



IGB NEWS

Upcoming Events

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Happenings at IGB

Image Of The Month

IP @ IGB

Administrative News

Volume 8, Number 1

UPCOMING EVENTS

Lunch With The Core

Super Resolution Structured Illumination
February 25, 2015, 12:00 p.m.
612 Carl R. Woese Institute for Genomic Biology

Austin Cyphersmith, PhD
Research Specialist in Life Sciences
University of Illinois at Urbana-Champaign

Pioneers Seminar (BSD)

Engineering the Human Microbiome and the Future of Microbiome-Based Medicine
March 3, 2015, 12:00 p.m.
612 Carl R. Woese Institute for Genomic Biology

Eric Alm, PhD
Massachusetts Institute of Technology
Department of Biological Engineering

IGB Seminar (EBI)

Sequestered: The Assembly and Function of Protein Organelles
March 17, 2015, 12:00 p.m.
612 Carl R. Woese Institute for Genomic Biology

David F. Savage, PhD
University of California, Berkeley
Departments of Biochemistry, Biophysics, and Structural Biology

Art of Science 5.0

Images from the Carl R. Woese Institute for Genomic Biology
April 23, 2015, 6:00 p.m. reception
Exhibit on display through April 27
indi go Artist Co-Op
9 E University Ave, Champaign, Illinois 61820

FEATURED NEWS



2

Harnessing the Power of Big Data



4

IGB Establishing New Research Theme



5

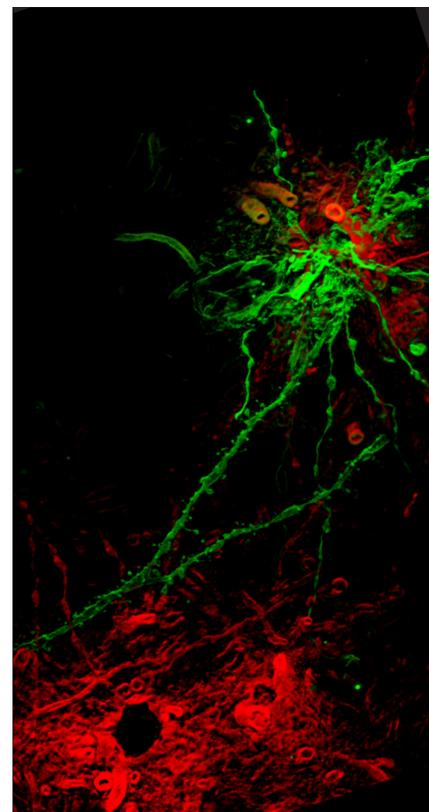
Profile: Jonathan Sweedler



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On the Grid: Happenings at IGB

IMAGE OF THE MONTH



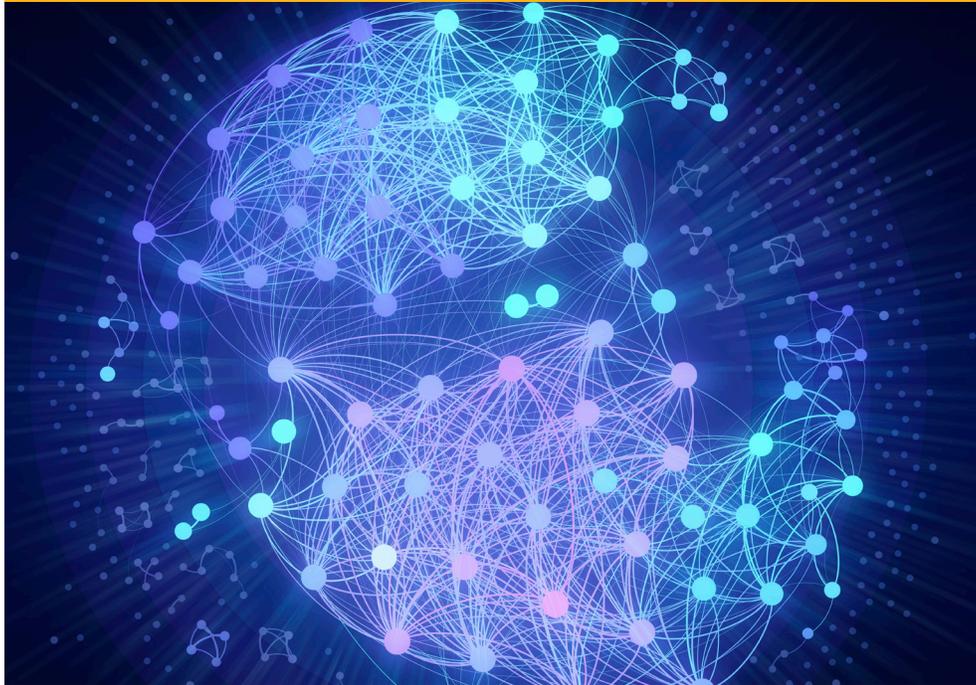
This month's image features Glial cells from Jennifer Mitchell of the Martha Gillette Lab.

This image was created using the SR-SIM Four laser structured illumination super resolution system, and is provided courtesy of IGB Core Facilities.

IGB News

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

FEATURE



Harnessing the Power of Big Data: A Revolution in Genomic Data Analysis

Internet search engines like Google allow us to search and parse the collective knowledge of the world—they anticipate the user's questions, remember preferences, deliver information quickly and clearly. Why can't researchers trying to discover the most effective disease treatment employ the same analytical power to the knowledge discovery challenges of their work?

To a team of biologists, computer scientists, and bioinformaticians from the University of Illinois at Urbana-Champaign and Mayo Clinic, this question sounds like an exciting opportunity. Supported by one of the first awards from a recently established National Institutes of Health initiative, the group has begun work on a tool, the Knowledge Engine for Genomics (KnowEnG), that interprets new results by leveraging community knowledge of how genes interact with each other.

Converting Big Data to better knowledge

The Illinois-Mayo effort aims to address one component of a broad and pressing issue faced by the biomedical research field. Rapid advances in laboratory technology have made it possible for investigators to collect once unheard-of amounts of data in a single experiment, whether those data are high-resolution brain images, interactions within a social network, or expression levels of thousands of genes.

The problem with such large-scale experiments is that the resulting data sets—termed “Big Data”—

are only valuable if they can be translated into more knowledge, and the tools used to handle all this information haven't improved quickly enough.

To address this issue, the National Institutes of Health created the Big Data to Knowledge (BD2K) initiative in 2012. The goals of the initiative are to promote the development of better methods to manage very large data sets, develop better analytical tools, train researchers in the use of those tools, and shift the culture of the scientific community to make these and related activities more successful.

As part of the first wave of BD2K funding announced in October 2014, the University of Illinois at Urbana-Champaign and Mayo Clinic received a \$9.34M, 4-year award to create one of 11 new Centers of Excellence for Big Data Computing. The Illinois-Mayo Center focuses on a specific class of Big Data: the rapidly growing body of genomic and transcriptomic data produced by genome-wide, high-throughput experimental technologies.

Computer scientist and IGB affiliate Jiawei Han is the Center's Program Director. Other Principal Investigators are computer scientist and IGB member Saurabh Sinha; physicist, bioengineer and IGB member Jun Song; and Richard Weinsilboum, M.D., interim director of the Mayo Clinic Center for Individualized Medicine and director of the center's Pharmacogenomics Translational Program. IGB and NCSA Director of Bioinformatics and Director of the High-Performance Biological Computing

Group C. Victor Jongeneel is Executive Director.

“By integrating multiple analytical methods derived from the most advanced data mining and machine learning research, KnowEnG will transform the way biomedical researchers analyze their genome-wide data,” said Program Director Jiawei Han, describing the software tool under development. “The Center will leverage the latest computational techniques used to mine corporate or Internet data to enable the intuitive analysis and exploration of biomedical Big Data.”

The Center combines the expertise of many units across the U of I campus, including the Carl R. Woese Institute for Genomic Biology (IGB), the Department of Computer Science, the Coordinated Science Laboratory, the College of Engineering, and the National Center for Supercomputing Applications (NCSA). As a leader of biomedical research and structured data collection, Mayo Clinic plays a vital role in design, testing, and refinement. The Breast Cancer Genome-Guided Therapy (BEAUTY) study at the Mayo Clinic will be the first to benefit from the KnowEnG technology.

KnowEnG: a tool to harness community knowledge

Results of biomedical genomic studies often come in the form of a list of genes—genes that differ in sequence or activity in healthy and diseased individuals, for example. Researchers would like to translate that list of genes into a better understanding of how

KNOWENG

BIG DATA TO KNOWLEDGE CENTER OF EXCELLENCE

disease works: How does a particular disease compare to other diseases at a cellular level? Are there specific functions inside the cell that are most affected? How are they affected? This type of knowledge could help predict disease risk, or lead to new ideas for treatment.

Traditional tools used to interpret genomic data have relied on making comparisons between a researcher's gene list, and a database containing a specific type of information about genes. It is up to the researcher to identify what comparisons will be helpful, and integrate the outputs of many different analytical tools into a coherent interpretation.

Newer tools aggregate different types of gene-related information from multiple sources, but the difficult task of synthesizing how these relate to a specific list of genes is still up to the researcher. When completed, KnowEnG will be unique in its integration of many disparate sources of gene-related data into one enormous network, a comprehensive guide against which a researcher's specific results can then be compared.

"We'd like to take community knowledge and datasets in this richer representation, this format of a network of gene-gene relationships, gene-gene functional relationships, protein-protein relationships and so on, and allow the user to do their analysis in the context of that community knowledge," said Sinha, who leads the research arm of the project. The team is also designing KnowEnG to accommodate future growth in size and scope of the network, as the scientific community continues to learn about the relationships among genes.

In addition to development of KnowEnG, the Center is developing a training framework that empowers researchers to use the new tool and engage in bioinformatics research, regardless of their prior computational knowledge. The Center has also begun participation in a nation-wide consortium, composed of all the BD2K Centers of Excellence established by the NIH initiative, to exchange insights, contribute to standards for tool develop-

ment, and help set broad goals for the future of work on Big Data.

"Ideally, undergraduates would be trained in both biology and computer science" before engaging in biomedical genomics research, said Song, who leads the training and community activities of the Center. Because most of today's biomedical researchers did not have access to extensive formal training in computation, Song explained, the Center's training resources will be carefully designed to build users' understanding of computational questions in a visual, intuitive way.

Strengthening interdisciplinary connections

The Center relies on communication between interface design experts at Illinois and biomedical researchers at Mayo Clinic, who represent KnowEnG's intended users. Feedback among these Center members ensures that the completed tool will be valuable, intuitive, and customizable for use in a broad array of experimental contexts.

"A major challenge is to understand the language and culture of each group so that we can communicate effectively, and make the tools that are developed at Illinois accessible to the biomedical audience," said Weinshilboum, who oversees the evaluation of KnowEnG's functionality. "The biomedical staff will communicate back to Illinois about what is helpful in terms of advancing their research and their understanding."

Mayo researchers will test the mettle of initial versions of KnowEnG, employing it in two large-scale investigations of the genomics of cancer treatment. KnowEnG's success in constructing functional conclusions from patients' genetic background, gene expression, responses to treatment, and many other measures will provide important benchmarks of performance during its development.

"All the institutional signals are agreeing; the computer scientists are really excited about doing this, and the biologists also behind it," said Jongeneel, reflecting on the culture of collaboration that has

made the Center's conception possible. "We have a fantastic partnership with Mayo."

Analysis of several biological experiments at Illinois will also be used to gauge performance. Cell and developmental biologist Lisa Stubbs, along with Sinha and Robinson, will use KnowEnG in a project investigating the relationship between gene regulation and social behavior in animal models and humans. Stubbs is also the leader of the Gene Networks of Developmental and Neural Plasticity Research Theme at the IGB, which is the official host of the Center.

Microbiologist Bill Metcalf, leader of the IGB's Mining Microbial Genomes Research Theme, will work with Sinha to improve the ability to draw relationships between an organism's genome sequence and its physical characteristics, providing a major plank of the evaluation strategy for the KnowEnG system.

The Center also represents another step forward for Illinois' CompGen Initiative, a campus effort led by the Coordinated Science Laboratory and the IGB whose goal is to forge new connections between expertise in information technology and biological Big Data.

"Receiving this NIH BD2K Center of Excellence award from NIH is another feather in the cap of the CompGen Initiative," said IGB Director Gene Robinson. "CompGen has enabled over 50 computer scientists, computer engineers, bioinformaticians and genomic biologists to come together and forge the close collaborative relationships necessary to spark the brilliant ideas that animate the proposal."

Altogether, the project promises both incredible intellectual challenges, and the possibility of great advances in genomics and Big Data.

"There's a lot to do, and obvious challenges to overcome, and we're looking forward to those challenges," said Sinha. "What I'm most excited about is the actual possibility that this could be a tool which everybody uses in the world." ■

Written by Claudia Lutz.

RESEARCH



Derek Wildman, Professor of Molecular and Integrative Physiology, is leading the effort to create a new computational genomic medicine research theme at the IGB.

IGB Establishing Research Theme in Computational Genomic Medicine

Medicine is in the midst of a flood of genomic data. From the genomes of individuals to the genomes of our microbiomes there is an increasing need to develop computational methods to analyze medical data.

“The forefront of medicine appreciates that health and treatment of disease is not a ‘one size fits all’ solution,” said Derek Wildman, Professor of Molecular and Integrative Physiology, who is leading the effort to create a new research theme at the Carl R. Woese Institute for Genomic Biology (IGB). “The promise of precision medicine is to develop treatments that are directed to each individual’s genetic and physical makeup. Precision medicine requires Big Data solutions, and the new theme in conjunction with other IGB themes and University wide initiatives such as CompGen will tackle the challenges associated with the analysis of thousands of genomes and the vast array of data contained in electronic health records.”

Currently, a tumor genome takes several months to analyze, during which time patients are at continued risk. Fetal DNA testing during pregnancy is now recognized as a safer alternative to amniocentesis. Genetic risk assessment through genotyping of DNA variants that are associated with breast and ovarian cancers, Alzheimer’s disease, and cystic fibrosis are now conducted on a daily basis. Insight into complex diseases such as diabetes, mental health disorders, and global health crises in infectious disease is gained through genomic and epigenomic approaches.

“One area of research focus is women’s and children’s health issues such as preterm birth,” said Wildman. “This devastating syndrome occurs in one of every nine U.S. pregnancies and comes at

a cost of \$26 billion per year. Infants born prematurely are at greater risk for developing a large range of health problems later in life, and prematurity is a leading cause of infant mortality and morbidity. Because there is no single cause for preterm birth, a precision medicine approach is necessary to reduce its incidence.”

Combining genetic data with the multitude of different environmental exposures each individual faces throughout their life requires computational breakthroughs that have the possibility to change

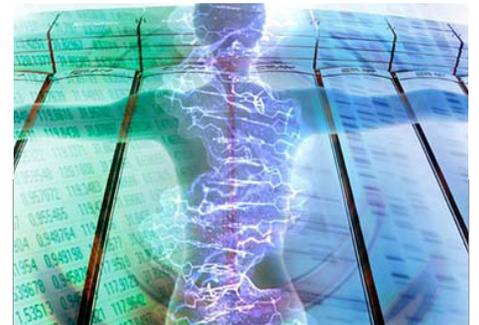
“Precision medicine requires Big Data solutions, and the new theme in conjunction with other IGB themes and University wide initiatives such as CompGen will tackle the challenges associated with the analysis of thousands of genomes.”

how medicine is treated and even conceived. This new theme will be dedicated to improving the lives of individuals in Illinois and across the globe through genomic research. It will use techniques in statistics, evolutionary biology, and medicine to unravel the complex interactions between human behavior and genetics that ultimately result in resilience or susceptibility to disease, and employ comparative and evolutionary genomic techniques

to understand the origins and histories of human health and disease.

“Computational genomic medicine sits directly at the interface where science meets society,” said Wildman. “Members of this new theme are eager to make a lasting impact on the health of Illinois residents as well as in the rest of the world.” ■

Photo by Kathryn Coulter.



IGB is a key partner in the CompGen initiative, which seeks to combine the collective strengths of Illinois’ genomic research with its prowess in large-scale parallel systems and big data to develop new technology that enables future genomic breakthroughs. As part of the initiative, researchers aim to build an instrument that allows scientists to manage and process genomic information and algorithm development.

PROFILE



Jonathan Sweedler is the James R. Eiszner Family Endowed Chair in Chemistry and Director of the School of Chemical Sciences.

Jonathan Sweedler: Exploring the Brain's Frontier

Jonathan Sweedler uses grapefruit-sized sea slugs—that can weigh more than four pounds—to study how chemicals, like serotonin and dopamine, enable brain cell interactions.

These “big, disgusting, gooey-looking” mollusks are surprisingly complex. They are capable of learning and long-term memory, but their neural networks are simple enough that the team is able to draw conclusions about how chemicals in the brain work.

“Sometimes people like to make statements that neuropeptides, which modulate behavior, are responsible for four of the seven deadly sins,” said Sweedler, the James R. Eiszner Family Endowed Chair in Chemistry. “These molecules change the way we think, the way we feel, and whether we are hungry or not. They are really important in a lot of ways, and surprisingly, a lot of them aren’t known.”

Sweedler explores the brain’s frontier, seeking out new neurochemicals that signal between and amongst brain cells to encode memories or change behavior. To better understand this process, his lab has developed new tools to analyze the neurochemical differences in nearby cells.

“We have used these tools and come up with a list of hundreds of new peptides,” Sweedler said. “To discover new molecules that weren’t known before and learn what they do is very satisfying.”

His group’s tools are widely used by scientists and pharmaceutical companies today. Scientists are closer now to having what they need to discover the link between neurochemicals and mental illness, like serotonin and depression as well as dopamine and attention deficient disorder.

When Sweedler joined the University of Illinois in 1991, he did not think he would be studying neurochemicals amidst cornfields for nearly 25 years.

Over this period of time, he has picked up an impressive string of titles, duties, and affiliations. In addition to holding a chair in chemistry, he is the

Director of the School of Chemical Sciences. He is also affiliated with the Biotechnology Center, Neuroscience Program, and Bioengineering Program and is a member of the Carl R. Woese Institute for Genomic Biology (IGB) and the Beckman Institute for Advanced Science and Technology. In addition, he is editor of *Analytical Chemistry*.

Sweedler isn’t a stranger to long work days. But at the end of the day, he says he leaves his work at the office. He doesn’t consider the one or two hours he

“These molecules change the way we think, the way we feel, and whether we are hungry or not. They are really important in a lot of ways, and surprisingly, a lot of them aren’t known.”

spends each night reading journal submissions or the additional tasks required to run a 15-30 member lab group to be “work.”

“I may have a nine-to-five job, but then I have my hobby, which is research,” Sweedler said. “I work on my hobby at night and on the weekends: reading about research, writing papers, or meeting with students.”

More than 100 students have been a part of Sweedler’s lab, each leaving their mark “figuratively and literally” he said, referring to their scientific accomplishments and the various snail memorabilia they have donated to his ever growing office collection.

“They have been very successful in all sorts of areas,” he said. “My former students continuously reinvent

themselves and that has been one of the most exciting aspects of my career.”

Sweedler received his bachelor’s degree in chemistry from the University of California at Davis in 1983. He went on to earn a doctorate from the University of Arizona in chemistry in 1989 followed by a National Science Foundation Postdoctoral Fellowship at Stanford University in neuroscience and chemistry. ■

Written by Claire Sturgeon. Photo by L. Brian Stauffer.



Shown here is the marine mollusk Aplysia californica. The Aplysia’s simple nervous system is comprised of approximately 10,000 neurons, almost 10 million times fewer than what’s found in a human brain - yet still capable of long-term memory and a variety of learning tasks.

Aplysia offers researchers advantages like large, easily accessible neurons, and the chemicals and molecular scale processes found in the sea slug are the same ones at work in higher-end brains like those in mice and humans.

ON THE GRID HAPPENINGS AT THE IGB

AWARDS



GENE ROBINSON

Gene Robinson (IGB Director) was conferred the degree of Doctor Philosophiae Honoris Causa of the Hebrew University of Jerusalem.



RASHID BASHIR

Rashid Bashir, Bioengineering Professor and Department Head (Regenerative Biology & Tissue Engineering) has been elected a Fellow of the International Academy of Medical and Biological Engineering (IAMBE).



BRENDAN HARLEY, JIAN MA

Brendan Harley, Professor of Chemical and Biomolecular Engineering (Regenerative Biology & Tissue Engineering) and Jian Ma, Assistant Professor of Bioengineering (Cellular Decision Making in Cancer, Gene Networks in Neural & Developmental Plasticity, Biosystems Design) were named as 2015-16 Center for Advanced Study Fellows.



YANG LI, TONG SI

Yang Li, PhD Candidate, Department of Bioengineering, Jian Ma Lab, and Tong Si, IGB Fellow, Biosystems Design, will receive the highly competitive 2014 Chinese Government Award for Outstanding Self-Financed Students Abroad, sponsored by the Chinese Ministry of Education.



DOUGLAS MITCHELL, KAREN SEARS

Douglas Mitchell, Assistant Professor of Chemistry (Mining Microbial Genomes) and Karen Sears, Assistant Professor of the School of Integrative Biology (Regenerative Biology & Tissue Engineering) have been named 2015-2016 Helen Corley Petit Scholars.

ART EXHIBIT



ART OF SCIENCE 5.0

Save the date for the next show of the IGB's Art of Science exhibit!

Opening Reception is Thursday, April 23, from 6:00 to 8:00pm at the indi go gallery. The exhibit will run through April 27.

RENAMING

CARL R. WOESE INSTITUTE FOR GENOMIC BIOLOGY

Where Science Meets Society

IGB OFFICIALLY RENAMED

After obtaining approval from the University Senate, the Board of Trustees and Illinois Board of Higher Education, the Institute for Genomic Biology has officially been renamed.

We honor an individual who made legendary contributions to science, served as a University of Illinois Microbiology faculty member for nearly 50 years, and was a founding member who paved the way for the IGB to emerge as a leader in advancing life sciences. The institute will now be known as the Carl R. Woese Institute for Genomic Biology.

We proudly carry on the spirit of discovery, dedication, and determination so well embodied by Carl, his legacy now an indivisible part of our history.

BAKE OFF



IGB BAKE-OFF

Monday, February 16
Array Café, 4:00pm

Showcase your delicious recipe at the IGB Bake-Off. Email darci@illinois.edu with the name of your sweet and/or savory dish.

Mark your calendar and save the date!

ON THE GRID HAPPENINGS AT THE IGB

HEALTH



MEDICAL INFORMATION

Bruce Schatz, a medical information scientist and IGB affiliate, and researchers have created Move Sense, an app that turns your smartphone into a useful medical device. The app uses a smartphone's accelerometer motion sensors to measure a person's gait, or walking pattern, which can tell doctors about a patient's heart and lung health status.

View a video on the research [here](#).

GIVING



WALK OF LIFE

The double helix—the classically beautiful twisting ladder that forms the shape of DNA—is beautifully depicted within the landscape of the IGB.

Located to the west of the IGB building, adjacent to the historic Morrow Plots, the Walk of Life pays tribute to the historical discoveries that enable our work on the cutting edge of genomic research. Contributing to the Walk of Life is a unique opportunity to simultaneously support our mission and become a permanent part of IGB history.

Contact Melissa McKillip at mmckilli@illinois.edu or find more information at www.igb.illinois.edu/about/giving.

GRANT PROPOSAL SUPPORT



IGB GRANT PROPOSAL TEAM

For those submitting a grant proposal, members of the IGB Business Office, Communications group, and Outreach group are available to help.

The business office is available for submission training or to help you navigate forms, prepare subcontract documents, and by liaising between OSPRA and the Sponsor Grants Management Office. The Communications and Outreach groups can assist you with incorporating outreach activities, editing your proposal, and other needs.

For more information please visit <http://www.igb.illinois.edu/content/grant-proposal-team>.

BLOOD DRIVE



IGB BLOOD DRIVE RESULTS

Thanks to all who volunteered—Community Blood Services of Illinois collected 33 pints of lifesaving blood on our on January 23 blood drive.

The results are listed below:

Goal	25
Donors Registered	40
Temporary Deferrals	7
First time donors	10!

The next IGB blood drive is scheduled for April 22, 2015.

IP @ IGB



ILLINOIS PROOF OF CONCEPT FUND PRE-PROPOSAL APPLICATIONS

Pre-proposal applications for funding are being accepted now through February 27, 2015.

This program helps bridge the gap between University innovations and the marketplace by funding development that will demonstrate an innovation's market viability to potential investors and partners.

I-POC projects consist of a defined set of milestones that, when completed, help overcome a specific hurdle to an innovation's transfer outside of the University.

The I-POC Fund is currently made possible by contributions from the following colleges & units and matching funds from the Office of the Vice Chancellor for Research. The Office of Technology Management will work with campus alumni and development officers to create an ongoing and sustainable source of funding.

The I-POC Fund is currently open to projects that originate from a participating college or unit. However, if you would like to apply for funding and do not see your college listed, please contact the Office of Technology Management.

Submitting a pre-proposal is the first step in applying for this new round of funding.

For more information or questions please contact: Nicole Nair at nnair@illinois.edu. Please submit pre-proposals to: IllinoisPOC@illinois.edu (you should receive an acknowledgment within 1-2 days. If you do not, please contact Nicole Nair).

For full details please visit <http://otm.illinois.edu/IPOC>.

ADMINISTRATIVE NEWS

BUSINESS

PROPOSAL AND AWARD POLICIES AND PROCEDURES GUIDE (PAPPG) REVISED VERSION

A revised PAPPG was issued on November 20, 2014, which incorporates OMB's Uniform Administrative Requirements, Cost Principles, and Audit Requirements for Federal Awards (Uniform Guidance), as well as other policy updates. Below we have outlined important new changes to be aware of.

Automated Compliance Checks

FastLane will begin to run an additional 24 automated compliance checks on proposals to ensure they comply with requirements outlined in the PAPPG, Chapter II.C.2 of the Grants Proposal Guide (GPG). These checks will validate a proposal for compliance with page count, proposal sections per type of funding mechanism and budget related rules for proposals submitted in response to the GPG, Program Announcements and Program Descriptions. At this time, these checks will not be enforced for proposals submitted in response to Program Solicitations.

- **Page Count:** Page count rules will be enforced on the following proposal sections:
 - **Project Description:** 15-page limit [exceptions: 8-page limit for Early-Concept Grants for Exploratory Research (EAGER), and 5-page limit for Rapid Response Research (RAPID)]
 - **Budget Justification:** 3-page limit for the proposing institution and a separate, 3-page limit for each sub-recipient organization
 - **Mentoring Plan:** 1-page limit
 - **Data Management Plan:** 2-page limit
- **Budget:** Budget-related checks will focus primarily on proposal duration and requested amount. For example, the system will enforce a maximum requested amount of \$200,000 for a RAPID proposal and \$300,000 for an EAGER proposal.
- **Proposal Section:** Proposal sections will be enforced by their funding mechanism for Program Announcement, Program Description and other GPG-type funding opportunities. For example, an error message will appear if a Project Description was not provided for an EAGER proposal.

The checks detailed above will be triggered when the "Check Proposal," "Forward to SPO," or "Submit Proposal" functions are selected by a proposer or proposing organization. Depending on the rule being checked, a warning or error message will display when a proposal is found to be non-compliant. If an error message appears, the organization will not be able to submit the proposal until it is compliant. To view a detailed list of all compliance checks, click [here](#).

We encourage you to share this information with your respective organization. View the complete guide [here](#). Please contact policy@nsf.gov for any further questions. ■

UNIVERSITY LIBRARY

REQUEST A SAVVY RESEARCHER WORKSHOP

While you may already know about the Library's Savvy Researcher workshop series (<http://illinois.edu/calendar/list/4068>), did you know that you can request a Savvy Researcher workshop to be taught at a lab or research group meeting? Since the scheduled workshops may not be at a convenient time and/or location, the Library offers to take the workshops on the road! Just submit a request (<https://illinois.edu/fb/sec/6094473>), and the instructor who teaches the workshop you selected will respond to find a convenient time and location.

The free workshops are 50 minutes and cover a variety of tools and topics to improve research and information management skills. Below are some of the sessions that might be of particular interest to researchers at the IGB, but be sure to look at the online schedule for a complete list of sessions, with descriptions.

- The ORCID Identifier: The Free iD Number that Ensures You Get Credit for ALL of Your Research
- Introduction to Data Management
- Documentation and Organization for Data and Processes
- Making Research Data Public: Why, What, and How
- PubMed – Beyond the Basics
- Using GitHub for Scholarly Publishing and Collaboration
- Getting Organized with Mendeley
- Drowning in Citations and PDFs? EndNote Can Help! ■

COMMUNICATIONS

IGB RENAMING GUIDELINES

Now that the IGB has been officially renamed to the Carl R. Woese Institute for Genomic Biology, please be aware there are many areas that pertain to your information that may need to be updated. Some examples of these areas could include:

- Email signature
- Office nameplate
- Title of personal, lab, or project web page
- Business cards
- Nametag
- CV
- Poster
- Powerpoint slides

The Communications group is available to provide guidance in any of these areas, and has access to templates and file formats to assist you. If you have any questions, please don't hesitate to contact Nicholas Vasi at nvasi@illinois.edu. ■

ADMINISTRATIVE NEWS

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.

Huang Z, Wang KK, Lee J, van der Donk WA. Biosynthesis of fosfazinomycin is a convergent process. *Chem Sci*. 2015;6(2):1282-1287.

Gundling WE, Jr, Wildman DE. A review of inter- and intraspecific variation in the eutherian placenta. *Philos Trans R Soc Lond B Biol Sci*. 2015;370(1663):20140072.

Chau A, Kalsotra A. Developmental insights into the pathology of and therapeutic strategies for DM1: Back to the basics. *Dev Dyn*. 2015.

Zhang H, Luo Q, Gao H, Feng Y. A new regulatory mechanism for bacterial lipoic acid synthesis. *MicrobiologyOpen*. 2015.

Caliari SR, Weisgerber DW, Grier WK, Mahmassani Z, Boppart MD, Harley BAC. Collagen scaffolds incorporating coincident gradations of instructive structural and biochemical cues for osteotendinous junction engineering. *Adv Healthc Mater*. 2015.

Kim T-, Zheng S, Sun J, et al. Dynamic visualization of α -catenin reveals rapid, reversible conformation switching between tension states. *Curr Biol*. 2015;25(2):218-224.

Denard CA, Ren H, Zhao H. Improving and repurposing biocatalysts via directed evolution. *Curr Opin Chem Biol*. 2015;25C:55-64.

Cobb RE, Bae B, Li Z, DeSieno MA, Nair SK, Zhao H. Structure-guided design and biosynthesis of a novel FR-900098 analogue as a potent *Plasmodium falciparum* 1-deoxy-d-xylulose-5-phosphate reductoisomerase (dxr) inhibitor. *Chem Commun (Camb)*. 2015.

Kim T-, Oh EJ, Jin Y-, Oh M-. Improved resistance against oxidative stress of engineered cellobiose-fermenting *Saccharomyces cerevisiae* revealed by metabolite profiling. *Biotechnol Bioprocess Eng*. 2015;19(6):951-957.

Metelev M, Tietz J, Melby J, et al. Structure, bioactivity, and resistance mechanism of streptomonicin, an unusual lasso peptide from an understudied halophilic actinomycete. *Chem Biol*. 2015.

Bhatia S, Prabhu PN, Benefiel AC, et al. Galacto-oligosaccharides may directly enhance intestinal barrier function through the modulation of goblet cells. *Mol Nutr Food Res*. 2015.

Shattuck MR, Satkoski-Trask J, Deinard A, et al. Patterns of genetic variation and the role of selection in HTR1A and HTR1B in macaques (*Macaca*). *BMC Genet*. 2014;15:116.

Doroghazi JR, Buckley DH. Intraspecies comparison of *Streptomyces pratensis* genomes reveals high levels of recombination and gene conservation between strains of disparate geographic origin. *BMC Genomics*. 2014;15:970.

Carr-Markell MK, Robinson GE. Comparing reversal-learning abilities, sucrose responsiveness, and foraging experience between scout and non-scout honey bee (*Apis mellifera*) foragers. *J Insect Behav*. 2014;27(6):736-752.

Bouvier J, Groninger-Poe F, Vetting M, Almo S, Gerlt J. The discovery of a lactone isomerase involved in pectin degradation. *FASEB J*. 2014;28(1).

Markelz RJC, Vosseller LN, Leakey ADB. Developmental stage specificity of transcriptional, biochemical and CO₂ efflux responses of leaf dark respiration to growth of *Arabidopsis thaliana* at elevated [CO₂]. *Plant Cell Environ*. 2014;37(11):2542-2552.

Kim SR, Xu H, Lesmana A, et al. Deletion of PHO13 encoding HAD type IIA phosphatase results in upregulation of the pentose phosphate pathway in yeast. *Appl Environ Microbiol*. 2014.

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