



IGB NEWS

Upcoming Events
Monthly Profiles
Happenings at IGB

Image Of The Month
IP @ IGB
Department Announcements

Volume 9 Number 7

UPCOMING EVENTS

IGB Seminar (BCXT)

*CRISPR Surveillance of the
Microbial Pan-Genome*

November 29, 2016, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Rachel Whitaker, Ph.D.

University of Illinois, Urbana-Champaign

Department of Microbiology

Lunch With The Core

New Instrumentation from Zeiss

November 30, 2016, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Lunch and learn hosted by IGB Core Facilities.

Joe Huff

Carl Zeiss Microscopy

IGB Seminar (BCXT)

*Invisible Influence: How the Indoor Microbiome
Influences Health*

December 6, 2016, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Jack A. Gilbert, PhD

Department of Surgery

University of Chicago

IGB Seminar (GEGC)

TBA

January 17, 2017, 12:00 p.m.

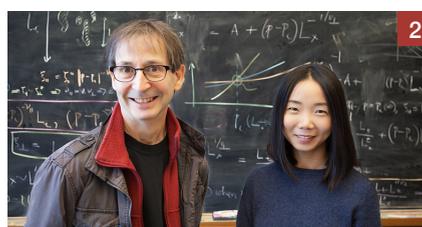
612 Carl R. Woese Institute for Genomic Biology

Patrick J. Brown, PhD

University of Illinois Urbana-Champaign

Department of Crop Sciences

FEATURED NEWS



2
Slow motion waves of jumping
genes in the human genome



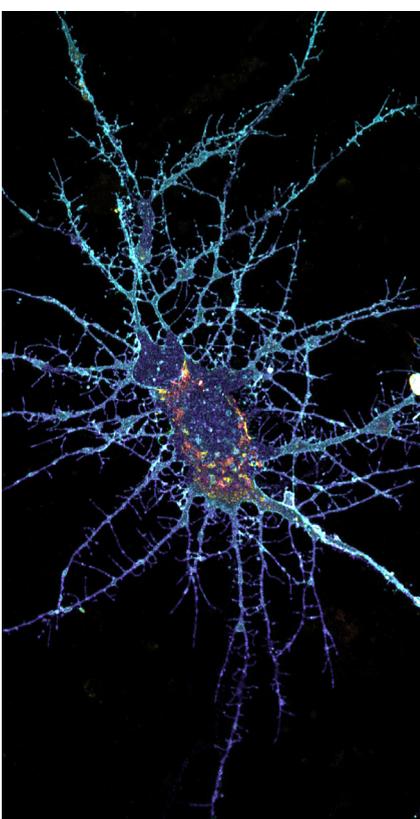
3
Future drought will offset benefits
of higher CO2 on soybean yields



4
Monthly Profile:
Pablo Perez-Pinera



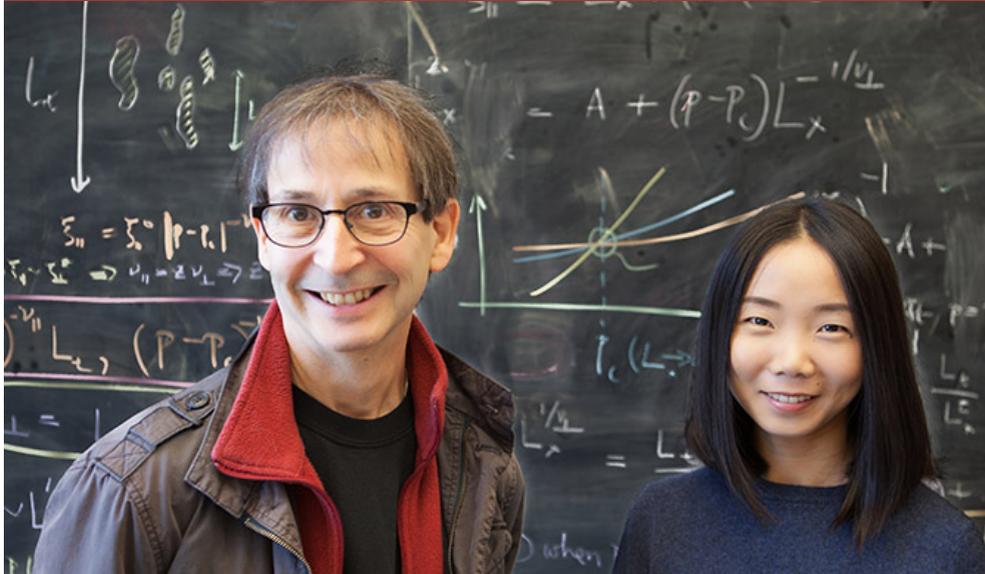
5
On the Grid:
Happenings at IGB



This month's image uses the LSM Fast Mode to study how inhibiting miR-125b affects the structure of dendritic filopodia and dendrites themselves. Here, cultured hippocampal neurons are treated with a peptide nucleic acid (PNA) inhibitor of miR-125b, and transfected with a BacMam 2.0 cell membrane-GFP virus. This allows visualization of the morphology of these neurons, and specifically study features of dendrites and filopodia at a high resolution. Image courtesy of Rajashekar Iyer of Martha Gillette's Lab.

IGB News

Share your news with the IGB. Send ideas on stories, articles, and features to nvasi@illinois.edu.



Slow motion waves of jumping genes in the human genome

Nature is full of parasites—organisms that flourish and proliferate at the expense of another species. Surprisingly, these same competing roles of parasite and host can be found in the microscopic molecular world of the cell. A new study by two Illinois researchers has demonstrated that dynamic elements within the human genome interact with each other in a way that strongly resembles the patterns seen in populations of predators and prey.

The findings, published in *Physical Review Letters* by physicists Chi Xue and Nigel Goldenfeld, ([DOI: 10.1103/PhysRevLett.117.208101](https://doi.org/10.1103/PhysRevLett.117.208101)) are an important step toward understanding the complex ways that genomes change over the lifetime of individual organisms, and how they evolve over generations.

“These are genes that are active and are doing genome editing in real time in living cells, and this is a start of trying to really understand them in much more detail than has been done before,” said Goldenfeld, who leads the Biocomplexity research theme at the Carl R. Woese Institute for Universal Biology (IGB). “This is helping us understand the evolution of complexity and the evolution of genomes.”

The study was supported by Center for the Physics of Living Cells, a Physics Frontiers Center at Illinois supported by the National Science Foundation, and the NASA Astrobiology Institute for Universal Biology at Illinois, which Goldenfeld directs.

Goldenfeld and Xue embarked on this work because of their interest in transposons, small regions of DNA that can move themselves from one part of the genome to another during the lifetime of a cell—a capability that has earned them the name “jumping genes.” Collectively, various types of transposons make up almost half of the human genome. When they move around, they may cre-

ate mutations in or alter the activity of a functional gene; transposons can therefore create new genetic profiles in a population for natural selection to act on, in either a positive or negative way.

The Illinois researchers wanted to learn more about how evolution works on this level, the level of whole organisms, by looking at the metaphorical ecosys-

Physicists Nigel Goldenfeld (left) and Chi Xue have made detailed predictions about an intriguing mechanism of genomic evolution.

tem of the human genome. In this view, the physical structure of the DNA that makes up the genome acts like an environment, in which two types of transposons, long interspersed nuclear elements (LINEs) and short interspersed nuclear elements (SINEs), have a competitive relationship with one another. In order to replicate, SINEs steal the molecular machinery that LINEs use to copy themselves, somewhat like a cuckoo bird tricks other birds into raising her chicks for her while abandoning their own.

With help from Oleg Simakov, a researcher at the Okinawa Institute of Science and Technology, Xue and Goldenfeld focused on the biology of L1 elements and Alu elements, respectively common types of LINEs and SINEs in the human genome.

The researchers adopted methods from modern statistical physics and modeled the interaction between Alu and L1 elements mathematically as a stochastic process—a process created from chance interactions. This method has been successfully applied in ecology to describe predator-prey interactions; Xue and Goldenfeld simulated the move-

ments of transposons within the human genome with the same mathematical method. Their models included a detailed accounting for how Alu elements steal the molecular machinery L1 elements use to copy themselves.

Xue and Goldenfeld’s results predicted that populations of LINE and SINE elements in the genome are expected to oscillate the way those of, for example, wolves and rabbits might.

“We realized that the transposons’ interaction actually was pretty much like the predator-prey interaction in ecology,” said Xue. “We came up with the idea, why don’t we apply the same idea of predator-prey dynamics . . . we expected to see the oscillations we see in the predator-prey model. So we first did the simulation and we saw the oscillations we expected, and we got really excited.”

In other words, too many SINEs and the LINEs start to suffer, and soon there are not enough for all the SINEs to exploit. SINEs start to suffer, and the LINEs make a come-back. Xue and Goldenfeld’s model made the surprising prediction that these oscillations occur over a timescale that is longer than the human lifespan—waves of Alu elements and L1 elements pushing and pulling at each other in slow motion across generations of the human genomes that carry them.

“The most enlightening aspect of the study for me was the fact that we could really compute the timescales, and see that it is possible that we could observe these things,” said Goldenfeld. “We have a prediction for what happens in single cells, and we may be able to actually do an experiment to observe these things, though the period is longer than the lifetime of a single cell.” ■

Written by Claudia Lutz. Photo by Kathryn Faith.

RESEARCH



Future drought will offset benefits of higher CO₂ on soybean yields

An eight-year study of soybeans grown outdoors in a carbon dioxide-rich atmosphere like that expected by 2050 has yielded a new and worrisome finding: Higher atmospheric CO₂ concentrations will boost plant growth under ideal growing conditions, but drought—expected to worsen as the climate warms and rainfall patterns change—will outweigh those benefits and cause yield losses much sooner than anticipated.

The new discovery, reported in the journal *Nature Plants*, contradicts a widely accepted hypothesis about how climate change will affect food production, said University of Illinois plant biology professor Andrew Leakey, who led the new research.

“If you read the most recent Intergovernmental Panel on Climate Change reports and if you read the scientific literature on the subject for the last 30 years, the concluding statement is nearly always that elevated carbon dioxide will ameliorate drought stress in crops,” Leakey said.

Numerous laboratory and field studies have supported this assessment: In many scenarios, elevated carbon dioxide acts as a fertilizer, boosting plant growth. Plants exposed to high CO₂ also reduce the size of the pores in their leaves, lessening the exchange of gases with the atmosphere. This helps plants use less water from the soil.

Such findings strongly suggested that elevated CO₂ would help plants better withstand drought, Leakey said.

“This was consistent with what we saw with our own experiments the first four years, the relatively wet years,” Leakey said. “But when the growing seasons were hot and dry, that pattern broke down.”

To make this discovery, Leakey and his colleagues relied on an unusual technology that enables them to simulate future climate conditions in actual farm fields. The Soybean Free Air Concentration Enrichment facility uses high-tech sensors to determine wind speed and direction, and a computer to regu-

*Professor of Plant Biology
Andrew Leakey (above) at the
Soybean Free Air Concentration
Enrichment system, which allows
researchers to simulate future
atmospheric conditions to
determine their effects on plants.*

late the release of gases to expose the crop plants to a given set of climate conditions.

Under hot and dry conditions at elevated CO₂, the plants in the SoyFACE experiments used more, not less, water than those grown under current atmospheric conditions, the researchers found.

“What we think is happening is that early in the growing season, when the plant has enough water, it’s able to photosynthesize more as a result of the higher CO₂ levels. It’s got more sugars to play with, it grows more, it creates all this extra leaf area,” Leakey said. “But when it gets dry, the plant has overextended itself, so later in the season it’s now using more water.”

Two other plant responses also contribute to the problem, the researchers found.

“At elevated CO₂, there are changes in certain hormones the plant uses to signal between the roots and shoots,” Leakey said. “The plant becomes more sensitive to that signal at elevated CO₂, and that causes photosynthesis to decline more in response to drought than it would do at ambient CO₂ levels.”

Elevated CO₂ and drought together also influence soybean’s ability to fix nitrogen through nodules formed on its roots. These nodules harbor bacteria that help the plant capture and convert atmospheric nitrogen into a form the plants can metabolize.

Under elevated CO₂ and drought, the number of beneficial nodules on the soybean roots increases, Leakey said.

“But what we find is that they put all these extra nodules on in relatively shallow soil layers. And the nodules don’t work well when they’re in dry soil.”

The new findings, from soybeans grown in one of the most productive regions of the planet, suggest climate-related declines in soybean yields will occur sooner than previously thought, Leakey said.

“All of the model predictions up to this point were assuming that in 2050, elevated CO₂ was going to give us a 15 percent increase in yield over what we had at the beginning of this century,” he said. “And what we’re seeing is that as it gets hotter and drier, that number diminishes to zero. No gain.”

The U.S. Department of Agriculture’s National Institute of Food and Agriculture, the U.S. Department of Energy and the USDA Agricultural Research Service funded this research, along with a gift from David Sigman to the U. of I. at Urbana-Champaign. ■

Written by Diana Yates. Photos by L. Brian Stauffer.

MONTHLY PROFILE



Pablo Perez-Pinera is an assistant professor of bioengineering whose synthetic biology lab works to develop new applications for drug production, gene therapy, and regenerative medicine.

Pablo Perez-Pinera: Finding the Common Thread through Genetic Disease

Research at the IGB is diverse: From plant structure to life on other planets, genomic study tackles it all. Few scientists, however, maintain as many varied lines of research as Assistant Professor of Bioengineering Pablo Perez-Pinera (ACPP). His lab works to develop strategies to improve drug biomanufacturing, create new gene therapy approaches, and better understand how cancer can be fought at the cellular level—all with gene editing tools.

Perez Pinera's overarching interest in gene editing comes in part from his time in medical school. "I was fascinated by emerging treatments that were customized to target the molecular basis of a disease, as opposed to drugs that simply alleviate their symptoms," he recounts, "which consequently stimulated my interest in pursuing a Ph.D. in molecular biology and a career in science."

After earning an M.D. and Ph.D. at the Universidad de Oviedo in Spain, Perez-Pinera moved on to various research positions in the US; he spent several years at Scripps Research Institute, followed by shorter stays at Duke University and the Massachusetts Institute of Technology. "[In my] early career, I was confronted with important limitations in cancer research such as the lack of appropriate tools for genetic manipulations, which are necessary to develop cell models or even to test potential targets for therapeutic interventions in cancer," Perez-Pinera describes.

"For these reasons, I became extremely interested in gene editing and transcriptional regulation ... [which is now] the overall common theme in my research projects."

Perez-Pinera joined the Bioengineering faculty at the University of Illinois in 2014, thanks in part to Illinois' strong reputation for interdisciplinary study in biology and engineering. Though young, his research group is already exploring multiple

avenues of work, all of which focus on using and improving current genome and epigenome editing technologies.

Much of his previous research focused on developing gene therapy techniques for treating hereditary illnesses such as Duchenne Muscular Dystrophy.

"Understanding cancer itself and developing anti-cancer therapies requires an integrative approach, which necessitates expertise in molecular and cellular biology, computational biology, and chemistry. Here ... we have the benefit of interfacing with different groups that have experience in these areas, in addition to a common interest in cancer."

Though these techniques are very early stage due to the limitations of current gene editing technology, Perez-Pinera believes they hold great promise.

"One important problem with current generations of gene therapy is the potential to introduce unintended mutations," Perez-Pinera explains. "This problem prevents the development of clinical applications at the moment, but a lot of research is focused on creating safer techniques for manipulating DNA ... [my lab is] focusing a lot on technology development to improve the efficiency and specificity of gene editing."

"In effect, I think that we will see gene therapies entering clinical practice within the next decade."

Another facet of Perez-Pinera's research deals with cancer; he joined the IGB as one of the four original members of the Anticancer Discovery from Pets to People research theme in January of this year. "Understanding cancer itself and developing anti-cancer therapies requires an integrative approach, which necessitates expertise in molecular and cellular biology, computational biology, and chemistry," said Perez-Pinera. "Here ... we have the benefit of interfacing with different groups that have experience in these areas, in addition to a common interest in cancer."

Unlike some other members of the theme who focus on target identification or screening large libraries of potential drugs, Perez-Pinera's research extends into genetic engineering, including producing better cell models and identifying new genes that contribute to cancer growth, progression and spreading, with the ultimate goal of developing novel anti-cancer drugs.

Through all of his lines of research, Perez-Pinera has maintained a deep interest in the multifold potential of gene editing. "My laboratory is fairly new in its inception [...] as such, we are now just beginning to explore projects including gene therapies to correct primary immunodeficiencies and identification of new targets for treatment of cancer using genetic screenings," he describes.

"It is fascinating to me to be able to use the basic building blocks of biology to develop model cell lines, correct disease-causing mutations, or even to create transgenic animals with unprecedented speed and precision." ■

Written by Kathryne Metcalf. Photo courtesy of Department of Bioengineering.

ON THE GRID HAPPENINGS AT THE IGB

AWARDS



GENE ROBINSON

Gene Robinson (IGB Director) was elected as Chair of the National Academy of Sciences Section 27, Evolutionary Biology.



RASHID BASHIR

Rashid Bashir, Bioengineering Professor and Department Head (Regenerative Biology & Tissue Engineering) was named as the first Grainger Distinguished Chair in Engineering.

EVENT



GENOME DAY GRAND SUCCESS

Our 2016 Genome Day was a very successful event, with over 550 attendees participating in 18 educational activities. Our thanks to Dr. Sandra Rodriguez-Zas, Professor of Animal Sciences (GNNDP) and to the over 130 volunteers from the IGB research themes, all the activity leaders, members of the IGB staff, HPCBio, NCSA, Center for the Physics of Living Cells, the Biomedical Engineering Society, and our translators from the Society for Advancement of Chicanos/Hispanics and Native Americans in Science and the Chinese Students and Scholars Association.

NEW ARRIVALS



MICHAEL SPINELLA

Professor Michael Spinella has joined the IGB as a faculty member in the Anticancer Discovery from Pets to People (ACPP) Research Theme. He is a faculty member in the Department of Comparative Biosciences in the College of Veterinary Medicine. Prior to joining the University of Illinois in the Fall of 2016, he was on the faculty at the Dartmouth Geisel School of Medicine. His research focuses on molecular mechanisms of cancer therapy and mechanism of chemoresistance.



STANLEY AMBROSE

Professor Stanley Ambrose has joined the IGB as an affiliate member in the Microbiome Metabolic Engineering (MME) Research Theme. He is a faculty member in the Department of Anthropology. He received his M.A. and Ph.D. from the University of California, Berkeley. His research interests focus on diet, climate, environment and habitat reconstruction with stable carbon, nitrogen, oxygen and strontium isotope ratios of human and other animal bones, teeth and soft tissues.



HANNAH HOLSCHER

Professor Hannah Holscher has joined the IGB as an affiliate member in the Microbiome Metabolic Engineering (MME) Research Theme. She joined the Department of Food Science and Human Nutrition as a faculty member in 2015. She received her Ph.D. in Nutritional Sciences from the University of Illinois, and served as a postdoctoral research associate at the University of Illinois from 2012 to 2015. Her research interests focus on clinical applications of nutritional sciences with an overarching goal of improving human health through dietary modulation of the gastrointestinal microbiome.



LORI RAETZMAN

Professor Lori Raetzman has joined the IGB as an affiliate member in the Gene Networks in Neural and Developmental Plasticity (GNNDP) Research Theme. She is a faculty member in the Department of Molecular and Integrative Physiology. She received her Ph.D. at Case Western Reserve University, and was a postdoctoral research associate at the University of Michigan. Her research focuses on the notch signaling pathway in hypothalamic-pituitary gland development and disease.

EVENT



DECEMBER SCIENCE CAFE

Join us on Wednesday, December 7th, 5:30pm at Pizza-M in Urbana for a talk from Joaquin Vieira entitled "Telescopes: Past and Future" As always there will be first come first served pizza provided by our fabulous host!

DEPARTMENT ANNOUNCEMENTS

UNIVERSITY LIBRARY

IDEA LAB AT GRAINGER ENGINEERING LIBRARY

The Grainger Engineering Library has opened a new space – the IDEA Lab. The Lab supports collaboration, innovation and entrepreneurship with state-of-the-art facilities and technology, including:

- Visualization wall
- Informatics labs
- 3D printing
- Presentation spaces
- Innovator design rooms
- Collaboration equipment

Access to the IDEA Lab is currently limited to individuals and groups working on innovation projects, but if you are working on such a project, you can request access via the Lab website. For more information or to request access, go to the IDEA Lab website: go.illinois.edu/idealab. ■

BUSINESS OFFICE

HOLIDAY BREAK REDUCED SERVICE DAYS

As we approach the holiday season we are providing a reminder of the upcoming holiday schedule and the accompanying reduced service days.

Friday, December 23, 2016

1/2 Gift Day (from Chancellor and the President) and 1/2 Excused Day p.m.

Monday, December 26, 2016

Christmas Day Observed

Tuesday, December 27, 2016

Day after Christmas Holiday Observed – Designated Holiday

Wednesday, December 28, 2016

Reduced Service Day

Thursday, December 29, 2016

Reduced Service Day

Friday, December 30, 2016

Reduced Service Day

Monday, January 2, 2017

New Year's Day Holiday Observed

Reduced Service Days:

As in the past, IGB will be closed starting December 23, 2016 thru January 2, 2017 and most employees will not be working those three days. Employees may use floating holidays, vacation, or take time without pay, or any combination thereof.

Questions regarding reduced service days, please contact Jacinda King at 244-2276 or jkking@igb.illinois.edu. ■

RECENT PUBLICATIONS

Please include your connection to the IGB in your author byline when submitting publications, as it will greatly help track potential newsworthy items and increase the possibility of coverage.

Lee, T. G., Diers, B. W., & Hudson, M. E. (2016). An efficient method for measuring copy number variation applied to improvement of nematode resistance in soybean. *Plant Journal*, 88(1), 143-153. DOI: 10.1111/tj.13240

Kim, S. M., Dien, B. S., & Singh, V. (2016). Promise of combined hydrothermal/chemical and mechanical refining for pretreatment of woody and herbaceous biomass. *Biotechnology for Biofuels*, 9(1), [97]. DOI: 10.1186/s13068-016-0505-2

Koeln, J. P., & Alleyne, A. G. (2016). Event-based hierarchical control for power flow in vehicle systems. In 2016 American Control Conference, ACC 2016. (Vol. 2016-July, pp. 569-574). [7524974] Institute of Electrical and Electronics Engineers Inc.. DOI: 10.1109/ACC.2016.7524974

Keating, B. D., & Alleyne, A. (2016). Combining self-optimizing control and extremum seeking for online optimization with application to Vapor Compression cycles. In 2016 American Control Conference, ACC 2016. (Vol. 2016-July, pp. 6085-6090). [7526625] Institute of Electrical and Electronics Engineers Inc.. DOI: 10.1109/ACC.2016.7526625

Schatz, B. R. (2015). National surveys of population health: Big data analytics for mobile health monitors. *Big Data*, 3(4), 219-229. DOI: 10.1089/big.2015.0021

Xie, Q., Pundir, M., Lu, Y., Abad, C. L., & Campbell, R. H. (2016). Pandas: Robust Locality-Aware Scheduling with Stochastic Delay Optimality. *IEEE/ACM Transactions on Networking*, PP(99), [7582519]. DOI: 10.1109/TNET.2016.2606900

Kumar, D., & Singh, V. (2016). Dry-grind processing using amylase corn and superior yeast to reduce the exogenous enzyme requirements in bioethanol production. *Biotechnology for Biofuels*, 9(1), 1-12. DOI: 10.1186/s13068-016-0648-1

Wang, R., Zhang, J., Yin, Q., Xu, Y., Cheng, J., & Tong, R. (2016). Controlled Ring-Opening Polymerization of O-Carboxyanhydrides Using a β -Diiminate Zinc Catalyst. *Angewandte Chemie - International Edition*, 55(42), 13010-13014. DOI: 10.1002/anie.201605508

Pangborn, H., & Alleyne, A. G. (2016). Switched linear control of vapor compression systems under highly transient conditions. In 2016 American Control Conference, ACC 2016. (Vol. 2016-July, pp. 543-548). [7524970] Institute of Electrical and Electronics Engineers Inc.. DOI: 10.1109/ACC.2016.7524970

Guerra, A. S., Eckerlin, R. P., Dowling, A. P. G., Durden, L. A., Robbins, R. G., Dittmar, K., ... Young, H. S. (2016). Host-Parasite Associations in Small Mammal Communities in Semiarid Savanna Ecosystems of East Africa. *Journal of Medical Entomology*, 53(4), 851-860. DOI: 10.1093/jme/tjw048 ■



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Contact Nicholas Vasi (nvasi@illinois.edu)
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RECENT PUBLICATIONS

Please include your connection to the IGB in your author byline when submitting publications, as it will greatly help track potential newsworthy items and increase the possibility of coverage.

Gabrys, R., & Milenkovic, O. (2016). Balanced permutation codes. In Proceedings - ISIT 2016; 2016 IEEE International Symposium on Information Theory. (Vol. 2016-August, pp. 390-394). [7541327] *Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/ISIT.2016.7541327

Sanogo, Y. O., & Bell, A. M. (2016). Molecular mechanisms and the conflict between courtship and aggression in three-spined sticklebacks. *Molecular Ecology*, 25(17), 4368-4376. DOI: 10.1111/mec.13766

Hossein, S. M., Yazdi, T., Kiah, H. M., & Milenkovic, O. (2016). Weakly mutually uncorrelated codes. In Proceedings - ISIT 2016; 2016 IEEE International Symposium on Information Theory. (Vol. 2016-August, pp. 2649-2653). [7541779] *Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/ISIT.2016.7541779

Bhaduri, B., Nolan, R. M., Shelton, R. L., Pilutti, L. A., Motl, R. W., & Boppart, S. A. (2016). Ratiometric analysis of in vivo retinal layer thicknesses in multiple sclerosis. *Journal of Biomedical Optics*, 21(9), [09S001]. DOI: 10.1117/1.JBO.21.9.09S001

Gabrys, R., Yaakobi, E., & Milenkovic, O. (2016). Codes in the damerau distance for DNA storage. In Proceedings - ISIT 2016; 2016 IEEE International Symposium on Information Theory. (Vol. 2016-August, pp. 2644-2648). [7541778] *Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/ISIT.2016.7541778

Sweedler, J. V. (2016). Our evolving editorial team. *Analytical Chemistry*, 88(17), 8347. DOI: 10.1021/acs.analchem.6b03222

Leblanc, A. K., Mazcko, C., Brown, D. E., Koehler, J. W., Miller, A. D., Miller, C. R., ... Gilbert, M. R. (2016). Creation of an NCI comparative brain tumor consortium: Informing the translation of new knowledge from canine to human brain tumor patients. *Neuro-Oncology*, 18(9), 1209-1218. DOI: 10.1093/neuonc/now051

Peh, J., Fan, T. M., Wycislo, K. L., Roth, H. S., & Hergenrother, P. J. (2016). The combination of vemurafenib and procaspase-3 activation is synergistic in mutant BRAF melanomas. *Molecular Cancer Therapeutics*, 15(8), 1859-1869. DOI: 10.1158/1535-7163.MCT-16-0025

You, S., Tu, H., Zhao, Y., Liu, Y., Chaney, E. J., Marjanovic, M., & Boppart, S. A. (2016). Raman Spectroscopic Analysis Reveals Abnormal Fatty Acid Composition in Tumor Micro- and Macroenvironments in Human Breast and Rat Mammary Cancer. *Scientific Reports*, 6, [32922]. DOI: 10.1038/srep32922

Dau, S. H., & Milenkovic, O. (2016). Inference of latent network features via co-intersection representations of graphs. In Proceedings - ISIT 2016; 2016 IEEE International Symposium on Information Theory. (Vol. 2016-August, pp. 1351-1355). [7541519] *Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/ISIT.2016.7541519

Zhang, C., Zhang, K., Yuan, Q., Zhang, L., Hanratty, T., & Han, J. (2016). GMove: Group-level mobility modeling using geo-tagged social media. In KDD 2016 - Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. (Vol. 13-17-Au-

gust-2016, pp. 1305-1314). *Association for Computing Machinery*. DOI: 10.1145/2939672.2939793

Li, J., Pincu, Y., Marjanovic, M., Bower, A. J., Chaney, E. J., Jensen, T., ... Boppart, S. A. (2016). In vivo evaluation of adipose- and muscle-derived stem cells as a treatment for nonhealing diabetic wounds using multimodal microscopy. *Journal of Biomedical Optics*, 21(8), [086006]. DOI: 10.1117/1.JBO.21.8.086006

Thiaville, J. J., Flood, J., Yurgel, S., Prunetti, L., Elbadawi-Sidhu, M., Hutinet, G., ... De Crécy-Lagard, V. (2016). Members of a Novel Kinase Family (DUF1537) Can Recycle Toxic Intermediates into an Essential Metabolite. *ACS Chemical Biology*, 11(8), 2304-2311. DOI: 10.1021/acscchembio.6b00279

Price, N. P. J., Labeda, D. P., Naumann, T. A., Vermillion, K. E., Bowman, M. J., Berhow, M. A., ... Bischoff, K. M. (2016). Quinovosamycins: New tunicamycin-type antibiotics in which the α , β -1',11'-linked N-acetylglucosamine residue is replaced by N-acetylquinovosamine. *Journal of Antibiotics*, 69(8), 637-646. DOI: 10.1038/ja.2016.49

Wei, J., McFarlin, B. L., & Wagoner Johnson, A. J. (2016). A multi-indent approach to detect the surface of soft materials during nanoindentation. *Journal of Materials Research*, 31(17), 2672-2685. DOI: 10.1557/jmr.2016.265

Xia, P. F., Zhang, G. C., Liu, J. J., Kwak, S., Tsai, C. S., Kong, I. I., ... Jin, Y. S. (2016). GroE chaperonins assisted functional expression of bacterial enzymes in *Saccharomyces cerevisiae*. *Biotechnology and Bioengineering*, 113(10), 2149-2155. DOI: 10.1002/bit.25980

Sakoda, K., Tanaka, Y., Long, S. P., & Shiraiwa, T. (2016). Genetic and physiological diversity in the leaf photosynthetic capacity of soybean. *Crop Science*, 56(5), 2731-2741. DOI: 10.2135/cropsci2016.02.0122

Ren, X., He, W., Qu, M., Voss, C. R., Ji, H., & Han, J. (2016). Label noise reduction in entity typing by heterogeneous partial-label embedding. In KDD 2016 - Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. (Vol. 13-17-August-2016, pp. 1825-1834). *Association for Computing Machinery*. DOI: 10.1145/2939672.2939822

Yu, N., Lee, T. G., Rosa, D. P., Hudson, M., & Diers, B. W. (2016). Impact of Rhg1 copy number, type, and interaction with Rhg4 on resistance to *Heterodera glycines* in soybean. *Theoretical And Applied Genetics*, 1-10. DOI: 10.1007/s00122-016-2779-y

Browne, P., Tamaki, H., Kyrpides, N., Woyke, T., Goodwin, L., Imachi, H., ... Cadillo-Quiroz, H. (2016). Genomic composition and dynamics among Methanomicrobiales predict adaptation to contrasting environments. *ISME Journal*. DOI: 10.1038/ismej.2016.104 ■



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