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News, Opportunities and Deadlines for January 2020

18th LBRN Annual Meeting Success!



Our 18th Annual LBRN Meeting was held at LSU this January 17th and 18th at the LSU Theater and Cotillion Ballroom to over 150 participants. 33 talks began with a keynote talk from the Director of the Stanley S. Scott Cancer, Dr. Augusto Ochoa, MD., from the LSU Health Sciences Center on the *Transformational Effects of COBRE Research in Louisiana*. We also hosted a special session for IDeA COBRE and CTR Programs for each of the COBRE and CTR programs in Louisiana by each Program PI or Representative to the LBRN participants. We had talks from our funded partner campus project investigators for translational, full, and pilot projects, and eight 2019 summer graduate students. Participants came from: LSU Shreveport, Grambling University, Louisiana TECH, University of Louisiana at Monroe, Southern University in Baton Rouge, Southeastern Louisiana University, Xavier University; as well as our Mentoring campuses: LSU Health Science Center in Shreveport and New Orleans, Pennington Biomedical Research

Center. A dinner and poster session was hosted with 60 poster presentations by LBRN 2019 Project PI's, Summer Graduate and Undergraduate program participants with awards given to the following:

Winners - The Undergraduate Awards

Placement	First Name	Last Name	Institution	Poster Title
1st	Prerana	Ramesh	Louisiana State University Shreveport	How to Train Your AI: Quantification of R-Loop Expression in Anaplastic Thyroid Carcinoma using Immunohistochemistry and Automated Cell Segmentation Software
2nd	Brennen	Murphy	Louisiana State University Shreveport	Reverse Phase Protein Array Analysis of FC101m Treated TNBC and ATC Cell Lines
3rd	Jacqueline	Dennis	Louisiana State University Shreveport	Anticancer Activities from Camptothecin-Related Iridoids from Medicinal Plant Camptotheca acuminata

Winners - The Graduate Awards

Placement	First Name	Last Name	Institution	Poster Title
1st	Adeola	Adedokun-Afolayan	Louisiana State University Shreveport	Fabrication of Human-Scaled Biliary Trees Surgical Replacements through 3D Printing
2nd	Camaray	Rouse	Louisiana State University Shreveport	In Silico Analysis for Characterization of Glucosidases from Anticancer Alkaloid-producing Medicinal Plants
3rd	Shilpa	Thota	Southern University and A&M College	PENTACHLOROPHENOL-MEDIATED INDUCTION OF INFLAMMATORY RESPONSES IN ALVEOLAR EPITHELIAL AND LIVER CARCINOMA CELLS
Honorable Mentions	A K M Nawshad	Hossian	University of Louisiana at Monroe	Novel nanocarrier based on Vitamin E derivatives for nucleic acid delivery
Honorable Mentions	Haley	Barnett	Louisiana Tech University	Tunable Biomimetic Scaffolds for Directing Stem Cell Growth and Differentiation for Tissue Regeneration Applications
Honorable Mentions	Onyekachi	Idigo	Louisiana Tech University	The role of MED12 in adipogenesis of human adipose stem cells (hASCs)
Honorable Mentions	Sree	Venigalla	Louisiana Tech University	Expression levels of Mediator kinase module subunits and their interaction with transcription factors in mouse adipose tissue
Honorable Mentions	Yaswanthi	Yanamadala	Louisiana Tech University	Folate receptor targeted release of Anti-inflammatory peptide from reducible thermosensitive nano-particles for treatment of Inflammatory diseases

It was a special weekend, as we were joined by our former INBRE grant Project Investigators, Dr. Harold Silverman (LSU Emeritus) and Dr. Thomas Klei (LSU Emeritus) during the opening meeting day and LSU was celebrating the National Championship win in SEC Football during our LBRN Annual Meeting at LSU. Needless to say, a day of festivities was going on all around the meeting! Participants were given the chance to join the parade briefly when we decided to alter our schedule to allow for the lunch break at the same time as the 11am parade. Later we were able to show some short video clips from the Pete Maravich Assembly Center (PMAC) taken by our PI, Dr. Gus Kousoulas with one of our EAC members, Dr. Stephen Cutler who was ‘high fived’ by the LSU Mascot, Mike the Tiger on the PMAC floor.

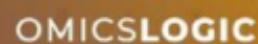
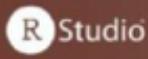
This is the 18th year that Louisiana has benefitted by the NIH General Medical Sciences (NIGMS) Institutional Development Award (IDeA) Networks of Biomedical Research (INBRE). In that time, it has fostered an atmosphere of biomedical research across all our current and former partner

campuses by improving infrastructure, research enablement in the administrations of these campuses, and overall access to quality mentoring and opportunities for research across the state in this field at the following institutions for junior faculty, graduate students and undergraduates at: LSU-Shreveport, Grambling University, Louisiana Tech University, University of Louisiana at Monroe, Southern University in Baton Rouge, Southern University in New Orleans, Southeastern Louisiana University, Xavier University and including all our Undergraduate Summer program campuses in addition to our partner campuses: Baton Rouge Community College, Centenary College, Dillard University, Louisiana College, LSU Alexandria, McNeese State University, Nicholls State University, Northwestern State University, Franciscan Missionaries of Our Lady University (formerly Our Lady of the Lake College), Southern University at Shreveport, University of Louisiana at Lafayette, and University of New Orleans. We welcome the excellence of those students from all these campuses each year. We thank NIGMS for the grant funding the Louisiana INBRE that enable these partner campuses and project investigators to further research and the Louisiana Board of Regents for whom we receive the summer program funds to at our partner campuses and all the students from all the Louisiana campuses to bring excellence in biomedical research to the state of Louisiana.

LSU / LBRN Graduate Transcriptomics Course

ANALYSIS OF TRANSCRIPTOMIC DATA

PBS 7003: Section 1 (Kousoulas)
From Introduction to Bioinformatics to Single Cell Transcriptomics
(Offered in PUI campuses -check with BBC Coordinators)



The LSU/LBRN Graduate Transcriptomics Course will start January 16, 2020. You can register for a local course in one of the LBRN participating PUIs to receive credit, or can access the course online and receive a certificate of participation from LBRN. Attendance of the Q&A sessions is open to all (faculty, postdocs, staff, students). Attendance for the full course is by permission from BioMMED/LBRN after each interested person has been registered. To register you can fill out the form found here: <https://edu.tbioinfo.com/lbrn-transcriptomics-spring2020>

General Information: Spring Session Graduate Course on Transcriptomic Data Analysis: Applied Bioinformatics Concepts for Life Science Research led by Dr. Gus Kousoulas, Dr. Ramesh Subramanian and Dr. Lyndon Coghill at LSU Baton Rouge with the participation of the LBRN BBC (Dr. Chris Taylor, Dr. Urska Svek). In this course, we will explore how gene expression can be studied using high throughput sequencing data by leveraging principles of bioinformatics. The course will cover essential steps of processing, analysis and interpretation of such data using commercial solutions for high performance computing (T-BioInfo) and open source applications (R). A video overview for the program topics can be seen here: <https://youtu.be/S2gDviol3eM>.

Spring session graduate Course: Analysis of Transcriptomic Data (January 13 - April 16) LSU PBS 7003 course - 2 credits (Online Coursework and scheduled review sessions every 2-3 weeks

on Thursdays at 3 PM, SVM room 3511). The program schedule is here: <https://lbrn.t-bio.info/>

Grading: bi-weekly quizzes and final exam, course participation, in-class discussion

Program length: 3 months

A BioMMED/LBRN certificate of completion will be awarded by BioMMED/LBRN to all attendees that successfully complete all exams and homework assignments.

The registration cut-off day will be January 30th !



LBRN Summer Research Program - 2020

LBRN Summer Research Program

for Undergraduate and Graduate students

May 25 — July 31, 2020*



AWARDS

- Undergraduate and Graduate students will receive support of \$4,000 and \$6,000 respectively
- Housing is provided, if needed

APPLICATION DEADLINE

- If you would like to know more about this program, please go to Research Programs at: <https://lbrn.lsu.edu/summer-research-program.html>
- If you have any questions, please contact Alexis M. White at lbrn@lsu.edu
- Phone: (225) 578-9683
- Email: lbrn@lsu.edu
- Web: <https://lbrn.lsu.edu/>



Louisiana Biomedical Research Network

The Louisiana Biomedical Research Network (LBRN) sponsors a summer research program in support of undergraduate students, graduate students and faculty from any Louisiana institute. We offer qualified participants the opportunity to work in established research laboratories at Louisiana State University, LSU Health Sciences Center in New Orleans, LSU Health Sciences Center in Shreveport, Tulane Medical Center, or Tulane National Primate Research Center. The goal of our program and funding is to support biomedical research through an increase in graduate school admissions in these scientific fields and make Louisiana researchers more competitive in obtaining federal funding for research.

The schedule for undergraduate students covers ten weeks during the summer; the summer program dates are May 25 - July 31, 2020. The schedule for graduate students and faculty is more flexible.

Please see our website for support details and program requirements for each application type, applications are open on our [LBRN Summer Program Webpage](#) now. Deadline for applications is

February 14, 2020.

LOUISIANA CANCER RESEARCH CONSORTIUM SCIENTIFIC RETREAT



-- Call for Abstracts--

The 2020 Louisiana Cancer Research Consortium Scientific Retreat has been scheduled for **Friday, March 13, 2020**, at Xavier University of Louisiana.

Abstracts are now being accepted for participation in this year's event. The guidelines for formatting and submission can be found at

<http://www.louisianacancercenter.org/news-events/guidelines-deadlines/>

Please note, the deadline for submitting an abstract is **Friday, January 31, 2020**.

Other Important Retreat Dates/Deadlines:

January 31, 2020 – DEADLINE to submit abstracts

February 10, 2020 – DEADLINE to submit Core posters ONLY for inclusion in abstract booklet

February 20, 2020 – Notifications will be sent to all poster/podium presenters

February 21, 2020 – DEADLINE to register

March 6, 2020 – DEADLINE for podium presenters to submit slides

March 13, 2020 – 2020 LCRC Scientific Retreat

Additional retreat information is available at <http://www.louisianacancercenter.org/news-events/guidelines-deadlines/>. Please check in periodically for the latest on the **2020 LCRC Scientific Retreat**.

CPRIT Summer Undergraduate Program

**\$6000
10-week
stipend**

Undergraduate Summer Research Experience

UTHealth Innovation in Cancer
Prevention Research
June 1 - August 7, 2020

Do you want to develop out-of-the-box thinking?

This program offers training in evidence-based tools for innovative thinking and placements with accomplished cancer researchers at McGovern Medical School (Houston) ■ MD Anderson Cancer Center UTHealth Graduate School of Biomedical Sciences (Houston) ■ School of Biomedical Informatics (Houston) ■ School of Public Health (Houston, Austin, Dallas, San Antonio, Brownsville, and El Paso)

Applications now available!
bitly.com/cpritsummer2020

Applications and supplemental materials due at
11:59 PM (CST) on January 20, 2020

For more information, visit bit.ly/cpritsummer



CANCER PREVENTION & RESEARCH
INSTITUTE OF TEXAS

LSU HPC Training: Introduction to Linux

The schedule for the Spring 2020 HPC Training is available at <http://www.hpc.lsu.edu/training/tutorials.php>.

Our first HPC training will be held on Wednesday, January 29 at 9:00 AM in 307 Frey Computing Service Center and broadcast online for remote users.

Note that all HPC trainings will start at 9:00AM.

Wednesday, January 29, 2020: Introduction to Linux

The aim of this training is to get users familiar with using Linux systems e.g. the HPC resources. This training will cover basic Linux commands and editors (emacs and vi) on Linux systems. Anyone who is interested in learning about using a Linux based computer is encouraged to attend. If you are not familiar with using a Linux system particularly creating/writing files then this course is a prerequisite for the forthcoming training on HPC User Environment 1 & 2. This training is *mandatory* for HPC users who are not familiar with using a Linux/Unix system. Prerequisite: Access to a Linux/Unix based computer i.e. Linux (VirtualBox images), Mac OSX and Windows with Cygwin or Bash installed.

Next two HPC Trainings:

Wednesday, February 5, 2020: HPC User Environment 1, Job Management with PBS

Wednesday, February 12, 2020: HPC User Environment 2, Job Management with PBS

This training provides an overview of the HPC/LONI general account and allocation policies, hardware and software environments, queuing system, compiling programs, writing submit scripts, running and monitoring jobs on HPC systems.

This training is a *mandatory* two day training event for all HPC/LONI new users held on February 5 and February 12.

Prerequisite: Familiarity with Linux/Unix commands and editors

Please visit <http://www.hpc.lsu.edu/training/tutorials.php> for more details and register using the link provided. Users who plan on joining remotely will be provided with a zoom link in their registration confirmation email. Please see the system requirements at <https://support.zoom.us/hc/en-us/articles/201362023-System-Requirements-for-PC-Mac-and-Linux>.

IDeA Co-Funding



The IDeA program managed by NIGMS is pleased to announce the 2020 co-funding opportunity for investigators in IDeA-eligible states whose R01 or R15 applications scored well but fall just outside of an IC's funding range. The IDeA program provides a maximum of \$320K in total costs for each of the first two consecutive years of a selected award. Nominations are made by the NIH IC that has the primary assignment for the application. PIs wishing to be considered for IDeA co-funding should contact directly the program officer at the IC assigned to the application.

IDeA co-funding is conducted once per year, and the nomination period will close in early April. Final selections will be made in June of 2020. Please visit <https://www.nigms.nih.gov/Research/DRCB/IDeA/Pages/IDeA-Co-funding.aspx> for further information about this initiative.

GeneLab Launched Two New Illumina Sequencing Machines

GeneLab (School of Veterinary Medicine - Louisiana State University) is a multi-faceted core laboratory directed by the Division of BIOMMED in the School of Veterinary Medicine at Louisiana State University. GeneLab engages in specific research and training projects, which require expertise in Next-Generation Sequencing, traditional DNA sequencing, gene cloning, PCR, gene expression and other molecular methods. The goal of GeneLab is to facilitate the utilization of the state-of-the-art technologies in genomics research by LSU faculty and researchers nationwide at a competitive price and in a timely fashion.

The primary focus of GeneLab is its portfolio of sequencing capabilities. Currently, two Next Generation Sequencing instruments, the Illumina NextSeq, the Illumina MiSeq and 10X Genomics Chromium Controller along with bioinformatics support for NGS data are provided to the research

community and offering will be extended rapidly as NGS and other emerging sequencing technologies are evolving.

Illumina NextSeq

The Illumina NextSeq System is a desktop sequencer with power and flexibility to carry out applications such as whole genome sequencing, exome sequencing, whole transcriptome sequencing, mRNA-Seq, and others. In one run it can sequence a full human genome at 30x coverage. Users can choose between high output or mid output flow cell configurations. At high output, up to 800 million paired end reads can be generated (at 150 bp read length) to produce up to 120 Gb of data in 29 hours. The Illumina sequencing systems utilize a well-established sequencing by synthesis (SBS) method and patented cluster generation technology in which fluorescently labeled nucleotide bases are detected as they are incorporated into DNA template strands. All four reversible terminator-bound dNTPs are present in each sequencing cycle.



Illumina MiSeq

Cluster generation, sequencing, and analysis are all done on a single instrument. The sequencing process takes place on a flow cell with 1 channel. Multiple samples can be run at once by using indices for each sample. 2x300bp reads are supported on the MiSeq and takes ~3 days to run. With v.3 kits the MiSeq can produce >25 million reads or 15GB per run. With v.2 kits the MiSeq can produce >15 million reads or 7.5 GB per run with standard flow cells. There is also the option of using micro and nano flow cells which produce up to 4 million and 1 million reads per run (1.2Gb & 500Mb). Actual output can vary depending on cluster density.



10X Genomics Chromium Controller

Go beyond traditional gene expression analysis to characterize cell populations, cell types, cell states, and more on a cell-by-cell basis. From assessing tumor heterogeneity and stem cell composition, to dissecting neuronal populations—the technological advancements provided by the Chromium Single Cell Gene Expression Solution allow the creation of high complexity libraries from single cells to maximize insight from any sample type.



Services and collaboration can be delivered through the LBRN cores.

CFA for Short Term Core Projects



Molecular Cell Biology Research Resources Core (**MCBRC**) and Bioinformatics, Biostatistics, and Computational Biology Core (**BBCC**) are calling for proposals to carry out short term projects in collaboration with the Cores. All LBRN researchers can submit a proposal for a defined project that can be carried out in collaboration with the Core facilities listed in the attached Call for Proposals (CFP) on a competitive basis. Each selected project will be allocated \$1,500 to fully or partially offset Core expenses. More details can be found in the attached CFP.

[More details can be found in the attached CFP.](#)

BBC Core Educational Resource



The BBC Core provides introductory educational lecture series on informatics topics that are recorded and streamed. Prior offerings that are available for on demand streaming include;

- An Introduction to Computers and Informatics in the Health Sciences

<http://metagenomics.lsuhsc.edu/lectures/introinformatics/>

- An Introduction to Microbial Community Sequencing and Analysis

<http://metagenomics.lsuhsc.edu/lectures/intromicrobiota/>

On demand streaming links are available by each lecture along with downloadable lecture slides.

LONI HPC Allocation for LBRN



To support the LBRN / BBC Core community on LONI HPC systems, we have renewed our high-performance computing allocation for 2019/2020.

This can be utilized in lieu of individual investigators having to apply for and acquire their own allocations to access the HPC resources. If any of your campus members need access to high performance computing, please have them interface with [Dr. Nayong Kim](#).

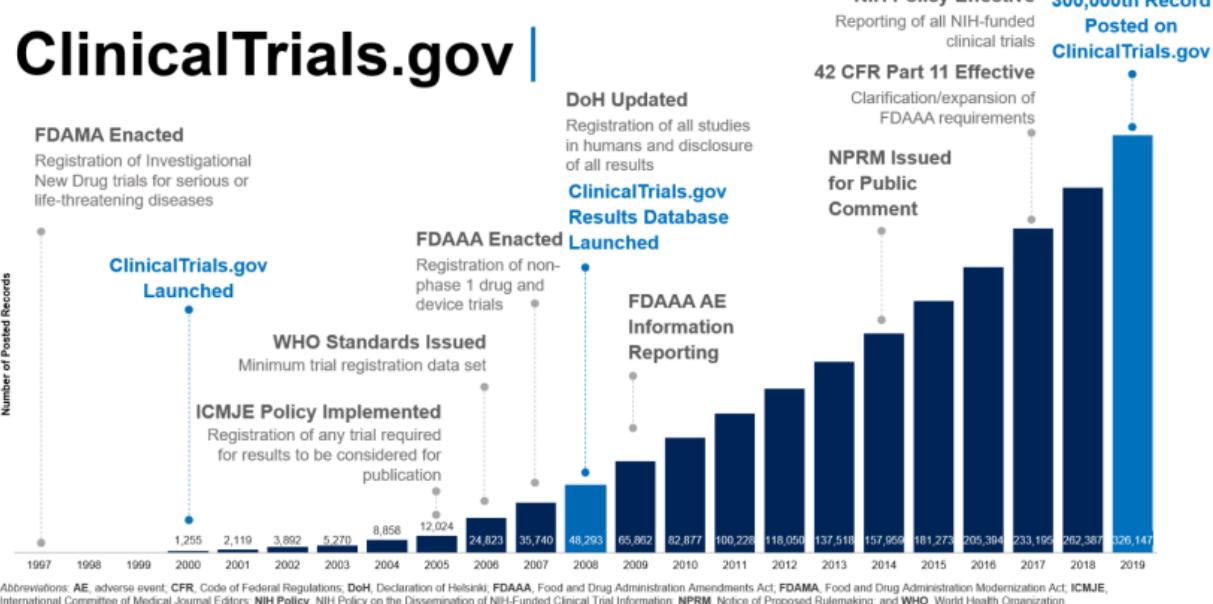


• Celebrating 20 Years of ClinicalTrials.gov and Looking to the Future

As [ClinicalTrials.gov](#) celebrates its 20th anniversary on February 29, 2020, we're asking for your input on how it can best continue to serve your needs for many more years to come.

ClinicalTrials.gov is the world's largest public clinical research registry and results database, giving patients, families, health care providers, researchers, and others easy access to information on clinical studies relating to a wide range of diseases and conditions. This online resource, which has more than 145,000 unique visitors every day, is operated by NLM and makes available information provided directly by the sponsors and investigators conducting the research.

NLM has launched an effort to [modernize ClinicalTrials.gov](#) to deliver an improved user experience on an updated platform that will accommodate growth and enhance efficiency. Creating a roadmap for modernization requires feedback from a wide array of stakeholders on how to continue serving, balancing, and prioritizing their varied information needs. These stakeholders include sponsors and investigators who submit clinical trial information to the site, academic institutions, nonprofit and advocacy organizations, government agencies, and the public, all of whom can access and use the information that ClinicalTrials.gov contains free of charge.



To obtain timely, detailed, and actionable input, we have issued a [Request for Information \(RFI\)](#) to solicit comments on the following topics: website functionality, information submission processes,

and use of data standards.

Recognizing that ClinicalTrials.gov supports a network of stakeholders who contribute to, and rely on, clinical research, our aim is to understand how the system can better support this network and to identify opportunities for improving its compatibility with existing clinical trial management tools and processes. It is important to note that this RFI focuses on the functionality of ClinicalTrials.gov and is not intended to modify existing legal and policy requirements for clinical trial registration and results submission.

Over its 20-year history, ClinicalTrials.gov has helped shape the way in which clinical trial information is made transparent and discoverable to the public (see figure 1). In 2000, sponsors and investigators began submitting structured summaries of clinical trial protocols for the public to view. Over time, new policies and laws reinforced this practice, and ClinicalTrials.gov now contains over 320,000 study listings, with 56,000 studies currently seeking participants.

[...Continue reading](#)

• Data are Available on NIH Funding Plans

The [NIH-Wide Strategic Plan for Fiscal Years \(FYs 2016-2020\)](#) laid the groundwork for discussing data on our funding strategies—see page 28 for example data on R01 applications across peer review percentiles in FY 2014. The 21st Century Cures Act recognized the value of reporting such information. Building on what we have blogged on before (see [here](#), [here](#), [here](#), and [here](#)), let's talk more about how we make funding decisions and show some data as well.

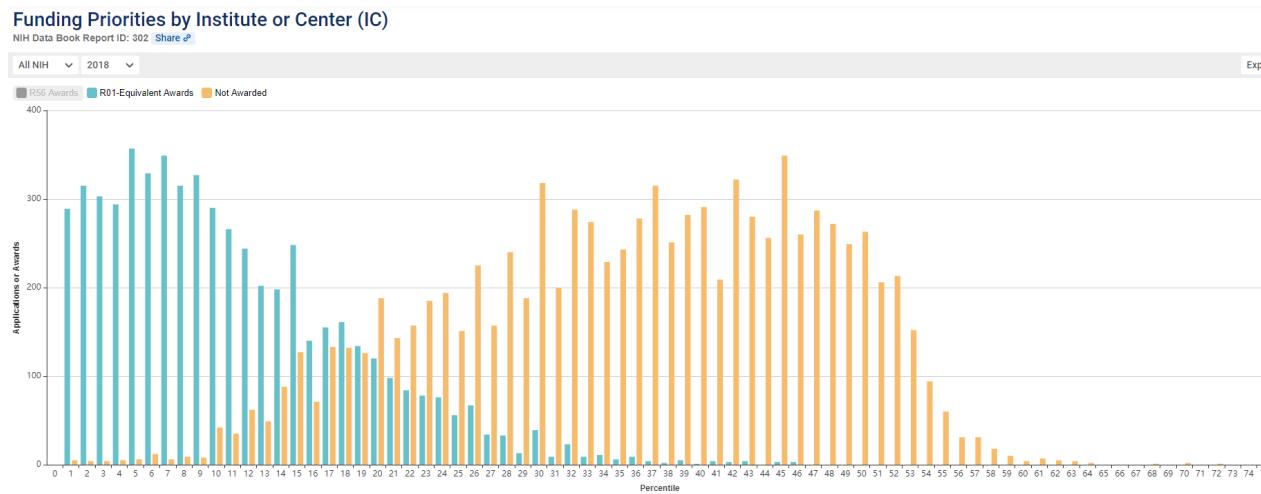
Funding decisions rely heavily on peer review scores, but there is more to the story. NIH Institutes and Centers (ICs) weigh those scores together with ensuring their entire research portfolio addresses the wide array of diseases, conditions, or other research areas within its mission. They also account for unmet scientific needs and build on recent unexpected breakthroughs as part of prudent planning. When public health needs emerge, such as for the opioid epidemic or a microbial outbreak, ICs must be nimble enough to respond. Training, work force, and infrastructure needs are also thrown into the mix. Want more? See our [NIH Funding Strategies page](#) and find [individual IC strategic plans on NIH RePORT](#).

Some ICs, though not all, set percentile-based paylines each fiscal year. R01 applications that fall below the payline are likely to be funded, while those above may not. Moreover, not every application scored within the payline, it should be noted, may be selected for funding (see [here for some reasons why](#)). ICs can also use a small portion of their discretionary annual budget to support meritorious applications that did not meet the payline, a process called select pay.

Expanding on what was provided in the NIH Strategic Plan, we present FY 2018 data here on R01-

equivalent applications (which include R37-MERIT), and [R56-Bridge awards](#). These data ([available here](#) in the [NIH Data Book](#)) are restricted to those investigator-initiated R01 applications or awards reviewed by a study section and which received a percentile score.

In FY 2018, NIH issued 5,710 R01-equivalent grant awards, while 9,309 applications were not funded. As shown in Figure 1, these R01-equivalent awards were generally within the 1st–36th percentiles of all applications (light blue bars). Unfunded applications fell in the higher percentiles (yellow bars).



For those at higher percentiles in Figure 1, an IC may have opted to fund these applications for reasons such as supporting early stage investigators, addressing a gap in scientific knowledge, responding to an emerging health threat, or fostering an innovative approach.

[...Continue reading.](#)

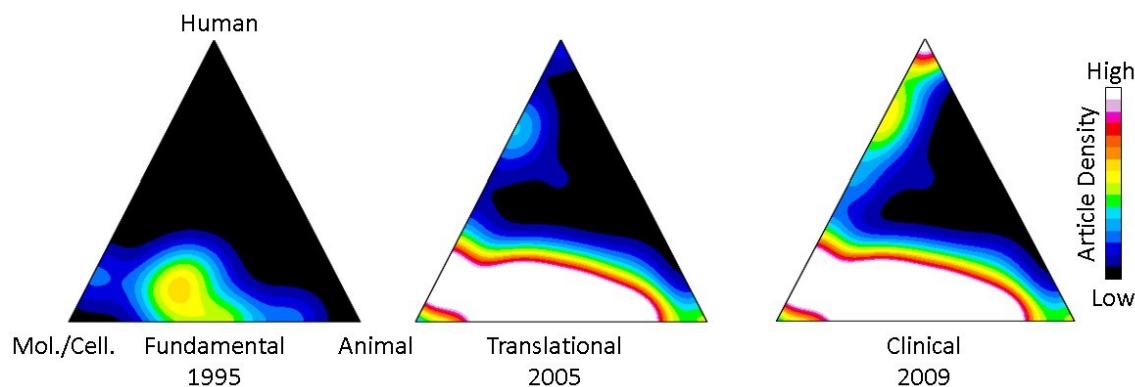
• Predicting Translational Progress from Citations of NIH-Supported Fundamental Research

By looking to the past we may be able to better understand the flow of scientific knowledge going forward, and possibly even predict translational research outcomes. In their [October PLOS Biology paper](#), Drs. Ian Hutchins and George Santangelo from the NIH's Office of Portfolio Analysis devised a machine-learning strategy that taps into the trajectory of science by tracking knowledge flow from bench to bedside.

Their approach stems from a computational process, [first described in 2013](#), that uses each paper's Medical Subject Heading (MeSH) keywords to classify and quantify publications in PubMed according to three domains: human, animal, and/or molecular/cellular. Once classified, groups of papers can be visualized on a “triangle of biomedicine” with three vertices representing these three domains (Figure 1). Fundamental research papers are characterized by a heavy focus

on molecular/cellular biology and animal research and appear toward the bottom of the triangle, while translational work is characterized by a stronger human focus and appear toward the top.

Figure 1 displays a representative example of knowledge flow from fundamental to translational research for immunotherapy papers that led to Nobel prize-winning cancer treatments. The “hotter” colors relate to higher densities of publications. The resulting density map depicts, in the authors’ words, “the translational potential of publications across the entire biomedical research landscape.” The earliest work was fundamental, primarily centered between the molecular cellular/animal vertices of the triangle of biomedicine (left). Ten years later, translational studies were beginning to populate the region just below the human vertex (middle), and research culminated in clinical studies several years later at the top (right).



Citation metrics historically focused primarily on the quantity of citations, which are easy to count. However, we can glean more information – including translational potential — by not only counting citations but also by assessing the nature of citing papers. Fundamental papers with a pattern of being cited by more human-focused articles might be more predictive of being cited by a future clinical article. This may be because those fundamental research papers cited by progressively more human-oriented papers are beginning to find a use among clinical researchers.

To test this hypothesis, the authors used machine learning to gain insight into the trajectory of knowledge flow from cited articles to citing articles. The machine learning algorithm considers papers published within the last 20 years available in the NIH’s Open Citation Collection (see [here for more](#)) and the features of the papers citing them to determine which papers are more likely to be cited by a clinical trial or guideline, which is an early indicator of translation. The machine was trained on a dataset of 100,000 papers with a binary indicator of whether each paper had ever received a citation by a clinical trial or guideline.

[...Continue reading](#)

- ## • Important Reminders for Fellowship and Career Development Applicants

Planning to apply for a fellowship or career development award? If so, don't forget your ORCID iD.

We encourage everybody from graduate students to senior scientists to [register for an ORCID account](#) and [link it to their eRA Commons personal profile](#) (see this [eRA video](#) for a quick step-by-step). But for some grant applicants, it's an absolute *must*. ORCID iDs are *required* for PD/PIs on individual fellowship and career development applications submitted for due dates on or after January 25, 2020. Our eRA systems will check the PD/PI eRA Commons IDs on all submitted fellowship and career development applications. If there isn't a linked ORCID iD, an error will be generated preventing the application from moving forward to NIH for consideration. For more details, see the full [Guide Notice](#) or the [Open Mike blog](#) on this topic.

While in your eRA Commons profile linking your ORCID iD, take the opportunity to make sure all your profile information is current. If you selected "Do not wish to provide" in the demographics section, please consider revising your selection. The information you provide will be kept confidential and used for aggregate statistical reporting only. Reports generated from this demographic data assist us in evaluating the impact of our efforts to improve diversity in the scientific workforce.

- ## • How NIH Can Support Your Career Path

Thinking about a career in research or wondering how to move forward in your journey to becoming an independent researcher? Check out these interactive guides that walk you through how NIH programs can support you at different career steps on the path to becoming a:

- [Physician-Scientist](#),
- [Veterinarian-Scientist](#),
- [Dentist-Scientist](#), or
- [Research-Scientist](#).

Take a scroll and click on the links under each career stage to learn more about the NIH programs available that may be right for you.

- ## • Need Help Determining If Your Research Involves

Human Subjects?

NIH has updated its [human subjects research decision tool](#) to reflect changes effective in the 2018 [Revised Common Rule](#). Answer a few quick questions to find out if your research could be considered human subjects research or if it may be exempt from federal regulations.

- **NIH & You: Join Us at the 2020 NIH Regional Seminars in Baltimore & Nashville**

If the year 2020 has you looking for an opportunity to learn more about working with NIH extramural research, then consider the NIH Regional Seminar on Program Funding and Grants Administration. These unique and informative seminars will provide you with the latest policy and process information, as well as guidance and resources directly from NIH & HHS experts. Interested? Read on!

Two NIH Regional Seminars will be held this year:

April 20-22: Baltimore, MD ([Registration Open](#))

Oct 28-30: Nashville, TN ([Registration Opens Late January](#))

- **75 NIH presenters:** Review, program, grants management and policy officials ready to meet you at the seminar.
- **HHS experts:** Hear from and talk to experts from the Office of Human Research Protections (OHRP), Office of Inspector General (OIG) & Office of Research Integrity (ORI).
- **1:1 Meet the Experts:** Many of our experts will be available for 20-minute conversations throughout the seminar to help provide more personal guidance.
- **3 Tracks and over 45 different topics:** With tracks for Administrators, New Investigators and All Interests and 6-7 sessions available for each timeslot, you'll find multiple topics of interest. (Check out the sample [2-Day Seminar Agenda](#).)
- **Optional Pre-Seminar Workshops:** Looking for more in-depth learning opportunities on specific subjects? Consider these workshops on topics like electronic Research Administration (eRA), Intellectual Property, OHRP & NIH Human Subjects Review, and Administrator's Boot Camp. ([Overview of Optional Workshops](#).)

Information on the Baltimore seminar, optional workshops, discounted hotel room block can be found on [the Baltimore 2020 seminar site](#). Details for Nashville will be available by the end of this month on [the NIH Regional Seminars page](#). **We hope to see you in 2020!**

NIH LBRN Acknowledgement

So that we can most effectively communicate the scope and results of our funding support, we would like to know when you are planning news announcements about IDeA awards or program activities and achievements...

When you produce such material, please be sure to identify the IDeA program, not just the INBRE, COBRE or sub-program, and to provide context about the program's goals along the lines of:

The University of _____ has received \$XXX from the National Institutes of Health (NIH) to support an Institutional Development Award (IDeA) Center of Biomedical Research Excellence. The IDeA program builds research capacities in states that historically have had low levels of NIH funding by supporting basic, clinical and translational research; faculty development; and infrastructure improvements.

In journal articles, news releases, or other materials about your program's activities or achievements, please use funding acknowledgement language such as:

Research reported in this {publication, release} was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number 5 P20 GM103424-18 and 3 P20 GM103424-15S1.

- In journal articles, oral or poster presentations, news releases, news and feature articles, interviews with reporters and other communications, acknowledge the IDeA program's full or partial support of the research. The citation in scientific publications should use the following format:

Research reported in this publication was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM12345.

- If you wish to acknowledge NIH/NIGMS funding on your Web site or other communication product, you may use wording such as:

Funded by an Institutional Development Award (IDeA) from the National Institutes of Health.
or

Funded by the LBRN (P20 GM103424-18) an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health.

Please do not use the NIH or NIGMS logo to acknowledge funding, as these logos are only to be used for material produced by NIH and its components.



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