerges from an agenda-less meeting and an open exchange of ideas.

All three researchers study collective behaviors that allow microbial communities to adapt to their environment, and how to engineer microbial communities to fulfill complex functions such as seeding a healthy microbiome in the gut of a human patient or synthesizing biofuels (page 16). The ongoing conversation among Lu and his IGB colleagues has already led to projects that are strengthened by each researcher's unique background and research area. The broader collaboration within the Biosystems Design research theme, led by Steven L. Miller Chair Professor of Chemical and Biomolecular Engineering Huimin Zhao, is jointly developing a biological foundry that will make it possible to engage in this type of work on a massive scale.

"The IGB is really designed in a way to facilitate collaboration and get people to work together . . . there was no reason why I should not join," says Lu, commenting on his appreciation of the academic community he has discovered here. "It is very unique, and we are really appealing because we foster that collaboration."



IGB travels to Shenzen, China for BGI workshop

go.igb.illinois.edu/BGIworkshop

As part of an international exchange of knowledge and ideas, members of the IGB traveled to BGI (formerly known as the Beijing Genomics Institute) for a learning and discussion workshop in January 2015. The week-long workshop was an opportunity for BGI and IGB researchers to share views on new developments and technologies in genomic research and foster the collaboration between the two institutes.

Founded in Beijing with a mission to support science and technology development, build strong research teams, and promote scientific partnership in genomics, BGI's headquarters were later relocated to Shenzhen as the first citizen-managed, non-profit research institution in China. BGI engages in large-scale, high-accuracy projects, and has sequenced over 50 plant and animal genomes and over 1,000 bacterial genomes.

Genomics among the biggest of Big Data, experts say

go.igb.illinois.edu/BigDataGenomics

Almost every microscopic cell contains its own complete genome, and the information packed into just a few DNA molecules could fill a hard drive. As more people have their DNA sequenced, those data will require massive computational and storage capabilities beyond anything previously anticipated, said computational biologists and computer scientists at the IGB and Cold Spring Harbor Laboratory.

The team of experts, including IGB Director and Swanlund Professor of Entomology Gene Robinson and Associate Professor of Computer Science Saurabh Sinha (BSD/GNDP), compared the data needs of genomics with those of three of the biggest players in Big Data: astronomy, Twitter and YouTube. They projected growth in each area through the year 2025 and predicted that genomics is poised to place the heaviest demands on data acquisition, storage, distribution and analysis technologies. The team's assessment was published in the journal *PLOS Biology*.

"Genomics will soon pose some of the most severe computational challenges that we have ever experienced," Robinson said.

"If genomics is to realize the promise of having a transformative positive impact on medicine, agriculture, energy production and our understanding of life itself, there must be dramatic innovations in computing. Now is the time to start."

Scientists find DNA is packaged like a yoyo

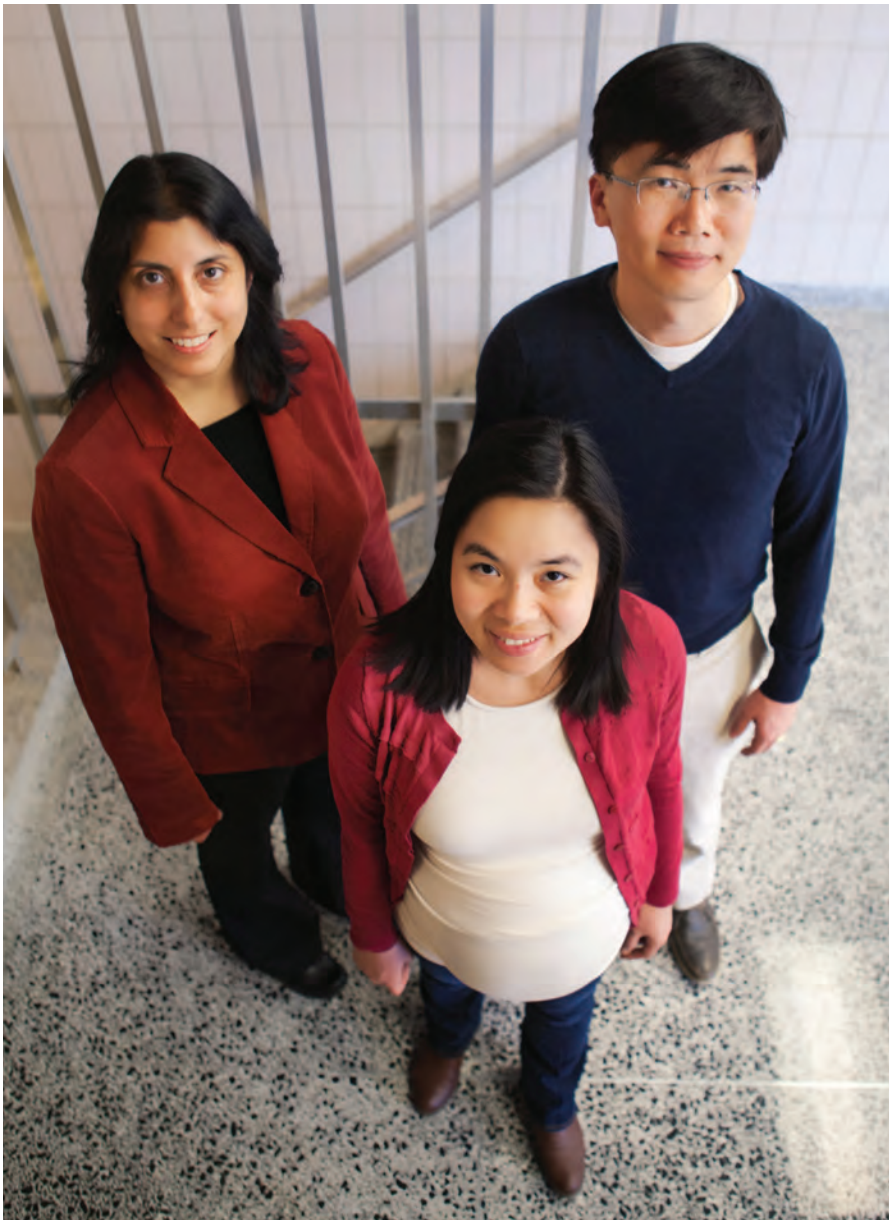
go.igb.illinois.edu/DNAPackaging

How a region of DNA is packaged inside the cell—and importantly, in what ways it can be easily unpackaged—depends on its sequence, scientists reported in *Cell*. The work was supported by the NSF, the NIH, and the HHMI.

"We discovered this interesting physics of DNA that its sequence determines the flexibility and thus the stability of the DNA package inside the cell," said Gutgsell Endowed Professor of Physics Taekjip Ha (CDMC Theme Leader). "There are still surprises in the physics of DNA."

DNA is packaged into chromosomes, which resemble beaded bracelets. The rope ladder-like structure of DNA is coiled around bead-shaped proteins called histones to create nucleosomes. Scientists expected that either end of a strand of DNA could be uncoiled with equal ease from the nucleosome.

Ha and his colleagues instead found that if the sequence at one end made that end of the strand more flexible, that



Left page, left | *Shenzhen High-Tech Industrial Park.*

Left page, right | *Associate Professor of Computer Science Saurabh Sinha and colleagues found that genomics data will likely surpass other Big Data in scale.*

Above | *Research Assistant Professor and CPLC Director of Education and Outreach Jaya Yodh, graduate research assistant Thuy Ngo, and Gutgsell Endowed Professor of Physics Taekjip Ha.*

end clung more tightly to the nucleosome. If uncoiling began at the other end, this flexible end would act like the attachment of a string to a yoyo, forming an anchor and enabling the opposite end to unwind more easily.

This relationship between DNA sequence and stability of the nucleosome may imply a new facet of disease-causing mutations: a change in sequence might affect a gene's activity by making it easier or harder to access.

Glacial moraines influence new techniques in biomedicine

go.igb.illinois.edu/Glaciers

A recent piece of biomedical research has drawn extensively from an unexpected source: the geological remnants left behind by glaciers. By mimicking structural properties of the ice, researchers were able to design an implantable gel that delivers therapeutic agents to healing tissues with precision.

Associate Professor of Chemical and Biomolecular Engineering Hyunjoon Kong (RBTE) and his team wanted to control both the speed with which a drug is released and the spatial pattern of its distribution inside the body. This type of control is important, especially when trying to replicate the release of growth factors and other naturally produced chemicals that promote healing.

Kong was inspired by a phenomenon that accompanies glacial movement. As glaciers advance across landscapes over hundreds of years, the forces within the ice gather soil and rocks that have become trapped and push them to the front. When the glaciers recede, these piles of rocky materials, called moraines, are left behind.

Left | *Associate Professor of Chemical and Biomolecular Engineering Hyunjoon Kong.*

Right page | *Chemical and biomolecular engineering professors Huimin Zhao and Charles Schroeder, with graduate students Luke Cuculis and Zhanar Abil.*

In an article published in Advanced Healthcare Materials, *Kong and coauthors demonstrated that by freezing a hydrogel loaded with nanoparticles carrying therapeutic growth factor, they could create tiny channels within the hydrogel, much like those within glaciers, that facilitated better contact between the growth factor and blood cells when the gels were implanted in mice.*

The work was funded by the Korean Ministry of Science, ICT and Future Planning.

Genome-editing proteins seek and find with a slide and a hop

go.igb.illinois.edu/GenomeEditing

Searching a whole genome for one particular sequence is like trying to fish a specific piece from the box of a billion-piece puzzle. Using advanced imaging techniques, Illinois researchers have observed how one set of genome-editing proteins finds its specific targets, which could help them design better gene therapies to treat disease.

Chemical and biomolecular engineering professors Charles Schroeder (BSD) and Huimin Zhao (BSD Theme

Leader), along with graduate students Luke Cuculis and Zhanar Abil, published their work in the journal *Nature Communications*. The IGB and the David and Lucile Packard Foundation supported this work.

The structure of transcription activator-like effector proteins (TALE proteins) can be tweaked to recognize and bind to specific regions of DNA. TALE proteins are being used for techniques in synthetic biology, such as genome editing in plants or bacteria, and for gene therapy.

The researchers used imaging techniques that let them watch through a microscope how individual TALE proteins interacted with a strand of DNA. They observed that the proteins bind to the DNA and slide along the strand, performing frequent, short hops that allow them to move more efficiently without straying far from the DNA.

"It gives us a better understanding of the genome editing mechanism," Zhao said. "When we understand it better, it provides new insights for the design of the protein. If you really talk about therapeutic applications, it needs to be a specific design."

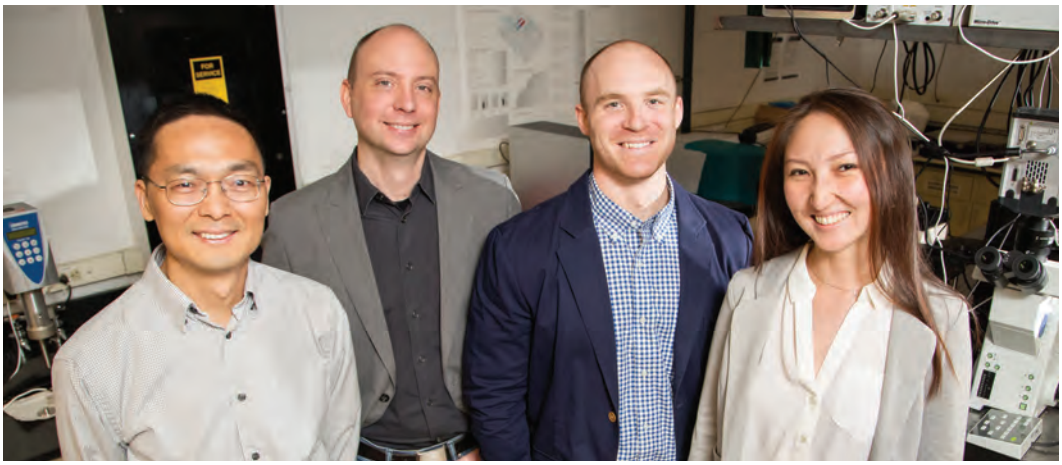
Many experiments for the price of one: breakthrough in the study of gene regulation

go.igb.illinois.edu/GeneRegulation

Inside every cell is a vast, dynamic network of information—the genome whose myriad genes allow that cell to function. In a study published as a Breakthrough Article in *Nucleic Acids Research*, computer scientists and molecular biologists demonstrated the utility of a novel approach to deciphering how networks of genes are regulated.

Computer scientist Saurabh Sinha (BSD/GNDP) and colleagues, including Scot Wolfe and Michael Brodsky at the University of Massachusetts Medical School, were led to this work by their fascination with interactions between DNA and proteins called transcription factors that help control when and where genes are expressed. Illinois computer science graduate student Charles Blatti played a major role in the study, which was funded by the NIH, NSF, and a Cohen Graduate Fellowship awarded to Blatti.

Researchers have previously relied on arduous, expensive



methods to determine where in the genome a particular transcription factor binds. Sinha and his collaborators realized that by combining information about how DNA was packaged throughout the genome with an algorithm that identified the DNA sequences a particular transcription factor would be attracted to, they could predict previously observed DNA-binding behavior of many transcription factors.

"In order to reconstruct a regulatory network in a new system, you don't necessarily have to do a whole lot of assays in the right cell types," Sinha said. "If you instead do an accessibility assay in those cell types and then overlay the motif information on top of it . . . these two together approximate the same information very well."

Illinois researchers build genomic platform to further understand E. coli

go.igb.illinois.edu/UnderstandingEColi

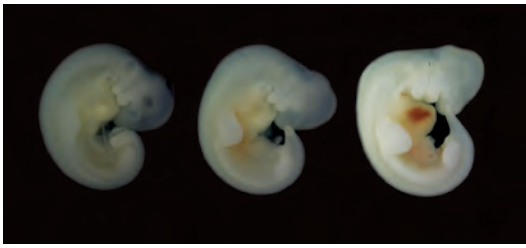
In August 2015, three children in three separate northern Indiana counties were sickened by *Escherichia coli* O157:H7, and one of them died. Bacterial outbreaks like these send public health officials into overdrive as they search for the source of the contamination. Was it undercooked meat, unwashed produce, juice that wasn't fully pasteurized? Did the children have contact with each other?

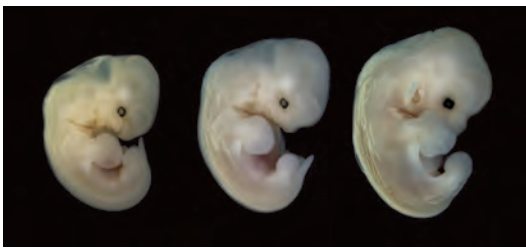
The difference between the potentially deadly O157:H7 strain and its more benign cousins stems from just a few genome sequence changes, explained Sergei Maslov (BCXT), a professor of bioengineering and Bliss Faculty Scholar. The team's research was published in the *Proceedings of the National Academy of Sciences* and funded by the Office of Biological and Environmental Research of the DOE and by Brookhaven National Laboratory, where Maslov holds a joint appointment.

Above | *Professor of Bioengineering and Bliss Faculty Scholar Sergei Maslov.*

Right page, left | *Karen Sears, Associate Professor at the School of Integrative Biology, coauthored the new study.*

Right page, right | *Embryonic development of the buffy flower bat,* Erophylla sezekorni, *showing the progressive growth and formation of the wings.*





Maslov, also an NCSA affiliate, and his colleagues, biophysicist William Studier, postdoctoral researcher Purushottam Dixit, and graduate student Tin Yau Pang of Brookhaven National Laboratory recently analyzed O157:H7 and 31 other *E. coli* strains to gain insights into the evolution of bacteria and the development of benign and pathogenic strains. They identified stretches of the *E. coli* genome that were present across all strains, and whose small variations in sequence could be used to characterize differences among existing or novel strains.

"This is key because, in the event of an outbreak of a new strain of pathogenic E. coli*, medical researchers will be able to run a single comparison of the new strain against this basic platform to quickly find what is new, what is lost or replaced by another strain," Maslov said.*

Before nature selects, gene networks steer a course for evolution

go.igb.illinois.edu/GeneNetworks

Natural selection is a race to reproduce, a competition between individuals with varying traits that helps direct the evolution of a species. As scientists begin to explore the complex networks of genes that shape the form and function of each individual, they can ask a new question about evolution: How do the structures of these gene networks determine which individuals appear on the starting line, silently influencing evolution before competition has even begun?

Animal biologist Karen Sears (GNDP/RBTE) and mathematician Zoi Rapti, along with collaborators at Illinois and four other institutions, have addressed this question by exploring the gene network that guides limb development in mammals.

They found that during early development when limbs are first forming, gene activity in this network varies little; later, when detailed limb structure is beginning to emerge, the network changes in structure and gene activity varies more widely. This pattern may make it easier for evolution to tweak, rather than remodel, limb structure.

"If early development is disrupted, limb development will be severely disrupted, and it is very unlikely that the resulting limb structure will be selectively advantageous," said Sears. "Later development, which doesn't have as many downstream impacts, might be expected to

be more free to vary because the consequences of that variation would be less dire."

Sears, Rapti, and coauthors were brought together by the Illinois BioMathematics Program, an NSF-funded project that promotes research collaboration among biology and mathematics undergraduates and faculty members. Their study was published in *PLOS Genetics*.

Study supports the validity of including viruses among living things

go.igb.illinois.edu/LivingViruses

A recently published analysis supports the concept of viruses as living entities that share a long evolutionary history with cells. The study offered the first reliable method for tracing viral evolution back to a time when neither viruses nor cells existed in the forms recognized today, the researchers said.

Their findings appeared in the journal *Science Advances*. The work was supported by the NSF, the USDA, the University of Illinois, and the French government.

The new study focused on the vast repertoire of protein structures, called "folds," that are encoded in the genes of all cells and viruses. Folds are the structural building blocks of proteins, giving them their complex, three-dimensional shapes. By comparing fold structures across different branches of the tree of life, researchers can reconstruct the evolutionary histories of the folds and of the organisms whose genomes code for them.

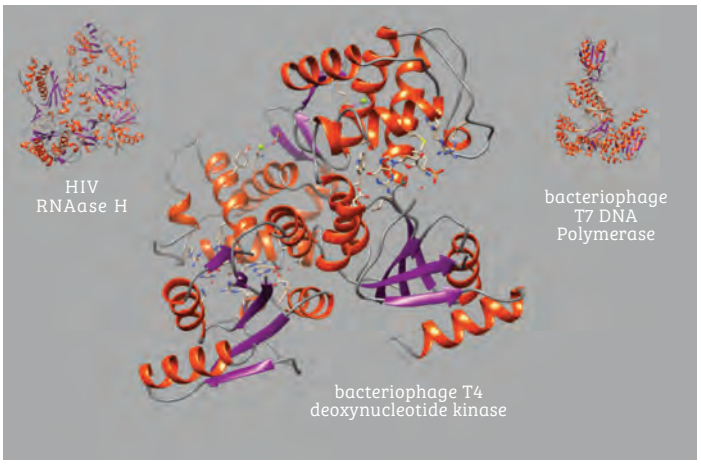
The data suggested "that viruses originated from multiple ancient cells ... and co-existed with the ancestors of modern cells," the researchers wrote. These ancient cells likely contained segmented RNA genomes, researcher said.

"Viruses now merit a place in the tree of life," said Professor of Crop Sciences Gustavo Caetano-Anollés (GEGC). "Obviously, there is much more to viruses than we once thought."

Straight up, with a twist: new model derives homochirality from the basic requirements for life

go.igb.illinois.edu/Homochirality

Life is quirky. Although the molecules that make up all living things obey physical and chemical laws, they do so with a puzzling twist. How did the distinctive molecular features of life emerge, and what can they tell us about life on Earth and elsewhere in the universe?



Left *The new study analyzes the distinct, three-dimensional structures found in proteins. These structures are called folds. Some folds are shared by all organisms, while others are unique to individual branches of the tree of life. Pictured here are folds found in several viral proteins.*

Swanlund Professor of Physics Nigel Goldenfeld (BCXT Theme Leader/CGRH/GNDP), graduate student Farshid Jafarpour, and postdoctoral researcher Tommaso Biancalani have made a breakthrough in one of the most central chemical quirks of life as we know it: homochirality, the uniform "left- or right-handedness" of biological molecules. Their new model addressing the emergence of this feature, published in *Physical Review Letters* and highlighted by *Physics*, suggested that homochirality can be used as a universal signature of life.

The team developed a model based on only the most basic properties of life: self-replication and disequilibrium. They showed that with only these minimal requirements, homochirality appears when self-replication is efficient enough. The work leads to a key conclusion: since homochirality depends only on the basic principles of life, it is expected to appear wherever life emerges, regardless of the surrounding conditions.

"For me, the most exciting thing is that this mechanism shows that homochirality is really a biosignature of life, a 100% signature, and should be expected anywhere life emerges," said Goldenfeld.

Research was made possible by funding from the IUB.

A pocket test for melamine-adulterated milk

go.igb.illinois.edu/MelamineMilk

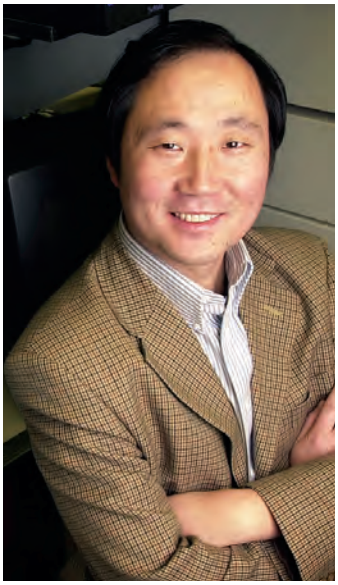
Researchers at Illinois and Beijing's Tsinghua University have developed a method for converting a personal glucose meter (PGM) into a portable tool for detecting melamine contamination in milk.

Melamine is used in the production of a variety of products but is not safe to eat. In 2008, the Chinese government discovered that some producers of powdered milk were using melamine to artificially inflate measurements of protein content.

A fast, portable test that could check for melamine adulteration anywhere along the chain of production would help manufacturers and consumers, said chemist Yi Lu (BSD). Lu's group had previously developed ways to use the PGM to detect metals, antibodies, and other molecules of interest.

The researchers identified a DNA sequence that binds to melamine; in their protocol, strands of DNA are added to the sample of milk to be tested, along with magnetic beads and a solution containing an enzyme, or protein catalyst, that converts sucrose to glucose. When melamine is absent, the sequence binds to both the bead and the enzyme and all three are removed from the solution. However, any melamine present will displace the enzyme, leaving it behind when the beads are removed. The more melamine, the more enzyme is left behind, and its presence can be detected by the PGM via the amount of converted glucose.

Initial research was supported by the NSF and the Major Scientific Equipment Development Project of China. GlucoSentient, a company Lu cofounded, is now working to commercialize the test. Lu and his colleagues described their method in *Analytical Chemistry*.



Left | *Jay and Ann Schenck Professor of Chemistry Yi Lu developed a new test to detect melamine contamination.*

Milenkovic looks for big data storage solution in DNA

go.igb.illinois.edu/DataStorage

While the cost of data storage has gone down in recent years, the difficulty of finding a storage medium that is nonvolatile, durable and large enough to meet today's big data needs has remained. A group of researchers, including several at Illinois, have taken a large step closer to a practical solution that comes from a surprising source.

To address the problem, Associate Professor of Electrical and Computer Engineering Olgica Milenkovic (GNDP/BSD) is exploring the use of DNA to store big data, in an attempt to replace devices such as flash drive memories, hard disks and magnetic recording devices. Compared with these technologies, DNA is durable and can achieve incredibly high storage densities: a single gram of DNA has the ability to store up to two terabytes of data.

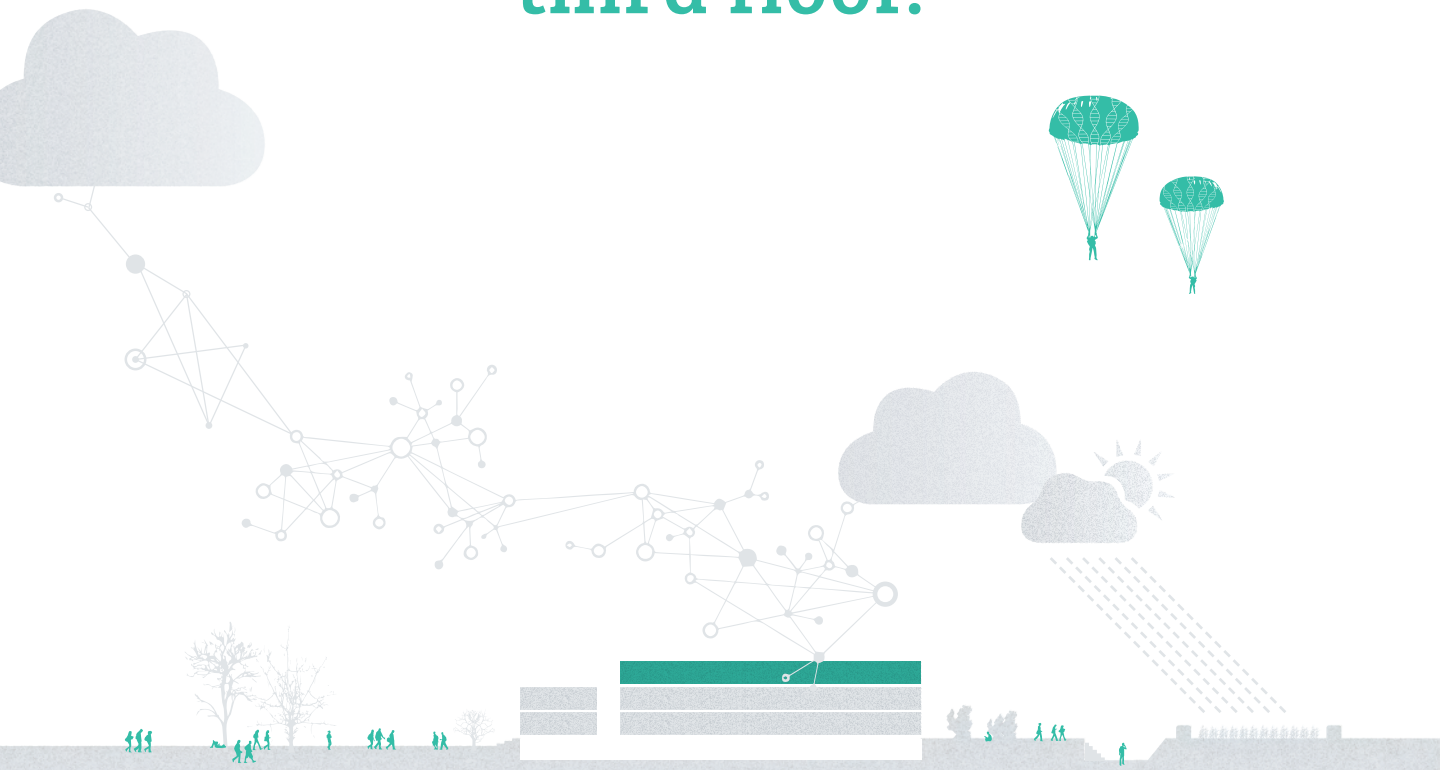
Milenkovic and colleagues have developed a novel DNA storage architecture, recently described in *Scientific Reports*, that allows for random access and rewrite capabilities. The work was supported by an NSF Science and Technology Center grant awarded to Purdue University; the project had previously been funded through a Strategic Research Initiative award.

"We are still finding bones from over 10,000 years ago from which we can extract DNA," Milenkovic said. "No other storage medium is that durable."

AWARDS

RASHID BASHIR was named a Fellow of the Biomedical Engineering Society (BMES). Fellow status is awarded to BMES members who demonstrate exceptional achievements and experience in the field of biomedical engineering with a record of membership and participation in the Society.	*Bioengineering Professor and Head, Department of Engineering (RBTE)*
JIANJUN CHENG was chosen as an American Institute for Medical and Biological Engineering (AIMBE) Fellow for outstanding contribution to the development of polymeric biomaterials and translational nanomedicine.	*Associate Professor of Materials Science and Engineering (RBTE)*
BRENDAN HARLEY was named a 2015-16 Center for Advanced Study Fellow. CAS Fellows are selected in an annual competition and are granted one semester of teaching release time to pursue an individual scholarly or creative project.	*Assistant Professor of Chemical & Biomolecular Engineering (RBTE Theme Leader)*
PAUL HERGENROTHER received the Innovation Transfer Award from the Innovation Celebration, a joint venture between the Champaign County Economic Development Corporation, University of Illinois, and Parkland College to recognize entrepreneurial spirit on campus and in the community.	*Professor of Chemistry (CDMC)*
JEFFREY MOORE was named the 2015 recipient of the Leete Award by the American Chemical Society Division of Organic Chemistry. The Leete Award recognizes outstanding contributions to teaching and research in organic chemistry.	*Murchison-Mallory Professor of Chemistry (BSD)*
CHARLES SCHROEDER was named a Dr. Ray and Beverly Mentzer Faculty Scholar, a position established through a gift from an alumnus of Chemical Engineering, Dr. Ray Mentzer and his wife Beverly Mentzer.	*Associate Professor of Chemical & Biomolecular Engineering (BSD)*
KAREN SEARS was named a 2015-2016 Helen Corley Petit Scholar, an honor given annually to exceptionally successful faculty members in the College of Liberal Arts and Sciences, based on their work as scholars and teachers.	*Assistant Professor of the School of Integrative Biology (GNDP/RBTE)*
TANDY WARNOW was named a 2015 Fellow of the Association for Computing Machinery (ACM), for contributions to mathematical theory, algorithms, and software for large-scale molecular phylogenetics and historical linguistics.	*Founder Professor of Bioengineering and Computer Science (BCXT/CGRH)*

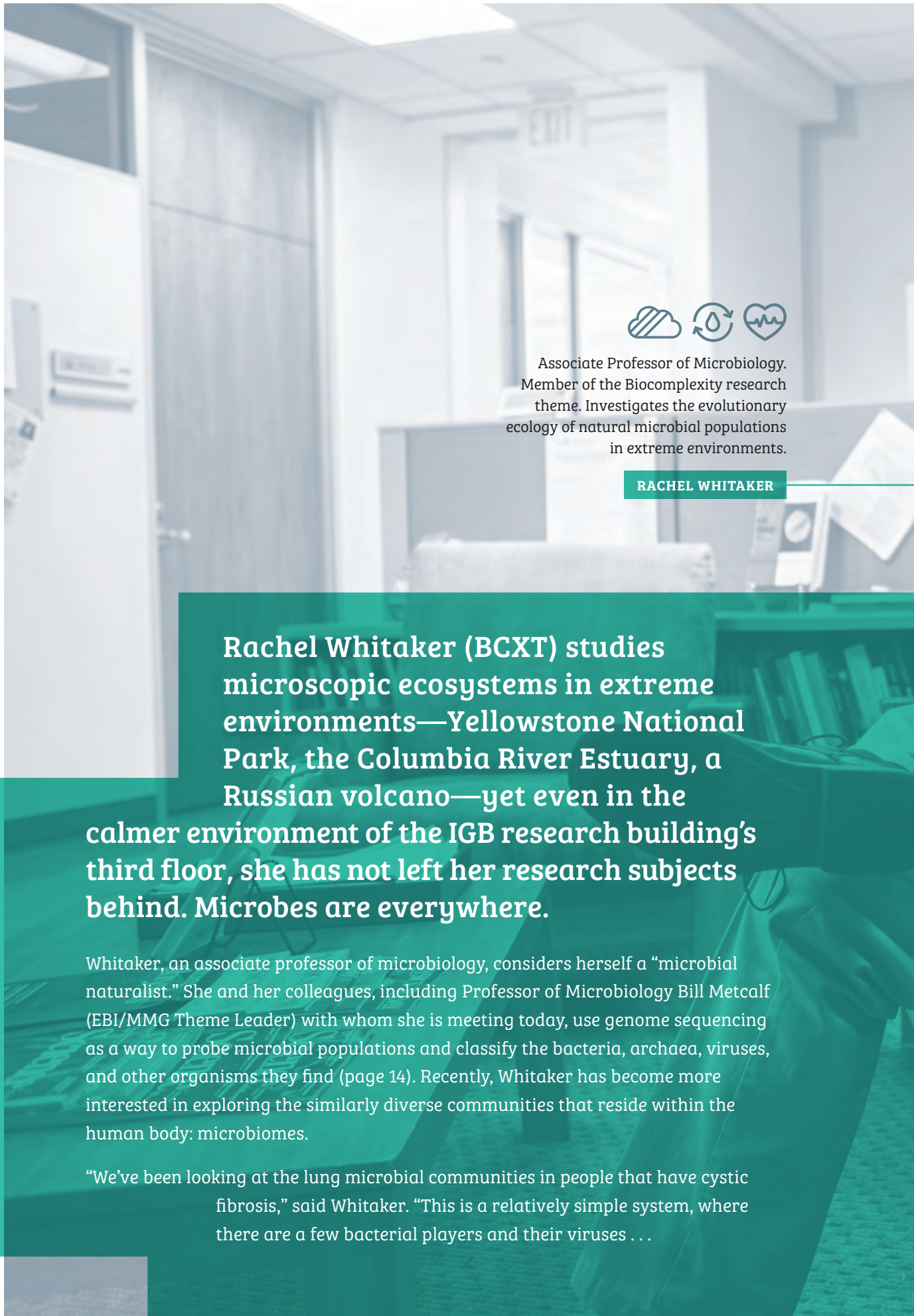
We're still in the Research Building. Now, join us on the third floor.



Every person or animal that suffers from ill health and every pathogen that causes disease has its own genome. Research in this area examines how genome function directs the development of healthy bodies and how disorders disrupt that function. Exploring the genomes of the microbes we live with also allows us to discover the molecular tools they use to aid or attack their hosts or to fight each other, knowledge that can act as a pathway to wellbeing.

ABOUT THE THIRD LEVEL, RESEARCH BUILDING

	34,564 SQ. FT.	101 OFFICE SPACES	2 THEMATIC LAB MODULES
PRESERVED OFFICE OF CARL WOESE	TEA TIME AREA	HISTORIC TIMELINE WALL	



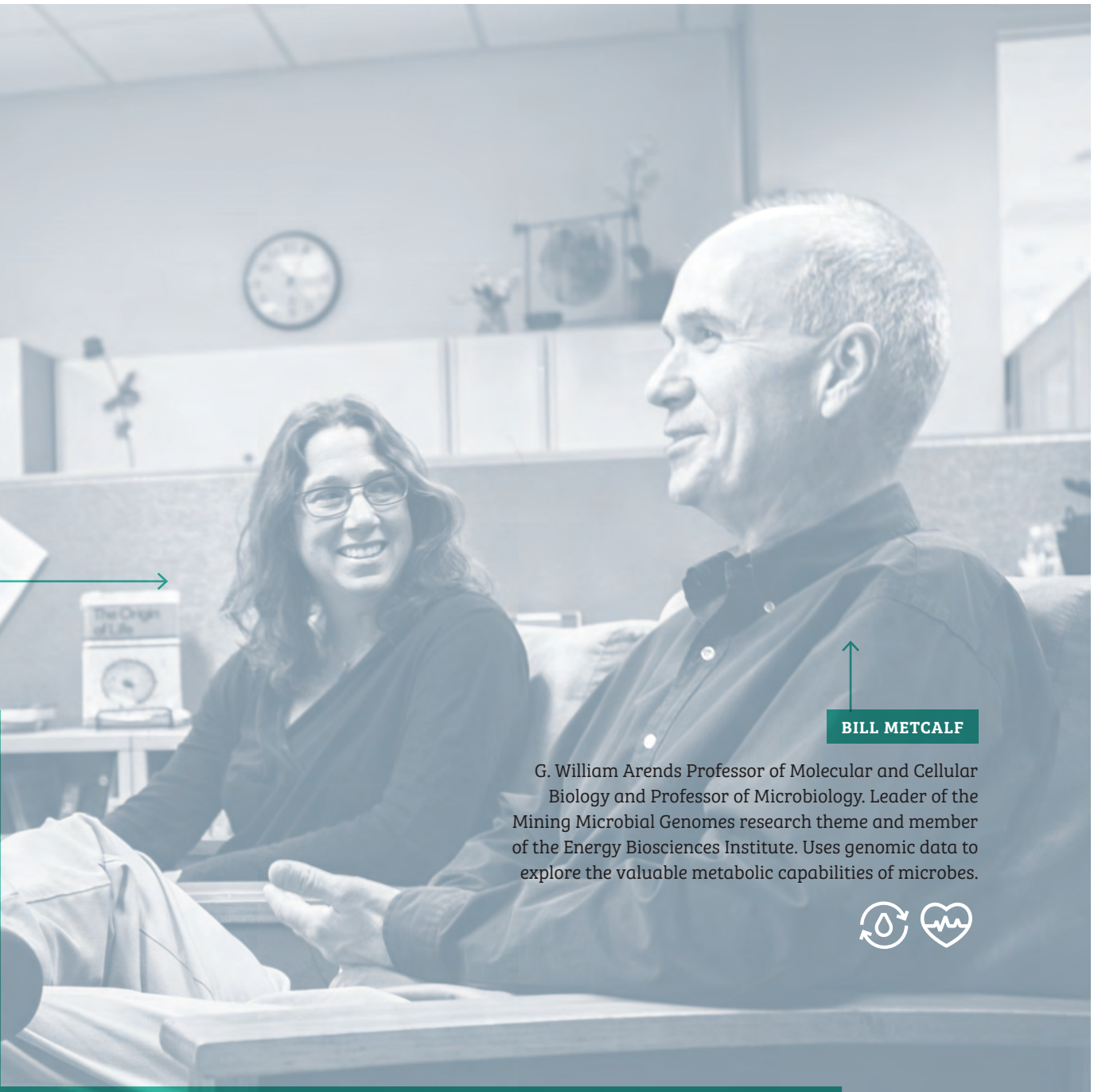
Associate Professor of Microbiology. Member of the Biocomplexity research theme. Investigates the evolutionary ecology of natural microbial populations in extreme environments.

RACHEL WHITAKER

Rachel Whitaker (BCXT) studies microscopic ecosystems in extreme environments—Yellowstone National Park, the Columbia River Estuary, a Russian volcano—yet even in the calmer environment of the IGB research building's third floor, she has not left her research subjects behind. Microbes are everywhere.

Whitaker, an associate professor of microbiology, considers herself a "microbial naturalist." She and her colleagues, including Professor of Microbiology Bill Metcalf (EBI/MMG Theme Leader) with whom she is meeting today, use genome sequencing as a way to probe microbial populations and classify the bacteria, archaea, viruses, and other organisms they find (page 14). Recently, Whitaker has become more interested in exploring the similarly diverse communities that reside within the human body: microbiomes.

"We've been looking at the lung microbial communities in people that have cystic fibrosis," said Whitaker. "This is a relatively simple system, where there are a few bacterial players and their viruses . . .

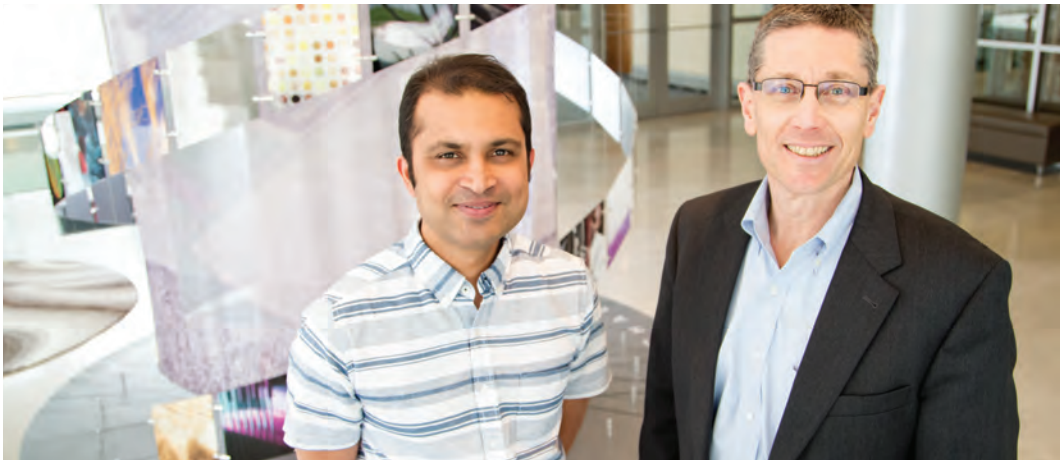


BILL METCALF

G. William Arends Professor of Molecular and Cellular Biology and Professor of Microbiology. Leader of the Mining Microbial Genomes research theme and member of the Energy Biosciences Institute. Uses genomic data to explore the valuable metabolic capabilities of microbes.

we're starting to look at that ecosystem in the same way as we've looked at other geothermal islands."

This view of each human body as a unique ecosystem is a powerful approach to health research, made possible by blending the traditional disciplines of ecology, genetics, microbiology, and pathology. The interdisciplinary environment of the IGB has allowed Whitaker, Metcalf and other faculty members to do exactly this, investigating the microbes we live with and those we can't live without; they are explorers of worlds on every scale.



Gene regulation underlies the evolution of social complexity in bees

go.igb.illinois.edu/BeeEvolution

A near-endless sequence of letters on a computer screen, representing the chemical structure of genomic DNA, seems far removed from the complex daily routine of a honey bee, bumble bee, or sweat bee.

Yet the small differences in the genome sequence of each bee species hide the key to understanding the much more visible differences in their social behaviors.

A genomic study of ten bee species representing a spectrum of social behavior from solitary living to large and highly organized colonies offered new insights into the genetic changes that accompany the evolution of bee behavior. Primary funding sources of the research, which was led by IGB Director and Swanlund Professor of Entomology Gene Robinson and published in *Science*, were the NIH, BGI, and the European Union Framework Programme for Research and Innovation.

By sequencing and comparing the genomes of ten bee species that vary in social complexity, the multi-institutional team of researchers found that some genomic features were consistently associated with social behaviors, while others varied according to differences in lifestyle or degree of social complexity. Genome sequence also evolved more slowly in social species, suggesting that social life may sometimes buffer the impact of natural selection.

New research theme focuses on computational genomic medicine

go.igb.illinois.edu/CGRHtheme

Every person is unique, and so are the individual health issues each may face. IGB's newly established research theme, Computing Genomes for Reproductive Health (CGRH), is aligned with efforts to translate genomic data into tailored medical approaches for individual needs.

"The forefront of medicine appreciates that health and treatment of disease is not a 'one size fits all' solution," said Derek Wildman, Professor of Molecular and Integrative Physiology, who leads the theme.

"The promise of precision medicine is to develop treatments that are directed

Left page — *Associate Professor of Computer Science Saurabh Sinha worked with IGB Director and Swanlund Professor of Entomology Gene Robinson and an international consortium of 52 scientists to discover that the evolution of bee societies is associated with increases in the complexity of gene regulation.*

Right — *The Lucy Islands in British Columbia, Canada were the discovery site for 6,000-year old skeletal remains. Pictured here is an ancient shell midden found on the islands.*

to each individual's genetic and physical makeup."

Combining genetic data with the multitude of different environmental exposures individuals face throughout their lives requires advanced computational strategies. CGRH researchers are using techniques in statistics, evolutionary biology, and medicine to unravel complex interactions between human behavior and genetics that lead to disorders of pregnancy and childbirth, as well as other health conditions.

Past and present genomes tell the story of Native American origins

go.igb.illinois.edu/NativeAmericanGenomics

The first human inhabitants of the Americas lived in a time thousands of years before the first written records, and the story of their transcontinental migration is the subject of ongoing debate and active research.

A study by a multi-institutional, international collaboration of researchers and published in Science *presents strong evidence, gleaned from ancient and modern DNA samples, that the ancestry of all Native Americans can be traced back to a single migration event, with subsequent gene flow between some groups and populations that are currently located in East Asia and Australia.*

The study was led by the Centre for GeoGenetics at the University of Copenhagen; more than 80 researchers contributed sequence data and analyses of key ancient individuals, and from living individuals in the Americas and possible ancestral regions. This breadth of sampling increased the power of the study to distinguish between alternative hypotheses for the timing and pattern of migration events. Ripan Malhi (CGRH/RBTE), an associate professor of anthropology and one of the senior coauthors, focused on genome sequence obtained from 6,000-year old skeletal remains found on Lucy Islands in British Columbia, Canada, and modern descendants of those individuals.

"There were multiple reasons why certain ancient individuals were selected," said Malhi. "We wanted a variety of locations as well as ages . . . individuals ranging from 6,000 years ago to more recent times show closer genetic affinity to the modern-day Native Americans in that same geographic region than anywhere else."

Study of ancient dogs in the Americas yields insights into human and dog migration

go.igb.illinois.edu/DogMigration

A study led by anthropologist Ripan Mali (CGRH/RBTE) and graduate student Kelsey Witt suggested that dogs may have first successfully migrated to the Americas only about 10,000 years ago, thousands of years after the first human migrants crossed a land bridge from Siberia to North America. The findings appeared in the *Journal of Human Evolution*.

The study, which looked at the genetic characteristics of 84 individual dogs from

more than a dozen sites in North and South America, was the largest analysis so far of ancient dogs in the Americas. Because the genetic samples were taken

Left page, top — *A ritual burial of two dogs at a site in Illinois near St. Louis suggests a special relationship between humans and dogs at this location and time (660 to 1350 years ago).*

Left page, bottom — *Graduate student Kelsey Witt conducted the largest genetic analysis so far of ancient dogs in the Americas.*

Right — *Associate Professor of Sociology, African American Studies, Urban and Regional Planning, and Social Work Ruby Mendenhall.*

from ancient city sites such as Janey B. Goode and Cahokia, their diversity speaks to the migrations and behavior of their human companions.

Human remains are not always available for study "because living populations who are very connected to their ancestors in some cases may be opposed to the destructive nature of genetic analysis," Witt said. Analysis of ancient dog remains is often permitted when analysis of human remains is not, she said.

"Dogs are one of the earliest organisms to have migrated with humans to every continent, and I think that says a lot about the relationship dogs have had with humans," Witt said. "They can be a powerful tool when you're looking at how human populations have moved around over time."

The University of Illinois provided funding for the study.

Ruby Mendenhall featured on spotlight on poverty and opportunity webcast

go.igb.illinois.edu/Opportunity

Ruby Mendenhall (GNDP), an associate professor of sociology, African American studies, urban and regional planning, and social work, was featured in a January webcast by *Spotlight on Poverty and Opportunity*, a web-based, non-partisan initiative to inform the policy debate about reducing poverty in the United States.

Mendenhall employs sociogenomics to explore how aspects of stress in urban environments "get under the skin" to affect health and wellness.

Sociogenomics highlights the dynamic nature of the genome and how environmental factors can influence gene expression patterns. Her work examines how the stress of living in neighborhoods with high levels of violence may affect the expression of genes that regulate the immune system and inflammation.

Mendenhall is working to establish an initiative called DREAM, Developing Responses to poverty through Education And Meaning. This initiative combines research, intervention and education to understand the experience and conditions of low income communities in Illinois, utilizing differences in genomic expression to evaluate factors such as stress, mental health, and environment.

Spotlight's Jodie Levin-Epstein talked with Mendenhall about the DREAM project; research on the Earned Income Tax Credit; and the Black Women's Network's impact on economic trajectories.

Cancer drug first tested in pet dogs begins human trials

go.igb.illinois.edu/PAC1Trial

A new drug that prompts cancer cells to self-destruct

Left *Veterinary clinical medicine professor Timothy Fan, left, and chemistry professor Paul Hergenrother tested an anti-cancer compound in pet dogs that will be used in human clinical trials.*

while sparing healthy cells has entered phase I clinical trials in humans.

Developed by Professor of Chemistry Paul Hergenrother (CDMC), the drug, named PAC-1, is moving toward testing in both human and canine brain cancer patients.

Early tests of the drug's effectiveness came when Hergenrother collaborated with Associate Professor of Veterinary Clinical Medicine Timothy Fan (CDMC), who tested PAC-1 in his canine cancer patients. These clinical trials helped the researchers find the best way to deliver the drugs—it is now in pill form for both human and canine patients—and led to new insights into the drug's activity and potential, Fan said.

The successes with dogs led to the formation of the Illinois-based company Vanquish Oncology to further develop the anti-cancer agent. Vanquish received initial support from the investment firm IllinoisVENTURES, and an anonymous "angel investor" provided the funding to move the drug through preclinical trials and gain Food and Drug Administration approval to begin a phase I clinical trial.

The trial, led by Dr. Oana Danciu of the University of Illinois Hospital and Health Sciences System in Chicago, opened enrollment last February to patients with advanced malignancies. Doctors will start the first patients at a low dose and gradually increase the dose and watch for side effects, the researchers said.

In the meantime, PAC-1 will enter clinical trials in pet dogs with brain cancer. That research will aid in understanding how human brain cancers may respond to the new treatment, Fan said.

Researchers look to HIV drug as a weapon against bacterial infections

go.igb.illinois.edu/FightingStrep

With antibiotic resistance on the rise, scientists are

looking for innovative ways to combat bacterial infections. A team of scientists led by Assistant Professor of Chemistry Douglas Mitchell (MMG) have found a tool that could help them fight one particularly resistant pathogen: a drug approved to treat HIV. Their work, which appeared in the journal *ACS Chemical Biology*, could lead to new antibacterial treatments.

Mitchell and colleagues pointed out that *Streptococcus pyogenes* is responsible for more than 600 million illnesses and 500,000 deaths globally every year. A major factor in the pathogen's ability to cause disease is its production of a toxin called streptolysin S, or SLS.

If scientists could figure out a way to jam the bacterial machinery that makes the compound, they could develop new therapies to fight the pathogen and slow the spread of antibiotic resistance.

But not much is known about how *S. pyogenes* makes SLS. Mitchell's team wanted to start filling in the blanks.

The researchers turned to an HIV drug called nelfinavir. Although the drug's target is an HIV protein, it is also known to incidentally block a key enzyme closely related to one in *S. pyogenes* that is critical for producing SLS. The scientists were able to make several nelfinavir-like compounds that stopped the bacteria from making the toxin in lab tests. They believe that the drug and its variants could help future efforts to understand how the deadly bacterium works and how to stop it. Their work was supported by the NIH and the University of Illinois.

Collaborative research team solves cancer cell mutation mystery

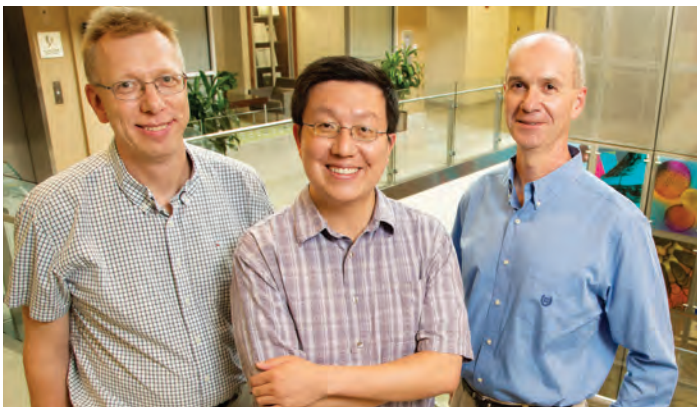
go.igb.illinois.edu/CancerMutation

More than 500,000 people in the United States die each year of cancer-related causes. Researchers have identified the mechanism behind one of the most common mutations that allows tumors to grow.

Approximately 85 percent of cancer cells obtain their limitless replicative potential through the reactivation of a specific protein called telomerase (TERT). Recent cancer research has shown that highly recurrent mutations in the promoter of the TERT gene are the most common genetic mutations in many cancers, including adult glioblastoma and hepatocellular carcinoma.

A collaborative team of researchers including Founder Professor of Bioengineering and Physics Jun Song (CDMC) and bioengineer Sua Myong (CDMC), supported by the University of Illinois and the University of California, San Francisco, uncovered the mechanisms by which these common mutations result in elevated TERT expression. Their findings, published in *Science*, have exciting implications for new, more precise and personalized cancer treatments with fewer side effects compared with current treatments.

The team found that TERT mutations act as a new binding site for a transcription factor that can then influence TERT expression. The newly identified transcription factor does not recognize the normal TERT promoter sequence, and thus, does not affect TERT expression in healthy tissue. Further work will test whether inhibiting the transcription factor activity would not only turn down TERT expression, but might also result in selective cancer cell death.



Right | *Chemistry professor Wilfred van der Donk (left), postdoctoral researcher Kou-San Ju, microbiology professor William Metcalf and their colleagues used genome mining to discover many new natural products quickly and inexpensively.*

New synthetic tumor environments make cancer research more realistic

go.igb.illinois.edu/SyntheticTumors

Tumors are notoriously difficult to study in their natural habitat—body tissues—but a new synthetic tissue environment may give cancer researchers the next-best look at tumor growth and behavior. Researchers have developed a new technique to quickly create a cell habitat that mimics tissue environments in the laboratory.

"This is really the first time that it's been demonstrated that you can use a rapid methodology like this to spatially define cancer cells," said Assistant Professor of Materials Science and Engineering Kristopher Kilian (RBTE). "That's important, because once you have that architecture, then you can ask fundamental biological questions."

To illustrate the potential of their more efficient and modifiable technique, Kilian, Professor of Chemistry Jeffrey Moore (BSD), graduate student Joshua Grolman, and colleagues mixed breast cancer cells with cells called macrophages, which signal cancer cells to spread and grow into a tumor. They were able to observe the cells' activity and growth within a hydrogel (a material similar to firm Jello), which mimics many properties of organ tissue.

Their research, supported by NSF and the American Cancer Society Illinois Division, was published in *Advanced Materials.*

"The long-term vision would be: A patient goes in and finds out they've been diagnosed with some sort of solid tumor," Kilian said. "You take a biopsy of those cells, you put it into this device, grow them and see how they respond to different treatments."

Genome mining effort discovers 19 new natural products in four years

go.igb.illinois.edu/GenomeMining

It took two postdoctoral researchers, a lab technician, four undergraduates and their faculty advisors only four years—a blink of an eye in the pharmaceutical industry—to scour a collection of 10,000 bacterial strains and isolate the genes responsible for making 19 unique, previously unknown phosphonate natural products. Each of these products is a potential new drug; one of them has already been identified as an antibiotic.

The researchers reported their findings in the *Proceedings of the National Academy of Sciences*, and were funded in part by the NSF.

Phosphonates are an abundant and diverse class of natural signaling molecules that have already proved useful to medicine and agriculture, said microbiology professor William Metcalf (EBI/MMG Theme Leader), who led the research with chemistry professor Wilfred van der Donk (MMG).

"We focused on phosphonates because we know they are strongly predisposed to have biological activity—antibiotic activity, antiviral activity, herbicidal activity," Metcalf said. Bacteria use these compounds to signal their presence to their microbial neighbors, or, at higher concentrations, to kill them, he said.

The researchers describe the new findings as a proof of concept that genome mining can be used on a scale that will speed the process of drug discovery, focusing on naturally produced compounds, which are among the most promising new drug leads.

Bacterial hole puncher could be new broad-spectrum antibiotic

go.igb.illinois.edu/Antimicrobials

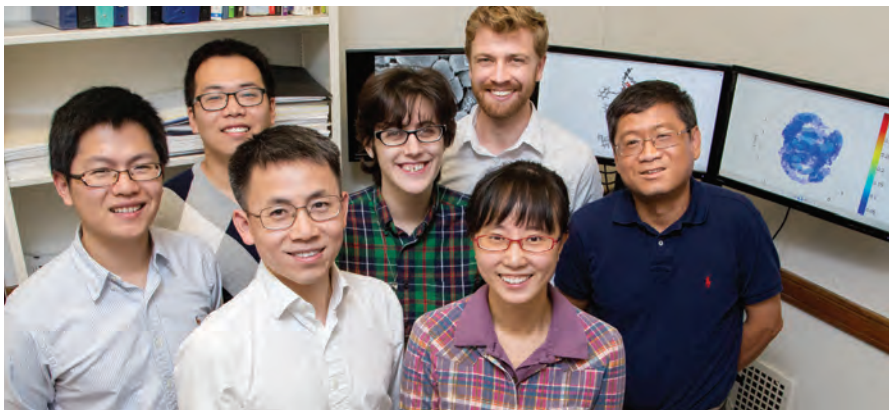
Bacteria have many methods of adapting to resist antibiotics, but a new class of spiral polypeptides developed at Illinois targets one thing no bacterium can live without: an outer membrane.

The polypeptides, which are short protein chains, act as bacterial hole-punchers, perforating the bacterial membrane until the cell falls apart. The antimicrobial agents are encased in a positively charged shell that lets them travel in body fluids and also attracts them to bacterial membranes.

Lead author and Professor of Materials Science and Engineering Jianjun Cheng (RBTE) and his fellow researchers published the findings in the *Proceedings of the National Academy of Sciences.* The NSF and NIH supported this work.

Many drugs are very targeted, interacting with a particular protein or interfering with a particular pathway in the bacterial cell. Bacteria can develop resistance to the antibiotic when alternative pathways evolve. The new antimicrobial polypeptides are specially designed to puncture the physical structure of the cell, making it much harder for bacteria to form resistance, postdoctoral researcher Menghua Xiong said. In addition, the new antimicrobial agents could be coupled with other, targeted drugs to enhance their effectiveness.

"The polypeptides punch holes in the membrane, which makes it very easy for other drugs to go through and bypass some of the



Right | *A team of researchers developed a new broad-spectrum antibiotic that kills bacteria by punching holes in their membranes. Front row, from left: materials science and engineering professor Jianjun Cheng and postdoctoral researcher Yan Bao. Back row, from left: postdoctoral researcher Menghua Xiong, graduate students Ziyuan Song and Rachael Mansbach, materials science and engineering professor Andrew Ferguson, and biochemistry Professor Lin-Feng Chen.*

drug-resistant mechanisms," Cheng said. "Together, they work even better than a single agent."

Wimps or warriors? Honey bee larvae absorb the social culture of the hive

go.igb.illinois.edu/SocialInformation

Even as larvae, honey bees are tuned in to the social culture of the hive, becoming more or less aggressive depending on who raises them, researchers described in a recent *Scientific Reports* article.

"We are interested in the general issue of how social information gets under the skin, and we decided to take a chance and ask about very young bees that are weeks away from adulthood," said IGB Director and Swanlund Professor of Entomology Gene Robinson, who performed the study with postdoctoral researcher Clare Rittschof and Pennsylvania State University Professor of Entomology Christina Grozinger.

The NSF-supported study examined the behavior of bees that were cross-fostered as larvae, moved from their native hive to a foster hive as they developed. Sister larvae were divided between high- and low-aggression colonies. The larvae were removed from their foster hives and put into a neutral laboratory environment one day before they emerged as adults, and later tested for aggressiveness.

The researchers were surprised to see that the bees retained the social information they had acquired as larvae. Those raised in aggressive colonies were 10 to 15 percent more aggressive than those raised in the gentler colonies. The finding was surprising in part because bee larvae undergo metamorphosis, which radically changes the structure of their bodies and brains.

"In mammals, including humans, the effects of early life social interactions often persist throughout adulthood despite additional social experiences," Rittschof said. "A similar pattern in honey bees has broad implications for our understanding of social behavior within the hive and in comparison with other species."

AWARDS

ALEKSEI AKSIMENTIEV was selected as a 2015-16 NCSA Faculty Fellow for his project "Patchwork Molecular Dynamics: A New Paradigm for Hardware-Accelerated Large-Scale All-Atom Simulations of Biological Systems."	*Associate Professor of Physics (CDMC)*
ARON BARBEY received an Outstanding Associate Editor Award from *Frontiers in Human Neuroscience.*	*Assistant Professor of Speech and Hearing Science (GNDP)*
BRIAN T. CUNNINGHAM was named Donald Biggar Willett Professor in the College of Engineering.	*Professor of Electrical and Computer Engineering (MMG)*
TAEKJIP HA was elected to the National Academy of Sciences, one of the highest professional honors a scientist can receive. He was also elected to the American Academy of Arts and Sciences.	*Gutgsell Endowed Professor of Physics (CDMC)*
JIAWEI HAN received the Engineering Council Award for Outstanding Advising.	*Abel Bliss Professor of Engineering (GNDP)*
AUINASH KALSOTRA was named a Center for Advanced Study Fellow.	*Assistant Professor of Biochemistry (GNDP)*
JIAN MA was named a 2015-16 Center for Advanced Study Fellow.	*Assistant Professor of Bioengineering (CDMC/GNDP/BSD)*
RUBY MENDENHALL was named a Center for Advanced Study Associate.	*Associate Professor, African American Studies of Sociology (GNDP)*
DOUGLAS MITCHELL received the National Fresenius Award, administered by the American Chemical Society. The award recognizes excellence in chemistry and is presented annually to an outstanding young scientist. He also received the 2015 Pfizer Award in Enzyme Chemistry from the American Chemical Society Division of Biological Chemistry and was named 2015-2016 Helen Corley Petit Scholar.	*Assistant Professor of Chemistry (MMG)*
SANDRA RODRIGUEZ-ZAS received the Senior Faculty Award for excellence in research from the College of Agricultural, Consumer and Environmental Sciences.	*Professor of Animal Sciences (GNDP)*
SAURABH SINHA was named Donald Biggar Willett Professor in the College of Engineering.	*Associate Professor of Computer Science (BSD/GNDP)*
DEREK WILDMAN received the International Federation of Placenta Associations (IFPA) Award in Placentology, bestowed for contributions to the field of placentology.	*Professor of Molecular and Integrative Physiology (CGRH)*

Next, follow us to the concourse level. This is where the two buildings connect.

New technologies let us see the physical world more clearly, in greater detail, in finer scales of space and time. Microscopes whose focus penetrates deeper or zooms closer than any before, analytical equipment that provides more accurate and precise quantitation of biological molecules, and software tools that refine and model larger volumes of data all represent new frontiers of research never before within reach.

ABOUT THE CONCOURSE LEVEL

	62,369 SQ. FT.	31 OFFICE SPACES	2 THEMATIC LAB MODULES	1 CAFÉ
	13 MICROSCOPES	1 NUCLEAR MAGNETIC RESONANCE SPECTROMETER (NMR)		

AUSTIN CYPHERSMITH

Senior Research Specialist in the IGB Core Facilities. Innovates new techniques, engineers and maintains equipment, trains and supports researchers.

KINGSLEY BOATENG

Senior Research Specialist in the IGB Core Facilities. Conducts research in molecular mechanisms of cell division. He also innovates new techniques, engineers and maintains equipment, and trains and supports researchers.

Kingsley Boateng, Senior Research Specialist in the IGB Core Facilities, doesn't get to see sunlight very much during his workday. Boateng's technical expertise is in microscopy, and he spends much of his time in darkened rooms, scrutinizing the glowing fluorescence of plant, animal, or microbial cells.

Today, though, the overhead light is on as he meets with Beryl Jones, a graduate student in Swanlund Professor of Entomology and IGB Director Gene Robinson's laboratory. They are discussing the operating features of the cryostat, a carefully calibrated piece of equipment used to slice frozen biological samples into incredibly thin sections—often thinner than a single sheet of paper.

Training researchers to use instruments and tailoring methods to fit their needs is an important component of Boateng's work at the IGB. Thanks to the dedicated efforts

PhD candidate in the Program of Ecology, Evolution and Conservation Biology. Works with Swanlund Professor of Entomology and IGB Director Gene Robinson to investigate the evolutionary origins and genomic mechanisms of reproductive division of labor in social insects.

BERYL JONES

and expertise of the Core Facilities staff, researchers across campus and beyond can use the cutting-edge equipment housed here to create and analyze high-resolution images or perform other specialty techniques (page 55).

Boateng also devotes time to his own research projects. He collaborates with Professor of Animal Sciences Isaac Cann (BCXT/EBI Deputy Director) to investigate the activity of proteins that regulate cell division in Archaea and pursues independent research on the formation of reproductive cells in mammals. He appreciates the ways in which his roles as a member of the Core Facilities and as a researcher harmonize with each other.

"Every day you have questions that you are trying to answer, even as you find more answers, more questions come up," he said. "I think the aspect that I enjoy the most is the ability to interact with people."

Travertine Reveals Ancient Roman Aqueduct Supply

go.igb.illinois.edu/Aqueduct

For hundreds of years, the Anio Novus aqueduct, built sometime between AD 38 and 52, carried water 54 miles from the Aniene River of the Apennine Mountains down into Rome. Modern scholars have struggled to determine how much water it supplied to the Eternal City, until now.

By studying the buildup of limestone deposits, called travertine, that formed as the water flowed within the aqueduct, researchers estimated the flow rate: 1.4 m^3/s (± 0.4), as reported in the *Journal of Archaeological Science*.

"At this rate, the aqueduct would have supplied the city with 370 gallons of water each second," said lead author Bruce Fouke (BCXT), Professor of Geology and Microbiology and Director of Carver Biotechnology Center.

"That's enough water per second to take a three-hour shower or to take seven baths."

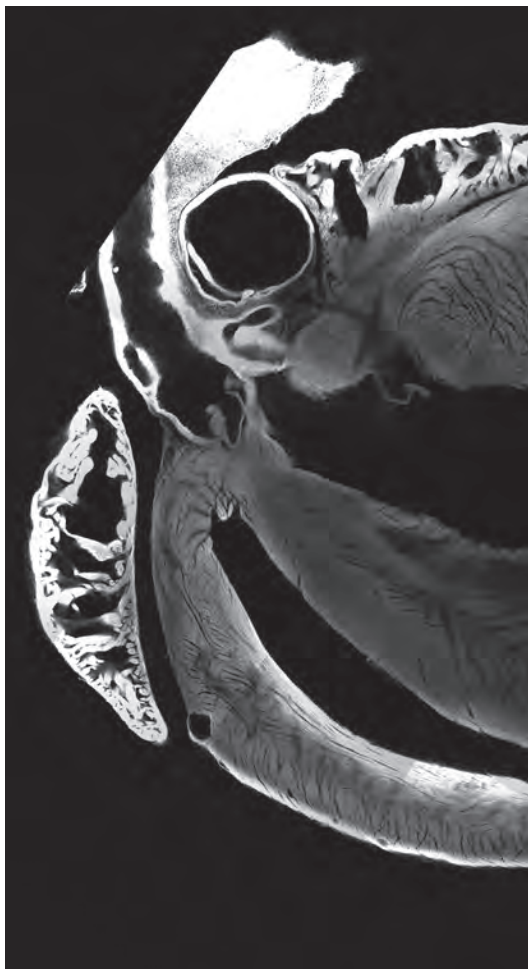
This estimate is significantly lower than previous estimates, which did not account for travertine deposits. The authors found that even a small amount of travertine reduced the water flow by 25 percent. Their work was supported by the Andrew W. Mellon Foundation; the Italian Government; the late Dr. William and Mrs. Janet Gale; Macquarie University; and the British Academy/British School at Rome. Their work was also made possible by the assistance of the Soprintendenza Speciale per i Beni Archeologici di Roma.

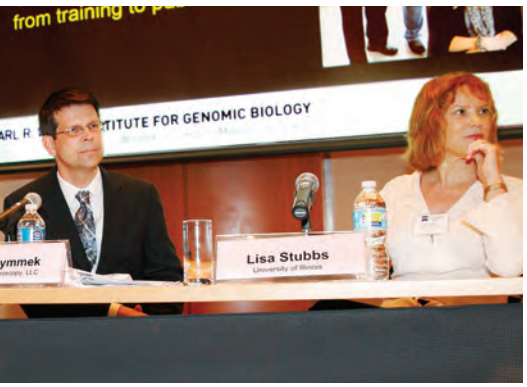
Art of Science extends its reach

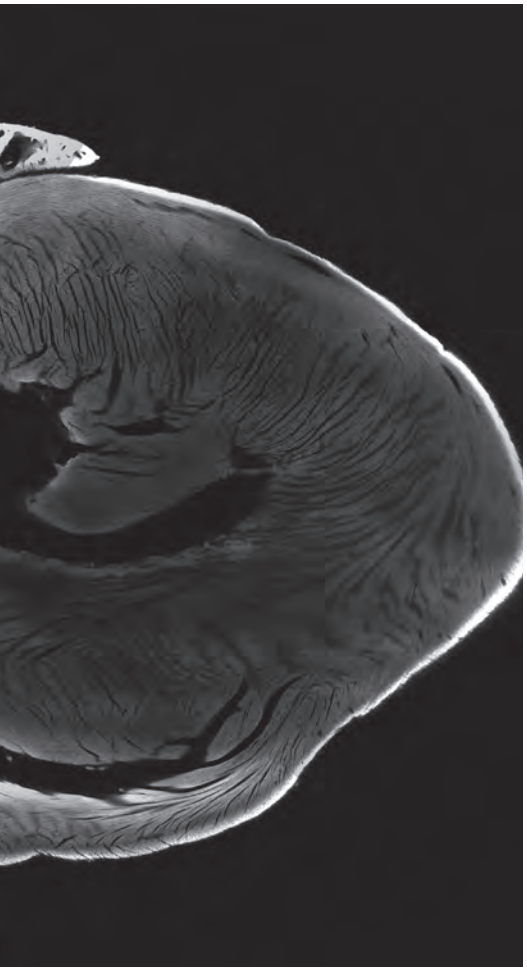
go.igb.illinois.edu/ArtofScience5

The Art of Science 5.0 exhibit opened at the Indi Go Artist Co-Op in April 2015, the show's fifth consecutive year. Managed by IGB Senior Multimedia Designer Kathryn Faith, the Art of Science is a celebration of common ground between science and art. Researchers and members of the public attended an all-ages opening reception, where they had the chance to view genomics through an unconventional lens.

The exhibition comprised images from research addressing significant challenges in the areas of environment, medicine, and energy use and production. Images were selected to highlight the beauty and fascination encountered daily in scientific endeavors.







Top | *IGB Senior Multimedia Designer Kathryn Faith, Director of Core Facilities Glenn Fried, and Professor of Cell and Developmental Biology Lisa Stubbs present on the Art of Science.*

Bottom | *A newly developed method yields detailed images of whole mouse hearts.*

Images from previous Art of Science exhibits have been showcased in diverse settings including the Alice Campbell Alumni center, the iHotel, Champaign's Willard Airport, and Chicago's O'Hare and Midway Airports. In June 2015, the German Center for Research and Innovation in New York hosted an exhibition entitled "Seeing the Art in Science" that featured Art of Science images. Presentations were given by Dr. Kirk Czymmek, Director of Carl Zeiss Microscopy North American Applications and Labs, as well as several representatives from the IGB: Faith, Director of Core Facilities Glenn Fried, and Professor of Cell and Developmental Biology Lisa Stubbs (GNDP Theme Leader).

New microscopy technique allows a clearer view of matters of the heart

go.igb.illinois.edu/CardiacImaging

Imaging heart tissue at high resolution is a critical component of cardiac research, allowing scientists to visualize the physical changes that characterize different diseases. However, current methods are labor-intensive and time-consuming, requiring physical sectioning, alignment, and 3D reconstruction to produce a comprehensive model of the heart. A new technique pioneered by IGB researchers has dramatically simplified this process while increasing resolution.

The team, led by Director of Core Facilities Glenn Fried and Assistant Director of Core Facilities Mayandi Sivaguru, used an unconventional staining method to label intact mouse hearts, rather than tissue sections on slides. The heart was then imaged with an innovative combination of microscopy techniques, allowing for deeper tissue penetration and image construction.

Their technique produced models of the heart that were not only three dimensional, but detailed at the cellular level, providing a high level of resolution and information previously difficult to achieve. The team validated their method by using these models to visualize the differences between healthy hearts and those that had undergone heart failure, noting differences in ventricular shape, volume, and wall thickness among other abnormalities.

The work was funded by the NIH and NSF and published in *BioTechniques*.

Head upstairs.
We are now in the Gatehouse Building.

Research at our Institute uses the science of genomes to address the pressing challenges faced by our society. By engaging with the public through programs and events, publications, and citizen science efforts, we ensure that our work continues to be relevant and impactful, a force for positive change in the wider world. Our interactions with the public are a source of motivation and inspiration; we hope and believe that many of our visitors feel the same.

ABOUT THE GATEHOUSE BUILDING

14,793 SQ. FT.	2 LEVELS	37 OFFICE SPACES	1 CARL R. WOESE MEMORIAL EXHIBIT

JESSICA WEDOW

Master's student in the Department of Plant Biology. Works with Associate Professor of Plant Biology Lisa Ainsworth (GEGC) to investigate the genomic response of C4 grasses to global climate change.

MELISSA MCKILLIP

Director of Public Engagement and External Relations. Oversees programs and events that foster a stronger connection between the IGB and the broader community.

On a warm day in midsummer, Melissa McKillip, director of public engagement and external relations, stands on the DNA-inspired walkway across from the plaza of the IGB. The flickering shadows cast by growing corn of the Morrow Plots are emblematic of the growth of science and science of growth that she and her coworkers are trying to encourage.

McKillip's role positions her at the interface of the Institute's scientific and societal aims, managing a diverse portfolio of outreach programs and events that have become self-

ILSE BARRIOS PEREZ

Master's student in the Department of Crop Sciences. Works with Assistant Professor of Crop Sciences Patrick Brown (EBI/GEGC) to characterize interactions between ozone-induced oxidative stress and fungal crop disease.

POLLEN POWER! CAMPERS

Area middle school girls with a passion for plant biology, climate science, pollination, and learning new things!

sustaining beyond her tenure at the IGB. Like a skilled interpreter, she has learned to navigate the quirky vocabularies and cultures of researchers, administrators, and stakeholders. Her flexibility and enthusiasm find a physical representation in her office two floors up, which contains everything from detailed budget information to bins of craft materials and candy for constructing models of cells and DNA.

Today and for the rest of Melissa's week, the concourse level of the IGB, with its classrooms, wet lab, and open spaces, are hosting over 20 middle school girls for Pollen Power!, the annual plant science day camp (page 63). McKillip, along with graduate students and camp counselors Ilse Barrios Perez and Jessica Wedow, is working with other IGB members to orchestrate the hands-on activities that will help girls who attend the camp understand connections between climate change and the biology of pollination.

McKillip's proficiency in moving projects from vision to reality has laid the groundwork as the IGB continues to engage with the public. With each new person impacted by the IGB's work, whether a middle school girl, an Illinois judge, a prospective faculty member, or a citizen scientist, an ever-strengthening connection is formed between science and society.

Exploring the intersection of genomics and heritage

go.igb.illinois.edu/SING

A group of young scientists representing more than 15 Native American communities traveled to Illinois this August for the fifth annual Summer Internship for Native Americans in Genomics (SING) workshop at the IGB. Participants discussed genomic research and technology, as well as their potential impacts on indigenous communities. The workshop is sponsored by the NIH, NSF, University of Illinois, University of Texas at Austin, and University of Copenhagen.

"We don't just focus on the lab work or the science, per se. We also discuss the ethical, legal and social implications of doing genomic research in indigenous communities," said Associate Professor of Anthropology Ripan Malhi (CGRH/RBTE), founding director of the workshop.

"What we wanted to do is have more indigenous scientists start doing this research, instead of non-indigenous scientists that go to the community and don't really have an understanding of the history and socio-political concerns within that community," Malhi said.

This year's workshop activities, many of which were led by Native American researchers, included

Left page — *Participants of the Summer Internship for Native Americans in Genomics workshop take notes in the laboratory classroom.*

Right — *Neil H. Shubin, Robert R. Bensley Distinguished Service Professor of Organismal Biology and Anatomy at the University of Chicago and host, PBS,* Your Inner Fish.

hands-on laboratory and bioinformatics training; conversations focused on genomics, communities, identity and ethics; and professional development sessions. Next year's workshop, which will be hosted by the University of Wisconsin, will be a reunion event for alumni from the first five years of SING.

IGB contributes exhibits to Caribbean Marine Education Center

go.igb.illinois.edu/CARMABI

Roy J. Carver Biotechnology Center Director and Professor of Geology and Microbiology Bruce Fouke (BCXT) and members of the IGB Communications Group contributed displays to a new Marine Education Center in Curaçao. The Center is part of the Caribbean Research and Management of Biodiversity Foundation (CARMABI), which is responsible for managing Curaçao's national parks, conducting marine and terrestrial ecological research, educating the public about nature and the environment, and advising the government and others on nature-related issues.

The recently inaugurated Marine Education Center is a small but high-quality museum exhibiting information on local marine life, particularly the coral reef surrounding the island where Fouke is conducting research. It is part of a broader education program aimed at increasing awareness of the natural beauty of coral reefs, as well as the key roles they play in the marine ecosystem.

Neil Shubin, host of PBS show Your Inner Fish, speaks at Illinois

go.igb.illinois.edu/YourInnerFish

Have you ever wondered why animals look the way they do?

It took more than 350 million years of evolutionary time for the bodies of humans and other animals to take shape. Hidden within each one is a story of life on Earth.

These ideas and others were explored by Neil Shubin, the Robert R. Bensley Distinguished Service Professor of Organismal Biology and Anatomy at University of Chicago and host of the PBS show *Your Inner Fish*, when he spoke as part of IGB's Genomics and Society lecture series on April 14, 2015. Shubin told the story of one of his most significant discoveries,

the 375-million-year-old *Tiktaalik roseae* fossil, which is considered an important transitional form between fish and land animals. He also described how diverse fossil findings are used to better understand the genetic and developmental processes that led to anatomical transformations in the evolution of animals.

The tone and accessibility of Shubin's talk reflected his strong commitment to sharing the importance of science with the public. He has authored two popular science books: *The Universe Within: The Deep History of the Human Body* (2013) and the best-selling *Your Inner Fish: A Journey into the 3.5-Billion-Year History of the Human Body* (2008).

Lifelong learning meets life-changing research

go.igb.illinois.edu/OLLI

How relevant are obscure-sounding topics such as cell division, genomics of plant breeding, and bioengineering for the daily lives of local community members?

A group of University of Illinois Osher Lifelong Learning Institute (OLLI) students discovered the everyday importance of genomics through a course offered by OLLI last spring, "How Genomics is Changing Everything." OLLI is a member-driven learning community for people over the age of 50 that offers classes in a wide variety of subjects, as well as a citizen scientist program. It is supported by the Bernard Osher Foundation, the Illinois Office of the Provost, and community members.

"It is such a pleasure to have an opportunity to interact with students in the OLLI community," said animal biologist Alison Bell (GNDP), who designed the course and coordinated guest presentations by other IGB faculty.

"They are inquisitive and ask razor-sharp questions that kept all of the instructors on their toes," Bell said.

Participants praised both the scientific content and its societal relevance in post-course feedback. One called the course a "mind-bending view of a changing

Left page, left — *Osher Lifelong Learning Institute (OLLI) students take courses on a variety of topics and volunteer in citizen scientist positions.*

Left page, right — *Associate Professor of Animal Biology Alison Bell.*

Right — *Department Head and Swanlund Professor of Entomology May Berenbaum shares science and stories with Pollen Power! campers.*

field," while another stated that they most enjoyed "the varied areas genomics is involved in, [and] how it touches all our lives in myriad ways."

Pollen Power! camp participants forecast a bright future for women in plant science

go.igb.illinois.edu/PollenPower

Does facetime with female researcher role models make a difference to middle school girls with an interest in science? For those who converged on the Carl R. Woese Institute for Genomic Biology (IGB) last July to learn about plants, pollination and technology, the answer was a cheerful yes.

"I liked talking with scientists. I talked to May Berenbaum," said Aisha DeSouza, 13, referring to a lunchtime conversation with the Entomology Department Head and IGB member (GEGC) who won a National Medal of Science Award in 2014. "Her story and what she studies were cool."

DeSouza was one of 24 girls who attended Pollen Power!, a week-long science day camp, participated in laboratories, presentations and activities at the IGB as well as other University of Illinois science and technology facilities, including Champaign-Urbana Community FabLab, the Plant Biology greenhouse, and the Pollinatarium. Campers learned about the science of plant response to global climate change by engaging directly with scientists and the tools and methods they use.

The camp, which is funded in part by the National Science Foundation, is co-organized by plant biologists Andrew Leakey (EBI/GEGC) and Lisa Ainsworth (GEGC), as well as IGB Core Facilities and Outreach staff. Many other IGB members contributed their time and efforts to camp activities.

iGEM team wins silver medal

go.igb.illinois.edu/iGEM

The goal of the 2015 Illinois International Genetically Engineered Machine (iGEM) team was to create a biosensor, a novel genetic component that would allow bacteria to record their

environment in analog. Their completed project, SCRIBE (Synthetic Cellular Recorders Integrating Biological Events), received a silver medal at the iGEM Giant Jamboree in Boston last fall.

The Illinois iGEM team, hosted by the IGB, is now in its eighth year, and has won several medals at both the regional and international level. The 2015 team consisted of ten undergraduate students from six departments, including three returning members. Their research was conducted in the Biosystems Design research theme laboratory under Associate Professor of Food Microbiology Yong-Su Jin (BSD/EBI), with the mentorship and assistance of graduate advisors from a number of departments.

Whereas traditional biosensors only signal the presence or absence of a compound or condition, SCRIBE causes the cell to add a detectable mutation to its chromosome, which is then passed to daughter cells. By "counting" the number of recombination events in cells from subsequent generations, it is possible to determine how much of the inducing substance was in their environment. Team member Caroline Blassick suggested one potential application for SCRIBE: testing for groundwater contaminants.

"SCRIBE could become a cost-effective, long term, and durable solution for testing environmental contaminants" that does not require frequent resampling as traditional monitoring does, said Blassick.

Left | *A young Genome Day attendee identifies differences between drought-sensitive and drought-tolerant plants.*

The iGEM Foundation is a non-profit organization that promotes synthetic biology technologies and collaborative, open-sourced study in the context of high school and undergraduate education. Funding for the Illinois iGEM team was provided in part by the IGB, the Departments of Bioengineering, Agricultural & Biological Engineering, and Chemical and Biomolecular Engineering, and the Roy J. Carver Biotechnology Center.

Families explore a world of science at Genome Day

go.igb.illinois.edu/GenomeDay

Reconstructing animal skeletons from a pile of bones, creating a shimmering necklace pendant by extracting DNA from strawberries, constructing a model of a double helix out of candy—these were a few of their favorite things.

So said children and parents who attended the IGB's fourth annual Genome Day, an open-house event for community members of all ages to learn about genomes, genes, DNA, and evolution. The annual event is hosted by the Orpheum Children's Science Museum in Champaign.

"I like it because it explains about genomes in a simple way," said one young participant. Activities were designed to engage people of all ages, and to cover a wide range of topics related to genomic research.

As in previous years, volunteers from SACNAS (Society for Advancement of Chicanos and Native Americans in Science) provided language assistance for Spanish-speaking attendees.

Illinois and AAAS co-sponsor bioengineering panel

go.igb.illinois.edu/BioengineeringPanel

One of the greatest strengths of biomedical engineering is also the source of one of its greatest challenges: its defiance of traditional disciplinary boundaries. In a panel hosted by the American Association for the Advancement of Science, Swanlund Chair Professor of Entomology and IGB Director Gene Robinson, Swanlund Chair Professor of Materials Science and Engineering John Rogers, Professor of Bioengineering Rashid Bashir (RBTE), and University of California, San Diego, Professor of Bioengineering Todd Coleman discussed how the increasing interdisciplinarity of biomedical engineering enables more innovative research, but can be harder to match with traditional funding sources. The

Left | *Professor of Microbiology and Animal Sciences Isaac Cann and Professor of Chemical and Biomolecular Engineering Paul Kenis exchange thoughts at the symposium.*

panel, entitled "Visionary Frontiers at the Convergence of Biology, Medicine and Engineering," was held in Washington, D.C on January 14, 2015.

In recent years, bioengineering has led to the development of integrated devices for diagnosing and treating diseases or improving health, including implantable, flexible electrodes that can monitor biological function or stimulate cell growth; "lab-on-a-chip" devices that can cheaply diagnose diseases; and better brain-computer interfaces that allow people to control prosthetics.

The panel, co-sponsored by Illinois and AAAS, emphasized the need for funding mechanisms that can support the type of large-scale, interdisciplinary research efforts that produced these technologies.

IGB honors renaming with symposium in memory of Carl Woese

go.igb.illinois.edu/WoeseSymposium

In September 2015, the IGB celebrated the memory of Carl Woese with a three-day symposium, "Looking in the right direction: Carl Woese and the New Biology." The symposium's agenda showcased Woese's resilient and dynamic legacy: the many areas of valuable research his work made possible.

Woese, who passed away in 2012, was the first scientist to map out the evolutionary history of all life on Earth, overturning the once-accepted tree of life with his discovery of the third Domain, Archaea. His work fundamentally changed our understanding of evolutionary biology, and anticipated today's genomic biology decades before its rise.

The symposium attracted world-class scientists, friends and colleagues of Woese, and promising researchers from across the country.

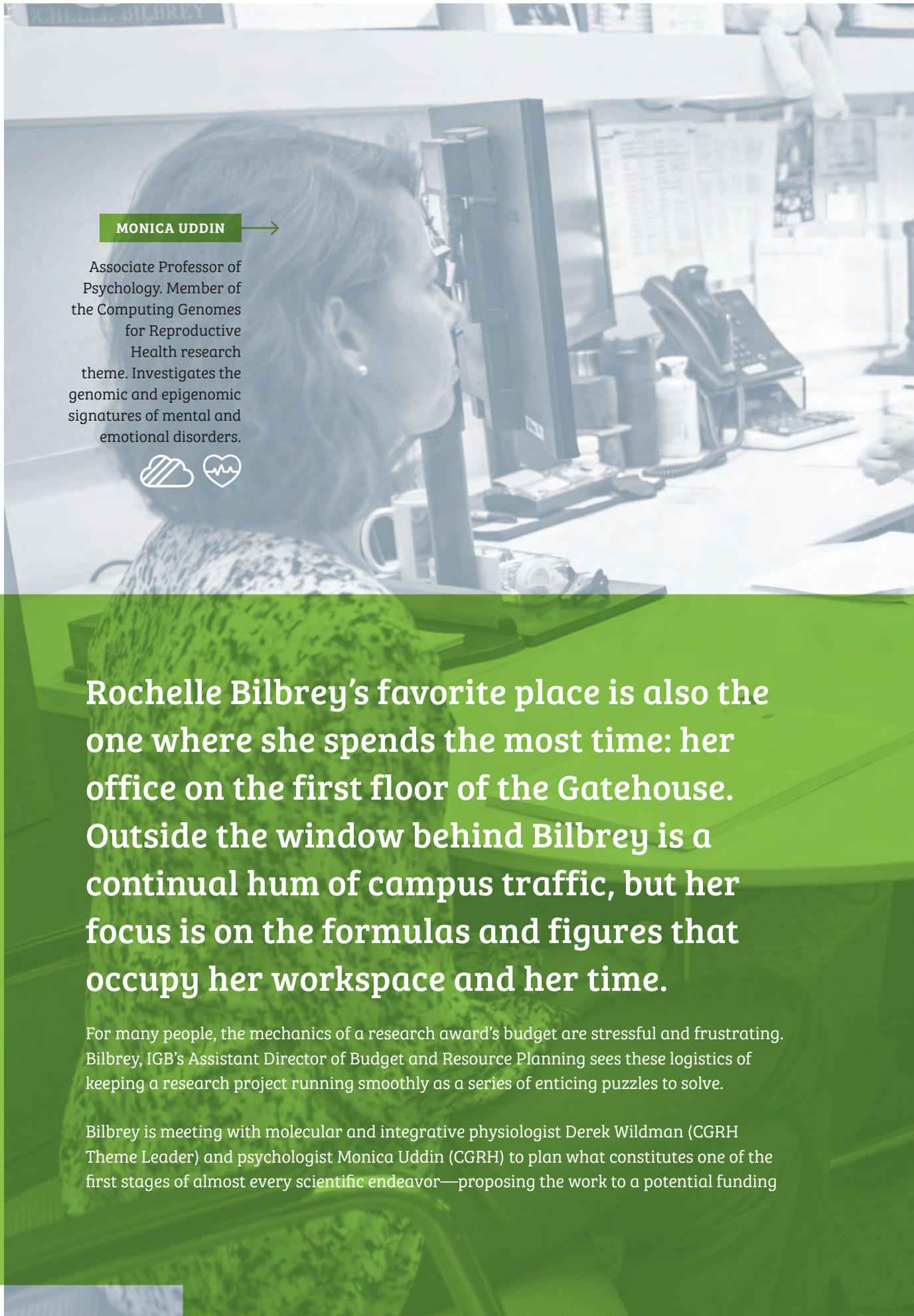
The six scientific sessions covered the scope of modern-day intersections between microbiology and genomics: the diversity of microbial ecosystems in the environment and within our own bodies; the details of molecular machinery and the evolution of the genome; the history of life's origins; and the future of synthetic biology.

Penny Chisholm, the Lee and Geraldine Martin Professor of Environmental Studies at the Massachusetts Institute of Technology, gave the opening lecture.

Many of the symposium's presentations are available online, including talks by University of California, San Diego Professor of Computer Science and Engineering Larry Smarr (founding director of Illinois' National Center for Supercomputing Applications) and University of Houston Professor of Biology and Biochemistry George Fox.

AWARDS

CLAIRE BENJAMIN received the inaugural 2015 Social Media Award from the office of Public Affairs. This Award for Communications & Marketing Excellence (ACME) is presented to an individual who brings innovation and quality content to their social media presence.	*Media Communications Specialist*
LEE DEVILLE received the Distinguished Teaching Award in Mathematics for Tenured Faculty from the College of Liberal Arts and Sciences.	*Professor of Mathematics (BCXT)*
A. BRYAN ENDRES was among the faculty to receive the American Agricultural Economics Association Distinguished Extension/Outreach Program Group Award from the College of Agricultural, Consumer and Environmental Sciences.	*Associate Professor of Agriculture and Consumer Economics (EBI)*
BRENDAN HARLEY received the Everitt Award for Teaching Excellence.	*Assistant Professor of Chemical & Biomolecular Engineering (RBTE)*
DOKYOUNG LEE received the North American Colleges and Teachers of Agriculture Educator Award from the College of Agricultural, Consumer and Environmental Sciences.	*Professor of Crop Sciences (EBI)*
DOUGLAS MITCHELL received a Camille Dreyfus Teacher-Scholar Award from the Camille & Henry Dreyfus Foundation, for demonstrated commitment to education signaling the promise of continuing outstanding contributions to both research and teaching.	*Assistant Professor of Chemistry (MMG)*
GENE ROBINSON was appointed to the Board of Scientific Advisors (BSA) of the National Courts and Sciences Institute (NCSI), a judicially governed science and technology institute providing special training to state and federal court judges, Native American court judges, and administrative law judges of federal and state executive agencies and independent regulatory agencies.	*Swanlund Chair Professor of Entomology and IGB Director*



MONICA UDDIN

Associate Professor of Psychology. Member of the Computing Genomes for Reproductive Health research theme. Investigates the genomic and epigenomic signatures of mental and emotional disorders.

Rochelle Bilbrey's favorite place is also the one where she spends the most time: her office on the first floor of the Gatehouse. Outside the window behind Bilbrey is a continual hum of campus traffic, but her focus is on the formulas and figures that occupy her workspace and her time.

For many people, the mechanics of a research award's budget are stressful and frustrating. Bilbrey, IGB's Assistant Director of Budget and Resource Planning sees these logistics of keeping a research project running smoothly as a series of enticing puzzles to solve.

Bilbrey is meeting with molecular and integrative physiologist Derek Wildman (CGRH Theme Leader) and psychologist Monica Uddin (CGRH) to plan what constitutes one of the first stages of almost every scientific endeavor—proposing the work to a potential funding

ROCHELLE BILBREY

Assistant Director of Budget and Resource Planning-Sponsored Research Administration. Oversees budget matters for IGB research projects from proposal to completion.

DEREK WILDMAN

Professor of Molecular and Integrative Physiology. Leader of the Computing Genomes for Reproductive Health research theme. Studies the evolutionary history of mammals, particularly the origins and genomic mechanisms of pregnancy and disorders of pregnancy.

agency. She and the rest of her group assist members of the IGB with research projects at every stage, fitting the development and implementation of budgets to the guidelines provided.

Like the colored balls in the games of pool Bilbrey enjoys outside of work (on a nationally competitive team), the different components of a budget must be brought into line with each other to ensure that work continues uninterrupted. Acting as a point of contact to help researchers, agencies, institutions and other important players stay in synchrony with each other gives Bilbrey a sense of satisfaction.

"Through this office, externally, we touch corporations, federal institutions, foundations, other universities, we work with so many different places in the U.S. and overseas," Bilbrey says. "The IGB has a lot of great research going on . . . just learning about all the different types of research is exciting."

Researchers awarded $3.1M to develop robotic rovers for crop phenotyping

go.igb.illinois.edu/MEPPRover

Illinois was awarded a 2-year, $3.1-million grant from the Transportation Energy Resources from Renewable Agriculture (TERRA) program, part of the DOE Advanced Research Projects Agency-Energy (ARPA-E). Illinois will be the lead institution on the Mobile Energy-crop Phenotyping Platform (MEPP), working in partnership with researchers from Cornell University and Signetron Inc.

The researchers are developing all-terrain automated ground rovers designed to travel between rows in the crop fields, viewing each plant from below and above. These rovers will be able to assess crop growth and other indicators of performance. The team will also use these data, as well as genome sequence data, to create models of crop growth and discover associations between genes and improved crop performance to accelerate breeding of improved energy sorghum.

"High throughput field phenotyping is crucial to

Left page | *A prototype of an all-terrain automated ground rover, designed to assess experimental crop plants, explores the greenhouse.*

Right | *Associate Professor of Electrical and Computer Engineering Olgica Milenkovic.*

making full use of the current ability to re-sequence many genetically unique lines in breeding improved bioenergy crops," said principal investigator Stephen Long (BSD/EBI/GEGC), Gutsgell Endowed Professor of Plant Biology and Crop Sciences.

"These all-terrain robotic platforms have a much lower cost yet are easily transportable, so they will be within the reach of small breeding operations as well as the largest companies," Long said.

Cutting Big Data down to a usable size

go.igb.illinois.edu/BigDataCompression

Next generation DNA sequencing technologies have turned the vision of precision medicine into a plausible reality, but also threaten to overwhelm computing infrastructures with unprecedented volumes of data. A $1.3-million NIH award has now enabled researchers at the University of Illinois and Stanford to help address this challenge by developing novel data compression strategies.

Genomic data sets pose a unique set of challenges and opportunities for data compression, because they have a large amount of repetition and a very small alphabet: just four nucleotide bases, or "letters," in raw DNA sequence. Repetitions within sequenced data provide opportunities for shortcuts in representation.

Associate Professor of Electrical and Computer Engineering Olgica Milenkovic (GNDP) and Stanford Professor of Electrical Engineering Tsachy Weissman are co-PIs on the project. Electrical and computer engineers Deming Chen and Wen-Mei Hwu and bioengineer Jian Ma (BSD/CDMC/GNDP), now of Carnegie-Mellon, are co-investigators.

"Precision medicine requires that genomic, proteomic, and other types of health-care related data corresponding to many individuals be acquired, stored and archived for many years," said Milenkovic. "[Our goal is] to develop a suite of software solutions for the next generation of biological data repositories and labs, which are currently facing enormous challenges with data storage, transfer, visualization, and wrangling."

Plant biologists, computer scientists receive $1.8M to create data platform for Big Data in plant breeding

go.igb.illinois.edu/TERRABigData

Historically, successful trait selection in plant breeding has involved manual measurement of individual plants. This requirement limits the number of plants that can be evaluated, and the scope of properties that can be measured. A new grant from the DOE Advanced Research Projects Agency-Energy (ARPA-E) Transportation Energy Resources from Renewable Agriculture (TERRA) program is funding the development of a system to automate the measurement of plants using cameras and other sensors mounted on drones, tractors, and robots, as well as analysis of the resulting large data sets to

facilitate the development of high-yielding strains of sorghum, a key bioenergy crop.

The $8-million award was granted to a team of partnered institutions led by researchers at the Donald Danforth Plant Science Center. Of the total grant, $1.8 million will go to the NCSA at Illinois to establish a supercomputing pipeline for a reference sensing platform. Plant biologist David LeBauer (EBI) will act as principal investigator for this component of the project.

"[Our] goal is to reduce the overall program cost by providing a single large dataset and computing platform for all of the projects funded by the TERRA program," said LeBauer. "This reference data set will allow researchers to . . . develop smaller, less expensive platforms that more efficiently target the most useful observations."

Ultimately, he said, these tools will be used to develop plants strains that are able to tolerate stresses such as drought, temperature, and disease.

Creating bio-machines to improve health

go.igb.illinois.edu/BioMachines

By studying the behavior of living cells and combining them with synthetic tissue, researchers are creating biological machines—"biobots"—to deliver drugs more effectively, function as internal diagnostic tools, or serve as contaminant sensors in the field.

This work is facilitated by a multi-institution effort known as the Emergent Behaviors of Integrated Cellular Systems (EBICS), which will receive $25 million in NSF renewal funding over the next five years to build living, multi-cellular machines to solve environmental, health, and security problems. Illinois is one of several participating sites; the Massachusetts Institute of Technology is the lead institution.

Developing these biobots takes a wide range of expertise. Co-principal investigator Rashid Bashir (RBTE), Abel Bliss Professor of Engineering and Head, Department of Bioengineering, is joined on the EBICS team by cell and developmental biologist Martha Gillette (GNDP), mechanical engineer Taher Saif, biomolecular engineer Hyunjoon Kong (RBTE), and electrical and computer engineer Gabriel Popescu.

According to Bashir, the goal of the project is to build non-natural functions with cells.

"[For example,] what if we could take passive vascular cells and combine them with cardiac muscle cells to create vascular tissue that could pump?" asked Bashir. "Such devices would allow patients' own bodies to become part of the solution."

Left page — Left to right: Gabriel Popescu, Hyunjoon Kong, Martha Gillette, Taher Saif, EBICS Director Roger Kamm of MIT, Rashid Bashir, and Program Coordinator Carrie Kouadio.

Left — Andrew Leakey, Associate Professor of Plant Biology, will lead a multi-institutional team to increase the water use efficiency of sorghum.

Other proposed applications of the biobots include remotely controlled systems and environmental biosensors.

Go WEST: $5M to increase water use efficiency in bioenergy sorghum

go.igb.illinois.edu/SorghumWUE

The IGB was awarded a 3-year, $5-million grant from the DOE Advanced Research Projects Agency-Energy as part of its OPEN 2015 funding initiative (ARPA-E OPEN). Under plant biologist Andrew Leakey (EBI/GEGC), the interdisciplinary and multi-institutional team is increasing the water use efficiency (WUE) of sorghum, a valuable bioenergy crop.

Sorghum, like nearly all plants, transpires through stomata, small pores on the surface of the leaf that allow for gas exchange. By decreasing the number of stomata, researchers hope to increase WUE by reducing the amount of moisture lost. In addition, by shifting a larger percentage of photosynthetic activity to lower leaves, the higher local humidity will further reduce water loss.

By combining these approaches, the team predicts via its mathematical models that it may develop sorghum with a 40% improvement in WUE.

"That means that we should be able to expand the growing area into regions that are currently too dry to produce a profitable crop," said Leakey. "And in the areas that are already suitable for growing, plants will suffer less in drought years, and make more biomass with the water that there is."

All in all, this research could unlock more than nine million new acres currently unusable for energy crop production, and increase production on currently farmed land by nearly 30% on average. Much of the newly available land would be located to the west of sorghum's current range, inspiring the project's name, WEST (Water Efficient Sorghum Technologies).

Interdisciplinary team receives $8M from NIH to study nuclear structure

go.igb.illinois.edu/NuclearStructure

For years, genome-mapping technology has represented DNA as a linear code, but that's not how it exists in the cell. Genomic DNA is tangled up in three dimensions inside the nucleus, with higher- and lower-density areas. Gene clusters can also shift their positions over time. But what is the functional significance of this positioning, and what does it mean when it changes?

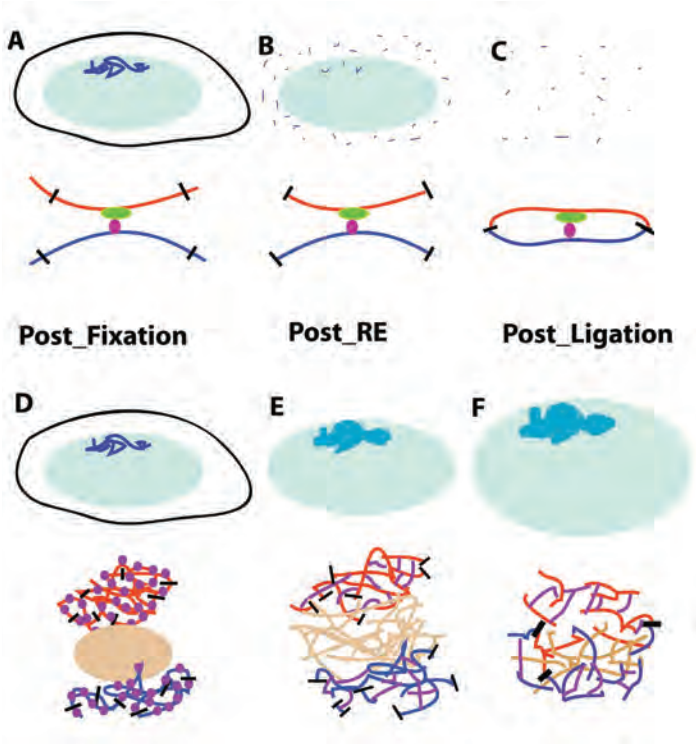
Professor of Cell and Developmental Biology Andrew Belmont (BSD) is heading a team that has been awarded an $8-million, five-year grant to study nuclear structure from the NIH Common Fund as part of the recently-unveiled 4D Nucleome Program. Other members on the project include Centennial Endowed Chair Professor of Chemical and Biomolecular Engineering Huimin Zhao (BSD Theme Leader/EBI/MMG), biomolecular engineer Jian Ma (BSD/GNDP), and collaborators at Florida State University and the Netherlands Cancer Institute.

Determining the position of the genome within the nucleus and creating a functional map are major project goals. The team will also model the relationships between DNA sequence, nuclear position, and gene function. By inserting large pieces of synthesized DNA, they will "rewire" chromosome regions to different nuclear locations and then determine the functional consequences of this rewiring.

Belmont believes this and other 4D Nucleome projects will dramatically further our understanding of the connections between nuclear organization and genomic function.

"The 4D Nucleome Program's longer-term goal is then to apply these new technologies and insights in order to ask how nuclear organization changes during development and in human disease," Belmont said. "Understanding nuclear structure at this level is an important first step."

Bottom | *A newer molecular technique for examining chromosome structure may reveal functional interactions between different regions of the genome.*



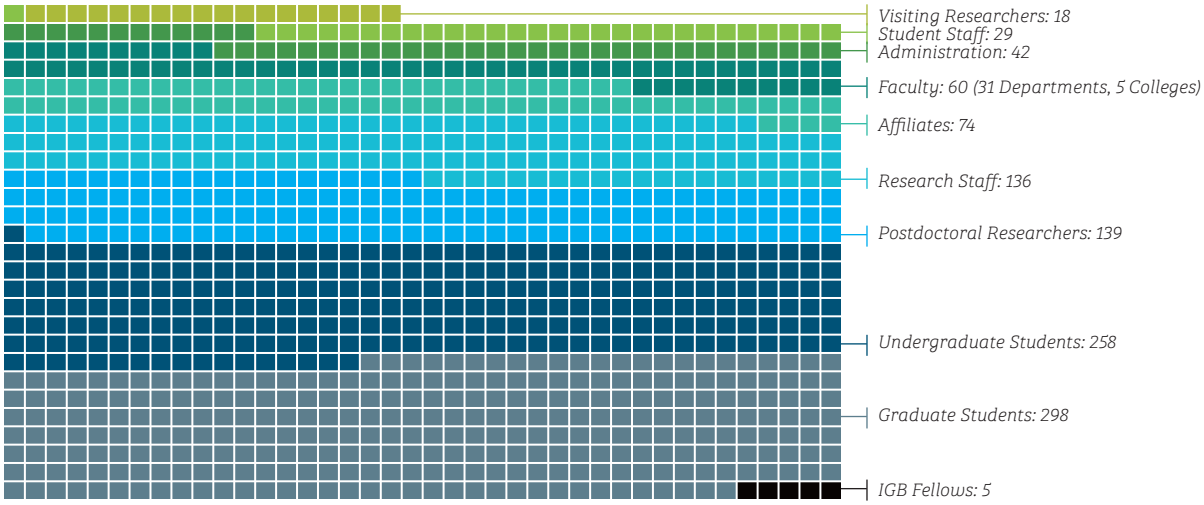
AWARDS

JESSE BLACK was selected as a 2015 award recipient of the American Society for Microbiology (ASM) Undergraduate Research Fellowship, aimed at highly competitive students who wish to pursue graduate careers in microbiology.	*Microbiology, Whitaker Lab*
PATRICIA BLAIR was selected to receive an ACS Division of Medicinal Chemistry Predoctoral Fellowship, a prestigious award given annually since 1991. The award recognizes superior achievement as a predoctoral student and the potential to become an independent investigator.	*Graduate student, organic chemistry, Douglas Mitchell Lab*
PRINCESS IMOUKHUEDE received a Scientist Development Grant from the American Heart Association, given to highly promising scientists with research broadly related to cardiovascular function, bioengineering, biotechnology, and public health problems. She was also named a 2015 Young Innovator of Cellular and Molecular Bioengineering, which highlights the best and brightest young faculty working in the area of cellular and molecular bioengineering.	*Assistant Professor of Bioengineering (RBTE)*
KRISTOPHER KILIAN received a National Science Foundation CAREER Award for his work in regenerative medicine and his initiative in educating students about stem cell engineering.	*Assistant Professor of Materials Science and Engineering (RBTE)*
YANG LI received a 2014 Chinese Government Award for Outstanding Self-Financed Students Abroad. Highly competitive, this award is sponsored by the Chinese Ministry of Education and recognizes the academic excellence of self-financed (non-government sponsored) Chinese students pursuing a PhD across all fields of study overseas.	*PhD Candidate, Department of Bioengineering, Jian Ma Lab*
DIPTI NAYAK was chosen as a 2015 Life Sciences Research Foundation Fellow, an organization which funds outstanding postdoctoral fellows in all areas of the life sciences.	*IGB Fellow (BCXT)*
JAMES O'DWYER was selected for a Simons Foundation Investigator Award. The Simons Investigators program provides a stable base of support for outstanding scientists, enabling them to undertake long-term study of fundamental questions.	*Assistant Professor of Plant Biology (BCXT)*
TONG SI received a 2014 Chinese Government Award for Outstanding Self-Financed Students Abroad. Highly competitive, this award is sponsored by the Chinese Ministry of Education and recognizes the academic excellence of self-financed (non-government sponsored) Chinese students pursuing a PhD across all fields of study overseas.	*IGB Fellow (BSD)*

IGB Numbers of 2015

In science and in communication, we use stories—like the ones we've shared here about our work this year—to create a feeling for something, to provide examples that build a common understanding. Metrics convey meaning in a different way. We reflect on the numbers associated with our Institute's structure and function to gauge our progress so far and to set meaningful goals for the future. In their own way, they paint a clear picture of who we are.

PEOPLE TOTAL: 1059



IGB FY15 PUBLICATIONS 289 PAPERS PUBLISHED, 10 IN *SCIENCE/NATURE*

SCIENCE 9

IGB members in bold

S. Arslan, R. Khafizov, C. D. Thomas, Y. R. Chemla and **T. Ha**, "Engineering of a superhelicase through conformational control," *Science*, vol. 348, pp. 344-347, 2015.

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M. J. Comstock, K. D. Whitley, H. Jia, J. Sokoloski, T. M. Lohman, **T. Ha** and Y. R. Chemla, "Direct observation of structure-function relationship in a nucleic acid-processing enzyme," *Science*, vol. 348, pp. 352-354, 2015.

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Z. L. P. Simões, K. Hartfelder, J. D. Evans, S. M. Barribeau, R. M. Johnson, J. H. Massey, B. R. Southey, M. Hasselmann, D. Hamacher, M. Biewer, C. F. Kent, A. Zayed, **C. Blatti III**, **S. Sinha**, J. S. Johnston, S. J. Hanrahan, S. D. Kocher, J. Wang, **G. E. Robinson** and G. Zhang, "Genomic signatures of evolutionary transitions from solitary to group living," *Science*, vol. 348, 2015.

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NATURE | 1

IGB members in bold

M. Rasmussen, M. Sikora, A. Albrechtsen, T. S. Korneliussen, J. V. Moreno-Mayar, G. D. Poznik, C. P. E. Zollikofer, M. S. Ponce De León, M. E. Allentoft, I. Moltke, H. Jónsson, C. Valdiosera, **R. S. Malhi**, L. Orlando, C. D. Bustamante, T. W. Stafford Jr., D. J. Meltzer, R. Nielsen and E. Willerslev, "The ancestry and affiliations of Kennewick Man," *Nature*, vol. 523, pp. 455-458, 2015.

IGB CORE FACILITIES USAGE

FY15 USERS

127 Research Groups, 342 active users

ECONOMIC DEVELOPMENT

PATENT APPLICATIONS	FY15:7	69 TOTAL (17 EBI)
DISCLOSURES	11	108
LICENSES OPTIONED	9	
PATENTS ISSUED	4	14

"Complete Hemicellulose Degrading Enzyme Cocktail"
Isaac K. O. Cann, Roderick I. Mackie, Dylan Dodd, Yejun Han, Shinichi Kiyonari

"Discovery and Characterization of Novel Pentose-Specific Transporters for Biofuels Production" (2 divisional patents)
Huimin Zhao, Yong-Su Jin, Suk-jin Ha, Soo Rin Kim, Jing Du, N. Louise Glass, Sijin Li, Jin Ho Choi, Chaoguang Tian, William T. Beeson

"Selective Apoptotic Induction in Cancer Cells"
Paul J. Hergenrother, Karson S. Putt, Diana C. West, Quinn P. Peterson, Steven J. Penner, Grace Chen, Ted Tarasow, Jennifer M. Pearson

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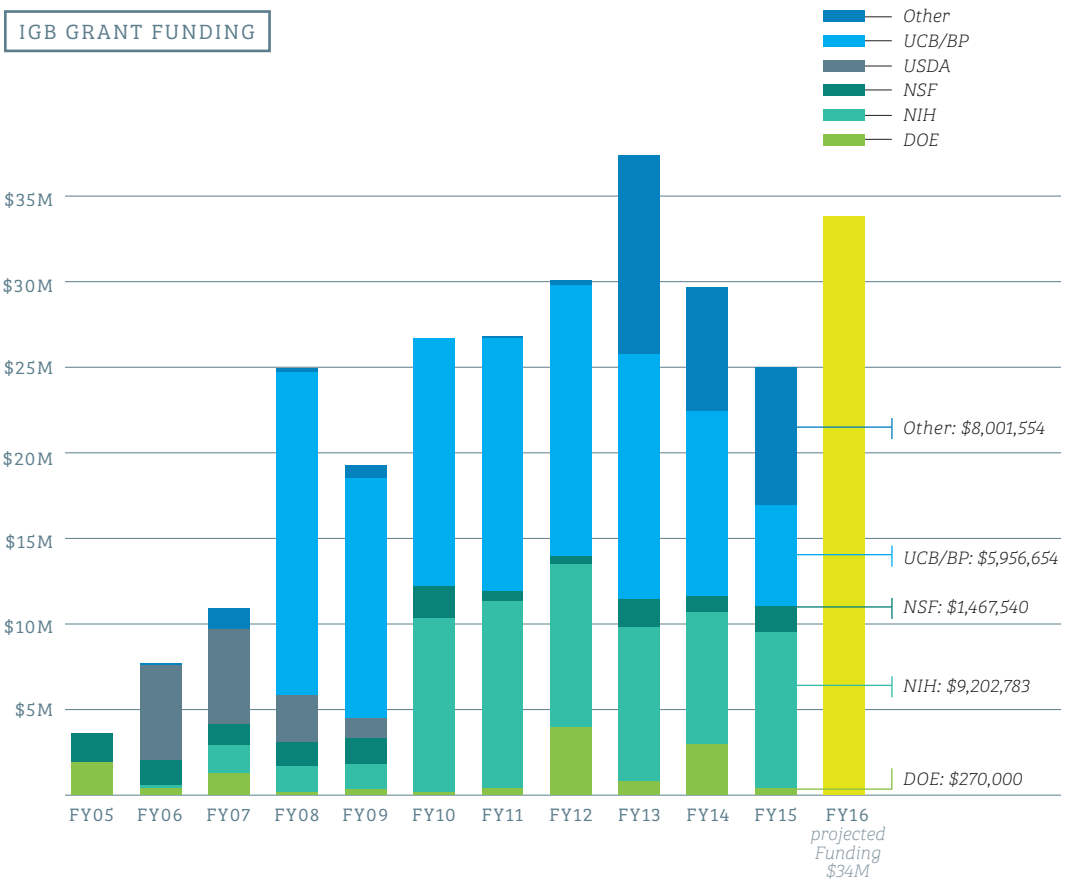

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