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Anybody
out there?



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berkeley science review

from the editor

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DEAR READERS,

Welcome to the 19th issue of the *Berkeley Science Review*. In this era of Facebook and Twitter, I feel a bit anachronistic introducing you to an honest-to-goodness paper and ink magazine that only appears twice per year. Indeed, information technology is dramatically influencing the research appearing in our pages, much of which focuses on finding connections buried in huge swaths of data that would surely be beyond the reach of human comprehension without computational assistance.

On page 30, Sisi Chen tells us how even the most fundamental assumptions about the origins of different classes of life are breaking down as we catalogue more and more of the Earth's genomic diversity. Phuongmai Truong describes the new SynBERC synthetic biology center (p. 36), which aims to nurture a field dedicated to building biological devices from the huge collection of genetic parts being discovered. For decades astrobiologists have been using distributed computing to search for signs of life elsewhere in the cosmos, as Naomi Ondrasek tells us on page 40. According to Crystal Chaw, such tools are also giving researchers new insights into the workings of Jupiter, our solar system's largest and most mysterious planet (p. 17). Finally, Alireza Moharrer writes that the power grids of the future will make use of Internet technology to intelligently balance the availability of electricity and consumer demand in real-time (p. 24).

Nevertheless, there are still many examples of scientists doing things the old-fashioned way, combining exciting observations, plain clever ideas, and careful experiments. Azeen Ghorayshi describes a sharp-eyed researcher's accidental discovery of a new water-splitting catalyst (p. 12), and Sebastien Lounis writes of an elegant optimization of solar-panel technology using simple geometrical principles and nanotechnology (p. 10). In the realms of psychology and the brain, we learn that there is a surprising link between hormonal cycles and cognition from Ginger Jui (p. 16) and that our emotional state is strongly affected by our perception of the passage of time from James McGann (p. 14).

In an effort to adapt to a world of ever-more rapidly expanding information, the *Berkeley Science Review* is proud to announce the launch of our new blog (p. 22), which will serve as a continuous source of BSR content between print issues. We are also introducing a new back page column, "Toolbox," where Robert Gibboni will describe methodological tools that have revolutionized science (p. 51). We hope to achieve a balance between our slow and steady print-magazine habits and the turbo-charged pace of the Internet to provide the best experience to you, our readers.

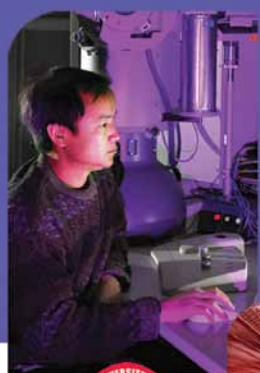
I would like to thank my predecessor Hania Köver for helping me survive my delicate early larval stage as Editor in Chief, Marek Jakubowski for a beautifully redesigned layout, and our new Web Editor Anna Goldstein for making the long-imagined blog a reality. I would also like to thank Rachel Bernstein for her continued commitment to making our organization actually function, and the authors, editors, and layout staff for their hard work and dedication.

Enjoy the issue,

Greg Alushin

Editor in Chief

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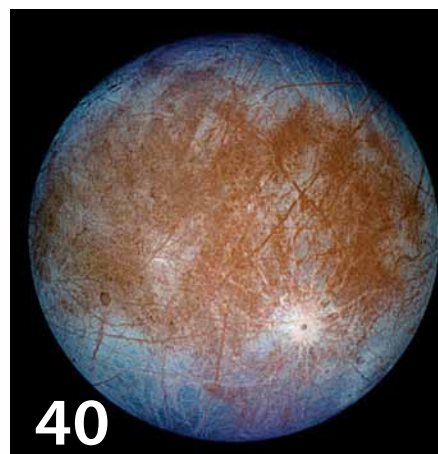
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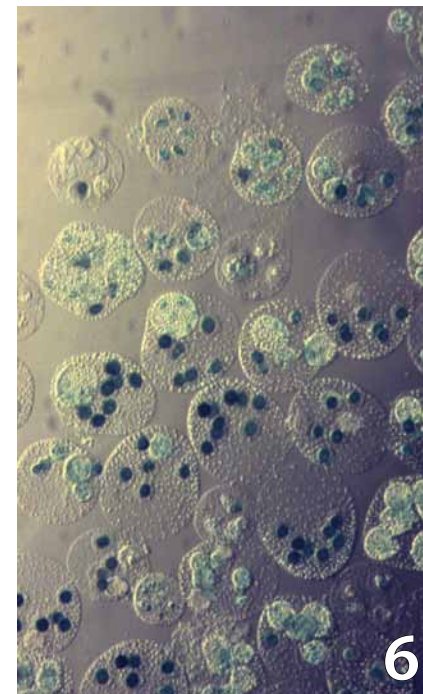
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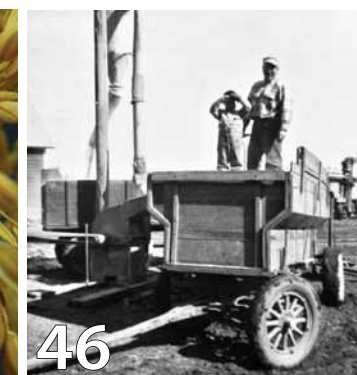
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Labscopes

Color my world

Which color do you like more—blue or red? The majority of people choose blue. However, recent research from the psychology department suggests that if you are in the same camp as most of the other people reading this article, you probably like blue even better than you did a few years ago because you attend UC Berkeley instead of that other university across the bay. Graduate student Karen Schloss and Professor Stephen Palmer have proposed an Ecological Valence Theory, which states that a person's color preference is based on how much he or she likes objects associated with that color. "When we were describing the data that we got," explained Professor Palmer, "we naturally started telling a little just-so story. People like blue because there are good blue things: clear blue skies, clean water, etc. Whereas dark yellow is rotting food, human waste—'yuck' stuff." To test this theory, the team had a large number of people list objects associated with a given color, and rank how positively they felt about the objects and how well they were described by the color. The researchers then compared these object preference data with the subjects' previous color preference data. "The amazing thing was it just worked," said Schloss. The correlations between the theoretical ideas and the actual preference data were outstanding. So, positive feelings toward your alma mater may help explain why you just chose to paint your walls blue or buy those gold shoes. The lab is currently expanding their study by collecting data from institutions across the globe to see how well their theory can explain cross-cultural differences in color preference.

-Colleen Kirkhart



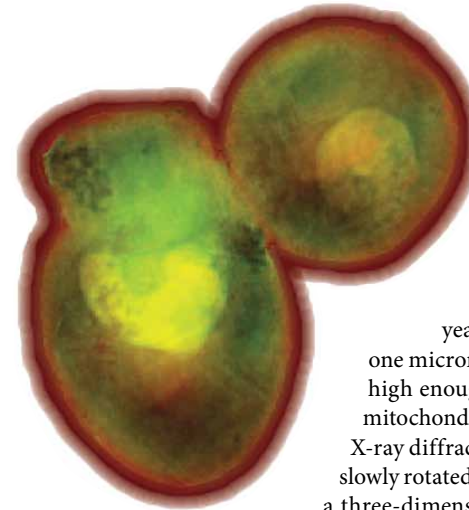
Vision²

In a little more than half a day your brain will have processed enough visual information to take up all of the available hard drive space on two computers. How does the brain do it? Imagine a digital image of a landscape. A computer stores this picture as a set of pixels; a human observer, on the other hand, perceives various shadows, textures, and shapes. The brain identifies and sorts all of this data by converting signals received by the eye, which essentially encode a set of pixels, into more and more abstract forms through various layers of neural networks. Using computational modeling, UC Berkeley Associate Professor of Vision Science Bruno Olshausen is creating maps that show what the data output from each of these layers might look like. The model consists of simulated neurons, organized into two different layers. The dots on the map represent different contrast elements captured by neurons in the first layer, their position connects contrast data collected to actual locations in the image, and the colors correlate data transfer from the first to the second layer of processing. The color scheme ranges from red to blue, where red indicates a positive correlation, blue a negative one, and gray indicates no correlation. This model successfully combines features output from first-layer neurons into a second layer, much like researchers think the brain's visual processing scheme would. If the model agrees with data from brain imaging experiments, it could be an important advance in understanding how our brains analyze what we see.

-Claudia Avalos

FROM TOP: ESTER IMBAR, DAVID SHANKBONE, BRUNO OLSHAUSEN AND CHARLES CADIEU

FROM TOP: LBL AND CHARLES LINDEM



Diffract this

Although microbes such as bacteria are tiny, their cells have elaborate three-dimensional structures that vary wildly across species. Using electron microscopy, scientists have previously imaged many different types of bacteria in 3D at molecular resolution, which has led to a far better understanding of how these organisms function. Eukaryotic cells, of which animals like humans are composed, are too large for this technique to work. Recently, however, a group of LBL researchers and their collaborators from Stony Brook University have crossed this barrier and successfully imaged an entire eukaryotic yeast cell (three to four micrometers in diameter, whereas most bacteria are smaller than one micrometer) at the highest resolution (11-13 nanometers) ever achieved. The resolution is high enough to visualize details of internal cellular structures like the nucleus, vacuoles, and mitochondria. Working at the LBL's Advanced Light Source, they used an imaging method called X-ray diffraction microscopy, recording a series of diffraction patterns from a single cell as it was slowly rotated, which were then combined through sophisticated computational analysis to produce a three-dimensional image. A major limitation of this method is that extended exposure to X-ray radiation will damage a specimen. The biological samples in this study were dehydrated and frozen before observation to reduce radiation damage. Other studies have used frozen hydrated cells, but the images obtained from these cells were of lower resolution. In the future, scientists hope to obtain higher resolution images from the frozen hydrated specimens, which best approximate the natural state of the cell.

-Sharmistha Majumdar

Gecko-nation

A patch of forest next to a shopping mall is just one example of forest fragmentation, or the division of forest habitat by human residential communities, farmland, or other developed areas. As forests become more and more fragmented, biodiversity is lost and studying the biodiversity that remains grows more urgent. Matt Fujita and Adam Leache, both former graduate students in UC Berkeley's Department of Integrative Biology, decided to study *Hemidactylus fasciatus*, a gecko species distributed over a fragmented forest habitat. They found that what was originally thought to be one species is actually four. The pair sequenced DNA regions from 51 geckos representing ten populations from rainforest fragments in Equatorial Guinea, Gabon, Ghana, Nigeria, Cameroon, and Congo. Using a statistical approach called Bayesian species delimitation, they then assessed the number of species present in the sample. This method first poses a "guide tree" model of possible speciation events, and then evaluates the probability of each node in the guide tree (the probability of each speciation event) by taking into account multiple factors including genetic sequence data, population size, and divergence times. Although traditional methods of classifying species are based on morphology, this statistical approach is valuable because it provides an objective and quantitative assessment. Indeed, Fujita and Leache hope their study will spark more discussion about using this method to evaluate visually indistinguishable diversity revealed by genetic studies. For now, their study is encouraging because it indicates that there may be more diversity in forests than previously expected. As Fujita says, "There is a lot more to discover, and we need to do that soon, before it is too late and the forests are gone."

-Mary Grace Lin



Beyond Watson and Crick

Untangling the role of methylation in DNA function

Generations of biology students have been taught that the instructions for creating an organism are completely contained in its DNA. The sequence of our DNA, the order of letters representing its chemical constituents, is what we inherit and in turn pass down as the template our cells use for creating the tools they need to carry out their functions. It is reassuring, really, to know that modifications we make to ourselves that don't change our DNA sequence won't be passed on. For example, our children will not, thankfully, be born with any of our tattoos, piercings, or other physical manifestations of our youthful indiscretions.

However, our DNA sequence is only a tiny part of what makes us who we are. What may be even more important is how our cells' use of DNA is regulated, a process that is still mysterious. For example, at conception an embryo receives genetic information from both parents, some of which may give conflicting instructions. How does it decide which to use during development? Additionally, since almost all cells in an organism have the same DNA, how do some turn into fingernails and others into a spleen? Finally, many organisms (including humans) have vast stretches of DNA that either have no known function or that can be harmful (some of those harmful bits are called transposons, elements that hop around the genome indiscriminately, potentially destroying important genes in the process).

So, how does a cell find and express only the DNA relevant to its role in an organism?

The answers to these questions lie in epigenetics (meaning "above genetics")—the study of phenomena that regulate gene expression without altering the underlying DNA sequence. One crucial component of this kind of regulation is methylation, the attachment of a methyl group (represented as "CH₃," one carbon and three hydrogen atoms) to cytosine, one of the chemical constituents of DNA. DNA methylation was originally thought primarily to turn genes off, a process key to development (choosing between genes from mom and dad), cell differentiation (turning off fingernail genes in the spleen), and healthy cell function (inactivating those pesky transposons). Levels of methylation can change over time under the influence

of environmental factors. If methyl groups are added to the wrong bits of DNA (or are absent in tumor suppressor genes), they can lead to cancer.

The pattern of DNA methylation found in a genome is known to be heritable in plants, and there are tantalizing hints that the same is true for humans. Methylation is thus like a genetic tattoo, but one that actually does get passed on to offspring—an acquired characteristic that is heritable. However, this seemingly essential form of DNA regulation has some mysterious properties. For example, it does not always act to silence genes—it can also be found in the middle of genes that are turned on and being actively expressed, where it causes mutations. It is also stunningly absent in some of biology's most beloved model organisms, including the worm *Caenorhabditis elegans*, the fly *Drosophila melanogaster*, and the yeast *Saccharomyces cerevisiae*.

Because of these puzzling inconsistencies, the general importance of DNA methylation tended, until quite recently, to be discounted. The data, "seemed like a real mess," says Daniel Zilberman, professor of plant and microbial biology at UC Berkeley. "The roots of these phenomena are not understood. We know they happen. How they happen is a mystery." He himself had found DNA methylation in the actively expressed genes of his favorite model organism, the mustard weed *Arabidopsis thaliana*, which "suggested that DNA methylation had a function we didn't know about." But because of the phenomenon's lack of uniformity throughout the different kingdoms of life, he didn't know if he could extrapolate his results to other organisms. Thus, the Zilberman lab set out to untangle the roles and patterns of DNA methylation, attempting to address two major problems. First, there was no big picture understanding of how the use of methylation is related between different organisms, or if it is related at all.



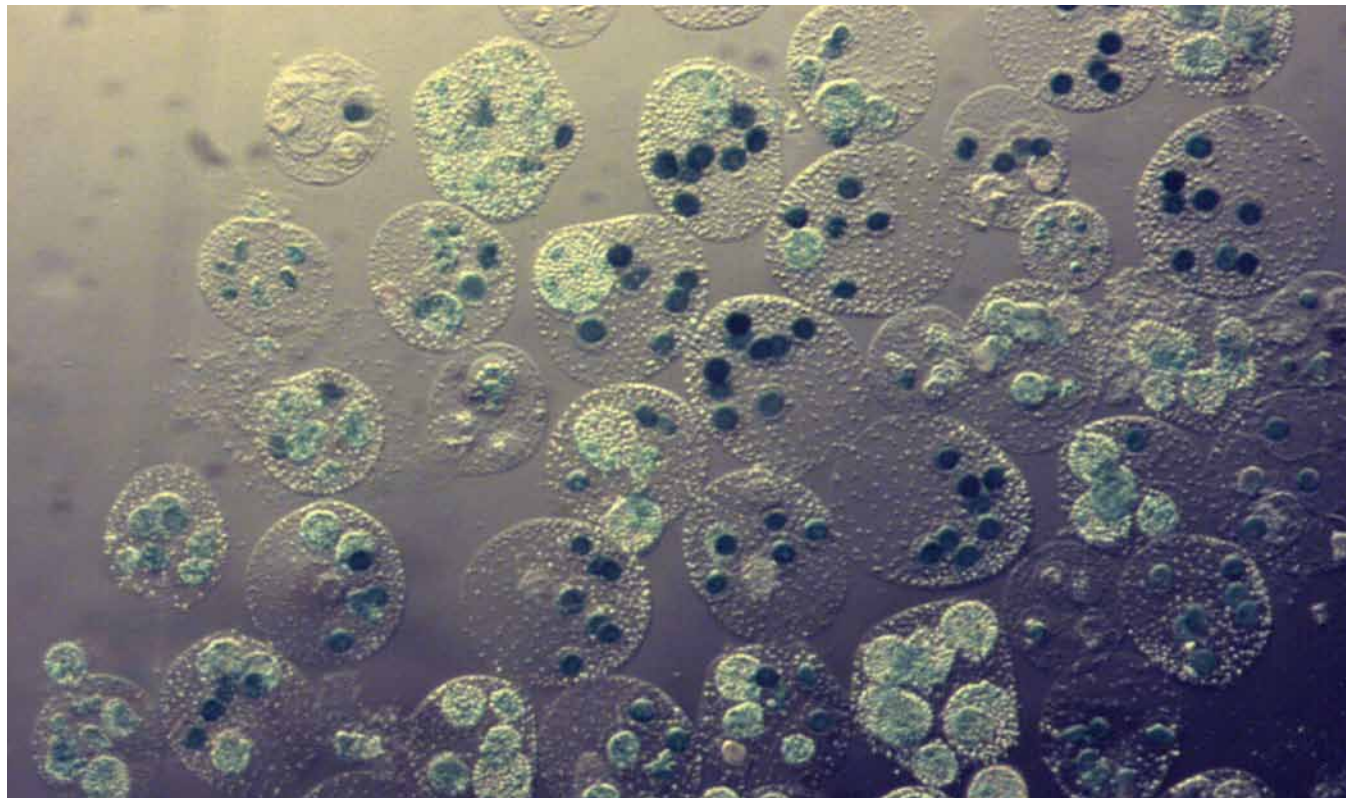
Rice was chosen for study because it is only distantly related to *Arabidopsis*, providing a useful point of comparison, and because of its importance as a food crop. It also has the smallest genome of any cereal, simplifying the analysis.

Second, there was no explanation for why methylation is present both in genes that need to be silenced and in active genes.

The team's key idea was that in order to properly investigate the pattern of DNA methylation between organisms, they would have to unravel the evolutionary context of the phenomenon. Therefore, they decided to study methylation in organisms at different points along the evolutionary tree. They evaluated 17 selected organisms with sequenced genomes: five plants, seven animals, and five fungi. Their menagerie included anemones, moss, green algae, puffer fish, honeybees, and rice. To quantify the methylation in each genome, the lab used a technique called deep bisulfite sequencing, which converts unmethylated cytosine into uracil (a genetic building block normally only found in RNA), while leaving methylated cytosine untouched. The methylated sites can then be read from the altered sequence. DNA methylation was correlated to gene expression by looking at messenger RNA levels (the presence of messenger RNA for a gene indicates that it is actually

expressed). This correlation was important for investigating whether methylation has a role in turning genes off in a particular region of DNA.

Even though they only needed less than one microgram (about two billionths of a pound) of tissue from each subject, obtaining samples of all these organisms was "a real adventure," says Assaf Zemach, a postdoctoral fellow in the lab, whose face lights up when describing his new collection. Learning to grow new organisms like algae was challenging but fun, whereas the animals, unfortunately, had to be sacrificed. "Some I had to kill as soon as I received them," he says, referring to the bags of swimming fugu fish and the boxes of honeybees that showed up in the mail, "but the rest...[now] I just grow them for fun in lab." Investigating such a diverse array of organisms paid off, as their results showed a coherent pattern of DNA methylation for the first time. While methylation is mostly absent in some classes of organisms (invertebrates and fungi), it is surprisingly consistent in others (plants and animals). Invertebrates and fungi show no



The name of *Volvox*, an algae, is derived from the Latin verb *volvere*, to roll. Each spherical microscopic plant, composed of hundreds of cells, can sense and swim toward light.

There's a fly in my water...

The discerning tastes of Drosophila

methylation of transposons (those bits of harmful DNA), but some methylation of active genes. On the other hand, plants and animals consistently show methylation of both transposons and active genes.

One of the most surprising results was that methylation of active genes appears to be an ancient property that can be traced all the way back to anemones and down the plant lineage. It was most likely present in the last common ancestor of plants and animals. Genes transcribed into mRNA at a modest level are most likely to be methylated while genes transcribed at high or low levels are least likely to be methylated, a parabolic relationship. Essentially the same kinds of genes tend to be methylated across plants and animals. “We are looking at a conserved phenomenon,” says Zilberman, “so we can use *Arabidopsis* to look at DNA methylation.” What they learn from this plant is relevant to other organisms, including humans.

While the role of DNA methylation in active genes remains a major unsolved problem, its function in gene silencing is becoming clear, and it all comes down to sex. Those nasty bits of harmful DNA, transposons, require sexual reproduction with another individual in order to spread, so organisms that reproduce asexually don't need to worry about them. Plants and animals are obligate sexual outcrossers, which means that they have to reproduce through sex with another individual, whereas fungi mostly reproduce asexually. Invertebrates do sexually outcross; however, Zilberman postulates that invertebrates lost the ability to use DNA methylation to silence transposons early in evolution when they were still single-celled organisms that reproduced asexually. Ultimately, this study underscores the importance of studying complicated biological phenomena through the lens of evolution. As Zilberman says, “The trend toward using a few model organisms was good and important, but organismal biology that provides an evolutionary context is also very important because biology doesn't make sense if you don't understand its evolution.”

Jessica Harvey is a postdoctoral fellow at UCSF in chemistry and cell biology.

Imagine yourself at a barbecue on a hot summer weekend. You're grilling burgers and hot dogs, eating potato salad, and indulging in a slice of watermelon. Let's say that you've chosen the sweetest slice of watermelon and you think to yourself, “What makes this watermelon taste so delicious?” The answer, in part, is that the sugars in the watermelon are stimulating the taste buds on your tongue and those sensations are being relayed to the brain via neurons, where the sweet taste is processed and identified as a source of energy. As far as we know, humans have taste buds for five categories of compounds, or modalities of taste: sweet, salty, bitter, sour, and umami, or savory. It's the discrete combination of these taste modalities, along with the smells and textures of foods, that actually produces flavor. But suppose there are more elements to our palate? Recent research at UC Berkeley confirms that we are still identifying new taste receptors that behave in unique ways compared to conventional ones. Researchers have found a gene in fruit flies responsible for tasting water, a modality that has not yet been identified in any other organism. Adding to the intrigue, this taste modality functions in a novel manner: rather than sensing individual molecules or ions as a sweet or salty taste receptor does, it instead senses the purity—or osmolarity—of water. In the example of our hypothetical summer barbecue, imagine a particularly thirsty fruit fly buzzing by and alighting on your sweet watermelon slice. It would taste both the sugars and juice and the high osmolarity of the water, and might decide to move on to a more watery meal to slake its thirst.

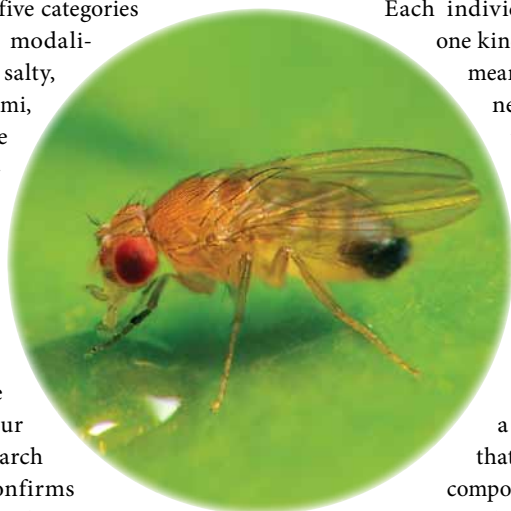
In a recent *Nature* paper, Kristin Scott, Associate Professor of Genetics, Genomics and Development and an affiliate of the

Neurobiology Department, and her colleagues at UC Berkeley show evidence of a previously undiscovered taste receptor in *Drosophila melanogaster*, the common fruit fly. Scott and her colleagues are studying how taste works in flies and have shown that the way a fly tastes food is slightly different from the way people do. “In *Drosophila*, there are taste bristles located on the legs, the wings, the proboscis and the internal mouth parts,” explains Dr. Peter Cameron, the lead author on the paper and a recent graduate student in Scott's lab. “Each taste bristle contains two to four taste neurons.” These neurons have receptors that come in contact with food on one end and, on the other, axons that extend to the fly brain to deliver taste information.

Each individual neuron has one kind of taste receptor, meaning that each taste neuron is specific to one taste. As Cameron says, “In *Drosophila* you have, for the most part, a class of neurons that respond specifically to sweet compounds, a class of neurons that respond to bitter compounds, and a class of neurons that respond to water.

There's even a class of neurons that respond to CO₂.”

For years, scientists have suspected that flies are able to taste water, distinguishing aqueous solutions from others. What Scott and her colleagues discovered was that flies are really using a single protein to determine the purity, or osmolarity, of water. The lower the osmolarity of the solution, the fewer the compounds and salts dissolved in it and the purer the water. Scott explains, “What was known were the results of electrophysiology experiments that monitor cell activity, and [we] could see that taste cells in the fly responded to water.” Despite the evidence, no one had been able to identify the protein responsible for the taste. The difficulty lay in the fact that the osmolarity sensor is relatively rare. The sweet and bitter receptor proteins, for example, had been relatively



PAVEL MASEK

easy to uncover because they belonged to a large family of receptors, whereas the water sensor belonged to a “lingering modality probably composed of a single receptor,” according to Scott. This needle-in-a-haystack search was rendered tractable by the use of recently-developed genetic tools. “There used to be very few ways to get at molecules expressed in only a few cells... but now, with the *Drosophila* genome sequenced, and with very sophisticated new molecular approaches, it's no longer as challenging as it once was,” Scott explains.

In order to pin down the osmolarity sensor protein, Cameron used DNA microarrays, diagnostic tools that compare the relative expression levels of all genes in a single cell. By comparing gene expression in the proboscis between a mutant fly that no longer had taste receptors and a normal (wild-type) fly, Cameron could sift through the genes and see which ones turned on due to the presence of a functioning taste receptor. Disregarding genes for known taste receptors, he focused on genes for receptors resembling ion channels, which, as the name suggests, are channels that control salts flowing in and out of the neuron. According to Scott, “ion channels had been implicated in salty and sour mammalian tastes, and because we didn't have any counterparts for salty and sour tastes in the fly, we thought looking at ion channels might be a good idea.” Cameron focused on a gene that encoded a protein in the cell membrane named Pick-Pocket 28—or PPK28—because it was present in cells where all other known taste receptors were absent, a good indication that PPK28 is responsible for a unique taste modality. As it turned out, Cameron's hunch was correct: PPK28 is responsible for osmosensation, a rare find, indeed.

The researchers next applied advanced molecular techniques to image the neural activity of individual flies. Using a cloning and imaging technique known as GCaMP imaging, they were able to make neurons that normally produce the protein PPK28 also produce a special fluorescent protein that responds to the influx of calcium into the cell, which is an indicator of neuronal activity. The term GCaMP refers to an engineered variant of green fluorescent protein (GFP) that is fused to the calcium sensitive protein

PETER CAMERON

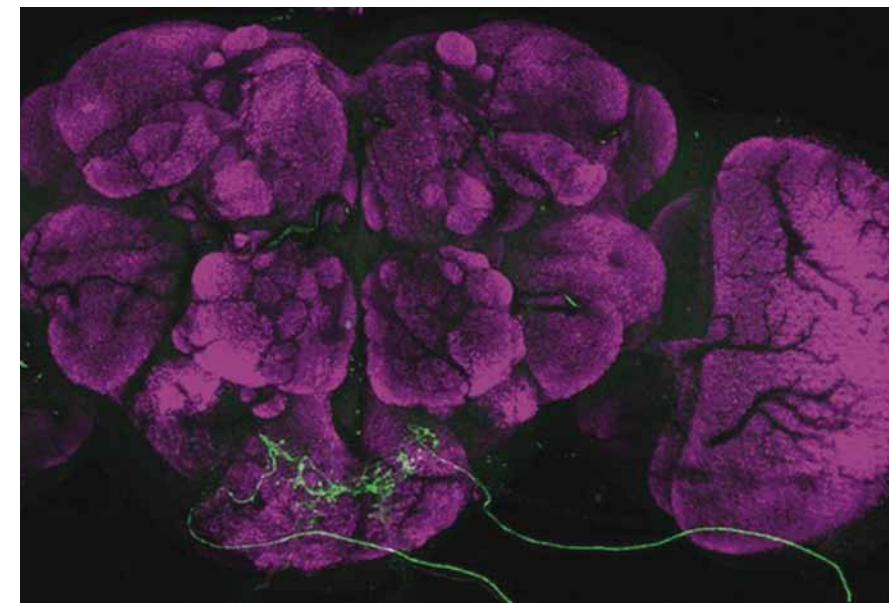
calmodulin (CaM), producing a protein that is only fluorescent in the presence of calcium. By immobilizing a fly and peeling off the cuticle above its brain, Cameron was able to see a green glow when the PPK28-positive neurons were stimulated. In the case of these neurons, the amount of fluorescence corresponded with how pure the solution was—the purer the water, the greater the activity. Scott explains, “With almost any solution, the cells responded, but the response decreased with increasing ion concentration. So that gave us one of our first clues that this might really be an osmosensitive ion channel that responds to low osmolarity.” That is to say, the protein is not so much a receptor, in the classical sense, but a sensor of water quality.

To test this hypothesis, Cameron generated mutant flies lacking the *ppk28* gene, and they behaved roughly like normal flies, except that they would drink much less water. Cameron was also able to reverse this defect in the mutant flies by having cells specifically express PPK28 again, causing the flies to behave normally. Electrophysiological experiments confirmed that PPK28-positive neurons respond specifically to low osmotic (highly pure) solutions.

The next step for the researchers is to characterize the mechanism by which PPK28 works. Scott already has a model in mind.

“We think [PPK28] may be just detecting membrane swelling: a hypoosmotic [purer] solution causes the cell membrane to expand, and the ion channel senses the expansion of the membrane, which causes a pore to open.” Scott also speculates that this discovery may lead to uncovering other osmosensitive proteins that might be important in maintaining cell homeostasis, not just in flies, but perhaps in mammals, too. “If we understand how PPK28 is opened and gated I think it will be important for studying osmosensation in other animals as well.” How organisms regulate water intake and distribution is incredibly important, and by studying PPK28 in fruit flies, we may learn more about the as-yet-unknown osmosensors that mammals and humans must possess. Do these osmosensors help us recognize water through a taste modality? As Scott puts it, “Maintaining water homeostasis is essential for all animals. PPK28 helps fruit flies do that, and I think that the modality is going to be more broadly conserved.” For now, the question remains: a fly can tell the difference between ultra-purified bottled water and water straight from the tap, but can you?

Hector Huang is a graduate student in molecular and cell biology.



Taste receptor PPK28 is labeled with GFP (green) in this image of a fly brain. Following the thread-like axons visible in such images helps researchers determine the receptor's neuronal interactions. Here, green labeling shows up in the taste-sensitive region of the brain, the subesophageal ganglion.

Can you second my emotion?

The genetic basis of empathy

Can you correctly identify the emotion depicted in the image? This is just one example from the “Reading the Mind in the Eyes Test” (RMET) designed to measure empathy, or the capacity to understand others’ emotions and body language. Levels of empathy vary widely throughout the population, with social butterflies breezing through social situations while others suffer from crippling



social awkwardness. What is responsible for these differences?

“Empathy is tricky,” explains Laura Saslow, a graduate student in the John and Keltner lab at UC Berkeley, because a complex system of hormones and neurotransmitters regulate our social behaviors. Nevertheless, recent research by Saslow and Sarina Rodrigues of Oregon State University suggests that minor variations in a single gene may strongly affect our capacity for empathy.

In the search for genes correlating with empathetic behaviors, Saslow and Rodrigues focused on oxytocin, a well-studied neurotransmitter known to modulate our daily social behaviors including stress, anxiety and empathy. Oxytocin, called the hormone of love, is crucial for its significance in reproduction and maternal behaviors. Oxytocin binds to receptors located in regions of the brain associated with social attachments, pair bonding, and prosocial behaviors.

Like all proteins, the blueprint for the oxytocin receptor is coded in our genes. Slight variations in this genetic sequence can lead to significant differences in the shape of the protein, which has dramatic effects on its functionality. In this case, a mutation at a single point in the genetic sequence—an adenine (A) in place of a guanine (G)—affects how oxytocin interacts with its receptor. In other words, there exist two forms of the oxytocin receptor gene, A and G alleles. Since one copy of the gene is inherited from the mother and another from the father, individuals possess either

two copies of the G or A allele (GG or AA homozygous), or a combination (AG/GA heterozygous). Previous research has found that AA homozygous individuals are more likely to be diagnosed with autism, a social impairment disorder.

Rodrigues and Saslow, curious to what extent genetic variation correlates with empathy, measured empathic behavior using RMET in 192 UC Berkeley undergraduate students. Along with a self-reported exam to probe empathy, students provided DNA

samples to test for the genetic variation. They found 25 percent of UC Berkeley students GG homozygous regardless of gender, while the rest either had one or two copies of the A allele. Individuals with the G allele scored 23 percent higher on the RMET, indicating they were more likely to identify the correct emotions shown in each snapshot. Even in the self-reported exam, GG individuals showed a higher level of disposition toward empathic behavior than AA/AG participants. They found that parental care and the individual’s home environment had little influence on their results.

How this particular mutation affects binding to oxytocin remains unclear. However, it does imply that the ability of oxytocin to bind its receptor plays a crucial role in regulating our social behaviors. While the RMET provides a standard by which to measure empathy, there is always room for improvement to the test, such as finding a way to incorporate body language.

What can we conclude from this research on empathic behavior and genetic variation? Empathy is a complex social behavior which is difficult to understand and is influenced by small genetic variations. This study reminds us that small changes within our genes can nontrivially impact our phenotypic behavior. Just as in the movie *Gattaca*, sequencing our DNA may become an integral measure for our behavior and capability.

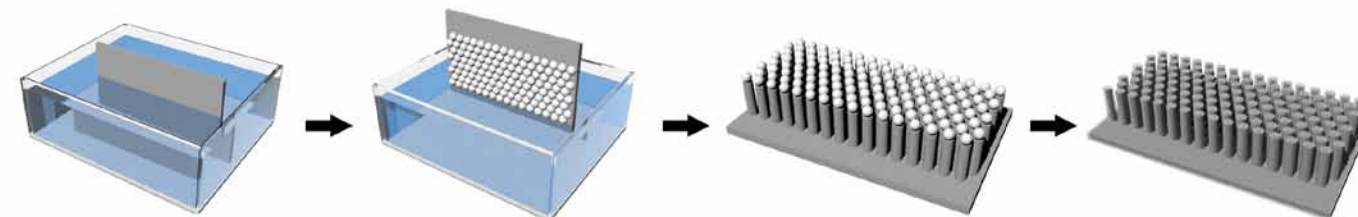
Maya Sen is a graduate student in chemistry.

Pillars of power

Nanotechnology creates new opportunities in solar energy

Solar energy has become a hot topic as public awareness of climate change and environmental degradation grow alongside political promises of a “green” rebirth of the struggling US economy. Solar cells, or photovoltaics, are able to convert the energy provided by the incoming rays of the sun directly to electricity. Given this ability to harness the vast and virtually untapped resource of solar radiation and turn it into useable power, photovoltaics seem poised to form the cornerstone of an evolving clean energy policy. However, ask any economist and you will discover that the costs associated with the materials, manufacturing, and installation of solar cells seriously limit their economic feasibility and necessitate the use of heavy government subsidies in order to keep the photovoltaic industry afloat. UC Berkeley professor Peidong Yang, along with his former student Erik Garnett, hopes to change this trend by using cutting-edge nanometer-scale fabrication techniques to significantly reduce the materials costs of silicon-based photovoltaic cells.

Most of the solar panels seen on buildings and homes today are made of silicon, the abundant and ubiquitous semiconductor that is the foundation of the modern computing industry. In fact, silicon solar panels make up about 70-80 percent of the worldwide market for photovoltaics. In a conventional cell, flat regions of electron-rich and electron-scarce silicon sit next to each other, forming what is known as a “planar p-n junction” (the p and n stand for positive and negative, respectively). As light from the sun strikes the cell perpendicular to the plane of the junction, the silicon must serve two purposes to allow efficient operation. First, in order to maximize the conversion of the sun’s energy to electricity, the cell must absorb as many of the incident photons as possible. Since silicon does not absorb light as well as some other semiconductors, a relatively thick layer is needed (imagine light shining through a thin sheet of paper: the thicker the stack of pages, the less light makes it through). Second, the silicon must allow electric charges to move effectively from the p-n junction to the surface of the cell where they can be connected to a circuit



This schematic shows the fabrication process for the silicon nanowires. A silicon wafer is first dipped into a liquid suspension of silica beads. When the wafer is removed from the liquid, the highly uniform beads—like tiny grains of sand—stick to the surface of the wafer in an ordered, closely packed pattern. The exposed areas of silicon are then etched away, leaving behind straight pillars. Finally, the silica beads are removed using hydrofluoric acid. The silicon nanowires remain intact, ready to be built into a solar cell.

and used. However, there is some resistance to this movement caused by impurities in the material and thus, the thinner and purer the layer of silicon, the more effectively it can transport electrons and electron vacancies (known as “holes”) to their destination.

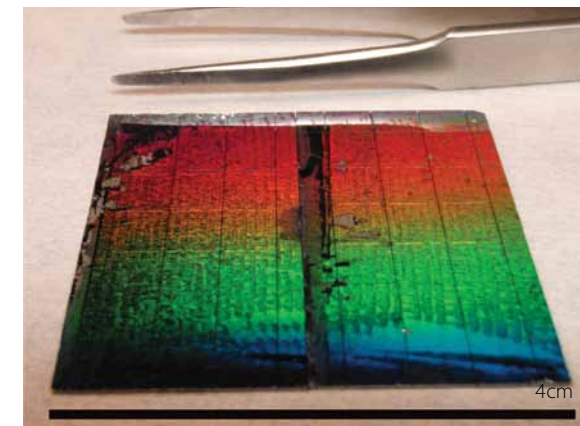
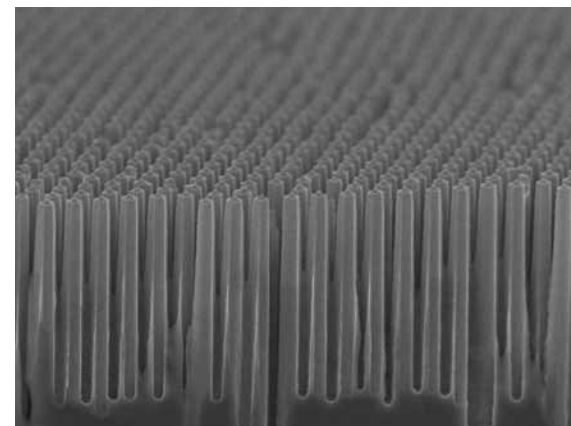
In a conventional planar cell, both absorption of light and movement of charge carriers occur in the same direction. The processes thus compete against one another—due to the thickness of the layer needed for adequate absorption, very pure silicon must be used to lower the resistance and allow the cell to operate efficiently. This is bad news in an industry where cost is everything: not only does one need a lot of silicon to absorb the right amount of light but that silicon must also be highly pure, which makes it drastically

more expensive. Yang and Garnett’s solution is to rethink the geometry of the solar cell so that absorption and charge movement happen in different directions. “By working with one-dimensional nanostructures, we can orthogonalize the light absorption and the charge separation,” says professor Yang. “This is an effective way of improving the movement of electric charge in the solar cell.”

Working with Dr. Garnett, Yang’s research group has developed a simple method for fabricating highly uniform silicon nanowires that could make solar cells significantly cheaper. This novel process makes wires that are typically about 400 nanometers in diameter—about 1000 times thinner than the average human hair—that stand up vertically like a nanoscale bed of nails. When a photovoltaic cell is made from

a surface covered in these miniature pillars, the p-n junction, instead of being a flat plane, is now in the shape of a cylinder centered on the axis of each individual nanowire. In this “radial p-n junction,” light is absorbed along the length of the wire—typically many micrometers, providing ample absorption—while charges are moved to the surface across its width. Since the electrons and holes must only move a few hundred nanometers in order to be used, there is less resistance due to impurities. Thus, the same relative level of performance can be achieved using less pure and significantly cheaper silicon, lowering the overall cost of the solar cell.

As an added benefit of the radial p-n junction design, Yang and Garnett discovered that, due to their periodic arrangement,



An image taken using a scanning electron microscope (left panel) shows the effectiveness of Yang and Garnett’s growth technique. The vertically aligned pillars are each approximately 400 nanometers in diameter and five micrometers in height. The excellent periodicity of the pillars is further demonstrated by the rainbow of colors seen in a tilted optical image of a nanowire solar cell (right panel). Because of their arrangement in rows, the nanowires disperse light much like a prism.

A catalytic conversion

The accidental discovery of a new way to split water

the silicon nanowires also trap much of the light that would usually be wasted by reflecting off the surface of the cell. Because of this enhanced absorption, thinner films of silicon can be used as the base for the nanowires—reducing the total amount of material needed and further bringing down the final cost of each cell.

Though it seems the advances made by Yang and Garnett have answered the major materials concerns with photovoltaics, much refinement is needed before nanowire solar cells will grace rooftops and provide cheap and clean energy for the everyday consumer. The best cells produced by the Berkeley researchers have an efficiency of around five percent—good for a budding laboratory technology but still far from the performance needed for a cost-effective product. For comparison, commercial planar silicon photovoltaics usually have a conversion efficiency of 15-20 percent. But if five percent seems like a meager result, consider that the first commercial silicon solar cells, developed in 1954, only achieved two percent efficiency. Nevertheless, the efficiency of the nanowire cells must be improved for commercialization to be realistic. Furthermore, the fabrication technique used to make the nanowire cells is also too costly to be viable beyond the laboratory scale. “Manufacturability is very important,” according to Garnett, “and adding one step [to the process] can be a major problem.” To address these problems, professor Yang’s research group is already looking at ways to improve device performance and make their cells cheaper to manufacture. For example, changing the size and shape of the nanowires to increase absorption and adding surface coatings to improve efficiency are potential strategies for bringing commercial nanowire solar cells to fruition. Dr. Garnett, who now works on nano-structured organic photovoltaics at Stanford, is cautiously optimistic: “I think the benefits of silicon nanowire solar cells are pretty significant,” he says. “We hope to dramatically increase efficiency but there’s still a lot of work to be done.”

Sebastien Lounis is a graduate student in applied science and technology.

In 1771, Italian physician Luigi Galvani was conducting a routine dissection of a frog leg when something unexpected occurred. Working at a table he had used earlier for some experiments on static electricity, Galvani picked up a metal scalpel that had accumulated charge while resting on the surface. When he touched the scalpel to the dead frog’s sciatic nerve, the leg twitched—Galvani had unintentionally discovered that nerves conduct electricity. Over two centuries later, biophysicist and Nobel Laureate Max Delbrück described accidents like Galvani’s as a necessary component of scientific discovery and thus coined his whimsical “Principle of Limited Sloppiness.” Defending his claim, Delbrück argued that science should be, “Sloppy enough so that unexpected things can occur, but not so sloppy that we can’t find out what happened.”

Fast-forward to UC Berkeley in 2009. Hemamala Karunadasa, a graduate student in the chemistry lab of Professor Jeff Long, had been conducting experiments using the heavy metal molybdenum, exploring



Chemistry graduate student Hemamala Karunadasa is continuing to investigate how her novel molybdenum-based catalyst splits water.

MAREK JAKUBOWSKI

its possibility for use as a single-molecule magnet. Because molybdenum is highly reactive, Karunadasa conducted all of her experiments in specialized tanks containing the inert gas nitrogen. However, at the end of the day as she was washing her glassware with water, she noticed a curious reaction taking place—tiny traces of her molybdenum compound, originally orange, appeared to be bubbling and turning green when exposed to the water. Karunadasa hypothesized that the compound was splitting water to produce hydrogen gas, resulting in the bubbling she observed.

If true, Karunadasa, like Galvani, had possibly made a very fortuitous discovery by accident, for hydrogen gas produced from water has been touted as an enticing green energy source. Though ideal in theory, the technology has been tough to implement in practice because of a couple knotty issues. First, producing hydrogen requires transferring electrons efficiently to water, which often requires very expensive metals such as platinum to act as catalysts, as well as electricity to power the reaction. Second, most catalysts discovered to date can only efficiently split water free of impurities, adding another costly step to hydrogen production. Nevertheless, water splitting is

one of the most common chemical reactions on Earth—it is the final step in photosynthesis—providing a tantalizing example of the potential to generate hydrogen from water and light if only the right catalyst could be discovered (also see “Photosynthesis,” BSR Spring 2009).

Before she could begin thinking about any far-reaching applications, Karunadasa first had to verify that hydrogen was being produced and was coming from water. By labeling the oxygen in water molecules with a heavy isotope, Karunadasa, Long, and their colleagues in chemistry professor Chris Chang’s lab demonstrated that hydroxide ions (and by extension hydrogen) were indeed produced in the reaction by splitting water. This proved successful, but Karunadasa points out that she was still skeptical of the reaction’s practicality. The question was, could they get the cycle to occur again and again without depleting the molybdenum compound? “We asked ourselves: can we take this molybdenum that has lost two electrons and pump in two new ones? And if we continuously add electrons, could this molecule continuously generate hydrogen?” says Karunadasa.

What they subsequently discovered was significant—the molybdenum compound was rare in that it could continually give up and accept up to three electrons, serving as a replenishable electron source. By using an external electron source known as a potentiostat, Karunadasa could pump the two electrons lost in the splitting reaction back into the molybdenum compound, restoring it to its original oxidation state and allowing the reaction to occur again from square one. Thus, the molybdenum compound’s role in the reaction was shown to be catalytic, making it a potentially invaluable reagent in the ongoing search for efficient energy sources.

While not yet as efficient at splitting water as current front-runner platinum, molybdenum may be a potential boon because it is significantly cheaper than its competitors and can even split our most abundant water source—seawater. The major disadvantage right now is the energy required to replenish the compound’s lost electrons after each cycle. “A lot of the reason people have been pursuing this kind of research is



The apparatus used for measuring the electrochemical parameters of the water-splitting reaction. The metallic mesh pictured is a platinum gauze, which serves as an electrode.

that it’s clear from biology that it’s possible to do this reaction effectively. Nature does this reaction at close to zero [energy loss]. We think we can try to match that,” says Long. One way the lab is currently attempting to tackle this issue is by tinkering with the geometry of the groups of atoms surrounding the molybdenum metal to try to lower the energy requirements for catalysis. The ideal scenario, however, would be to power the system using nature—which is why Long, Chang, and Karunadasa are collaborating with other groups to figure out a way to run the system using light energy. “If we can power this reaction with light, that would be great. After all, we’ll never run out of sunlight and seawater,” says Karunadasa. Because of her

fortuitous discovery, Karunadasa decided to remain at Berkeley for an extra year to continue her work with the molybdenum catalyst. Currently attempting to pick apart the mechanism for the reaction (“a bit of a black box,” she admits), Karunadasa is modest about her unexpected good fortune. Describing her sudden switch from studying magnets to trying to crack the renewable energy problem, Karunadasa exclaims, “I had to learn everything from scratch—this was completely accidental!” Max Delbrück may be grinning in his grave.

Azeen Ghorayshi is a research technician in molecular and cell biology.

MAREK JAKUBOWSKI

When time flies, you're having fun

How our perception of time affects enjoyment

We all know time flies when you're having fun: a day of skiing feels like it's gone too quickly; a great first date that comes and goes in a flash; a terrific party where dawn comes unexpectedly. But a recent study by Professor Leif Nelson of the Haas School of Business shows that we also think the reverse is true: if time feels like it flew by, we must have been having fun.

Dr. Nelson was originally researching what he calls "hedonic experiences" (or what you and I might call "fun") as a psychologist at NYU, investigating what factors might influence a person's enjoyment of various everyday stimuli, like listening to music. When trying to decide exactly how to set up the experiments, the question came up whether or not to have a timer on the display screen. No sooner had the decision been made to use the timer than Nelson, like any good scientist, thought, "We should manipulate that." So he sped up or slowed down the timer by 20 percent to simulate time

dragging or time flying, and asked people how much they liked the song after it ended. He found that when time dragged, evaluations of a song were worse, and when time went quickly, the ratings were better. This result indicates that people subconsciously believe that the faster something seems to happen, the more fun it must be.

One fascinating wrinkle to the experiment was that this difference in rating only occurred when the timer counted up, but not when the timer counted down. Nelson accounts for this finding by pointing out that if the timer counts down to reach zero as the song ends, our brain expects this result, no matter how much time has actually elapsed. And when expectations are met, no subconscious explanation is necessary, because in his words, "Our minds are incredibly lazy. If they don't have to think hard, they won't." But when the manipulated timer counts up, the song seems to end unexpectedly early (or late), resulting in a sense of surprise at the unexpected duration. Our brains then subconsciously grasp for an explanation to account for the disparity between expectation and result. The study suggests that the

explanation that made itself available to the subconscious minds of the test subjects is that "time flies when you're having fun," leading people to rank their experiences in accordance to the time distortion they felt. This type of everyday explanation that people have regarding their own conscious or subconscious thoughts is known in psychology as a "lay theory of metacognition."

Nelson tested how important the "time flies" lay theory actually was by giving subjects readings prior to the experiment challenging or supporting the theory. Those who read an article supporting the theory showed augmented differences in their music ratings compared to the first experiment. But for those who read an article refuting this theory, the differences in ratings between the "time flies" and "time drags" situations disappeared. In addition, he provided another group of subjects with an alternative (and somewhat preposterous) explanation for why time might feel distorted (blaming the headphones they were wearing), and again found that the difference in song ratings became negligible. Nelson concluded from these experiments that a belief in the 'time flies' theory was absolutely necessary for a person's enjoyment to be affected by a sense of time distortion.

Contrary to the critical readings Nelson provided to his subjects, the "time flies when you're having fun" theory is demonstrably true. Researchers have found that perception of time is indeed subjective and changes based on our activity and interest. What is fascinating about Nelson's study is that people apply the reverse theory: time appears to be flying, therefore I'm having fun. Although Nelson has no business applications in the works, one can only hope this understanding is an opportunity to improve those areas of life where time really seems to drag, like waiting for the BART or in line at the coffee shop. Simply distort the amount of elapsed time on the wall clock by changing how quickly the seconds tick by, and everyone will enjoy the experience more than they normally would—as long as they don't check their watches, of course.

James McGann is a postdoctoral fellow in molecular and cell biology.

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Hot flashes with a chance of brainstorms

The complex relationship between estrogen, dopamine, and cognition

Can estrogen boost your cognitive abilities? Estrogen, primarily known as the female sex hormone, also has broad effects on both the body and mind. For one, women are more prone to depression when they experience low levels of estrogen. And since the 1970s, estrogen has been lauded—and debated—as a prophylactic against the symptoms of mental and physical decline that accompany aging and menopause. Yet, until recently, neuroscientists have struggled to find a definitive link between estrogen and cognition.

“There were studies showing some change in working memory functions throughout a woman’s menstrual cycle, but no one had asked what the mechanism was,” says Emily Jacobs, a recent graduate of the Neuroscience Graduate Program at UC Berkeley. A recent study conducted by Jacobs and Dr. Mark D’Esposito, professor of neuroscience and psychology, suggests that dopamine, an important neurotransmitter, may be the missing link between estrogen and cognition in the human brain.

The UC Berkeley researchers had one important clue to the link between estrogen and cognition. They knew that working memory performance is critically dependent on dopamine—either too much or too little of the neurotransmitter would impair the ability to perform mental tasks. Working memory is the cognitive function used

to manipulate information in short-term memory tasks. As such, working memory is closely tied to attention span and the ability to focus. When she first began her research, Jacobs found, “Some studies showed that estrogen affects working memory but others got a null result and we wanted to know why. It turns out that if you think about it in terms of dopamine function, you can understand why some women improve when estrogen levels are high while other women are impaired.”

In their new study, Jacobs and D’Esposito found that women with different baseline levels of dopamine had predictably higher or lower cognitive performance depending on where they were in their menstrual cycle.

Jacobs separated the 24 women in her study into two groups based on whether they had naturally low or naturally high levels of dopamine, using both a chemical assay and a simple genetic test. Women with intermediate dopamine levels were not included in this initial study. Jacobs then tested the women’s ability to perform working memory tasks, such as memorizing a list of letters and then reciting them backwards.

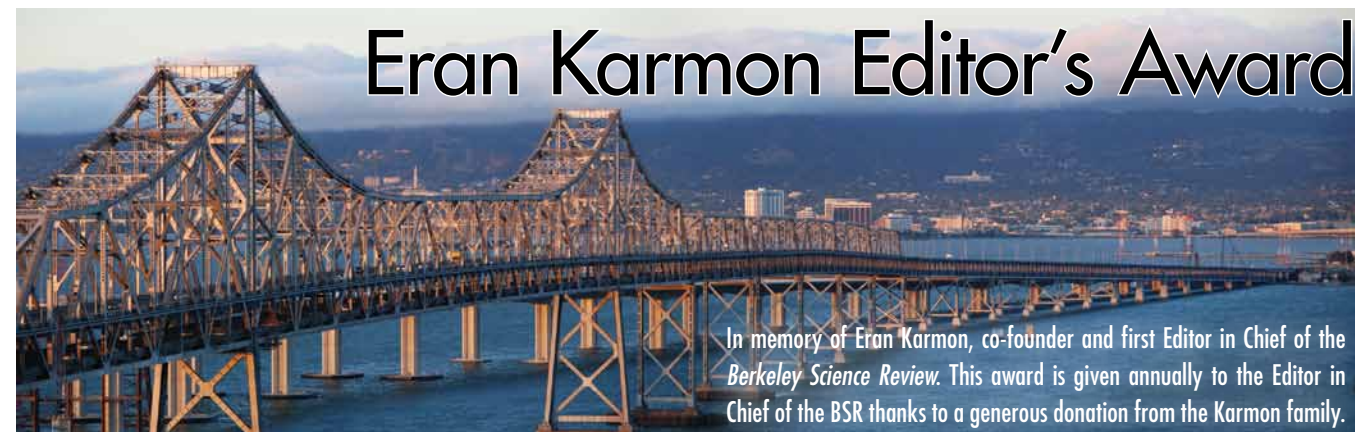
When Jacobs compared the results between the high and low dopamine groups, she found the women’s cognitive abilities changed throughout the menstrual cycle—but in opposite directions. When estrogen levels dropped just after menstruation, “high dopamine” women did well on working memory tasks, better than the “low dopamine” women. But when estrogen levels peak later in the cycle, during ovulation, the same “high dopamine” women took a dive in their ability to do tricky mental tasks, whereas the “low dopamine” women got a cognitive boost.

This is the first study to implicate dopamine in the link between estrogen and working memory in humans. Because estrogen levels change throughout the month—and over a woman’s lifetime—this finding suggests the link between dopamine and estrogen will refine our understanding of how estrogen affects cognitive function.

This research will also have broad implications for women’s health. Given the link between estrogen and dopamine, it would not be surprising to find that other behaviors affected by the neuroendocrine system also respond to hormonal fluctuations. A recent article in *Scientific American* (Emily Anthes, May 2010) reported on how the addictiveness of drugs, alcohol, and cigarettes changes throughout the menstrual cycle. Jacobs’ findings will likely impact how drugs targeting the dopaminergic system are administered. For example, an adolescent girl would need progressively lower doses of Ritalin as her estrogen levels increase through puberty—and the exact dose should change throughout her menstrual cycle. A better understanding of estrogen’s effect on the brain will also help the treatment of depression, anxiety, and chronic stress, which are just some of the neurological disorders that disproportionately affect women.

And let’s not forget that caffeine boosts dopamine levels as well. Does coffee help you focus some days but give you the jitters on others? Ladies, keep track of that extra cognitive boost—it could be that coffee time of the month.

Ginger Jui is a graduate student in integrative biology.



Eran Karmon Editor’s Award

In memory of Eran Karmon, co-founder and first Editor in Chief of the *Berkeley Science Review*. This award is given annually to the Editor in Chief of the BSR thanks to a generous donation from the Karmon family.

LEFT: MAREK JAKUBOWSKI; OPPOSITE: NASA

Juno’s revenge

Scientists probe Jupiter’s innermost secrets

by Crystal Chaw

It is the largest planet in our solar system, and one of the brightest objects in Earth's night sky. An enormous gaseous ball blanketed by reddish whorls and stripes, it has captivated humanity for centuries, featuring prominently in the astrology and mythology of ancient Babylonian, Chinese, Germanic, and Hindu cultures. Astronomers have watched Jupiter for as long as they have had telescopes: Galileo discovered its four largest moons in 1610. Modern technology has since revealed 59 more Jovian moons, and we now know that Jupiter's whorls are a cloud layer that includes ammonia, hydrogen, and helium. Some scientists suspect that Jupiter's strong gravitational field may protect the Earth from passing meteors and comets. According to Mike Wong, a research scientist in the Department of Astronomy at UC Berkeley, Jupiter also serves as a kind of "gravitational gas station for spacecraft," since by passing close to the planet, outward bound spacecraft can accelerate to even greater speeds.

Despite the progress we have made toward understanding some of Jupiter's mysteries, the great gas giant continues to baffle and inspire scientists. For example, Jupiter's Great Red Spot is a storm that has raged for at

least three hundred years—how does Jupiter's weather allow for such a phenomenon? How do elements commonly found on Earth like hydrogen and helium behave under Jupiter's extreme heat and pressure? How does Jupiter's atmosphere react to the impact of comets and meteors? Understanding these and other Jupiter-related phenomena is not only fascinating in itself, but may also yield important insights into the Universe, the Milky Way, our solar system, and the Earth itself. Work from many labs, including that of Geoff Marcy, professor of astronomy at UC Berkeley and adjunct professor of physics and astronomy at San Francisco State University, has revealed hundreds of Jupiter-like planets in the universe beyond our solar system (see "Strange new worlds," BSR Spring 2003). It thus appears that Jovian planets are fairly common in the galaxy—what remains to be seen is whether small rocky planets like Earth are as well. In addition, "Jupiter's sheer size, being far more massive than all the other planets of our solar system combined, means that understanding Jupiter and how it formed is a huge part of understanding the formation of our solar system, and of planetary systems in general," says Hugh Wilson, postdoctoral researcher in the Department of Earth and Planetary Science. According to

Philip Marcus, professor in the mechanical engineering department, studying physical phenomena on Jupiter is valuable because it provides additional data points that help us understand these phenomena on Earth. "Granted, we have historical information for the Earth which provides some additional data," says Marcus, "but the more planets we look at, the better."

No man's land

While studying Jupiter is conceptually appealing, in practice it poses significant challenges. As a gas giant, Jupiter has no solid surface—just layers of mixed elements in different phases. "Jupiter has a cold gaseous outer atmosphere, but as you go inwards it gets hotter and denser, eventually reaching a phase we just call fluid because the distinction between liquid and gas is lost at high pressures," says Wilson. "Eventually, you might hit a solid core made of rock and ice, but it will be tiny; probably only around five percent of the mass of the planet, and the pressure and temperature at that point would be ginormous." Indeed, Jupiter's interior is a pressure cooker that defies imagination. With temperatures of up to 20,000 Kelvin (approximately 35,000 degrees Fahrenheit) and pressures up to



A close-up view of the weather systems that give Jupiter its distinctive look. Red Spot Jr. is visible to the left of and below the Great Red Spot.

four terapascals (approximately 40,000,000 atmospheres—the Earth's surface is at about one atmosphere), no probe would survive a mission to Jupiter's deep interior. Instead, scientists must work with data such as telescopic observations, measurements of planetary emissions, and samples of Jupiter's atmosphere.

Centuries of storms

One of the planet's most striking features, Jupiter's Great Red Spot (GRS), was discovered in 1665. An incredibly stable storm, the GRS is perhaps the most famous example of Jupiter's baffling weather patterns. Marcus, trained as a physicist in fluid dynamics, was struck by Jupiter's weather early in his career. "Jupiter has 12 westward jet streams and 12 eastward jet streams," says Marcus, "and all along those jets there are rows of vortices," or swirling storms. From far away, the jet streams appear as distinctive stripes that cover the planet from pole to pole, and some storms appear as ovals of various sizes. The vortices are referred to as cyclones or anticyclones, depending on whether they spin in the same or opposite direction as the planet's spin (see sidebar). The GRS, for example, spins counter clockwise in Jupiter's southern hemisphere, making it a large anticyclone.

Until the early part of this century, data suggested that all the storms in a given jet stream spin in the same direction and are remarkably stable, sometimes lasting for hundreds of years. Beginning in 1998, however, several previously stable anticyclones merged to form "Oval BA," affectionately nicknamed Red Spot Jr. after it slowly changed from white to red in 2006. This sudden merging of previously separate

storms caused a flurry of excitement in the Jupiter research community. Marcus's focus on fluid dynamics gave him a unique perspective. "In studying fluids, vortices of the same sign merge like crazy all the time. So, to me, the question was why they were stable for a century—why didn't they merge in the first place?" says Marcus. He began asking how anticyclones could be relatively close to each other without merging, and found, surprisingly, that the answer lies in the presence of vortices spinning in the opposite direction: cyclones.

Long-lived cyclones were not previously known to exist on Jupiter. In part, this was because their presence is obscured by cloud patterns. "Using direct observation of clouds to try to understand what is going on can be really confusing," says Marcus. "Just because you can't see a storm doesn't mean it isn't there." Instead, Marcus used simulations to show that the presence of cyclone-anticyclone pairs could produce stable storms. Specifically, if you drop dye into a liquid with vortices that exist in a plus-minus configuration, with an anticyclone flanking each cyclone, the resulting "cloud" of color mimics the patterns seen on Jupiter. "These plus-minus pairs of vortices engage in a chaotic dance in which they are drawn together and then repel each other," says Marcus. This act hides the cyclones under chaotic clouds, keeps the anticyclones from merging, and causes Jupiter's cloud cover to be filled with its distinctive twists and whorls.

Global warming Jupiter style

While working on storm stability, it occurred to Marcus and his collaborators that the interaction between cyclones and anticyclones

might be directly involved in temperature dynamics on Jupiter. Measurements taken by spacecraft show that at the elevation of visible clouds, Jovian temperature is roughly the same across the planet. Uniform planetary temperature like Jupiter's is unusual—because the Sun's rays hit Jupiter's poles at a different angle than along its equator, the temperature at the equator should be higher than at the poles. To explain this temperature homogeneity, Marcus suggests that the

Classification: vortex

The difference between cyclones and anticyclones, the swirling storms that give Jupiter its distinctive oval spots, can be tricky. In simplest terms cyclones spin in the same direction as planetary spin, while the reverse is true of anticyclones. This seemingly simple definition, however, is complicated by the fact that apparent planetary spin depends on location: a planet that appears to spin counterclockwise from the northern hemisphere will appear to rotate clockwise in the southern hemisphere. Imagine a wheel rolling downhill. A person watching the wheel from one side, parallel to the wheel with his or her right hand uphill, would say that the wheel was rotating to the left—counterclockwise. By contrast, a person watching the same wheel from the opposite side would say that it was rotating to the right—clockwise. This difference also applies to rotating spheres, in this case, planets. As a result, cyclones in the northern hemisphere spin counterclockwise, whereas those in the southern hemisphere spin clockwise.

Galileo's namesake

The first orbiting spacecraft sent to Jupiter, Galileo began its 14-year mission in October of 1989. After its launch from the space shuttle Atlantis, a booster rocket propelled Galileo into interplanetary space, where it borrowed energy from the gravity of Venus (one flyby) and Earth (two flybys) to slingshot it to Jupiter. On the way, it passed through the asteroid belt separating Mars and Jupiter, and completed the first close studies of two asteroids, Gaspara and Ida. It spotted Dactyl, a tiny moon orbiting Ida, which was the first sighting of an asteroid moon. Already, Galileo was making discoveries.

Five years after launch, Galileo finally reached Jupiter, just in time to capture the only direct observations of the fragmented Shoemaker Levy-9 comet as it crashed into the planet. In July of 1995, it released a probe into Jupiter's atmosphere, which managed to make a few precious measurements before being destroyed by the planet's hostile environment. Researchers at UC Berkeley, including Mike Wong, worked with NASA on Galileo. "The probe entered a dry region," says Wong, "the equivalent of a desert in Jupiter's atmosphere so we never got to measure the abundance of water on the planet. However, Galileo made accurate measurements of other cloud-forming gases such as ammonia and hydrogen sulfide."

Meanwhile, the main spacecraft continued its orbital tour of the Jovian system, making discoveries that caused NASA to extend its stay an extra six years until 2003. In particular, NASA approved an extension to tour two large Jupiter moons—icy Europa and fiery Io. Data from this mission supports the idea that an ocean exists under Europa's icy crust. Io, on the other hand, remains the most volcanic body known, and Galileo flew close enough to photograph a lava fountain. Finally, in 2003, NASA crashed Galileo into Jupiter to avoid the possibility of contaminating Europa's ocean via a chance collision. The first probe of the Jovian system, Galileo revealed moons, winds, oceans, and fire. Surely, Galileo Galilei would be proud.



NASA

NASA, ESA, J. DE PATER, AND M.H. WONG

movement of cyclone-anticyclone pairs toward and away from each other results in a steady disruption of the cloud layer, acting like a giant mixing device that leads to an even temperature across the planet.

Based on the mixing hypothesis, Marcus and his collaborators made a number of predictions about what would happen after the 1998 merging of cyclones that created Oval BA. This merging meant a local loss of the special interaction between paired vortices—a loss of chaos, and therefore less mixing, which over time should lead to local differences in temperature. Indeed, in 2005, the color of Oval BA began changing from white to red. Although the cause of this color change remains unknown, Marcus, along with Wong and Imke de Pater, professor in the astronomy department, believe that it may be caused by a temperature increase which uncovers the reddish particles that some scientists believe inhabit Jupiter's atmosphere. These red specks, of unknown composition, may serve as nuclei around

which droplets of ammonia ice and other particles condense to form white Jovian clouds. As temperature increases, the droplets may no longer be able to coalesce, revealing the red particles and changing the color of a given storm from white to red. Marcus and his collaborators believe that events like the merging of cyclones and the changing of storm color may be part of a climate change cycle that has a period of hundreds of years.

Cloudy with a chance of helium

Jupiter's bizarre climate is not limited to surface patterns—on Jupiter, it rains helium. Helium and hydrogen are the most abundant substances in the universe, and appear in Earth's atmosphere as colorless, electrically insulating gases. Take Earth's atmospheric pressure and multiply by 40,000,000, however, and helium and hydrogen atoms behave very differently. Toward Jupiter's interior, helium forms a liquid while hydrogen forms a substance that is liquid and capable

of conducting electricity—a liquid metal. Recently, Wilson and Burkhard Militzer, professor of Earth and planetary sciences at UC Berkeley, showed that Jupiter's atmospheric helium forms liquid droplets that rain through a layer of metallic hydrogen.

Wilson and Militzer arrived at this insight by pursuing an unexpected result from the Galileo probe. Atmospheric data from the probe suggested that all noble gases were present in the amounts expected according to popular models except for two that were depleted—helium and neon. In particular, neon was depleted by a factor of 10. "Enrichment in a given element would not be strange because you can argue that Jupiter may have captured some comets or other objects," says Militzer. "A depletion, however, is unusual." Scientists struggled to explain the neon depletion. One controversial theory came from Caltech scientist David Stevenson, who suggested "helium rain."

Stevenson's hypothesis is based on two lines of reasoning. First, it depends on the theory that at certain pressures and temperatures, helium and hydrogen become immiscible. Several groups have confirmed that helium and hydrogen, when mixed as liquids, separate from each other. Liquid helium is denser than liquid hydrogen, so, when present in smaller quantities than hydrogen, helium should form tiny droplets and "rain" out of the mix. "It has been speculated for 30 years that in giant planets like Jupiter and Saturn, there might be a region where this process actually occurs," says Wilson.

The second important component of Stevenson's hypothesis is the solubility of neon in helium versus hydrogen. If helium rain is responsible for neon depletion, the expectation is that neon gas energetically "prefers" to be dissolved in helium over hydrogen. Then, as the helium droplets descend through the hydrogen soup, they would take neon out of the atmosphere with them. Until recently, scientists lacked the computational power to run accurate simulations testing neon's preferential solubility at the pressures and temperatures seen on Jupiter.

Now, technology has advanced such that it is possible to run such simulations. Using "very expensive computers," says Militzer, he and Wilson calculated the thermodynamic stability of dissolving neon into helium versus hydrogen given the conditions in



An image of Jupiter taken after the July 2009 impact. The scar left by the comet impact is visible as a dark splotch (indicated by box) in the planet's southern hemisphere.

Jupiter's interior. "Sure enough, it turned out that neon is more stable in helium than hydrogen, and the magnitude of this preference is exactly enough to explain the level of neon depletion that we observe," says Wilson. The calculated magnitude closely matches the observed difference in actual versus expected levels of neon, leading Wilson and Militzer to surmise that helium rain is occurring in Jupiter's interior.

Beware falling rocks

Aside from weather patterns and alien precipitation, Jupiter's eccentricities extend to how well it can take a hit. In the past 18 months, three objects have slammed into Jupiter—a surprisingly high number, given that the collision of objects in space is extremely rare. The 1994 collision of the fragmented Shoemaker-Levy 9 comet into Jupiter, for example, is described on NASA's website as "extraordinary," and "millennial." Unlike Shoemaker-Levy 9, which astronomers expected to impact Jupiter, no one expected any of these three recent impacts. "Everyone thought Shoemaker-Levy 9 was a once-in-a-lifetime event, but now, in just over a year, we have three more impacts," says de Pater.

De Pater and Wong are part of a large group of scientists studying these impacts. De Pater specializes in using radio emissions, both thermal emissions from the planet's deep atmosphere and X-rays emitted from the acceleration of charged particles (primarily electrons), to gain insight into planetary structure. As radiation moves through different substances, it is absorbed

or scattered depending on the characteristics of the environment. These effects can be described mathematically to provide a picture of the radiation's path. De Pater and Wong also capture and analyze different kinds of optical data. Infrared images from large land-based telescopes like the Keck telescope atop Mount Mauna Kea, Hawaii, complement images taken in the visible spectrum by telescopes like the Hubble space telescope. By combining data gathered from radio emissions and optical images, scientists deduce details about Jupiter's atmosphere and interior. In the case of collision events, data like these can reveal the components and size of the impacting object, the object's angle of entry, and any short- or long-term effects on Jupiter's atmosphere.

With the recent impacts, de Pater and Wong have an additional data set to consider—one from amateur astronomers. Remarkably, all three impacts were discovered by amateurs, not by professionals. The first impact was a comet strike that left an earth-sized scar—Anthony Wesley spotted the gash in July 2009. Since then, Wesley and another amateur astronomer, Christopher Go, independently witnessed and filmed another impact on June 3, 2010 (the videos can be seen on <http://www.youtube.com>, search: Jupiter impact). Finally, Masayuki Tachikawa and Aoki Kazuo witnessed and filmed a third event in August 2010. "Amateur astronomers now have access to extremely advanced equipment. They are wonderful collaborators," says de Pater.

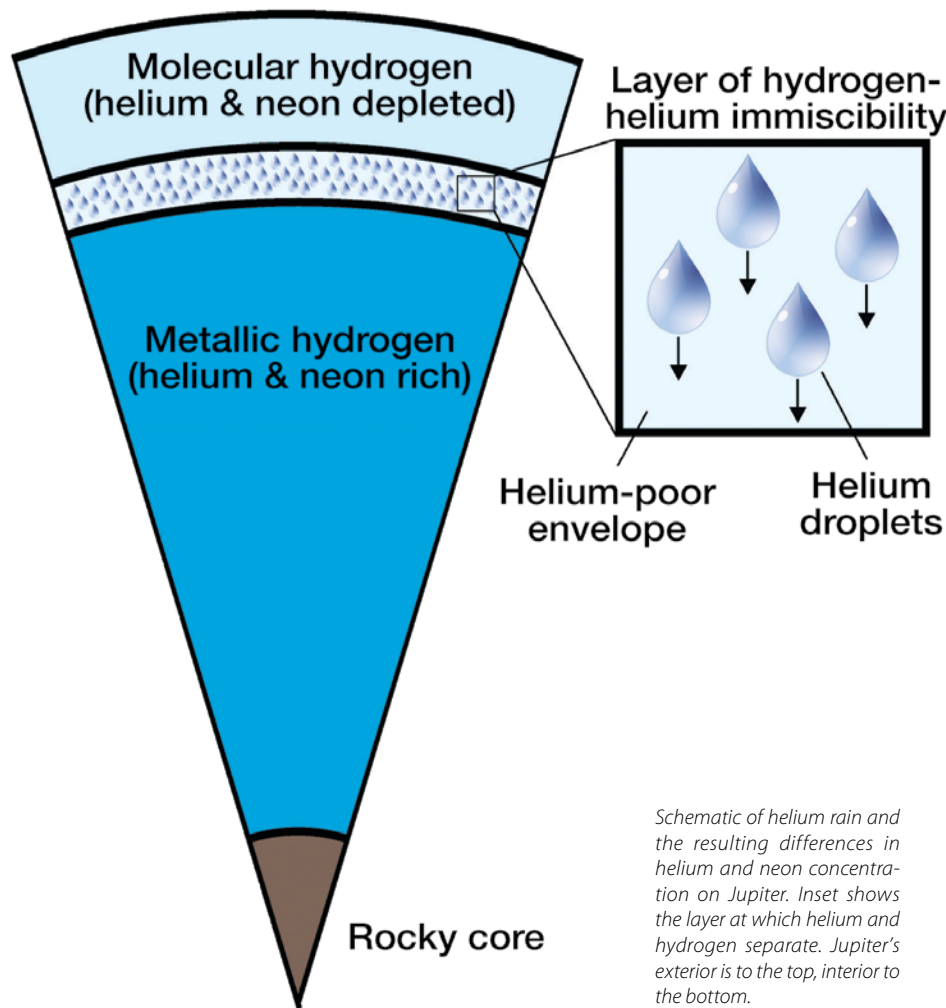
Using data from the amateur videos, as well as from several techniques de Pater

invented and refined during her extensive research on the Shoemaker-Levy-9 impact, de Pater, Wong, and their collaborators are contributing to growing scientific knowledge about impact events. Not only does this work inform a better understanding of Jupiter's composition, it also has potential ramifications for Earth. "The serendipitous recordings of these optical flashes by amateur astronomers may help us to quantify the number of bodies tens of meters in size in the outer solar system," says de Pater. "Such numbers will ultimately help to determine the threat of impacts on our own planet."

Looking ahead

At least three centuries after astronomers first observed features on Jupiter's surface, mankind remains fascinated by its enormous neighbor. The United States has sent eight spacecraft to Jupiter and will send another, Juno, in 2011. Like other planets in our solar system, Jupiter is named for a Roman god. In the mythology, Jupiter was a philanderer and his wife, Juno, was always trying to unravel his deceptions to reveal the truth. NASA's Juno probe will attempt to do the same with planet Jupiter. Juno's primary goals are to take accurate measurements of Jupiter's gravitational and magnetic fields and to probe the composition of its atmosphere. In addition to learning more from direct observation, these data will provide the basis for distinguishing between different models. Militzer is working with NASA scientists to generate solid theories for the behavior of hydrogen and helium to help interpret data from the probe. "You want to have the best models available," says Militzer. "Ideally, you have two well-tested competing models that data from the probe can resolve into right and wrong." Juno is set to launch in August of 2011, and will begin to send data after it reaches Jupiter in 2016. As they have for centuries, scientists in 2016 will excitedly gather to analyze the new data, discovering more mysteries even as they provide answers for others. Jupiter, in its aloof majesty, will likely continue to inspire mankind to ask questions about the Universe, the solar system, and the Earth for centuries to come.

Crystal Chaw is a graduate student in integrative biology.



Schematic of helium rain and the resulting differences in helium and neon concentration on Jupiter. Inset shows the layer at which helium and hydrogen separate. Jupiter's exterior is to the top, interior to the bottom.

BURKHARD MILITZER

NASA, ESA, M.H. WONG, H.B. HAMMEL, AND THE JUPITER IMPACT TEAM

Welcome to the BSR blog

Posted on July 11, 2010 by Anna Goldstein

Greetings, BSR readers! I'm your friendly neighborhood web editor. The BSR blog brings you the same high quality content you expect from the print edition, but without the long wait between issues. It's like a steady course of appetizers for the entrée that is the BSR. You can read about science news from Berkeley and around the world, information about science events around the Bay area, and much more.

Keep reading below for a taste test of what you can see at the blog. There are excerpts from a few stories published this fall, followed by a feature by Brian Lambson on nature-inspired photovoltaics. To read the rest of these stories, and many more, come visit us at sciencereview.berkeley.edu/blog.

Planting the SEED for Science Education

Posted on August 7, 2010 by Liz Boatman

About five years ago, the Berkeley Engineering Resources Collaborative (BERC) was born out of the collaborative minds of energy- and resource-interested students in the Haas School of Business. The founding goal of BERC was to promote collaboration among different departments and organizations at UC Berkeley. Today the Collaborative draws on mind-power from all over the UC Berkeley campus as well as Lawrence Berkeley National Laboratory (LBL).



A student demonstrates a homemade water mill at the SEED poster session in 2009. Photo credit: Will Regan.

The efforts of BERC extend beyond the higher-education and research community, however, with a unique outreach effort underway in local elementary schools: Students for Environmental Energy Development (SEED). SEED is run entirely by a group of science and engineering graduate students. Together, they have fully developed two complete after-school curricula: one on energy and one on water. During the school year, this same group of graduate students implements their lesson plans in classrooms at various schools in the Berkeley/Oakland area.

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Genomic analysis can be powerful—in the right hands

Posted on August 31, 2010 by Rachel Bernstein

You may have heard about the controversial genetics study connecting a set of 150 genetic markers to "exceptional longevity" (people living past 100). Everybody's interested in living longer, so it's not surprising that the work, published by Boston University researchers in July in the journal *Science*, was covered with much fanfare in many main-stream news outlets. *Science* even hosted a media teleconference to promote the story. Things took a turn about a week later, when *Newsweek* wrote a story about some deep flaws in the work, highlighting the potential pitfalls of genetic research that relies too heavily on statistics without experimental evidence to support the claims.

The longevity project comes from a relatively new field called "genome-wide association studies," or GWAS. Researchers in GWAS gather genetic data from thousands of individuals, sort them based on some characteristic, such as age or cholesterol levels, and see if there's a correlation. The first GWAS was done in 2005, and so far it has been shown that many traits and diseases, like height and diabetes, are correlated with hundreds of genetic markers. Some have doubted the utility of such studies, though, and the controversy surrounding the longevity study has only increased the scrutiny directed toward these projects.

Posted in In the news, Research highlights | Tagged cholesterol, GWAS, longevity | Leave a comment

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Going green... literally

Posted on September 15, 2010 by Brian Lambson

While impressive, the last few decades of human achievement in photovoltaics pale in comparison to nature's equivalent technology: photosynthesis. Just look at the numbers—every year photosynthesis produces about 3,000 exajoules (EJ) of chemical energy, or 7×10^{17} kilocalories, which equates to about half the total energy stored in the world's petroleum reserves (approximately the average daily caloric intake of eating champ Joey Chestnut). Compare this to the 0.1 EJ of electrical energy produced annually by man-made photovoltaics. Closing this gap is the key to a sustainable energy future, and unlike nature we don't have the luxury of waiting billions of years to get there.



As it turns out, we're not the first life form to unlock the secrets of quantum physics. Photo credit for Venus fly trap flower: Calyponte.

Researchers are increasingly trying to peek inside nature's bag of tricks and develop a new generation of biologically-inspired photovoltaics. Two recent discoveries represent significant progress toward this goal. The first of these papers (published in *Nature Physics* earlier this year) was from a group of UC Berkeley researchers, led by chemistry professors Graham Fleming and Birgitta Whaley. They demonstrated that chloroplasts make use of a quantum physical effect known as entanglement to transport solar energy from light-harvesting pigments to chemical reaction centers with extraordinary efficiency. Entanglement causes pairs of electrons that are spatially separated to behave like a single particle, meaning any change to one electron instantaneously affects the other. In plants, this effect allows solar energy to be stored in a high-energy electron configuration for a long enough period of time to be transferred to the chemical reaction centers before any of the energy has a chance to leak away.

Although their result lies in the realm of basic science, it may lead to the reality of utilizing quantum entanglement in man-made devices such as solar cells. It had previously been thought that the chaotic nature of high temperature systems at the molecular level would prohibit electrons from remaining entangled over a useful period of time. Now we know that you have to go no further than your windowsill to disprove this hypothesis; this is certain to change some minds and may lead to significant improvement to solar cell efficiency in the coming years.

The second recent innovation, made by a group led by Professor Michael Strano at MIT, is an artificial light-harvesting structure that has the ability to reassemble after its molecules have been broken apart by light. This mimics the mechanism used by plants to combat gradual reductions in conversion efficiency over time. In plants, proteins in the light-harvesting regions typically break apart and reassemble every 45 minutes, a process that maintains the health of the system year after year. Similarly, damaged structures in the MIT group's concoction reassemble whenever a surfactant is added to and subsequently removed from the solution. Thought to be the most complex man-made self-assembling system ever developed, their structure consists of seven different compounds, including carbon nanotubes, proteins, and phospholipids. Although their device isn't quite ready yet to compete with silicon-based solar cells, their work represents the first step toward developing long-lasting, low-cost solar cell materials using nature's own self-repairing approach.

It'll be interesting to see what comes next from this line of work. Self-installing solar arrays? Grid-connected rainforests? Photovoltaic jellyfish? Actually, my money is on an artificial Venus fly trap... it offers guaranteed savings on both your electric bill and exterminator bill.

Keep reading at:
sciencereview.berkeley.edu/blog



When the lights go out

Smart grids help us do **more** by consuming less

by Alireza Moharrer

Ask any of the people who were left idle at work and stranded on the hot and humid streets of New York City on the afternoon of August 14th, 2003 just how much electricity matters and one thing will be resoundingly clear: electricity powers our lives. The 2003 Northeast blackout left around 50 million people without power for four days and

caused 61,800 megawatts to be taken off the grid. When all was said and done, eight northeastern states and Ontario, Canada had lost power. Between four and ten billion dollars and the loss of nineteen million working hours were among the blackout's disastrous side effects, not to mention interruptions in transportation, communication, water supplies, and even sporadic cases of looting.

There was no warning before the chaos and no way to easily mitigate it once it began, but it could have been avoided had our electrical grid been supported by some form of adaptive intelligence to track and report on its operating conditions or, put simply, had the transmission grid been able to know what was happening over its system and why. Mary Ann Piette, a deputy staff scientist at Lawrence Berkeley National Lab (LBL) and research director of the California Energy Commission's (CEC) Public Interest Energy Research (PIER) Demand Response Research Center, hopes to create the essential elements of a system that will do just that. Part of a larger "smart grid" movement aimed at modernizing the national electricity grid, her technology, dubbed "OpenADR," forms the set of embedded instructions in a software package that will revolutionize the way the power grid transmits not only electricity but also information. As Piette points out, such a system could have averted the crisis in the northeast: "Had OpenADR been widely deployed during the 2003 electric grid crisis, the utilities could have issued automated demand response alerts to unload the electric grid and more quickly bring it back to stable operation."

Do ask, do tell

The 2003 blackout demonstrated that excessive load on the transmission grid can cause electric faults that cut through the protective systems in place today, leading to large-scale disaster. Official government investigation into its causes established

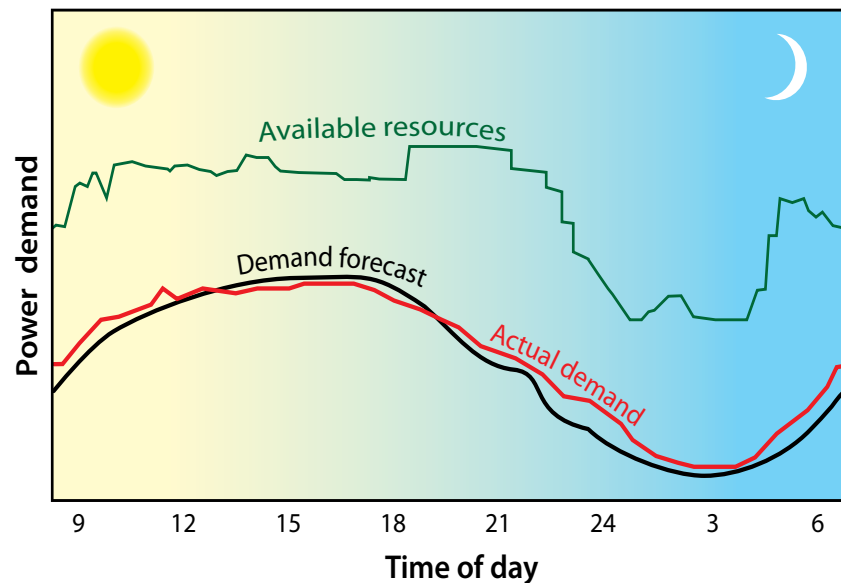
that overheating of transmission lines due to excessive load on the grid in Ohio caused the lines to expand and sag until they came into contact with adjacent trees and failed. Simultaneous monitoring system malfunctions eventually led to a cascade of rolling outages. Along with her colleagues at LBL and in industry, Piette has been working to resolve inadequacies in managing the load on the power grid to prevent future cascade events. Her goal is to create a system that is self-aware and can therefore avoid blackouts by fixing itself through demand management. The Automatic Demand-Response Open System Specification (OpenADR) is a piece of open-source software that implements a set of standardized price-modeling instructions and communicates them across the Internet to "smart" power management devices—like smart meters and programmable thermostats—in homes and buildings. OpenADR allows customers to play an active and responsive role in reducing their use of power and, in doing so, enables them to help control the large-scale movement of electricity through the power grid, reducing the peak load on the system in a way that was not possible in the past.

With control signals issued by OpenADR, consumers can be alerted to either reduce their unnecessary electricity usage at critical hours of the day or pay higher rates. Research indicates that when people are informed of grid overload conditions in advance, they tend to cooperate and take action to reduce their own consumption. This response translates into a significant relief of the peak load on the power grid, exactly the kind of relief that could have prevented the 2003 blackout. Moreover, from the viewpoint of utilities, standardized signaling from OpenADR can allow building and industrial power control systems to be pre-programmed, enabling a demand response event to be fully automated without human intervention.

As the load carried by our aging power grid continues to grow, more unpleasant surprises might be in store for consumers in the near future. However, in the next ten to 20 years our electrical power system will evolve such that the generation, transmission, distribution, and consumption of power will be governed by extensive, real-time communication among power system components. Software like OpenADR will be crucial to this self-aware, self-healing "smart grid." But why is our current grid so vulnerable?

All brawn, no brain

Although the size and complexity of the electric power system, as well as the total demand for electricity, have grown considerably over the past century, the operating principles of the power grid have remained more or less the same. Fundamentally, the power grid is a system that connects power generators with power users. Each individual power plant generates a huge amount of electricity, which must be distributed to millions of consumers. System designers usually locate power plants close to transmission lines that route electricity to the end-users' distribution grid. To efficiently send electricity over long distances, voltage is increased to anywhere from 135 kilovolts to as high as 500 kilovolts, thousands of times the voltage of a residential electrical socket. These high-voltage transmission lines run across the country, transporting power from power plants located in remote locations to the edge of urban areas. Once within city limits, the high transmission voltage is reduced to a safe distribution level that can vary from 12 kilovolts to as low as 110 volts for ordinary usage in our homes. This complex chain of transmission and distribution grid-lines, along with the interposed controlling and protective equipment, is what connects our homes and offices to power plants.



This figure shows an example of a typical “grid load profile” forecast, the actual power consumption over the course of a day, and the amount of power generation resources that are online to maintain reliability. Power system operators use this type of forecast to allocate resources. Technology like OpenADR can be used to lower the peak demand and flatten the overall shape of the profile, lessening the need for extra generation capacity.

Supervisory Control and Data Acquisition (SCADA) is the name of a large network of computers and automation devices that control and coordinate this supply chain. Using SCADA, human operators, like those working at the California Independent System Operator (CAISO), are continually watching the load on the grid and directing power plants to adjust their generation to meet power demand.

We are habitual creatures, and our use of electricity is no exception. When typical daily electricity consumption for millions of consumers is averaged, system operators can clearly see the growing cumulative demand on their computer displays. The load starts to build as people begin their day, eventually reaching a peak value that continues to hold from afternoon until late evening when it gradually begins to drop. This stable trend is called the “grid load profile,” and it tends to repeat predictably, allowing electric system planners to forecast how consumption patterns change on a day-by-day basis. It is here that human system operators play an essential role, balancing the amount of generated power supplied to the grid with the demand placed on it without overloading the system. The system operators are well trained to coordinate with power plant operators to continually accommodate the load profile with available power. However, on abnormally hot summer days or cold winter days, more people turn on air

conditioning devices or heaters, respectively. This leads to a greater demand for power that can put a lot of strain on the power grid and, in extreme cases (like at peak demand hours) system operators are more exposed to the risk of electric faults. Lacking the ability to communicate real-time demand information to consumers, SCADA is unable to reduce the overall grid load profile from dangerous levels in such extreme situations, sometimes leading to cascading outages like the 2003 blackout.

It is worth noting that our electric grid is highly reliable (power is available up to 99.97 percent of the time in a typical year) despite its vulnerability to extremes in peak demand. This is due to a large reserve of excess capacity that is built into the system. US Department of Energy data shows that over the course of the year, our power plants utilize, on average, only slightly more than 50 percent of their capacity. Some of the remaining capacity only comes online during peak demand hours of the day while the rest is in place in case of forced outages and other contingencies. This means our assets are often sitting idle and simply waiting to be used for the most demanding hours. While this reserve capacity provides an element of reliability, its brute-force approach is economically inefficient and, as previous catastrophes indicate, technologically insufficient in responding to peak load extremes. Given that the US Energy

Information Administration estimates that in the next 20 years, the country will consume 40 percent more electricity than in 2005, an upgraded and efficient power grid is becoming increasingly urgent.

One obvious and necessary upgrade to the current power grid is construction of newer, more efficient transmission lines to accommodate the projected increase in demand. However, such infrastructure is expensive to install: for a typical double circuit 220 kilovolt transmission line, the final installed cost can be as high as one million dollars per mile. A more effective, complementary strategy is to embed modern information management systems, like OpenADR and other smart grid technologies, in the architecture of the power system. These systems can sense and analyze performance characteristics of the power grid in real-time and quickly communicate the necessary actions to the devices that control its operation using the Internet. By making power use far more efficient from the demand side, smart grid systems can not only make the electric grid more reliable, but will also reduce the need for extra generation capacity and expensive new transmission lines.

Unfortunately there has been little investment in enabling the power grid with technologies that can intelligently direct the flow of electricity. In the current system, consumers have no knowledge of what is happening on the local grid: when it comes to using electricity, they simply plug in or flip a switch, with no regard for the time of day, current weather conditions, or total local demand for electricity. Furthermore, a lack of adequate investment in construction of new transmission lines has exacerbated the problem: over the past ten years, fewer than 700 miles of new interstate transmission were built. In order to achieve a more stable and uniform load profile, there is a clear need for new information technologies to improve the coordination between power supply and demand.

Enter the smart grid

The smart grid aims to remedy major demand problems by keeping electricity consumers informed of their usage. Power plants send electricity from remote locations out to a large network of users. Under the smart grid architecture, power will be routed through this network in the optimal way

and consumed as efficiently as possible. LBL, in cooperation with utility providers, has conducted a series of technology demonstrations by installing their demand response software on utilities’ supply automation servers (part of SCADA). These demonstrations have shown that when a communication link exists between these servers and end-use control systems like power management hardware at participating residential and commercial buildings, consumers will choose—either by pre-programming automated settings or direct user control—to cut down on unnecessary consumption rather than incur higher prices or suffer blackouts.

As a result of such studies, “demand response” has become the mantra of the smart grid movement. Demand response is defined as the ability of the power delivery system to continually measure its performance and respond to load changes by communicating the appropriate control actions to power management devices installed at consumers’ homes and businesses. Demand-response technology works by generating an online signal that is communicated to consumers to inform them of the conditions on the local grid and the corresponding effect on their electrical bill. Consumers can then choose to alter their behavior in response to this information. Under this scheme, the two ends of the supply and demand chain establish an interactive link via the Internet and are consequently able to behave symbiotically: utilities supply people with a reliable, efficient, and inexpensive source of power while simultaneously directing them to adjust their habitual power consumption to spare the local grid from unnecessary load.

With the knowledge of load and pricing conditions on the local grid, a power-management device installed in homes, commercial buildings, or industrial facilities is able to shave off unnecessary consumption (i.e. by turning off lamps, resetting thermostats or stopping some equipment) to help the local grid reduce its peak load. Alternatively, consumers can pre-program their load-management devices to run energy-intensive appliances like washing machines during off-peak hours, when the price of electricity will be lower. Consequently, the total load profile seen by the grid is smaller and more evenly spread throughout the day.

Future changes to power pricing schemes should encourage the adoption of such smart-grid technologies. As a recent

report by LBL indicates, electricity markets in California are making a transition toward dynamic pricing in response to the fact that the price of electricity and the stress on the electric grid are much higher during specific periods like hot summer days. These changes could significantly affect the cost of electricity for many facilities. In reducing usage during these peak periods, the smart grid can lower costs for customers, providing a strong incentive for its adoption.

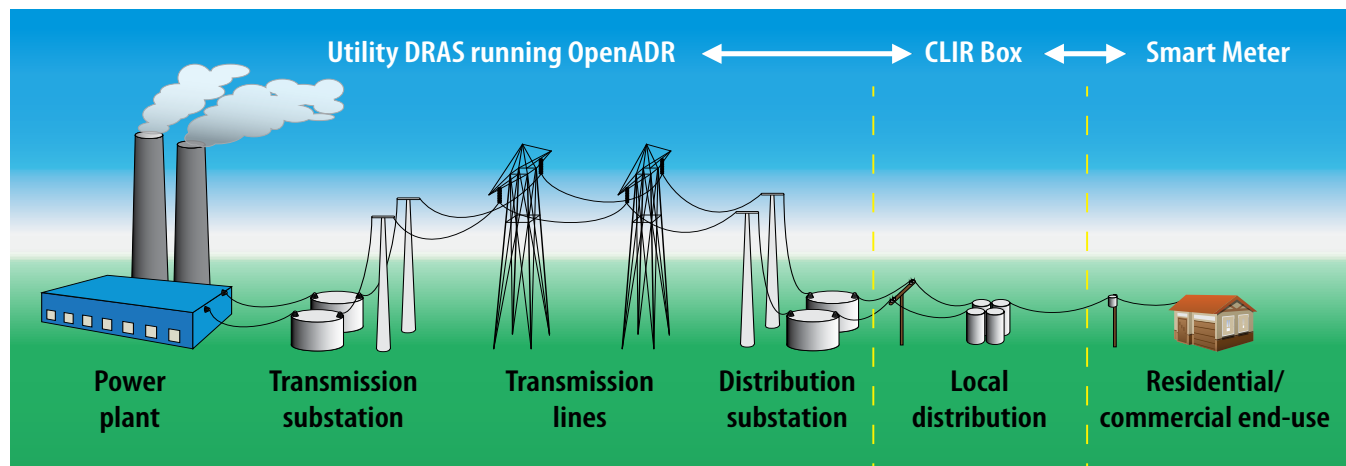
Putting the pieces in place

Over the past six years, with funding from the California Energy Commission, the Department of Energy, and major public utility companies, LBL’s PIER Demand Response Research Center has played a lead role in creating both the concepts and technology that will enable implementation of the smart grid. During this period, the center’s focus has been creating communication architectures, developing system specifications, and establishing operational and planning leadership for a consortium of academic and industry partners involved in the smart grid movement.

Coordination of millions of end-use electrical customers with utility providers is no easy endeavor; in reality, it is nothing short of sheer complexity. To tackle this task, Piette and her colleagues decided to develop the OpenADR specification, which serves as a facilitator for Internet communication of demand response instructions within the smart grid. Think of OpenADR software as an intelligent online middleman between supply and demand in the electric grid.

In technical terms, OpenADR is a proposed standard for exchanging information between a demand response automation server (DRAS) and a client that wants to receive and act on this information at the point of end-use. As such, OpenADR works in an Internet-based communication architecture and is intended to specify the various functions that must exist in a DRAS. These functions calculate the price of electricity based on power grid conditions for a particular time of day and historical information from the utilities and subsequently determine the effect on customers’ electrical bills. The DRAS then gives the customers’ power management devices a set of options to manage electrical loads. OpenADR also permits devices and software from external third parties such as utilities,





A schematic of the OpenADR communication architecture and power transmission. Using the Internet, supply and demand information and demand response actions are communicated between a utility's demand response automation server (DRAS) running OpenADR software and end-users' power management devices. An intermediary intelligent relay box (CLIR box) facilitates this communication. Based on real time instructions delivered by this system, power is routed through a series of transmission lines and substations to be used by consumers in their homes or commercial buildings.

facility managers, and hardware and software manufacturers to interface with and use the functions on the DRAS in order to customize demand response programs for specific applications.

Price signals in data models embedded in OpenADR are communicated to the DRAS via hardware like Ethernet cables or using wireless communication technology like Wi-Fi or ZigBee, a low-power wireless technology designed for monitoring and device control. The DRAS then communicates with the end-use load controllers either through the Internet or over electric power lines, instructing them to change settings on air conditioners, refrigerators, and other appliances and equipment. All of these

communications with a home or commercial building are automatic and pre-programmed.

Field trials conducted at LBL have already shown that OpenADR is able to help utilities deal with enhanced peak loads on cold winter mornings or hot summer days. In the summer of 2004, OpenADR was used to manage the electrical demand of several commercial buildings in California. Information provided by the local utility, Pacific Gas & Electric (PG&E), signaled the approach of peak load on the grid to power management devices in the buildings. These devices then automatically reset the building thermostats over a six-hour period and consequently shed approximately 100 kilowatts of load. This amounted to a 20 percent decrease in

peak load, twice the expected result. Much larger tests, with over one hundred large commercial buildings in California, have since been conducted and have demonstrated even larger load sheds. Due to these successes at LBL, the National Institute of Standards and Technology (NIST) has already adopted OpenADR as a key standard in the national smart grid initiative.

The adoption of OpenADR technology in California is critical to the successful implementation of the smart grid on a national scale. According to a report authored by Piette in 2009, California registered about 53,000 megawatts of peak electric demand on the hottest summer day of that year. Large buildings account for about 5,000 to 7,000 megawatts or five to ten percent of this peak load, while small commercial buildings account for 10,000 to 12,000 megawatts or 20 to 25 percent of the load. Much of the peak load is due to easily regulated processes like air conditioning, lighting, appliances, and other facility uses. This high concentration of demand in commercial buildings coupled with prior successful demonstrations using local utility companies makes California the ideal arena for a large-scale proof-of-concept for OpenADR. In playing this role, the state would not only gain the practical benefits of effective demand response technology but would also put itself at the forefront of the smart grid movement.

Smart grid = green grid

Beyond a more reliable power grid and reduced need for excess generation and

transmission capacity, demand response technology has the additional benefit of easing the implementation of renewable energy sources like solar cells and wind turbine generators. Intermittency presents an imposing barrier to the adoption of these technologies because the current power grid is designed for dispatchable sources of electricity that allow energy to be delivered within preselected hours based on advanced predictions. The output of solar and wind energy can vary drastically on short time scales throughout the day and thus, as no cost-effective means of energy storage currently exists, these technologies are difficult to dispatch in a reliable way. The valleys and peaks in power output due to shifting wind speed, cloud cover, and other environmental effects effectively prevent the integration of renewable energy technologies in the current grid.

In the smart grid, however, the distribution of load on the grid can be adjusted in a way that maximizes the usage and transmission of renewable energy sources. Demand response software, like OpenADR, can establish a real-time interface between consumer demand and output from solar and wind power plants, match them in an efficient way, and dispatch the energy they produce to the consumers that need it most. With the current push to slow global climate change and improve energy security by developing renewable sources of electricity, this added benefit of smart grid technology

should be a strong motivator for policy makers in shaping our future energy landscape. The broad reach of OpenADR is not lost on Piette: "Our hopes for the future of this technology is that it facilitates a low-cost, low-carbon future to help provide demand side load flexibility, reduce peak loads, and allow more intermittent renewables on the electric grid."

Looking forward

Despite significant progress in proving the efficacy of OpenADR in small-scale demonstrations, several key challenges need to be overcome to facilitate its integration into the electric grid at large. To begin with, OpenADR needs to be tested across a wider spectrum of building types, both commercial and residential, to ensure that it is versatile enough to adapt to the myriad properties and functions of buildings today and the disparate performance behaviors (in terms of energy use and efficiency) of buildings of different sizes. Equally important is the development of infrastructure that can respond to signaling from OpenADR and operate at high enough speeds along the entire signaling chain to take advantage of OpenADR's price communication capabilities. While the Internet provides a high-speed interface, more homes and buildings need to be equipped with smart power management devices and the DRAS needs to be updated to run OpenADR software. Finally, price modeling by the

electric utilities and the OpenADR software developers at LBL still needs to be refined and expanded to reflect real world data as accurately as possible across a broad array of scenarios. To begin addressing these needs, OpenADR is currently being implemented in a variety of programs in California, the Pacific Northwest, and Canada, and it is in development for a number of other demand response programs around the United States and abroad. The researchers at the PIER Demand Response Research Center are also constantly seeking new partnerships with utilities and updating their models in response to new experimental data.

Once the challenges facing OpenADR have been addressed and the combination of smart communication and smart devices has found its proper place across the power sector, the impact of this technology could be astronomical in scale. As much as the Internet has revolutionized communication, an Internet-enabled smart power grid will completely redefine the way people use electricity. This fusion of two immensely powerful systems will usher in an era where blackouts are a thing of the past, electric power is more affordable, renewable resources play a central role, and, sometimes, the lights will go out in order to keep the power on.

Alireza Moharrer works for the solar power company *Flagsol* in Oakland.



A bright bustling evening in Times Square (left) and the darkness of the 2003 blackout (right).

CLIR box

To facilitate machine-to-machine communication of demand response instructions, researchers at LBL have developed an intelligent relay box known as Client & Logic with Integrated Relay (CLIR). CLIR is a secure and self-configuring communication relay that sits between the demand response automation server running OpenADR software and the intelligent load controller in the end-user's building. It operates via Internet encryption protocols that are used for secure data transactions like online shopping or banking. This ensures that hackers do not jeopardize information exchange between a utility's servers and the computerized controller at the site of end-use.

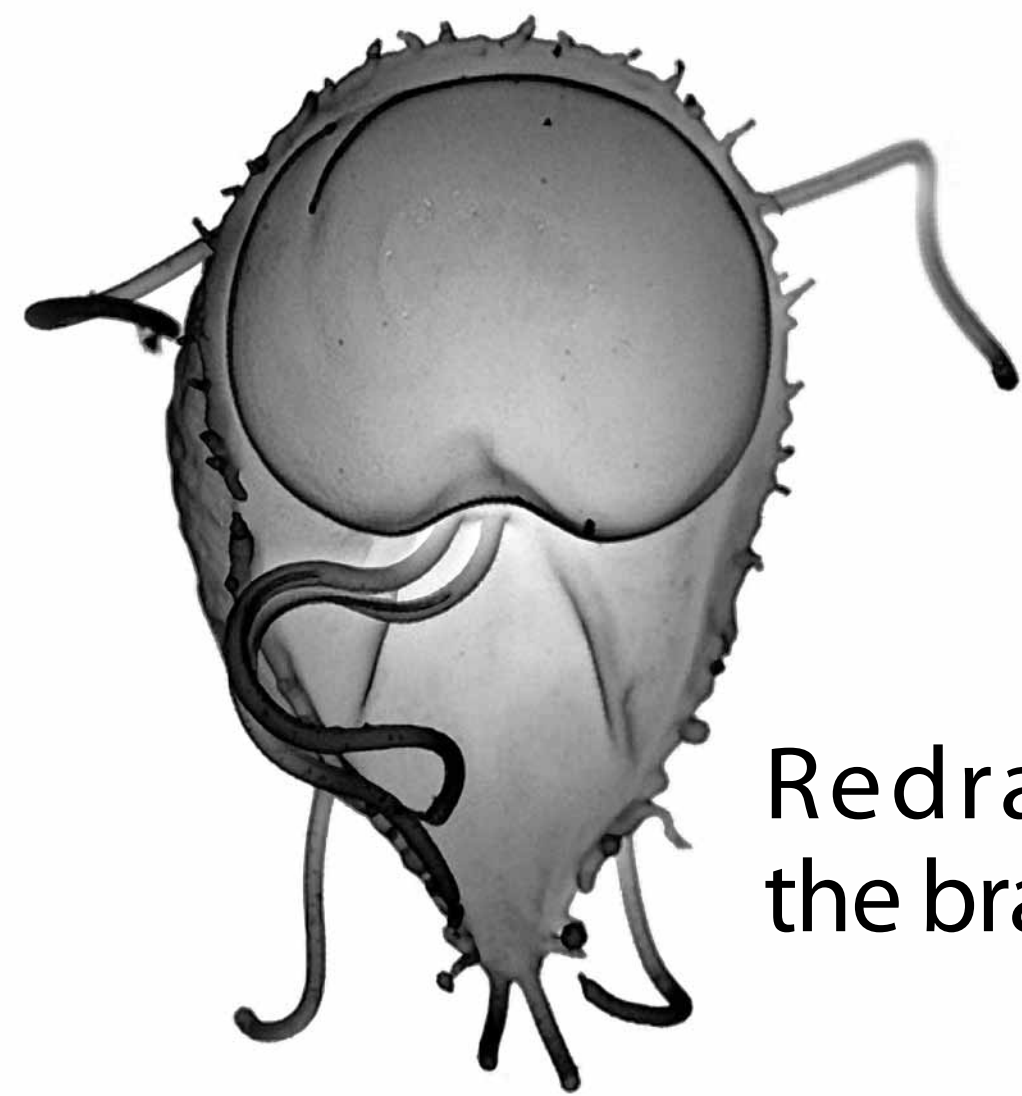
Once the CLIR box is powered on after installation, its status is visible via LCD display. Internet connectivity, time since last successful communication with the server, event modes, and other relevant data are shown on the display. An integrated keypad allows installers to set all relevant configurations without the use of a laptop or remote terminal. During an automated demand response event, the intelligent load controllers at the customers' building receive a signal from CLIR that causes the facility to automatically enter pre-configured low energy modes by adjusting air conditioning, lighting, and other energy intensive processes.

Through several major field tests with the participation of large commercial buildings, LBL has demonstrated that CLIR is capable of communicating OpenADR instructions to a load controller and reducing a building's total power demand. Relay boxes like CLIR will play an important role in the updated infrastructure of the smart grid.



TIMES SQUARE PHOTOS: ALAN WINNETT; ILLUSTRATION: MAREK JAKUBOWSKI

LBL



Redrawing the branches

by Sisi Chen

Phylogenomics sheds light on life's timeline

The human drive to categorize things is an impulse that's hard to suppress. In one famous example, Plato declared that man was "an animal, bipedal and featherless," receiving great public acclaim. Diogenes the cynic cleverly rebutted this claim by displaying a plucked chicken and proclaiming, "Behold! Here is Plato's man." Afterward, or so the story goes, Plato appended the definition to include "with flat broad nails."

Though comical, the allegory illustrates that taxonomy—the practice of finding, describing, and classifying organisms—is certainly an iterative sport. For most of human history, these classifications were based on morphological traits visible by eye or microscope. However, pitfalls abound when morphology is the sole criterion. After all, dogs belong to a single species but they

certainly aren't all cast from the same mold. By contrast, the deep sea floor is teeming with genetically diverse species of bacteria that all look pretty much the same.

These days, even the term "taxonomy" is a relic of the past, conjuring up visions of stuffed birds stashed in the dusty archives of natural history museums. The modern scientific practice—often known as phylogenetics—has evolved from taxonomy per se by its heavy reliance on using evolutionary relationships between species as the basis for classification. The end product of these investigations is often an evolutionary tree, a branching diagram showing the relationships between different species or genes. In fact, some of the first trees were drawn by Charles Darwin and were popularized by *The Origin of Species*.

Inferring evolutionary relationships is no easy task, especially in vast swaths of the tree of life that have no fossil record. That's where DNA can contribute; this latest iteration of taxonomic refinement relies heavily on sequencing genomes. In the past few decades, increasingly sophisticated molecular technologies have yielded a bounty of genetic information that speaks volumes about the relationships between species and their evolutionary heritage. Though the DNA transcript is traditionally perceived simply as the blueprint for proteins, it turns out that a compelling but tangled historical narrative is also scribbled into its margins.

The root of the story

Many key chapters have already been deciphered. One of the first examples harkens

JOEL MANGLISO

AMY ORSBORN

The making of a tree

Phylogenetic trees offer visually intuitive, information-rich representations of evolutionary history. Here, we highlight some of their most important features.

Each tip of the tree, called a taxon, represents a single organism or group of organisms. The node where branches split from each other represents the last common ancestor of both groups. In some trees, branch length is commensurate with real evolutionary time.

Trees are generally constructed with a few basic assumptions: that all organisms are related by descent from a common ancestor, that changes occur in lineages over time, and that new species emerge by the bifurcation of a lineage. Only the last assumption is controversial. It's true that for most organisms, new species arise when two subpopulations are subject to different environmental landscapes. However, in certain cases, many species can be generated simultaneously from one population, or near enough in time for the sequence of events to be irresolvable. The trifurcation between *Archaea*, *Eubacteria*, and *Eukaryota* may be one of these non-canonical splits.

Some trees are "rooted," meaning there is a node that represents the last common ancestor of all taxa in the tree. To determine the rooting scheme, phylogeneticists typically need to compare each taxon to the nearest outgroup, a taxon that is outside the tree of interest but close enough to allow meaningful comparisons. Choanoflagellates, for example, would be considered an outgroup of animals. However, sometimes no root can be identified robustly, as is the case for the eukaryotic tree, where definitive data are sparse.

from the dawn of genetic techniques in the 1970s. At the time, Carl Woese and his lab members at the University of Illinois set out to map evolutionary relationships between bacteria. They focused their attention on the sequence of ribosomal RNA, an essential component of the protein-assembling machinery in all cells. Because rRNA is so essential for life, its sequence changes very slowly, thus allowing comparisons between organisms that span billions of years of evolutionary time. In those days, the technology for sequencing nucleic acids was rudimentary, requiring tedious work to reconstruct the long 1500-nucleotide sequence from shorter sequences of six to 20 nucleotides. Woese was one of only a handful of people who could read the films necessary for deciphering the sequences. After a year of such labor, Woese stumbled upon a radical evolutionary schism in the world of bacteria. His results produced two very divergent sets of rRNA sequences, so different that he was compelled to partition bacterial life into two separate domains: *Eubacteria* and *Archaea*. Though recognition of his contribution was slow, Woese's initially controversial view is now universally accepted.

Applying similar modes of reasoning and vastly improved genetic tools, researchers at UC Berkeley have begun to probe other important transitions in our evolutionary history. These scientists strive to answer important questions about how multicellularity arose in animals and how eukaryotic life arose from the prokaryotic pool by sequencing entire genomes of organisms that have diverged around the time of these transitions. While

shedding light on some questions, they have also uncovered many more.

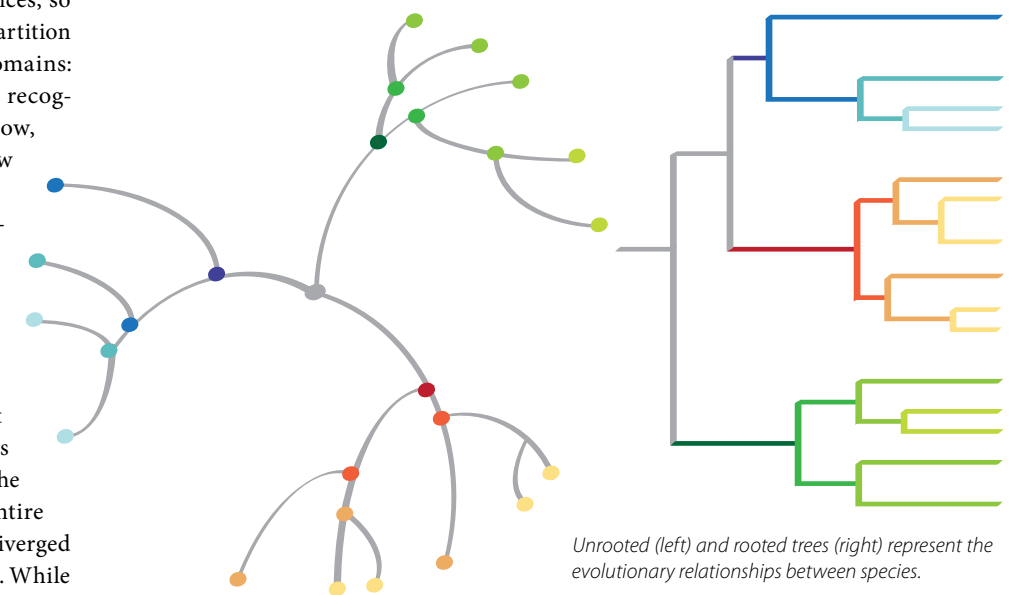
All for one

Since humans are animals, and egocentric ones at that, we are understandably curious about where animals came from. Animals are by definition multicellular, unlike plants or fungi which have unicellular members. Though the evolution of animal multicellularity is key to our existence, we have, at best, a cursory sketch of how it happened.

Multicellularity has arisen over 20 times in the tree of life, but only once in the history of animals. We know this because the trait is manifested the same way in all animals. All animals go through a single cell stage during their life cycles, usually when a sperm and an egg fuse. This single cell continually divides, migrates, changes shape, and differentiates to form intricately planned structures in a highly choreographed process called

development. The last common ancestor of all animals was almost certainly multicellular and the feature was never lost.

But how did it arise in the first place? To answer that question, scientists turn to tiny organisms called choanoflagellates, free-living water eukaryotes that resemble an inverted rocket anchored to a surface. Microvilli, which are small protrusions in a cell, line the choanoflagellates in a collar, surrounding a central undulating flagellum. By whipping the flagellum back and forth, the choanoflagellates can trap bacteria and other food particles against their collar, where they are then consumed. Their morphological similarity to the feeding cells of sponges piqued the interest of turn-of-the-century biologists, who believed they might be closely related to animals. In the last ten years, this relationship has been firmly cemented by the work of Nicole King, a professor in UC Berkeley's molecular and



Unrooted (left) and rooted trees (right) represent the evolutionary relationships between species.



A single choanoflagellate.

cellular biology department and a recipient of the MacArthur Fellowship.

Choanoflagellates are often found in a single-celled state, but some species can also exist in multicellular colonies, hinting at a close kinship with animals. However, since many other unicellular organisms also have the ability to form colonies, the choanoflagellate's link to animals was only putative until King began investigating specific protein sequences during her post-doctoral work in the lab of Sean Carroll at the University of Wisconsin.

At the time, people were comparing rRNA sequences (à la Woese) of choanoflagellates and animals, but failed to establish a definitive link. However, as King began investigating protein sequences, the choanoflagellates' sister status to animals became undeniably clear. She found that they contain a remarkable number of genes previously thought to be exclusive (and necessary) to animals. When King joined the faculty at UC Berkeley, she immediately set out to begin sequencing the first choanoflagellate genome, that of *Monosiga brevicollis*. Despite the fact that *Monosiga* is unicellular, its genome revealed that it contained a variety of signaling, cell-cell adhesion and development genes that are characteristic of animals (see "United we stand," BSR Spring 2006).

Since many species of choanoflagellates are typically in a unicellular state, consensus is that the last common ancestor between choanoflagellates and animals was most likely unicellular. Now that phylogenetic techniques have securely established choanoflagellates as our nearest unicellular eukaryotic cousins, King and her lab members are expanding their efforts to investigate the details of choanoflagellate multicellularity using other techniques.

Two crucial details have yet to be resolved. One is the question of genetic composition. Plenty of organisms can form colonies that are just motley crews, aggregates of many genetically distinct individuals or even different species. Animals, on the other hand, are composed of cells that are genetically identical, the result of many rounds of divisions from one starting cell. Are choanoflagellate colonies simply an amalgam of genetic strangers that collide and stick together? Or are they carefully constructed by reproducing a single cell over and over?

If the colonies are indeed composed of genetic clones, then the next important question is whether the cells are functionally the same. In animals like us, cells are manifestly different in their form and function. Although all cells in an animal are genetically identical, they take on different roles to perform specialized functions that benefit the individual as a whole. Do choanoflagellate colonies exhibit a similar division of labor?

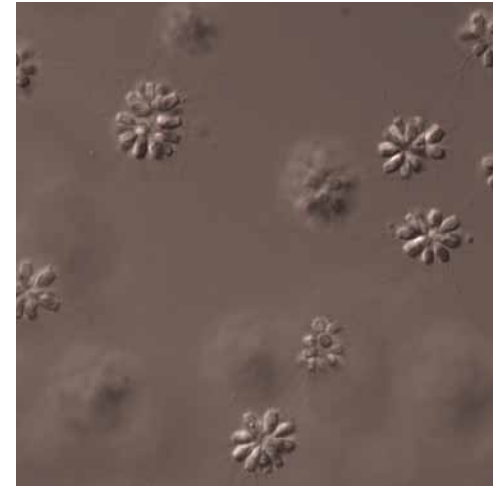
Though a far cry from the elaborately orchestrated processes of animal development, the idea that choanoflagellate colonies may form from a single cell and may divvy up tasks amongst colony members is intriguing. If both hypotheses were true, it would be an encouraging sign that choanoflagellate multicellularity may mirror animal multicellularity. Genome sequencing and cell biological studies of the colony-forming *Salpingoeca rosetta* can answer these questions, and thus tell us just how closely choanoflagellate multicellularity resembles our own.

What about Eu?

Not all key evolutionary transitions are lucky enough to have a modern-day "missing link." The appearance of eukaryotic life approximately 1.8 billion years ago is an evolutionary event that's still shrouded in mystery. Prokaryotes, or at least rudimentary fossils suggesting such, were already alive and kicking 1.7 billion years before eukaryotes first appeared, suggesting that eukaryotes evolved from prokaryotic ancestors. However, uncovering that narrative proves to be an elusive task.

Let us first clarify the difference between prokaryotes and eukaryotes. At the most superficial level, all bacteria (both *Eubacteria* and *Archaea*) are considered prokaryotes and all other forms of life are eukaryotes. Though this seems like an arbitrary division, the distinction is grounded in very sharp differences.

Prokaryotes are unicellular creatures with no nuclei or membrane-bound organelles. Eukaryotes, on the other hand, possess an eponymous "true nucleus," along with a host of other features. Prokaryotes have only one compartment within their outer cell wall, while eukaryotes divvy up their internal space into a baroque network of organelles that makes energy and stores, sorts, and transports molecules. While prokaryotes have one circular chromosome, eukaryotes



Understanding choanoflagellate colony formation may yield insights about animal multicellularity.

have varying numbers of linear chromosomes. Having a nucleus and more than one chromosome means that cell division is also complicated, necessitating the evolution of a highly choreographed process of sorting and physically separating duplicate copies of chromosomes to opposite poles of the cell before it divides. Eukaryotes also span a much wider size range, ranging from less than one micrometer to the size of a great whale.

How did eukaryotes, in all their intricacy, arise from their prokaryotic ancestors? That very question is one that is near and dear to the heart of Professor Zacheus Cande, a cell and evolutionary biologist in the molecular and cellular biology department. Cande has been active in genome sequencing projects of certain eukaryotes, such as *Giardia lamblia* and *Naegleria gruberi*, to gain a better understanding of the crucial mechanisms and unifying features of eukaryotic life. These organisms are considered basal, because their branches sit at the base of the eukaryotic tree. Because their forms are so incredibly divergent from other eukaryotes, they may yield insight into which features are necessary and which are not.

Parasitism's just another word for nothing left to lose

One particularly intriguing example is *Giardia*, a notorious water-borne parasite that can cause severe intestinal distress to unwitting drinkers at nature's watering holes. People discovered early on that *Giardia*'s ribosomal RNA bears closer resemblance to bacterial rRNA than eukaryotic rRNA.

For one, *Giardia* have no mitochondria, the organelles found in most eukaryotes that provide energy to the cell by cellular respiration. Along with chloroplasts, which are responsible for photosynthesis in most plants, mitochondria are believed to have evolved from an ancient free-living organism that long ago entered into a symbiotic relationship with the last common eukaryotic ancestor. These energy powerhouses are essentially ubiquitous among eukaryotes. However, the fact that *Giardia* has no mitochondria gives rise to the tantalizing idea that perhaps *Giardia* is a modern evolutionary descendant of the eukaryotic "chassis," the organism that engulfed the mitochondrial ancestor to become the modern-day eukaryote.

That hypothesis is tempting, but the genome begs to differ. Although mitochondria do carry some of their own DNA, the vast majority of genes necessary for mitochondrial function were slowly shuttled to the eukaryotic genome over hundreds of millions of years of evolution. A close inspection of *Giardia*'s sequence revealed a mitochondrial-like gene *cpn60* that hints at a mitochondria-containing ancestor, as well the presence of a mitochondria-related organelle, the mitosome, whose exact functions are a subject of continued inquiry. Genetically, it turns out that it is unlikely that *Giardia* diverged before the endosymbiotic event.

Besides *Giardia*, a few other basal eukaryotes have also been sequenced in the past few years. But like *Giardia*, they are all parasitic species, presumably chosen for their medical relevance. The problem with parasites is that they are known to be genomically streamlined.

"Parasites just chuck things out," explains Cande, "because they occupy such stable environmental niches." Thus, any comparisons between these organisms and other major eukaryotic branches may be incomplete because parasites have made so many genomic changes since their ancestors diverged from the main lineage.

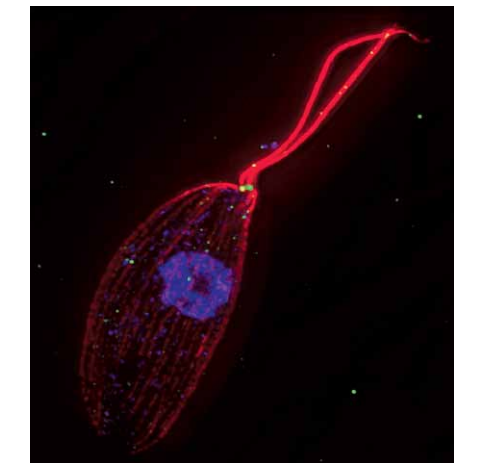
The independent lifestyle

That's where the sequence of *Naegleria* can contribute. *Naegleria* is considered a highly divergent eukaryote, meaning it's so different from other types of eukaryotes

that the lineage must have branched off very early in eukaryotic history. The lab strain was originally isolated from the eucalyptus grove abutting the Life Sciences Addition, but the species is ubiquitous across soil and freshwater habitats all over the world. Unlike its brain-eating cousin *N. fowleri*, which can cause fatal meningoencephalitis for unfortunate lake swimmers, *N. gruberi* is harmless. Its claim to fame is its locomotive versatility; it can reversibly switch from an amoeboid form to a flagellar form in less than an hour. Most importantly, as *Naegleria* is free-living and not a parasite, it is the first early eukaryote to be sequenced that did not have the luxury of shedding unnecessary portions of its genome.

Naegleria's independent lifestyle enables it to contribute significantly to our understanding of the central repertoire of eukaryotic genes. Using data from *Giardia*, only about 500 gene families were thought to be eukaryote-specific. Careful analysis of the *Naegleria* sequence increased this number to over 4,000. Over 40 percent of these genes have no recognizable homologs in prokaryotic ancestors, confirming that they must be novel inventions.

Its genome sheds light on the unifying features of eukaryotes, but is still relatively silent on what the evolutionary route to prokaryotes actually looked like. At the end of the day, *Naegleria* is still very much a true eukaryote, with all its hallmark features. A true intermediate between prokaryotes and eukaryotes, such as a eukaryote with a bacterial cell wall (plant cell walls are different) or a naked *Eubacteria* without one, would be ideal for solving this puzzle.



Naegleria in its flagellate form. The cell's DNA is shown in blue and its flagella in red. The bases of the flagella are highlighted in green.

FROM TOP: MARK J. DAVEL, LILLIAN FRITZ-LAYLIN

MARK J. DAVEL

Shaping the topiary

Such a chimera has not been yet found. One reason is that the transition may not have actually occurred, at least not with the linearity we suppose. “The prokaryotic-to-eukaryotic transition has become kind of a dirty word,” says Lillian Fritz-Laylin, the graduate student spearheading the *Naegleria* research.

First of all, true transitional forms may not exist because all eukaryotes have been evolving for the same period of time since the last common ancestor. Thus, *Naegleria* has been evolving for just as long as humans have been. We may like to think that it, or some other modern organism, has stayed true to the ancestral eukaryote, but this is unlikely. “Whatever happened, happened so long ago, you can’t actually find any transitional forms,” says Cande.

Eukaryotes have features stemming from both *Eubacterial* and *Archaeal* roots, inspiring two alternative theories about how eukaryotes arose. Some advocate the theory of the blessed event, in which some *Eubacteria* and *Archaea* fused to form eukaryotes, contributing the cytoplasm and nucleus, respectively. The alternative theory

is that because eukaryotes, *Eubacteria*, and *Archaea* are equally divergent from each other, the predecessors to all three groups split off at around the same time. In fact, this kind of trifurcation might even be an oversimplification. Unicellular organisms often reproduce asexually, opting instead to pick up genetic material from the environment to increase genetic diversity, a practice known as lateral gene transfer. For these organisms, the definition of a species is loose. The widespread occurrence of lateral gene transfer means that some evolutionary “trees” can look less like well-ordered branches and more like a tangle of yarn.

Because this transition or trifurcation happened over a billion years ago, any evidence is hazy. Genome sequences give us a better and more complete picture, but they don’t change the fact that the evolution of eukaryotic life may have been a messy, complicated affair, with few known modern descendants of the intermediate forms.

Since we can’t definitively describe how eukaryotic life progressed from ancestral forms, even deducing hierarchy solely within the eukaryotic tree is difficult. In fact, the eukaryotic tree of life is in such a constant

state of flux that it might as well be called a topiary, with competing sets of hands reaching for the shears.

“There’s this huge debate going on about how to root the eukaryotic tree,” says Fritz-Laylin. In the absence of definitive data, people may sometimes rely on gut instinct and personal preference. “What you would want is something that allows you to discriminate between one root or another,” says Cande. *Naegleria* itself, unfortunately, does not wield that kind of power, because more organisms are needed to get a sense of evolutionary context. “If we had more organisms to look at, and more genomes,” Cande adds, “we can have a better sense of it.”

More searchlights needed

As it turns out, recordkeeping is not one of Nature’s prerogatives; she’s just an accidental historian. The DNA transcript has provided many insights into life’s evolutionary history, but that information is not always easy to get. Major problems, like the abundance of lateral gene transfer in prokaryotes and some eukaryotes, make reconstructing the tree of life seem impossibly difficult. One can’t help but pose the question, “will we ever know?”

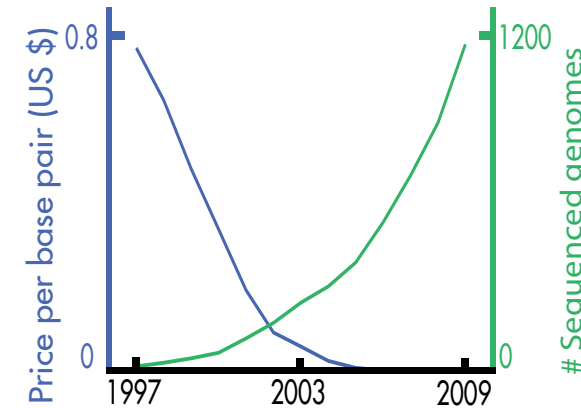
For sparsely sampled parts of the tree, like the sections Cande is investigating, the most crucial step might simply be more sequencing. Certainly the cost of genome sequencing is dropping rapidly. Two years ago, the *Monosiga* sequence cost approximately \$300k, but the upcoming *Salpingoeca* genome will only set the King lab back about \$40,000. The first human genome was a highly collaborative effort spanning ten years and costing over \$500 million. These days you can get your genome sequenced by Illumina for a mere \$15,000. That means even researchers with relatively limited funding can get their hands on a significant slice of the data pie.

The Department of Energy’s Joint Genome Institute, which is located partly at Lawrence Berkeley National Laboratory, was involved in the sequencing of both *Naegleria* and *Monosiga* and is ramping up plans to sequence more microbial genomes. In collaboration with Cande, they are also sequencing *Spironucleus vortens*, which is similar to *Giardia* in what it’s missing. Given that these organisms are only related very distantly (akin to the relationship between sea urchins and humans), the confirmation

of shared characteristics will be useful in understanding whether *Giardia*’s genomic minimalism is really a hallmark of early eukaryotes or simply an artifact of parasitism.

Cheaper sequencing is only part of the puzzle. Often the bigger challenge is simply collecting enough raw genetic material. Many free-living microbes are too difficult to grow in the lab. The web of life at that scale is delicate and can be impossibly complicated to replicate in vitro. Even if a species’ food source can be identified, it may be technically challenging to separate the species of interest from its prey, thus complicating genetic analyses. The proliferation of automated, high-throughput technologies may help future researchers quickly identify the proper culture conditions to grow and purify these fussy microbes.

Our technological future is poised to reveal much about our evolutionary past. However, the paramount goal is not really



As the price of sequencing decreases rapidly, more and more genomes are being sequenced.

to catalog all of life’s genomic sequences in exquisitely arranged phylogenetic trees. Rather, both genomic sequencing and phylogenetics can be considered colossal searchlights, scanning the landscape of biological complexity for salient features to be investigated further. Together, they illuminate a much broader field.

Sisi Chen is a graduate student in bioengineering.

GRAPHICS: AMY ORSBORN; DATA: GREGORY, T.R. (2005). ANIMAL GENOME SIZE DATABASE (GENOMESIZE.COM) AND ROB CARLSON (SYNTHESIS.CO)

The shotgun approach

In 1994, Craig Venter and his colleagues applied for an NIH grant to sequence the genome of *Haemophilus influenzae* using a then-untested technique called “whole genome shotgun sequencing.” At that time, the NIH was already four years into the Human Genome Project using a different methodology that systematically divides the genome into manageable pieces to be sequenced

individually. The team of experts reviewing Venter’s application deemed it unfeasible, believing the technique would produce a hopeless jumble of data that would be impossible to piece together.

Little did the NIH know that the gun was already loaded. Only a month after the NIH rejection letter arrived, *Science* published Venter’s complete sequence of the *H. influenzae* genome, the first complete genome ever to be deciphered. Since then, genome sequencing has experienced explosive growth, largely due to the rapid efficiency of the whole genome shotgun method.

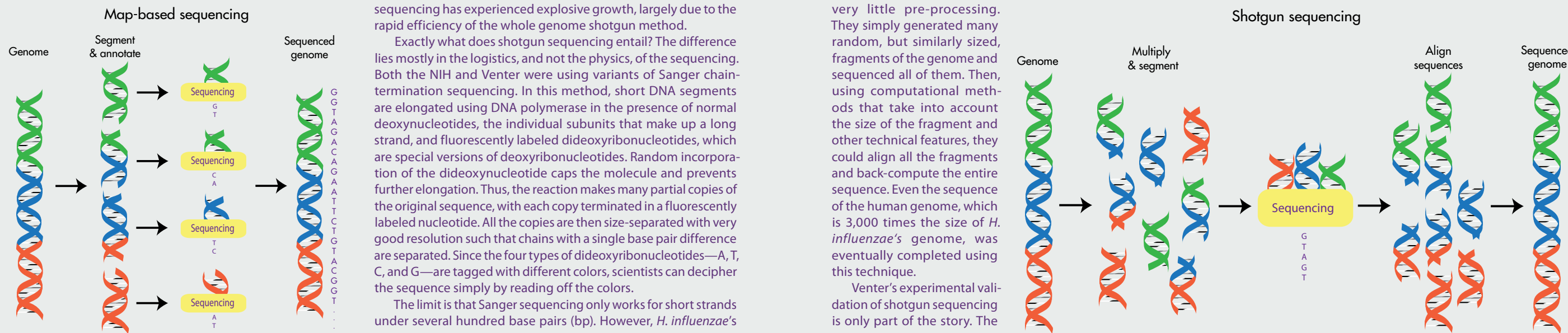
Exactly what does shotgun sequencing entail? The difference lies mostly in the logistics, and not the physics, of the sequencing. Both the NIH and Venter were using variants of Sanger chain-termination sequencing. In this method, short DNA segments are elongated using DNA polymerase in the presence of normal deoxynucleotides, the individual subunits that make up a long strand, and fluorescently labeled dideoxynucleotides, which are special versions of deoxyribonucleotides. Random incorporation of the dideoxynucleotide caps the molecule and prevents further elongation. Thus, the reaction makes many partial copies of the original sequence, with each copy terminated in a fluorescently labeled nucleotide. All the copies are then size-separated with very good resolution such that chains with a single base pair difference are separated. Since the four types of dideoxynucleotides—A, T, C, and G—are tagged with different colors, scientists can decipher the sequence simply by reading off the colors.

The limit is that Sanger sequencing only works for short strands under several hundred base pairs (bp). However, *H. influenzae*’s

genome is almost two million bp long and the human genome is over six billion bp long. The NIH tackled this problem by adopting the most straightforward approach—to neatly subdivide the giant tangle of genomic DNA into small parcels for sequential sequencing. However, the necessity of painstaking a priori annotation made this process excruciatingly slow. By contrast, the solution adopted by Venter’s team required very little pre-processing. They simply generated many random, but similarly sized, fragments of the genome and sequenced all of them. Then, using computational methods that take into account the size of the fragment and other technical features, they could align all the fragments and back-compute the entire sequence. Even the sequence of the human genome, which is 3,000 times the size of *H. influenzae*’s genome, was eventually completed using this technique.

Venter’s experimental validation of shotgun sequencing is only part of the story. The

success of whole genome sequencing is reliant upon a vast suite of diverse technologies, ranging from biochemical tags to automation to computational processing algorithms. Though shotgun sequencing has brought us a long way, so-called “next-generation” sequencing techniques promise even faster and cheaper results by sequencing arrays of many DNA strands in parallel.



THE FACTORY PHENOTYPE:

The rise of synthetic biology in the laboratory and the classroom

by Phuongmai Truong

Each year, 300 to 500 million cases of malaria are diagnosed worldwide, of which 1.5 to three million, mostly in children, result in death. Drugs to treat malaria are too expensive for people in developing countries, hence the lack of proper treatment and the high mortality rate. Fortunately, a new, much less expensive anti-malarial drug will surface in the market in 2012, thanks to synthetic biologist Jay Keasling and his team at UC Berkeley. Developing this product is just one among many goals of the Synthetic Biology Engineering Research Center (SynBERC), where scientists are working to create efficient biofuels, biosensors, and cures for cancer and HIV.

Synthetic biology in the past

Synthetic biology has its roots in early research on DNA manipulation. In 1970, Daniel Nathans, Werner Arber, and Hamilton Smith identified restriction

endonucleases, enzymes that can cut DNA strands at specific locations, which bacteria use as a defense mechanism against invading viruses. The discovery eventually led to the development of recombinant DNA techniques, which allow scientists to combine DNA sequences and introduce DNA from one organism into another. The term "synthetic biology" was first coined in 1974 by Waclaw Szybalski, now an oncology professor at University of Wisconsin-Madison Medical School, as he foresaw that the ability to build DNA sequences would eventually allow bioengineers to build "synthetic organisms," whose traits would be chosen by humans for useful applications.

Bringing ideas under one roof

In the summer of 2006, armed with a five-year, 16 million dollar grant from the National Science Foundation (NSF), bioengineers at UC Berkeley and other institutions across the United States formed SynBERC,

a collaborative funding initiative whose primary goal is to bring together experts in multiple disciplines to develop synthetic biology. In addition to its research efforts, the program also has a strong educational component. In Berkeley, SynBERC members reach out to local high school and undergraduate students with unique summer programs and competitions focusing on synthetic biology.

Synthetic biology today

The exact definition of synthetic biology varies depending on whom you ask, since each researcher's expertise and current project shape her view on the subject. The rapid growth of the field also makes it hard to label it with any specific stamp: a definition today may not apply to synthetic biology tomorrow. The backgrounds of synthetic biologists at SynBERC today are perhaps the best representation of this diverse and dynamic field of research.

Three main groups of scientists are joining the field: the protein engineers, who work with amino-acid building blocks; the metabolic engineers, whose focus is to regulate processes in cells to increase a cell's production of certain substances; and the computer scientists, whose knowledge of manipulating and interpreting large datasets is critical.

The numerous research projects of synthetic biology today have one goal in common: finding standardized processes to design biological systems with practical functions for our society's benefits.

Standardization is the key

As director of SynBERC, Professor Jay Keasling in the Department of Chemical and Biomolecular Engineering at UC Berkeley views synthetic biology as "the industrialization of biotechnology." Biotechnology, he claims, originally grew out of pharmaceuticals that were heavily restricted by patents, where each invention is independently made by individuals and is not readily available to be built upon by others. To overcome this obstacle to rapid progress, synthetic biology done at SynBERC is an open source, where scientists are free to learn from and build upon each other's results to speed up the research process.

Bioengineers have worked with different applications that, while sharing the same technical foundations and roadblocks, used tools that were particular to each research problem. Thus, synthetic biologists want to find a general procedure and to identify the circuitry rules that would guarantee a working system regardless of its application. A common but oversimplified analogy is that synthetic biology puts together biological parts just as electrical engineering and computer engineering put together an electronic circuit.

Part, device, chassis

Just as an electrical engineer needs resistors, capacitors, and inductors to make an electronic device, a synthetic biologist needs biological parts to build a biological device, usually in the form of bacteria or yeast that can produce certain chemicals or reactions to the environment. Biological parts

include protein-encoding DNA sequences and promoters, sequences that facilitate the expression of a gene. The parts need to be assembled and powered by an appropriate chassis to produce the desired outputs. This theoretical picture, however simple, encounters three main difficulties in practice.

First, biological parts, though numerous, are hardly categorized, and their functions under various laboratory conditions have not been well tested. Over the past 50 years, data accumulated from in vivo studies, as well as advances in DNA sequencing technology and computer analysis of genomes, have given considerable insight into the function of thousands of genes. However, similar to a toolbox full of nuts, bolts, screws, and nails all scrambled together rather than organized into compartments, there has been no systematic cataloging of genes and their characteristics for genetic engineering applications.

In December 2009, synthetic biologists Jay Keasling and Adam Arkin at UC Berkeley and Drew Endy at Stanford University launched the International Open Facility Advancing Biotechnology (BIOFAB) to professionally develop and characterize new

and existing biological parts. BIOFAB is the world's first biological design-build facility, funded by NSF in partnership with Lawrence Berkeley National Laboratory (LBL), the BioBricks Foundation (BBF), and SynBERC. Once fully operational, BIOFAB is expected to produce tens of thousands of parts each year, freely available to both academic and commercial users, while also providing the design essentials for partners like SynBERC.

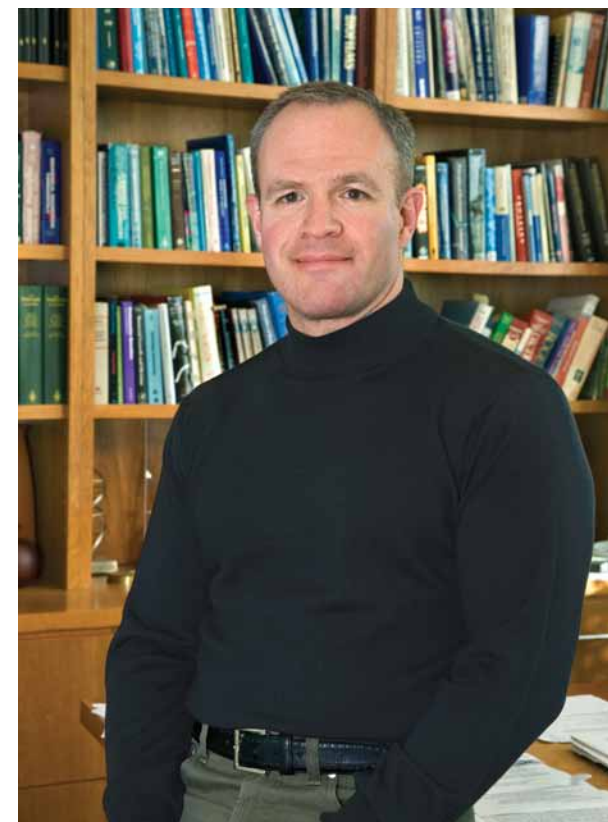
Second, biological systems are highly unpredictable. The complexities of life, such as the behavior of different possible combinations of four nucleotides A, T, C, and G in a piece of DNA, are not as well understood as the physical laws governing light bulbs and batteries. "50 percent of the time, you turn on a biological circuit, and it just doesn't work for no good reason," says Professor Christopher Anderson in UC Berkeley's Department of Bioengineering.

The third difficulty lies in constructing and testing complex multi-gene circuits. Larger circuits simply demand more effort. Most of the work in syn-bio research to date has been done manually, and an automatic process to combine the genetic parts would alleviate the load tremendously. To tackle

this, Anderson and his colleagues are working to engineer bacteria to assemble DNA pieces into useful circuits and select the successfully assembled products from among the unused DNA parts. The hope is that such automated systems can shorten the time needed for one assembly stage from a few days to a few hours.

Paging doctor bug

Keasling and colleagues are tackling the HIV problem. Human Immunodeficiency Virus (HIV) type I, the causative agent of AIDS, may be treated with various drugs to decrease its viral strength. The virus can remain latent in a patient's body for years. Because of its inactive state, latent HIV-1 is unaffected by current drugs and can later emerge to cause a full HIV infection or AIDS. Recent studies show that two related compounds, prostratin (12-deoxyphorbol 13-acetate) and DPP (12-deoxyphorbol 12-phenylacetate), have great potential to eliminate latent HIV. However, both only exist naturally in rare plants: prostratin is found



As director of SynBERC, Professor Jay Keasling hopes to engineer organisms to produce pathogen-fighting compounds.

in the bark of the Samoan mamala tree *Homalanthus nutans*, and DPP can only be extracted from the Moroccan spurge *Euphorbia resinifera* growing on the slopes of the Atlas Mountains in North Africa. As it is too inefficient to obtain the compounds for commercial HIV treatment in this way, the only hope is to engineer microorganisms to produce them. Keasling's team is in the process of locating and cloning the genes responsible for the synthesis of prostratin and DPP in the plants.

The biggest success contributing to UC Berkeley's placement on the worldwide syn-bio map is the yeast that can produce an anti-malaria compound, developed in Keasling's lab in late 2005 and recently perfected. This is the first example of synthetic biology actually producing a competitive product in the market. The malaria parasite develops inside red blood cells, where it accumulates iron, which makes it vulnerable to oxygen-based free radicals released from a scarce compound known as artemisinin. This compound is 100 percent effective against even the most lethal malaria parasite, *Plasmodium falciparum*. But before Keasling's process was developed, the compound could only be extracted from the plant *Artemisia annua*, a type of wormwood.

Anti-malaria drugs using plant-derived artemisinin cost \$2.40 per adult course (too expensive for people in developing countries), because of the low concentration of artemisinin found in wormwood. By inserting parts of the wormwood DNA into yeast DNA and reprogramming the cell's metabolic pathway,



The rare plant *Euphorbia resinifera* produces DPP, a compound SynBERC hopes to be able to synthesize for HIV treatment.

Keasling's team made yeast that can convert sugar into artemisinin in just a few hours. The laboratory success led to a contract between the research group and a start-up French pharmaceutical company, Sanofi-Aventis, in March 2010. The collaboration plans on releasing the synthetic artemisinin into world markets in 2012, at merely 1.5 cents per adult course, 160 times cheaper than the current price.

Also on the medical frontier is Anderson's new technique to combat cancer cells. The idea is to inject *E. coli* bacteria that can find and destroy cancerous cells into the bloodstream. The bacteria were first engineered to recognize tumors, which are characterized by high cell density and anaerobic growth. *E. coli* naturally possesses several genes, such as formate dehydrogenase (*fdhF*), that are strongly expressed when the bacteria are in a low-oxygen environment. Anderson's team then inserted a genetic circuit (*lux*) from the bacterium *Vibrio fischeri* to allow *E. coli* to distinguish between regions with low cell densities and those with high cell densities. Parallel to engineering these sensing circuits, the team inserted the *inv* gene from the bacteria *Y. pseudotuberculosis* into *E. coli* to allow *E. coli* to produce invasins, a protein that binds the bacteria to mammalian cells. Finally, the sensing circuits (*fdhF* and *lux*) were linked with the *inv* gene. The result is that only the low-oxygen, high-density environment of the tumor can trigger the bacteria to produce invasins, which in turn causes the cancerous cells to engulf the bacteria. The next step is to engineer *E.*

coli to release a toxin once inside the cancerous cells to kill them. By putting DNA pieces from different bacteria into *E. coli*, Anderson's team hopes to create intelligent toxin-carriers that actively look for and destroy tumors without affecting healthy cells. Currently, the separate parts have been built and tested successfully, and with further examination, it may be possible to apply the same technique to different applications with shared properties. For instance, researchers can use the parts developed

by Anderson to deliver medicine to HIV-infected white blood cells.

Energy applications

Following medical applications, the second most socially driven research area in synthetic biology is biofuels. The Berkeley SynBERC team carries out studies on this frontier at the Joint BioEnergy Institute (JBEI), a LBL-led scientific partnership between UC Berkeley, UC Davis, the Carnegie Institution for Science, Lawrence Livermore National Laboratory, and Sandia National Laboratory. Scientists at JBEI engineer microbes similar to yeast that can transform sugars from engineered plants into hydrocarbon-based fuels, such as butanol. The current highest production level for yeast is 2.5 mg of butanol per liter of growing substrate. Although this is still much lower than the 500 mg/l yield from engineered bacteria, researchers believe that yeast has high industrial value because of its robust growth and resistance to contamination.

Furthermore, Keasling announced in May 2010 that his team had successfully engineered *E. coli* to produce a biodiesel from hemicellulose, a sugar polymer present in large quantities in plant biomass. The engineered bacteria digest hemicellulose in such a way that the sugar is transformed into diesel, which is secreted by the cells and floats to the top of the culture where it can be collected. With very little purification, this diesel is ready for use.

Reaching out for more talents

As any ambitious goal requires a tremendous amount of work, SynBERC relies on collective effort to thrive. In terms of expertise, the field welcomes researchers from not only the biological sciences and engineering disciplines, but also humanities and anthropology. At SynBERC's Human Practices Lab (HPL), anthropology professor Paul Rabinow and his colleagues ponder the relations among biotechnological advances, politics, and security. As Gaymong Bennett, assistant director of HPL, put it, "the job of the ethicists and lawyers among others is to set up regulations on how your stuff can get used outside of the lab." Such study is necessary whenever there are concerns about the potential impacts of a newly developed technology.

In terms of finance and educational outreach, five institutions—UC Berkeley,

UC San Francisco, MIT, Harvard University, and Prairie View A&M University in Texas—and about twenty independent companies collaborate on funding and directing the research at SynBERC. As Anderson views it, the industry exposure also shows synthetic biology students the broad range of job opportunities available in the field, an important motivation for the pursuers of syn-bio study.

Get them while they're young...

At the high school level, SynBERC and JBEI, among other laboratories in the Bay Area, open doors both figuratively and literally to host six students and two high school teachers each year in an eight week paid summer internship known as the Introductory College Level Experience in Microbiology (iCLEM). The program, founded in 2008 by two of JBEI's postdoctoral researchers, Clem Fortman and James Carothers, gives the interns an opportunity to work with high-tech lab equipment and take part in the biofuel research at JBEI.

The goal of iCLEM is not to have results churned out by the end of each summer, but to arm the students and high school teachers with lab experience and research skills, while showing them the opportunities available in this new scientific field. Oakland Unity High School science department head

Rowan Driscoll, iCLEM 2009 participant, praised the opportunity: "As a biology and chemistry teacher, I want to make education as real and as practical as possible. I want to open doors, open eyes, and help my students find avenues to use science to make themselves useful to society."

For both teachers and students, the research does not stop when the internship ends. Berkeley High School science teacher Kate Trimlett, also a participant in iCLEM 2009, decided to start teaching about biofuels in her classroom, organizing her students to collect and analyze bacteria from a compost heap to test their ability to break down cellulose. Such classroom outreach embodies the goal of iCLEM: to raise the level of interest in science of Bay Area high school students,

and, hopefully, to inspire many of them to become future synthetic biologists. As Kate Spohr, SynBERC's education and outreach coordinator, said, "We want to get them while they're young."

...And they will revolutionize the way science is done

Beyond its presence in high school classrooms, SynBERC offers unparalleled opportunities for undergraduates to make a meaningful contribution to syn-bio research. Each year, five students are chosen to form the Berkeley International Genetically Engineered Machines (iGEM) competition team. The team is given a set of biological parts, with which they will build biological systems and operate them in living cells.



Undergraduates on the Berkeley International Genetically Engineered Machines (iGEM) team have the opportunity to participate in some of the most cutting-edge research in the field.

This is not just a menial practice project, but "part of cutting edge syn-bio research," says postdoctoral researcher Mariana Leguia. "The results they get will be used to advance the field." The iGEM team works full time in the summer, then present their results to other iGEM teams in an international competition held at MIT every November. Since its creation in 2004, the event has become an effective method to introduce undergraduates to synthetic biology research, and several winners have gone on to prestigious research institutions for their graduate study.

Berkeley iGEM teams have won gold medals in the past five competitions with their innovations such as Clonebots (2008), a collection of devices and DNA strains to aid part synthesis and analysis, and Bactoblood

(2007), a cost-effective red blood cell substitute constructed from engineered *E. coli*.

This year, the Berkeley iGEM team sets out to genetically engineer choanoflagellates (see "Redrawing the branches," current issue), single-celled organisms whose DNA is intractable by current methods in genetic engineering. "Since choanoflagellates eat bacteria, we plan on designing some bacteria that can do the job for us," says bioengineering major Christoph Neyer. The bacteria contain a set of proteins which are designed to insert a gene into the genome of the choanoflagellate once the bacteria get inside the choanoflagellate's food vacuole.

If carried out successfully, the experiment will lay the foundation for a new technique in genetic manipulation of choanoflagellates. "These species are interesting because they are the closest living relative to the microbial ancestor that became the first multicellular animal," says iGEM team member Conor McClune. To be able to genetically manipulate these little creatures would allow scientists to learn more about the transition from single-celled organisms to multicellular ones, an important step in evolution history.

More importantly, projects like this are the best representation of SynBERC and synthetic biology research in general, in which two main

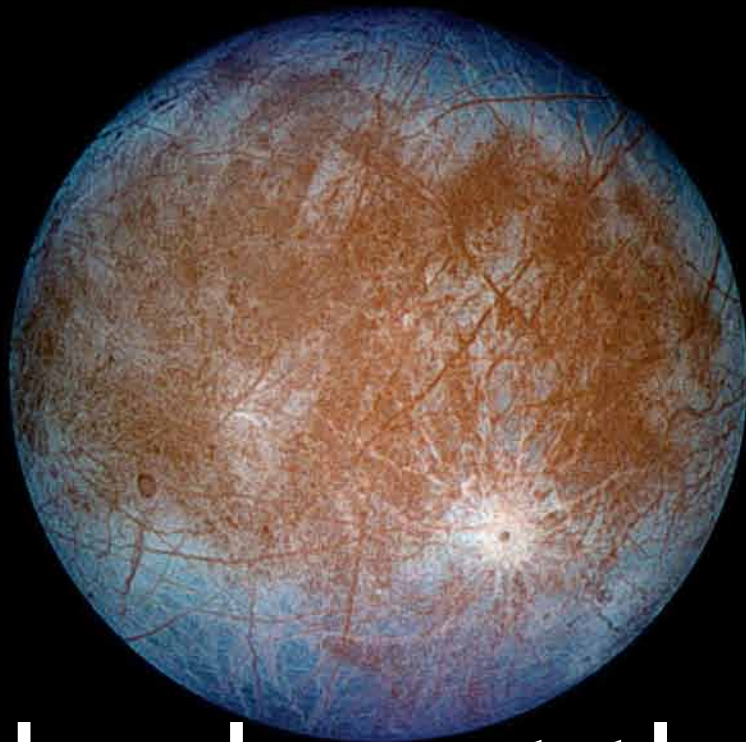
themes dominate. First, doing science is a collaborative effort in which participants are responsible for inventing individual parts, which are then standardized. Second, these parts must be open source and available to anyone who is interested, accelerating future developments. Once these two requirements are met, the possible applications are limitless, or as Amy Kristofferson, a fourth-year molecular and cell biology student, puts it, "[synthetic biology] is creating all sorts of applications for genetic engineering that are in turn revolutionizing the way in which science is done."

Phuongmai Truong is a graduate student in physics.

Anybody out there?

The search for extraterrestrial life begins at home

by Naomi Ondrasek



In 1980, astrophysicist Carl Sagan introduced people around the world to the possibilities of astrobiology—a scientific field dedicated to the search for life beyond our lonely blue planet—with a television series, *Cosmos: A Personal Voyage*. Wearing a scholarly beige jacket, Sagan traversed the universe, drawing viewers on a journey across the vastness of space and reviving interest in a question that had been brewing within humanity’s collective psyche since the beginning of civilization—has life arisen elsewhere in the Universe? With the maturation of space technology during the latter half of the 20th century, it finally became possible to begin a substantive investigation, but the road through astrobiology has not been without its rough stretches. Despite the revolutionary implications that astrobiology holds for humankind, scientists engaged in the search have occasionally encountered political and financial challenges. Through it all, UC Berkeley scientists scattered across numerous departments have been pursuing answers to some of the most profound questions our species has ever asked—what is life, how did it evolve, and are we alone?

Are we alone?

A committed quest to discover extraterrestrial life began in the 1960s with the birth of SETI (Search for Extraterrestrial Intelligence), a scientific field dedicated to scanning the sky for signals released into space by intelligent civilizations. Excited by SETI’s potential for discovery, on Columbus Day in 1992 NASA dedicated \$100 million to the endeavor, but rumblings within Congress about overspending soon made NASA reconsider its commitment. Targeted as an example of wasteful spending and mocked as the “search for little green men,” SETI lost NASA’s financial support, forcing researchers around the country to find other avenues for funding their work. “We all started scrambling around,” says SETI at Berkeley chief scientist Dan Werthimer, “but we got some private support, companies gave us money, and so we were able to keep going, keep innovating.”

Despite the occasional setbacks, Berkeley’s SETI scientists have become

pioneers in technological development and astronomical research. The scope of their creativity is reflected in their research programs—each with a different approach to tapping into the interstellar communications of distant civilizations—currently run by SETI at Berkeley. While they vary in their specific approaches, most of the projects work on the assumption that intelligent civilizations are emitting electromagnetic radiation into space, either intentionally to communicate with other intelligent beings, or accidentally as a byproduct of their daily lives. Electromagnetic radiation of varying energies corresponds to different types of detectable signals—radio waves, infrared waves, and visible light waves, to name a few. While waves from the entire electromagnetic spectrum are emitted by non-biological sources in the universe (radio waves, for instance, can be produced by stars and gases), SETI researchers argue that a concentrated, sustained, and repetitive release of waves from a narrow portion of the spectrum would suggest the presence of intelligent life. “We look for things that the universe doesn’t produce naturally,” says Andrew Siemion, a SETI graduate student from the Department of Electrical Engineering and

Computer Sciences. “It can be a lot of energy in a very narrow time window, or a lot of electromagnetic energy in a very narrow frequency window.”

At the lowest end of the spectrum are radio waves, which were among the first to be scanned by SETI scientists for signs of alien intelligence, in part because they travel through space relatively unimpeded. One of SETI’s largest and longest-running radio-based research programs is UC Berkeley’s SERENDIP (Search for Extraterrestrial Radio Emissions from Nearby Developed Intelligent Populations), which began sifting through radio waves for signs of intelligent life over 30 years ago. In 1992, SERENDIP was installed at the Arecibo radio telescope, the largest and most sensitive radio telescope in the world, located in Puerto Rico. Like other radio telescopes, Arecibo works by gathering radio signals with an enormous curved dish lined with mirrors. When the signals bounce off of the dish, they’re directed toward a receiver, which collects the data and sends it along to researchers.

While the vast majority of SETI studies focus on narrow portions of the electromagnetic spectrum or on specific regions in space, SERENDIP takes a broader approach. “We

try to look across the spectrum in the sense that we look at very long and very short wavelengths,” says Siemion. Werthimer adds, “There are different strategies in SETI. One of them is to find nearby stars that are kind of like our sun, point your telescope there, and look very carefully at that star. Our strategy typically is not to do that. We scan the sky, back and forth, looking at billions of stars, billions of galaxies.” While these tactics allow SERENDIP to search greater swathes of space and a wider portion of the electromagnetic spectrum, they have pitfalls—each region of space cannot be searched in fine detail, and with the influx of massive amounts of data, the system can only save the strongest signals for analysis, while the remaining majority of the data must be discarded. Berkeley’s SETI researchers responded to the latter challenge by creating SERENDIP’s complementary sibling project, SETI@home, which also collects data from the Arecibo radio telescope. While SERENDIP takes a rough look at a broad section,



Lake Tyrrell, a hypersaline lake in southeastern Australia (above); global view of Europa, taken by the NASA spacecraft Galileo (opposite).

or bandwidth, of radio frequencies, SETI@home scans a much smaller bandwidth in exquisite detail, allowing it to pick up weak radio signals. The data collected by SETI@home are sent out in small chunks around the world to millions of personal computers, which process the data while they're idle. Once finished, each computer sends its data back to SETI@home and receives a new data set to process. Since its inception in 1999, SETI@home has become the largest and most powerful supercomputer in the world, which has allowed it to facilitate the most sensitive SETI search in history.

Our microscopic neighbors

While SETI researchers seek signs of microscopic, intelligent life beyond our solar system, other scientists at UC Berkeley are hoping to find microscopic organisms on our neighboring planets and moons. In the Department of Chemistry, Professor Richard Mathies' group is developing the next iteration of the Mars Organic Analyzer (MOA), a miniaturized biochemical analyzer system with the ability to detect a variety of organic molecules with significant roles in life processes. The lab is especially interested in using the MOA to search for amino

acids—the building blocks of proteins—on Mars, since the chiral structure of these molecules can provide additional information about the presence or absence of life. Two molecules are said to be a chiral pair when they're mirror images of one another, asymmetrical, made of the same constituent elements, and non-superimposable (for an illustration of chirality, look at your hands—this is why chirality is also known as “handedness”). All known life on Earth uses left-handed amino acids. No one knows exactly why this is the case, but scientists agree that a mixture of left- and right-handed forms would probably interfere with biological processes, since combining the two types of amino acids creates a misshapen, tangled mess of a protein. In contrast, homochiral (all left-handed or all right-handed) amino acids can be strung into a well-defined and functional protein capable of carrying out life-sustaining reactions. When they're not being manipulated by organisms, amino acids tend to exist in a nearly equal mixture of left- and right-handed forms, a state known as heterochirality. With the MOA, an instrument compact enough to fit on a Mars-bound rover, but powerful enough to discern the presence and chirality of amino acids, future missions to Mars could determine if the planet harbors concentrated amounts of either left-handed or right-handed amino acids. A sample with a preponderance of either type of amino acid would suggest the presence of life and probably send more than one champagne cork flying into a laboratory ceiling.

In the field, the MOA separates out organic molecules using a microfluidic device, or chip (see “Lab on a chip,” *BSR* Spring 2009), which allows researchers to determine the make-up of a solution using a sample as small as one microliter (to give you an idea of how small that is, consider that it would take nearly 5,000 microliters to fill up one teaspoon). Similar in diameter to a Petri dish, the chip consists of a flexible membrane sandwiched between two glass plates. Etched into the glass are separation channels and holes, each corresponding to a valve that allows scientists (or a machine) to move a sample around on the chip using pressure and vacuums. To identify the molecules within a sample, the MOA begins by passing an electric current through the microfluidic device. Since many organic molecules carry different charges, the current

causes them to move down the separation channels at different rates, depending upon their charge-to-size ratio. At the end of the line, the molecules, which have been tagged using a fluorescent label, pass over a laser and fluoresce. A spectrometer then analyzes the signal and produces a spectrogram (a sort of identification key) for each molecule. “Basically, it's like being on a conveyor belt at an airport,” says Mathies Lab staff scientist Tom Chiesl. “Sometimes you get people that run forward on it, and other people want to go backwards, and some just sit there. Every different type of amino acid is moving at a different rate on a different type of conveyor belt. At the very end, they go by the laser and they fluoresce and then we see the signal.”

Until recently, the MOA had “flight status” designation, which essentially meant that the instrument was on the cusp of being installed on the upcoming ExoMars mission, a joint endeavor between NASA and the European Space Agency (ESA). With an intended launch date of 2018, the mission's goals are to search for signs of past or present life on Mars and to study the planet's geochemistry. During the planning process, officials at ESA were mulling over three different rover design options—large, medium, or small—and the respective benefits (bigger means more space for more instruments) and drawbacks (bigger means higher cost) of each. In the end, the economic downturn made the decision for them—ESA decided to proceed with the least expensive design, which placed real estate on the rover at a premium. With the need to include instruments built by European labs, ESA “descoped,” or bumped, the MOA from the 2018 mission. Despite this setback, Mathies lab staff scientist Tom Chiesl and graduate student Amanda Stockton are moving forward with their work and continue to envision an instrument that will eventually be more compact, lightweight, and someday get its first taste of Martian soil.

Unraveling the history of life

While some scientists dream of discovering life beyond Earth, other researchers are investigating the only model of life we have—that of our home planet—to unveil answers to two important astrobiological questions: what is life and how does it arise? In particular, astrobiologists are interested in extremophiles, organisms that thrive under harsh environmental conditions, because

many cosmic bodies harbor environments analogous to Earth's most extreme places. In addition, the most inhospitable locations on Earth are thought to closely resemble our planet's early history, when life first appeared. Studying Earth's hardest organisms provides scientists with an understanding of how life can emerge and survive on young or inhospitable planets, and offers a testing ground for the techniques that will allow us to detect life in other parts of the solar system and beyond.

In the Department of Earth and Planetary Science, members of Jill Banfield's lab are studying the lives and remains of extremophiles living in Lake Tyrrell, a hypersaline (very salty) lake in southeastern Australia. With a salt content ten times that of seawater, the lake is home to a community of resilient microbes and offers a treasure trove of information on palaeoenvironments (that is, very old environments) and their long gone inhabitants. One of Banfield's graduate students, Claudia Jones, is interested in characterizing the lake's microbial residents, both current and extinct. To determine what lived in the lake in the past, Jones uses lipid biomarkers, molecular fossils that can act as an identity card for ancient organisms. Although there are numerous types of biomarkers, lipids are especially useful because they can persist in the environment for billions of years. “Simply, you may die,” Jones explains, “but your fat lives on (nearly) forever.” The longevity of lipids results from the fact that they contain a large proportion of carbon-carbon bonds, which are extremely stable and resistant to degradation unless conditions are either severely hot or severely oxidizing. Lipid fossils are extracted from rock or sediment samples using organic solvents held under high temperature and pressure and then passed through a gas chromatograph, which separates the molecules by weight and charge. From there, the fossils are sent through a mass spectrometer in single file, where they are pelted by electrons and broken into pieces. When depicted on a spectrogram, these fragments can be reconstructed like a puzzle, allowing scientists to determine the molecule's

identity. Taking it a step farther, Jones also measures the ratio of carbon-13 to carbon-12 (the two types of carbon differ in the number of neutrons they possess) to identify the lipid's former owner. “These techniques tell us about the types of organisms extant in the geologic past, as well as the metabolic activities of those organisms,” says Jones. “Compound-specific isotopic measurements are important because some compounds, such as various fatty acids, can be produced by more than one type of organism. However, due to the different metabolic pathways by which microbes fix carbon and produce lipids, different ratios of carbon-13 to carbon-12 exist in the resulting molecules. In measuring this ratio, compound by compound, we can determine which type of organism produced which lipid.”

Using lipid biomarkers and geological data, Jones and her collaborators have managed to reconstruct Lake Tyrrell's past. Although the region has gone through several cycles of drying and wetting throughout its history, conventional thought says that in recent times, the cycles have become more extreme due to disturbances caused by humans. Surprisingly, Jones' findings suggest that in the distant past, the lake has been very similar to what it is now, both in terms of its aridness and its microbial communities. Discoveries like these show how it may someday be possible to use geological data and microbial fossils to reconstruct the evolution of habitats and organisms on other planets.

Another graduate student in the Banfield lab, Joanne Emerson, is helping to round out humanity's understanding of extremophiles



Located in Puerto Rico, the Arecibo radio telescope provides data for SETI at Berkeley's SERENDIP and SETI@home projects. With a diameter of 300 meters, the dish would hold ten billion bowls of corn flakes.



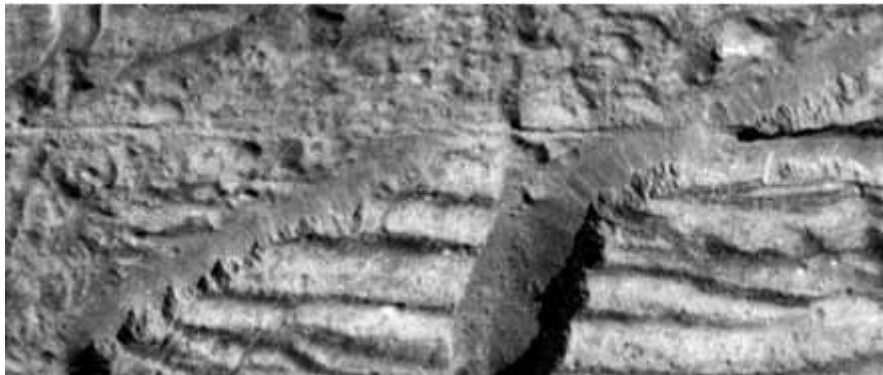
Halite, or rock salt, can be found abundantly in Lake Tyrrell. The pink coloration is due to the pigments of microorganisms living in the water.

by focusing on a less talked about class of microbe—viruses that infect bacteria and *Archaea* living in hypersaline environments. Since so little is known about these viruses, Emerson's goals are straightforward—she wants to characterize the viruses, figure out how they relate to other viruses, and understand their relationships with their hosts. Until very recently, biologists were unable to study 90 percent of the microorganisms living on Earth, since most are too poorly understood to be cultured in a laboratory. “We've been limited in our knowledge of microbiology based on what can be cultured, what can be grown in the lab, what can be manipulated,” says Emerson. “But with the advent of genome sequencing, we can actually go into an environment, take a sample, get all of the microbes on a filter, extract their DNA, sequence it, and then try to put the genomes back together again. In this manner, we can figure out who's there and what's going on without having to grow anybody in the lab.” These culture-independent techniques are especially exciting for the study of viruses since, until now, they could only be studied when their microbial hosts were thriving in a laboratory.

Although most speculations about the discovery of life on other planets have focused on bacteria, enhancing our understanding of viruses may prove equally important, since no one really knows what life outside of Earth will look like. In addition, viruses raise interesting questions regarding the definition of life and what it would mean to find a virus-like entity on another planet, as Jones points out: “Before we can discuss searching for life, we must specify what we mean by ‘life.’ A microbiologist would tell you that a virus is not technically alive: it cannot reproduce or replicate on its own, it lacks much of the internal machinery necessary to do so. However, viruses are organic in nature, respond to organic stimuli, and behave in the fashion of predators. It may at first seem frivolous, but without a strong definition of the term ‘life,’ or what we'd consider a smoking gun for the same, we are likely to neglect fruitful lines of research.”

Ice begets life

Searching for life on other cosmic bodies assumes that it has likely originated elsewhere in the solar system, which begs the question: if extraterrestrial life exists, where did it come from? In the Department of



Close-up of the Conamara Chaos region of Europa, taken by the NASA spacecraft Galileo. Professor Jere Lipps suggests that life could survive, hidden away and protected beneath the ice in some of Europa's surface features.

Integrative Biology, Professor Jere Lipps has used knowledge garnered from his research in Antarctica to develop the novel unconventional idea that life can begin in ice. While Lipps admits that he is not the first to suggest the concept, he is currently one of only a handful of scientists promoting the idea among astrobiologists. “There are two problems for the origin of life,” says Lipps. “The first is concentrating the elements of life. The second problem is having the energy to get it going.” The formation of ice solves at least one of these problems—when it freezes, water becomes a crystal that excludes foreign molecules, which are pushed into and concentrated in tiny rivulets, called brine channels (this is why icebergs formed from seawater produce freshwater when they melt). Provided that there's an energy source, like ultraviolet light, molecules squeezed together by freezing water may have created an ideal scenario for the appearance of the first amino acids and self-replicating nucleic acids, the building blocks of DNA.

Lipps began applying his knowledge and experience from working in icy environments to astrobiology when the Galileo spacecraft, launched in 1989 by NASA to investigate Jupiter and its moons, returned its first set of information on the moon Europa. Data from the spacecraft supported what planetary scientists had already suspected—that beneath its icy exterior, Europa possesses a salty ocean which likely holds about twice the amount of water contained in all of Earth's oceans. Images from Galileo also revealed a craggy, icy surface, crisscrossed by numerous cracks and dotted with pits and domes. When Lipps viewed these images, he felt right at home. Trained as a geologist and with years spent working as a biologist, he had extensive experience

using satellite images to identify sites that would likely harbor signs of life. “All of these geologic features fascinated me. This seemed to be an opportunity to look at the possibility of life based on my experience in Antarctica and to understand the geology and how we might be able to explore Europa for life.” While some scientists doubted that life could exist in the lightless environment beneath Europa's surface, Lipps's experiences in Antarctica told him otherwise. In the late 1970s, Lipps and a group of students drilled through 420 meters of ice on the Ross ice shelf (a mass of permanent, floating ice about the size of Texas) to determine what lived in the water beneath. Lowering a container filled with seal meat and a video camera, Lipps' group discovered an astonishing diversity of organisms—fish, microbes, large crustaceans, thousands of tiny crustaceans known as amphipods, and trilobite-like isopods previously documented only in shallow waters. In addition, he found that the underside of the ice, with its crevices and brine channels, functioned like a nursery, sheltering living organisms from the extremes in their environment. With these discoveries in mind, Lipps proposed that similar habitats could exist on Europa.

Despite the exciting potential for life in Europa's oceans, some significant challenges to conducting a search exist. To reach the European surface, spacecraft and their sensitive electronics would first have to survive the passage through the intense radiation surrounding Jupiter (see “Juno's revenge,” current issue). Protecting a European lander from radiation is possible, but the price tag increases by millions of dollars as the level of protection is enhanced. Compound this with the need to equip a lander with heavy-duty drilling equipment to breach the ice,

which is estimated to be many kilometers thick, and the cost for building a lander jumps even higher. Lipps suggests that it may be possible to reduce the hefty price of a mission to Europa by directing more effort to searching for life on the moon's surface. Europa lacks a protective atmosphere, so prolonged exposure to the radiation assaulting the moon's exterior would probably kill organisms dwelling in the open without at least 1.5 meters of ice overhead to shield them. But Lipps's discovery of a diverse biological community in the most inhospitable regions of Antarctica, along with findings made by other scientists that have revealed the existence of organisms thriving under other difficult conditions (extreme heat, pressure, salinity, and radiation to name a few) have convinced him that life could exist on Europa's surface, concealed and protected within caves and cracks, or beneath boulders and overhanging ledges. “Where there's an opportunity, even the smallest opportunity, life takes advantage of it,” Lipps says.

Along with other researchers from various institutions, Jere Lipps is a member of the Europa Task Force, which planned to put an instrument package into orbit around Europa or to fly by the moon if dealing with the radiation issue proved too costly. Collaborators from Lockheed Martin hoped to equip the spacecraft with a telescope capable of one centimeter resolution from 100 kilometers away (if you could eliminate the curvature of the Earth and all visual

obstructions, a telescope with this resolving power would allow you, while standing in Berkeley, to see a penny held out by your friend in Sacramento). Although the group received a grant to carry out their plans and move forward on the planned launch date in 2012, their contract was cancelled when President George W. Bush's administration postponed all outer planetary missions for 50 years or more. Planning meetings have continued, but Professor Lipps admits that they're of limited use: “How can you plan a mission in 50 years when you have no idea what kind of instrumentation there will be? What we can do is think about targets and objectives and keep them flexible, because those will probably change too, and then keep pushing to fly the mission.”

Why it matters

Despite the potentially revolutionary implications of astrobiology, its studies are often the first to lose funding during tough economic times. In defense of astrobiology, Professor Jere Lipps points out that the field has created an unprecedented platform for collaboration among scientists from many different disciplines and yielded advances that benefit non-astrobiological investigations. “If we discover life on another planet or moon,” he says, “we'll have added a big cherry on the top of a substantial cake of good science.” Some of the technology employed by Berkeley scientists for astrobiological research has proven useful for other

applications. The basic design of the Mars Organic Analyzer can be modified to aid in forensic investigations and identify medical conditions. Likewise, the technology used to create a massively powerful supercomputer, created for SETI@home, has benefited the study of other problems, like understanding cancer.

Some would also argue that astrobiology appeals to humanity for deeper reasons. “I think it's worth doing because it satisfies that fundamental curiosity that we all have, that sent Columbus to America and Magellan around the world. We've been doing this since the history of mankind started,” Lipps says. Werthimer provides another interesting perspective: “I think it's profound either way. If we find out that we are alone, the only intelligent civilization in the whole universe, that makes life on Earth an incredibly precious thing. If we find out that we're not alone and that we're part of a galactic club and thousands of civilizations are talking to each other, there's a lot we could learn.” When asked about the value of astrobiology, other Berkeley scientists echoed what Carl Sagan stated over 20 years ago on *Cosmos: A Personal Voyage*: “The nature of life on Earth and the search for life elsewhere are two sides of the same question—the search for who we are.”

Naomi Androsek is a graduate student in integrative biology.

Protecting the unknown

After centuries of ecological blunders, humankind has discovered the hard way that introducing invasive species—organisms that did not evolve within a particular ecosystem—can disrupt the delicate balance of relationships between native species, lead to declines in biodiversity, and spread disease. It's no wonder then that even during its earliest missions, NASA was deeply concerned about repeating the same mistakes on a much grander scale by depositing microbial stowaways on to other solar system bodies. Aside from disturbing the native ecology of other planets or moons, microbial contamination presents the additional problem of confusing efforts to identify new life-forms, necessitating the question, “Did that microorganism originate here, or did we plant it here by accident?”

To prevent the littlest Earthlings from hitching a ride to a new world, NASA enforces a set of rules known as its Planetary Protection Policy. Missions are divided into five categories, with increasingly stringent requirements for cleanliness depending upon the type of mission (lander, rover, orbiter, or flyby) and whether the destination is of astrobiological interest. Rovers and landers designed to seek signs of life or destined for places that may harbor life are placed into Category IV and subjected to strict cleaning protocols. As of now, NASA's only approved method for sterilizing an entire spacecraft is “dry heat microbial reduction”—to put it simply, the spacecraft is placed into a container resembling a giant casserole dish and then baked in an oven at 111.7 degrees Celsius (that's 233.1 degrees Fahrenheit) for 30 hours. Despite the best efforts of NASA scientists, a small number of spore-forming microorganisms survive the sterilization process, but spacecraft are generally considered safe to launch as long as they harbor an acceptably low microbial load.

Category V protection policies are designed to prevent the reverse situation—the contamination of our own planet by extraterrestrial life forms. We have yet to obtain terrestrial samples directly from a planet or moon (besides our own), but NASA is already brainstorming containment procedures, such as building specialized facilities for the storage and study of returned specimens, in preparation for the day when fragments from our celestial neighbors are delivered to Earth.

faculty profile



Ron Amundson *The Dakota Kid*

Not many professors can claim to be as adept with a pitchfork as they are with PowerPoint. But not many professors are Ron Amundson. The new chair and resident soil expert of the Department of Environmental Science, Policy, and Management (ESPM, in the College of Natural Resources), Amundson tilled the plains of South Dakota as a farmer long before he entered the world of lecture halls and committee meetings. He even looks like the landscape he comes from—floppy straw-colored hair and a long, wiry physique that gallops across campus. His research interests are many—the geology of lifeless environments, human degradation of ecosystems, the geological (and perhaps biological?) history of life on Mars—but his reach is much broader, incorporating music, art, and other forms of culture into his teaching and writing. So it should come as no surprise that his vision for ESPM and CNR is big, with an emphasis on bringing labs and people together to collaborate and maybe even have a little fun in the process.

BB: You've made a career out of studying dirt, or should I say, soil. What is so special about soil?

RA: Soil is the skin of the planet. The chemical compounds and stable isotopes found in soil provide a chemical history of the Earth's climate and biological processes. So, for example, we can use the ratio of oxygen isotopes found in certain soil compounds to approximate weather patterns that occurred hundreds of thousands or millions of years ago. Plus, soil harbors an enormous diversity of microorganisms which are poorly understood. There is a saying that "the soil is the poor man's rainforest," and I think it's true.

BB: Apparently you got bored with Earth, because now you have Mars as a field site. How did that come about?

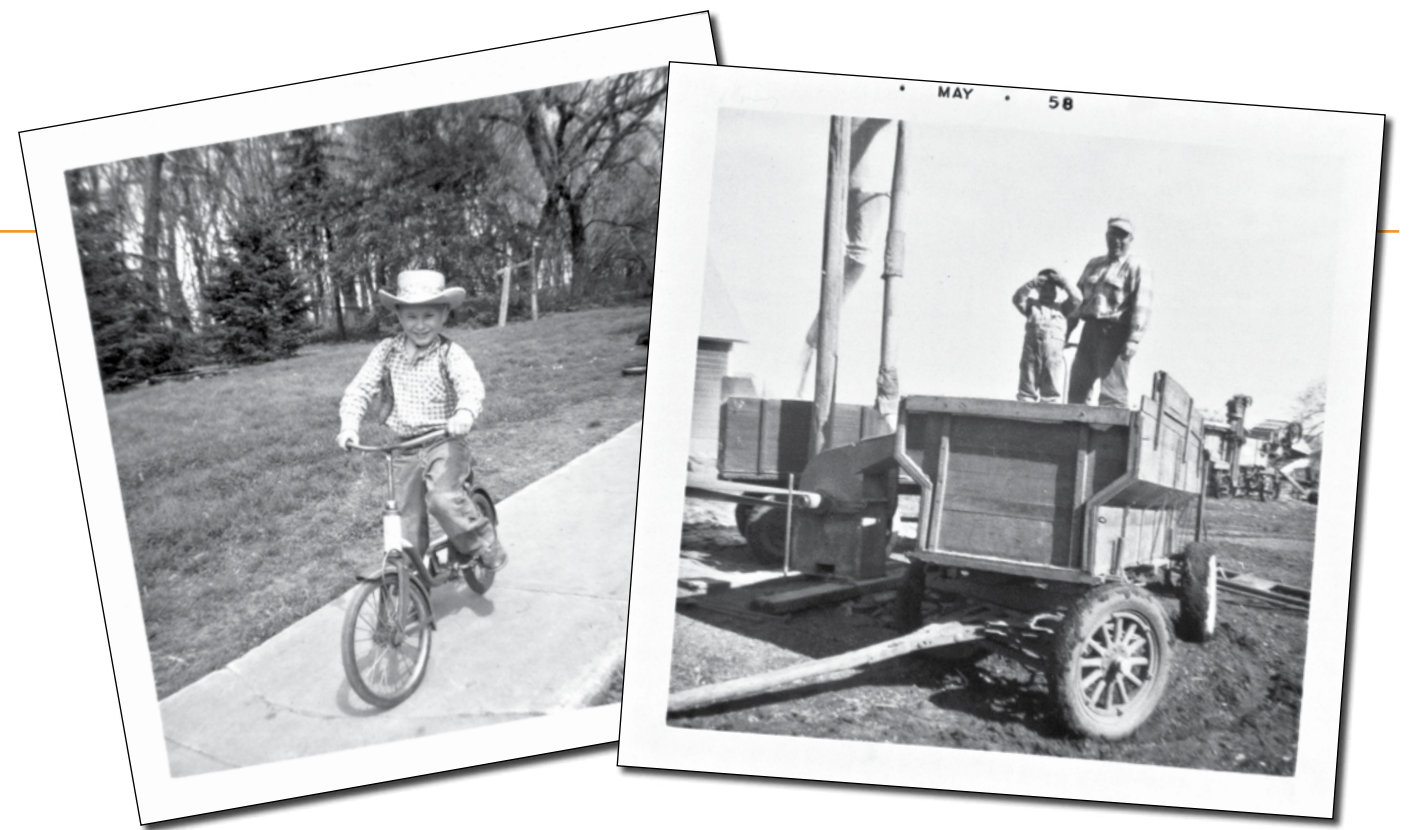
RA: I started working in the Atacama Desert in northern Chile several years ago because it is virtually lifeless, and I was interested in the geochemical properties of environments without life. It turns out

that rates of erosion and chemical changes in rock are much slower than elsewhere on Earth. We were also surprised to find that the soils there have rich accumulations of sulfate and chloride salts, much like those we have recently found on Mars. Also, isotopes of calcium, sulfur, and oxygen change composition in the Atacama, indicative of the slow, downward flow of water. This similarity is important for reconstructing the historical presence of water on Mars, which is currently a hotly debated topic.

BB: Do you think there was ever life on Mars?

RA: I would bet that there was life on Mars. And there may still be life on Mars underground. There are very peculiar and constant methane emissions on Mars that are at least suggestive of subsurface microbial life. And all the water that was on Mars early in its history and all the landscapes there that look so similar to Earth suggest that there was life at some point.

ARJUN HEIMSATH



BB: You're interested in finding out what Earth would look like without life.

RA: Mm-hmm.

BB: But don't you already know that? You did grow up in Canton, South Dakota, didn't you?

RA: *Laughs.* Well, Canton, South Dakota has lots of life. Lots of grass, before the corn was planted. And Canton is also the home to Berkeley's first Nobel Laureate, Ernest Lawrence. So it's quite an important place in Berkeley history.

BB: You're always looking for a way to innovate in your teaching. A perfect example is when you brought Roger McGuinn [of the classic rock band The Byrds] into your ESPM 10 [Environmental Issues] class as a guest lecturer. What does McGuinn have to do with environmental issues?

RA: I've always been inspired by things in my field in very unusual ways, and the arts and entertainment industries have been inspirational to me as well. As a grad student, the first Indiana Jones movie showed me that a career in earth science could be fun and creative. I feel that McGuinn in his music provided a broad context to the way the Earth works. The song *Turn, Turn, Turn!* is based on a biblical story about changes in the land over long time scales; it makes

ETHEL AMUNDSON

what could be a mundane or unappealing foray into geology more appealing.

BB: Is it true that during his acoustic guitar performance in the class that you were waving a lighter?

RA: *Laughs.* I was a bit nervous. The gravity of having a member of the Rock 'n' Roll Hall of Fame visit my classroom became clear to me as the lecture approached, and by that time, I was pretty nervous.

BB: Despite the potential for doom and gloom when talking about our environmental future, you always keep a sunny outlook. What and who give you hope?

RA: What has made the future important to me and what gives me a positive view about it is that I have a 13-year old son. I want to provide and inspire a future that is as good for him as it was for me. Also, when I walk in front of a class of 150 young students, all bright, talented, and enthusiastic, I realize that there's promise in the future with all the talents they offer. I feel an obligation not to just pass off a completely negative set of problems to them, and I want to pose it as an opportunity rather than as a disaster. Governor Schwarzenegger has also been something of a surprise. I certainly didn't vote for him the first time he ran for governor. What's been surprising to me is his forward-looking view and the fact that

he puts such a positive personal spin on it. I think he makes these problems seem tractable, and he's great at viewing these things not only as challenges but as opportunities.

BB: You are the new chair of ESPM. Congratulations. How much did you spend on the campaign?

RA: *Laughs.* These are jobs that people would spend money NOT to have.

BB: What are your major goals as chair?

RA: We're launching a major campaign to renovate Hilgard Hall and some of the other buildings in the college. We envision a world-class laboratory space with plenty of seating and an espresso lounge and high-tech video capability. The vision we have is to do modern science differently than the way we do it in our current structure, in which individual labs work in isolation from each other. I think we are committed to the idea that science has to be a little more collaborative and interactive, and we need a building to facilitate that. Most importantly, I think Berkeley is the ideal place for this new approach to science, and I look forward to seeing this happen.

Brad Balukjian is a graduate student in environmental science, policy and management.

Talks on rocks

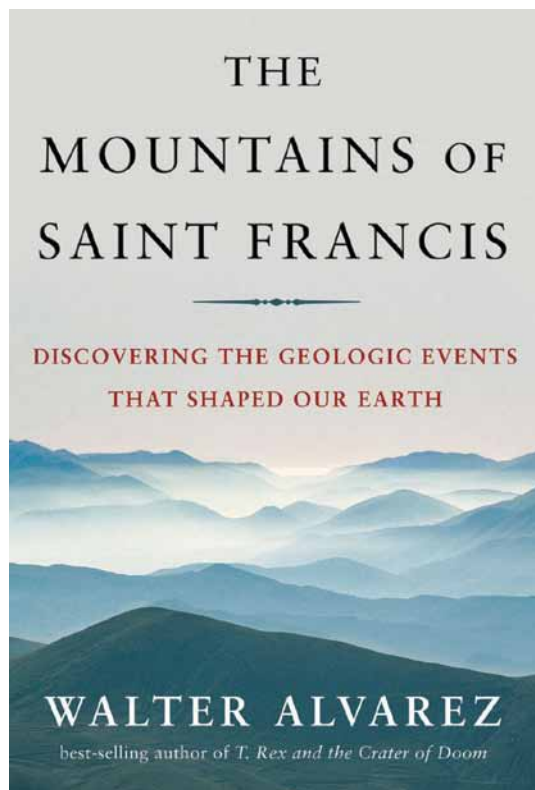
The Mountains of Saint Francis

by Walter Alvarez
W.W. Norton & Company
288 pages, \$25.95

“Written in the rocks, though not by a human hand, chronicles of strange and marvelous events await us,” writes UC Berkeley geology professor Walter Alvarez in his most recent book, *The Mountains of Saint Francis: Discovering the Geologic Events That Shaped Our Earth*. Taking the reader on a scientific tour of Italy, Alvarez explains how these “chronicles” can tell us about the formation of the Italian Apennine Mountains, sharing his enthusiasm for the many things we can learn from the study of rocks. The book weaves together the geological history of the mountain range with the human history that has unfolded there, and is peppered with personal anecdotes from Alvarez’s own experiences as a geologist in Italy.

“Let us begin by examining the pink-and-white Scaglia limestone very carefully,” Alvarez writes in the first chapter, going on to explain how this particular type of rock and the fossils preserved within bear witness to present-day Italy’s onetime submersion under the sea, the deformation of the Earth’s crust that produced the Apennine Mountains, and even provide observational evidence of evolution. Similar excursions to different sites throughout Italy introduce the reader to a range of geological concepts—from the simple, such as the three types of rock (igneous, sedimentary, and metamorphic), to more complex ones like thrust faults, deformations caused by the “crumpling up into folds” of the Earth’s crust.

Throughout, Alvarez makes a point of crediting European geologists, aiming to provide “an antidote to an Anglophone viewpoint that ignores many of our worthy scientific forebears from other countries.” He goes so far as to name Nicolaus Steno, a Danish scientist who researched in Florence, as the inventor of geology. He also uses the Italian, rather than English terms for rocks:



“Tufo rosso a scorie nere” sounds more beautiful than “red tuff with black scoria,” and underscores the historical context in which these two types of volcanic rock were described.

Contextualizing scientific discoveries is a central theme, and Alvarez emphasizes that scientific knowledge progresses in fits and starts, with more zigzagging and backtracking than unimpeded forward progress. For example, although one of the earliest tenets of geology states that “if a rock is on top, it is younger,” the order can sometimes be reversed through phenomena such as thrust faults, leading scientists to incorrectly infer the ages of rocks. Even correct theories can take years to be accepted, as was the case with the 18th century Italian abbot Ambrogio Soldani’s proposition that some rocks in the Apennine range were extraterrestrial. While this view initially “brought down upon him a barrage of ridicule,” chemical analysis later held up his interpretation.

The difficulties of building a complete geological timeline are many, as no place

on Earth has an intact stratigraphic sequence, with evidence for every historical phase. Geologists must cooperate with one another, as well as with other scientists to piece together information from different sites. Refreshingly, and in contrast to the frequent reports of antagonistic relationships between science and industry that one so often hears, Alvarez highlights how even oil companies have made valuable contributions by sharing geological data from around the world.

Though geology is no doubt a difficult science, one sometimes wonders whether Alvarez thinks that other fields are less challenging. Referring to the need to use indirect methods to infer the properties of the Earth’s interior, he claims that “we geologists can only envy astronomers who can actually see objects far across our galaxy and beyond,” failing to appreciate that astronomers must also use indirect

means to learn about stars. In another case, he argues that it was easier to work out the laws of motion (applied to the stars and planets) than the laws of geology because “these mathematical laws in no ways interfered with Christian beliefs”—the house arrest of Galileo serves as a striking counterexample to this assertion.

Despite these shortcomings, *The Mountains of Saint Francis* is nevertheless a good read for anyone seeking an introduction to geology or the history of the Apennine Mountains. Alvarez covers basic geological concepts in language that is easy to read and simple to understand—if at times slightly dry and nostalgic for the past. In the end, a shift in perspective is helpful—perhaps the best way to become invested in the story is to imagine that an avuncular relative is recounting the tale of how he and others before him pieced together the life story of the Mountains of Saint Francis.

Nicole Carlson is a graduate student in physics.

Things that repeat themselves abound in nature. The back-and-forth motion of a branch in the breeze, the repeating hexagons of a honeycomb, and the popularity of the 80s, are just a few examples. Despite living in a world of oscillations, for most of history people have lacked the tools to simply describe repetitive things. As early as 700 B.C., Babylonian astronomers were studying the movements of the Sun-Moon-Earth trio, a system rich in oscillations. They tracked numerous celestial events including the interval between moonset after a new moon and sunrise of the next day, shown as the jaggy black line in the figure.

The Babylonian data appears erratic because the subject of observation (the Moon) rotates around the observation platform (Earth), which itself rotates and orbits the Sun. Each of these oscillations expresses itself in the data, along with many other more subtle celestial motions. Wouldn’t it be nice if we could take this complex oscillation and uncover the simple oscillations that comprise it, like the Sun’s period? The bottom half of the figure shows just that; we break down the Babylonian data, a complex oscillation, into the simplest oscillators, sinusoids, with the largest peaks showing which oscillation periods are expressed most strongly in the signal. From this view, it is clear that the signal is dominated by two components—the Sun’s familiar 12-month period, elusive in

the original data, shows up as the largest peak and a prominent peak around 14 months signals the presence of another important astronomical period, the full moon cycle. We call this useful view the frequency domain representation, since our contributors are sinusoids of different frequencies. Importantly, the time and frequency domain representations are just different views of the same data, and as the upward arrow on the right indicates, we can move freely between the two.

The bridge between the domains is the Fourier Transform, but it wouldn’t be formulated until many centuries after the Babylonians. Eighteenth and 19th century brainiacs like Gauss and Bernoulli made big steps toward understanding how a signal could be deconstructed, but their solutions were not general enough. A one-size-fits-all method for most any imaginable signal was nowhere to be found. Many leading mathematicians doubted if such a thing existed.

Enter Jean Baptiste Joseph Fourier, a scientist-mathematician. Fourier followed a path not all that different from many of today’s highly motivated students. He took a prestigious internship in politics (as his town’s spokesperson during the French Revolution), attended university (to study under math legends Lagrange and Laplace), and even spent some time abroad doing international development work (as

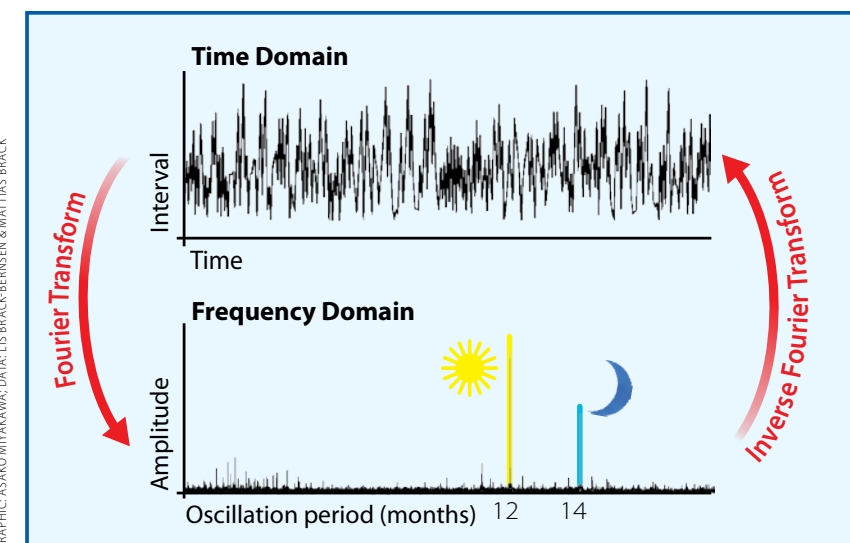
Napoleon’s scientific advisor, governor of Lower Egypt, and secretary of the Institut d’Egypte), although in those days, development looked a lot more like conquest.

After that, he settled down to formulate a complete mathematical description of heat transfer. Though he had the equation that describes how heat moves, solving it required performing precisely that dubious proposition of decomposing any signal into a sum of sinusoids. A tough break, indeed. But he kept at it long enough to devise an equation that did exactly that. This method is the core piece of math behind the Fourier Transform, the bridge between time and frequency domains.

The ability to hop in and out of the frequency domain revolutionized the analysis of oscillatory data. X-ray crystallographers study the structure of the molecules by coercing molecules into crystals, which are vast periodic structures. Geoffrey Feld, chemistry graduate student and crystallographer at UC Berkeley notes that “since we don’t have the ability to just take a picture of the atoms in their native state, we have to deduce it experimentally with math.” Whereas in the Babylonian data, the oscillations took place over time, like a swaying branch, crystals contain oscillations in space, like a honeycomb. Luckily, the math doesn’t mind either way, and we can leverage the same logic of Fourier’s method to understand the data.

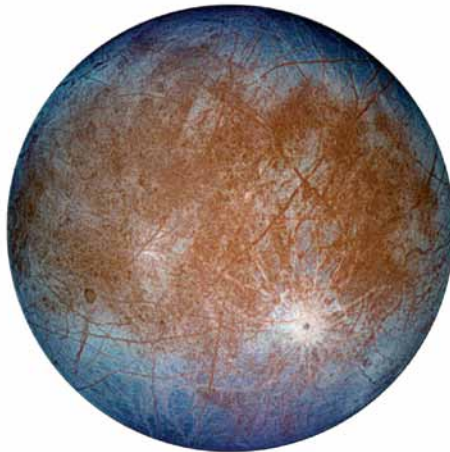
As mere humans with mere human senses, we rarely occupy the ideal vantage point for answering the questions we ask. The Babylonians were too close to their object of interest, and crystallographers are too far from theirs. In these cases, we can augment our senses with tools for making measurements and tools for making sense of those measurements. In the same way telescopes gave us eyes to see far away and microscopes gave us eyes to see very small things, Fourier’s method provides us with a mathematical lens to see the oscillations that fill our world.

Robert Gibboni is a graduate student in neuroscience.



GRAPHIC: ASAKO MIYAKAWA; DATA: LIS BRACK-BERSEN & MATTHIAS BRACK

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