News, Opportunities and Deadlines for December 2020

Happy Holidays!

SAVE the DATE !

19th LBRN Virtual Annual Meeting

LBRN is pleased to invite you to

the 19th LBRN Virtual Annual Meeting

February 12-13, 2021

Watch the LBRN Website & Social Media for Event information and registration.

We look forward to connecting with you for the 19th Annual Meeting!

Graduate Course on Bioinformatics for Infectious Diseases

Offered by the Department of Pathobiological Sciences (PBS), LSU School of Veterinary Medicine (SVM), Spring, 2021 session graduate course.

Details: PBS 7003 Special Topics, Section 2, Bioinformatics for Infectious Diseases (Kousoulas) - 3 credits (LSU Students), LBRN and other students will receive a certificate of completion from LBRN.

Online Materials: This course has been prepared and taught as a collaboration between the Louisiana Biomedical Research Network (LBRN), The SVM Division of Biotechnology & Molecular Medicine (BioMMED) and Pine Biotech.

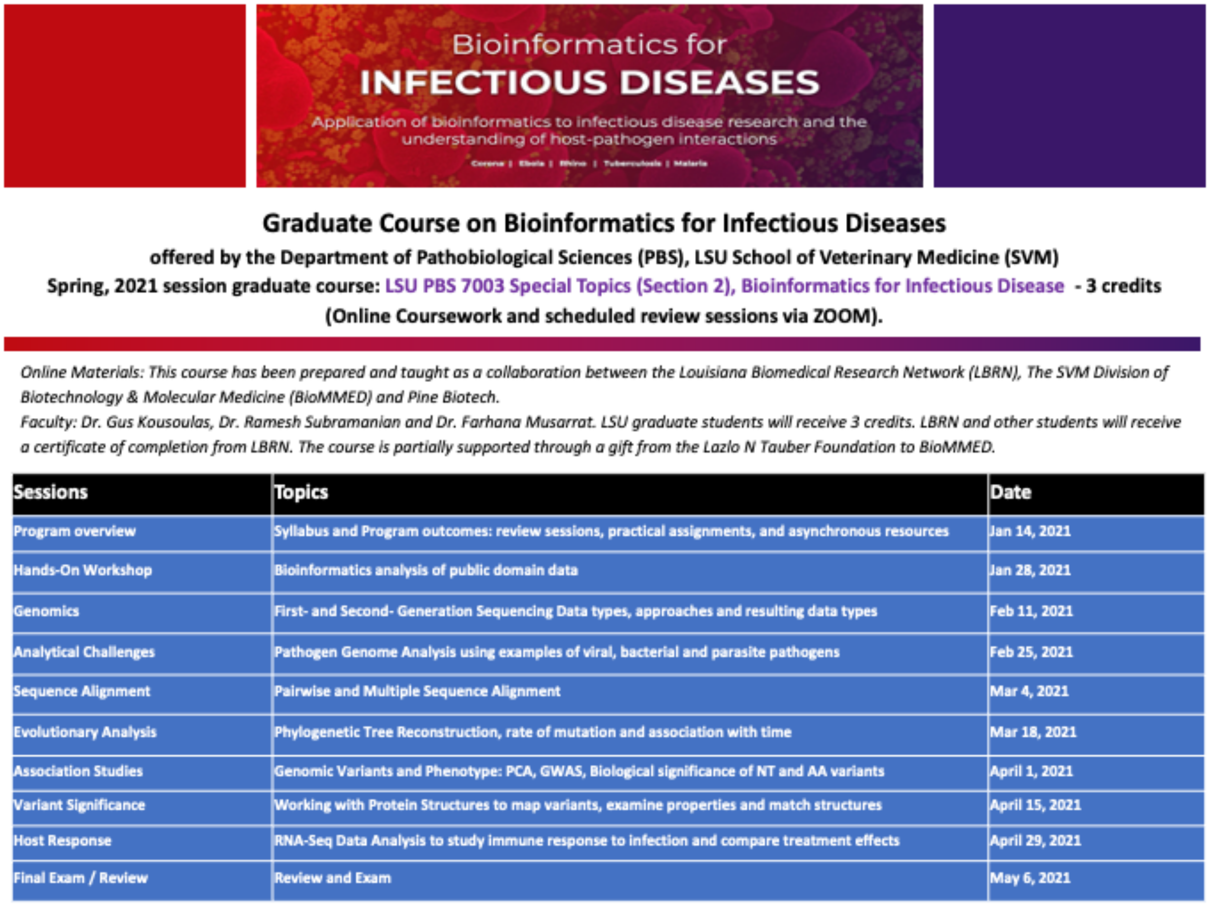
Faculty: Dr. Gus Kousoulas, Dr. Ramesh Subramanian and Dr. Farhana Musarrat.

The course is partially supported through a gift from the Lazlo N Tauber Foundation to BioMMED.

Registration Deadline: **January 4, 2021**.

Bioinformatics for Infectious Diseases Registration: Bioinformatics Registration

Flier and all the details of "Bioinformatics for Infectious Diseases" Information: Bioinformatics for Infectious Diseases



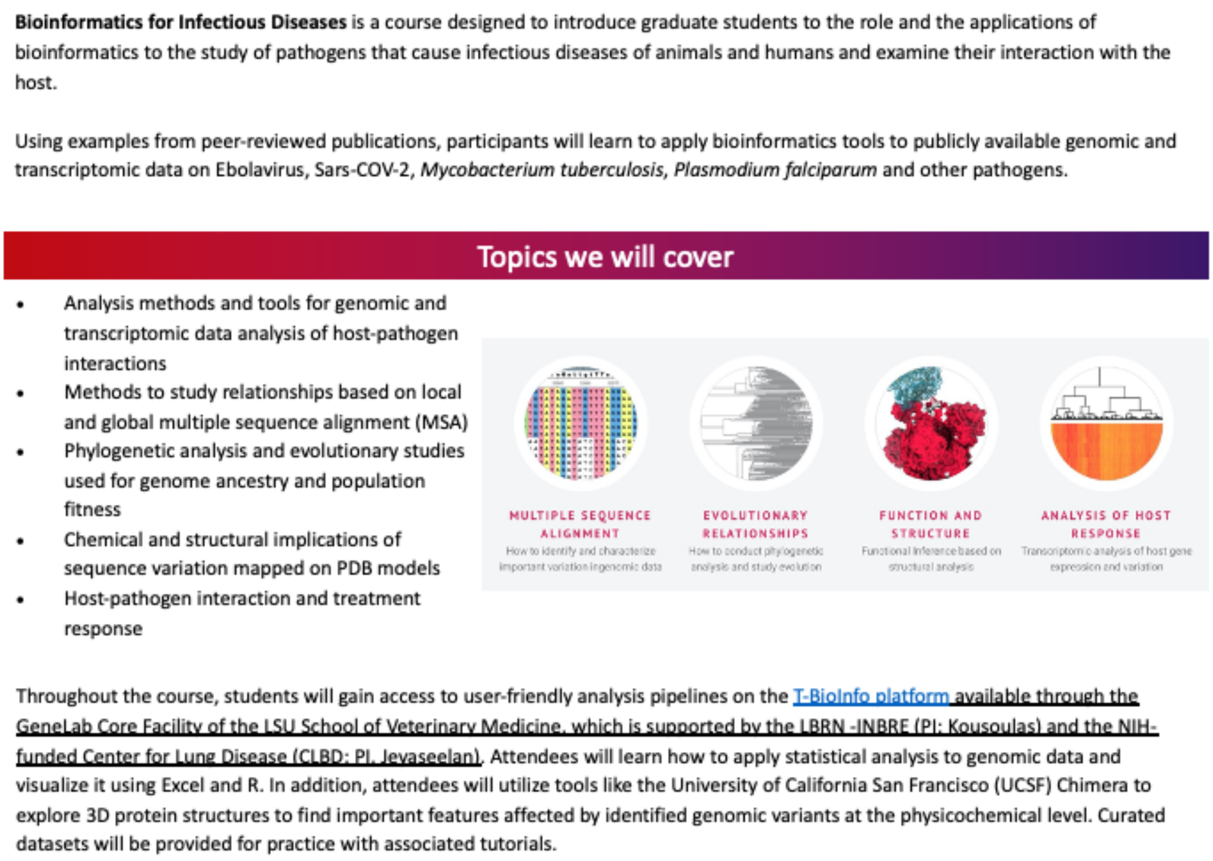
Bioinformatics for
INFECTIOUS DISEASES
Application of bioinformatics to infectious disease research and the understanding of host-pathogen interactions
Corona | Ebola | Rhino | Tuberculosis | Malaria

Graduate Course on Bioinformatics for Infectious Diseases

offered by the Department of Pathobiological Sciences (PBS), LSU School of Veterinary Medicine (SVM)
Spring, 2021 session graduate course: LSU PBS 7003 Special Topics (Section 2), Bioinformatics for Infectious Disease - 3 credits
(Online Coursework and scheduled review sessions via ZOOM).

Online Materials: This course has been prepared and taught as a collaboration between the Louisiana Biomedical Research Network (LBRN), The SVM Division of Biotechnology & Molecular Medicine (BioMMED) and Pine Biotech.
Faculty: Dr. Gus Kousoulas, Dr. Ramesh Subramanian and Dr. Farhana Musarrat. LSU graduate students will receive 3 credits. LBRN and other students will receive a certificate of completion from LBRN. The course is partially supported through a gift from the Lazlo N Tauber Foundation to BioMMED.

Sessions	Topics	Date
Program overview	Syllabus and Program outcomes: review sessions, practical assignments, and asynchronous resources	Jan 14, 2021
Hands-On Workshop	Bioinformatics analysis of public domain data	Jan 28, 2021
Genomics	First- and Second- Generation Sequencing Data types, approaches and resulting data types	Feb 11, 2021
Analytical Challenges	Pathogen Genome Analysis using examples of viral, bacterial and parasite pathogens	Feb 25, 2021
Sequence Alignment	Pairwise and Multiple Sequence Alignment	Mar 4, 2021
Evolutionary Analysis	Phylogenetic Tree Reconstruction, rate of mutation and association with time	Mar 18, 2021
Association Studies	Genomic Variants and Phenotype: PCA, GWAS, Biological significance of NT and AA variants	April 1, 2021
Variant Significance	Working with Protein Structures to map variants, examine properties and match structures	April 15, 2021
Host Response	RNA-Seq Data Analysis to study immune response to infection and compare treatment effects	April 29, 2021
Final Exam / Review	Review and Exam	May 6, 2021



Bioinformatics for Infectious Diseases is a course designed to introduce graduate students to the role and the applications of bioinformatics to the study of pathogens that cause infectious diseases of animals and humans and examine their interaction with the host.

Using examples from peer-reviewed publications, participants will learn to apply bioinformatics tools to publicly available genomic and transcriptomic data on Ebolavirus, Sars-COV-2, *Mycobacterium tuberculosis*, *Plasmodium falciparum* and other pathogens.

Topics we will cover

- Analysis methods and tools for genomic and transcriptomic data analysis of host-pathogen interactions
- Methods to study relationships based on local and global multiple sequence alignment (MSA)
- Phylogenetic analysis and evolutionary studies used for genome ancestry and population fitness
- Chemical and structural implications of sequence variation mapped on PDB models
- Host-pathogen interaction and treatment response

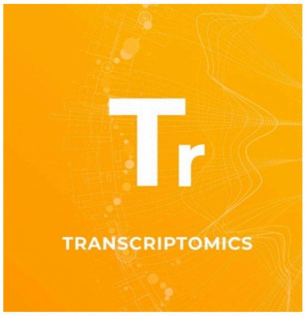
Throughout the course, students will gain access to user-friendly analysis pipelines on the T-BioInfo platform available through the GeneLab Core Facility of the LSU School of Veterinary Medicine, which is supported by the LBRN -INBRE (PI: Kousoulas) and the NIH-funded Center for Lung Disease (CLBD: PI. Jeyaseelan). Attendees will learn how to apply statistical analysis to genomic data and visualize it using Excel and R. In addition, attendees will utilize tools like the University of California San Francisco (UCSF) Chimera to explore 3D protein structures to find important features affected by identified genomic variants at the physicochemical level. Curated datasets will be provided for practice with associated tutorials.

LBRN Omics LOGIC Bioinformatics Training

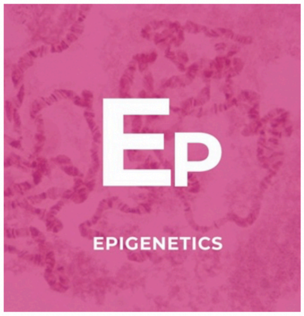
Omics LOGIC Bioinformatics Training has been developed by Pine Biotech to give students access to basic introductory to advanced analytical bioinformatics courses. The training is available through an online platform. The training is modeled after undergraduate and graduate course topics at LSU, Georgetown University Medical Center and other universities and was designed by faculty and researchers at the Tauber Bioinformatics Research Center.

Participation of a limited number of approved LBRN students is underwritten by LBRN and the Laszio N. Tauber Foundation in support of bioinformatics for the Division of Biotechnology & Molecular Medicine, School of Veterinary Medicine, Louisiana State University.

GENOMICS
DNA analysis using Exome and Genome Seq



TRANSCRIPTOMICS
Gene expression analysis RNA-seq (mRNA, miRNA)



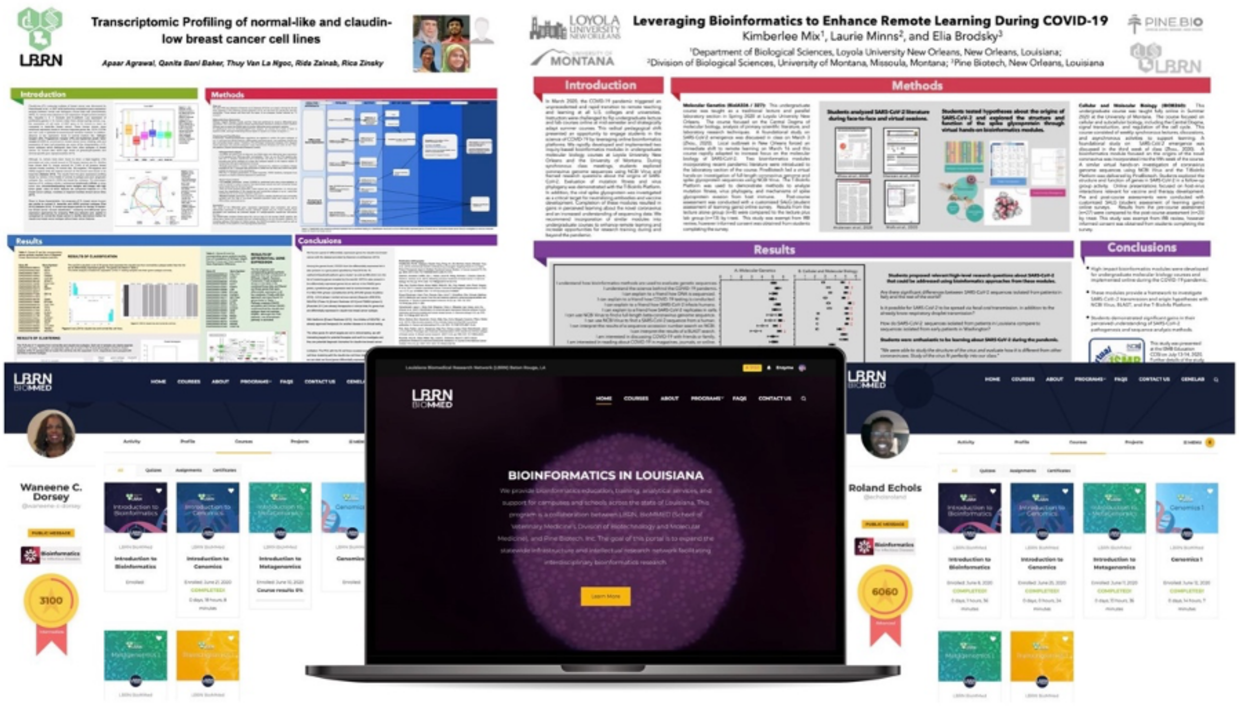
EPIGENOMICS
Non-genomic regulation using ChiP-Seq and WGBS

METAGENOMICS
16s rRNA processing and analysis

This online training is your opportunity to master BIOINFORMATICS as a supplement to other coursework and receive a certificate of Completion. Bioinformatics is a discipline that combines *Mathematics, Computer Science and Biology*.

By applying for this program, you will gain access to OMICS LOGIC resources on a monthly subscription which provides access to 12 online courses that cover various domains of Big Data Bioinformatics. The same license also enables participants to access the AI guided and user-friendly T-BioInfo platform for hands-on analytical experience and practice.

Many of the courses are introductory and are suited for undergraduate students that are interested to learn about the impact of Big Data and High-throughput Experiments across Life Science Domains, including Biomedical Research, Biotechnology and Agro-biological Studies. The coursework will be effective for students pursuing undergraduate life sciences degrees and pre-medical students.



The world of big data is constantly changing as technologies to generate new data open new perspectives for molecular precision and detail in life sciences. This exponential growth in knowledge is accompanied with the need for scientist from all backgrounds to find ways to integrate these concepts to their own research studies and allow them to identify new, meaningful information with either new or old data. This training and associated research resources help students and scientist of all backgrounds to leverage big OMICS data in an efficient way. Many students have applied the learned skills to develop independent research projects after completing this training.

Learn more and register on this link: https://edu.tbioinfo.com/lbrn-2020-1

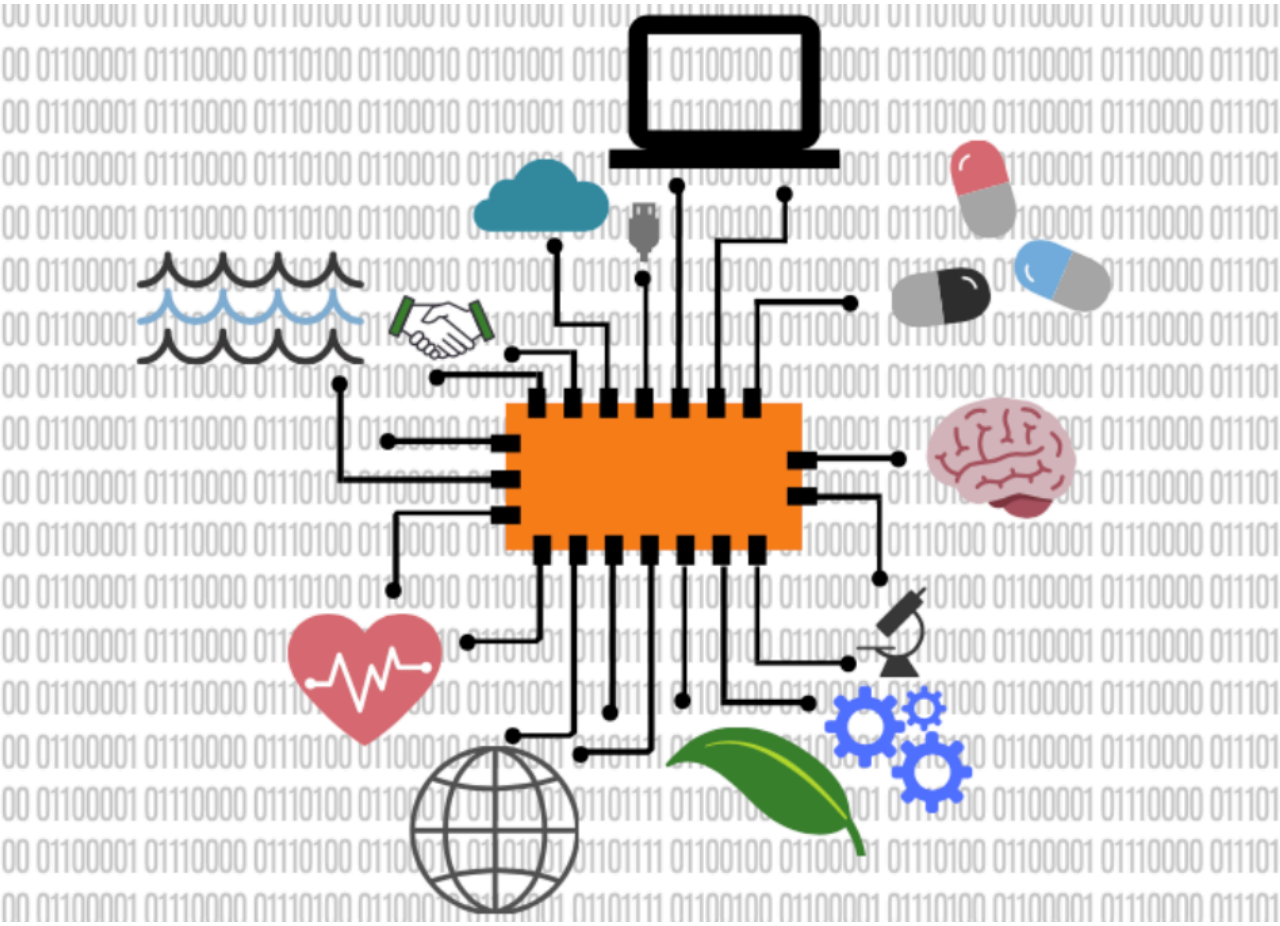
Flier for all the details. OmicsLOGIC Bioinformatics Training: **Omics LOGIC Bioinformatics Training**

LBRN Bioinformatics Needs Survey

This survey is conducted by the **Division of Biotechnology & Molecular Medicine (BioMMED**) of the **LSU School of Veterinary Medicine (SVM**). The Division operates the core facility **GeneLab** that currently conducts illumina-based Next Gen

Sequencing, Single-Cell Gene Expression (10X Genomics) and the **Protein Laboratory** that provides protein production, and purification, and antibody production and characterization. These Core Laboratories are supported by SVM, the Louisiana Biomedical Research Network (LBRN) and the Center for Lung Biology and Disease (CLBD). Current Bioinformatics support is provided through arrangements with **Pine Biotech Inc** through GeneLab. The Pine Biotech proprietary pipelines are available through GeneLab as fee-for-service for a specified time interval. The Illumina BaseSpace Sequence Hub is expected to be available in February, 2021 for all GeneLab clients.

LBRN Bioinformatics Needs Survey: Take Survey Here



Please fill out and also disseminate to appropriate researchers who are requiring bioinformatics services

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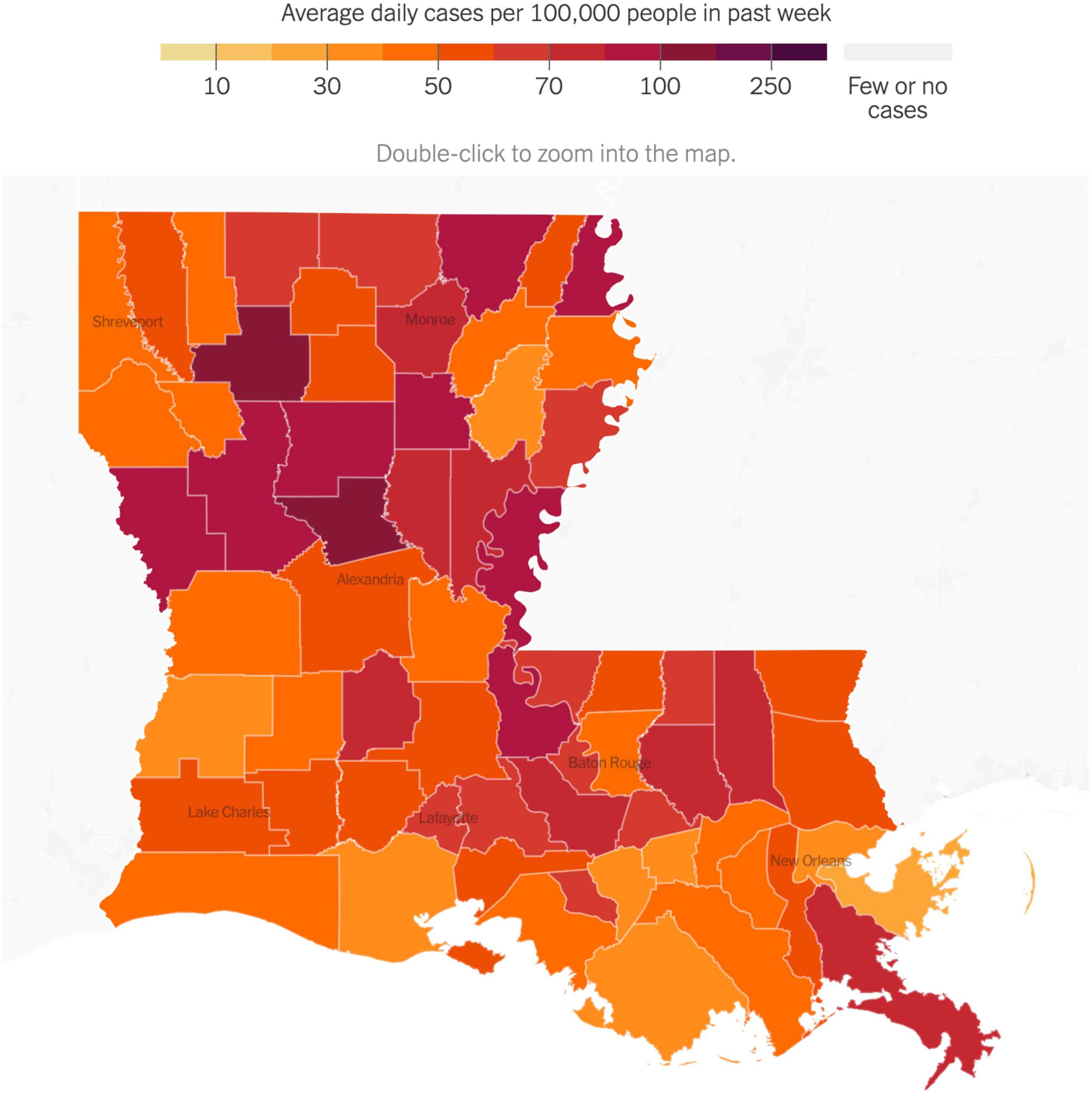
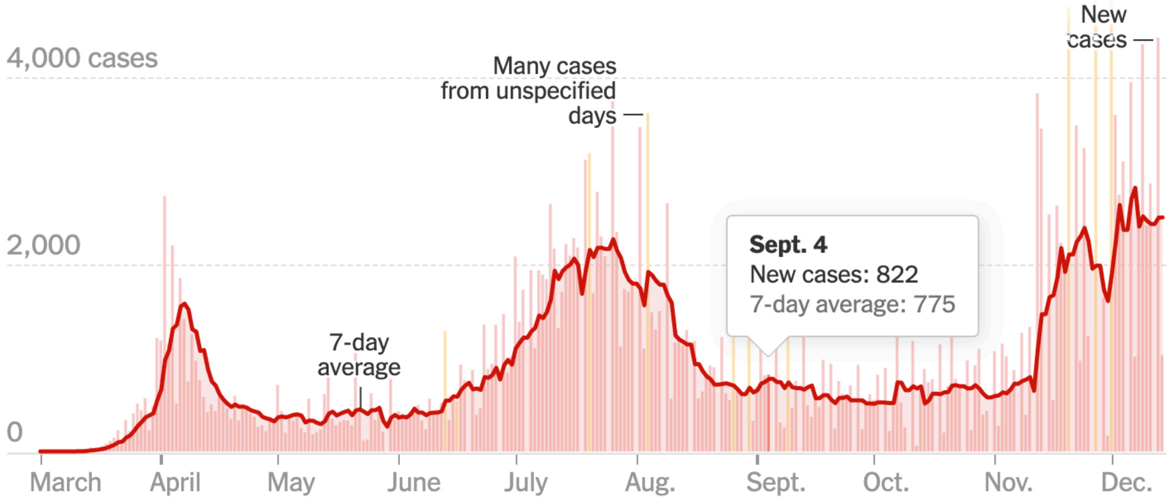
Louisiana Coronavirus (COVID-19) Information

The following information was provided by The New York Times Interactive Coronavirus website.

Average daily cases per 100,000 in Louisiana



Daily reported new cases



	TOTAL REPORTED	ON DEC. 14	14-DAY CHANGE
Cases	269,643	1,030	+56%
Deaths	6,845	27	+75%
Hospitalized		1,527	+39%

🟨 Day with reporting anomaly. Hospitalization data from the Covid Tracking Project; 14-day change trends use 7-day averages.

We want to remind everyone to continue practicing safety with regards to prevention of spreading and contracting the COVID-19 virus.

We remind everyone of the information provided here on our website: LBRN COVID-19.

The National Research Mentoring Network

NRMN
Mentoring to Diversify the Biomedical Workforce

Diversity Funding Opportunities

NIH- National Human Genome Research Institute:

NHGRI Training Mission: Prepare a diverse and talented genomics workforce that is operating at the forefront of genomics in order to accelerate scientific and medical breakthroughs to improve human health.

The National Human Genome Research Institute (NHGRI) provides both institutional and individual funding to help scientists develop their skills as researchers and professionals. Our programs offer opportunities at the undergraduate, postbaccalaureate, graduate, postdoctoral and faculty levels.

Mentoring Month Webinars - Thursdays from 11 - 1pm CST

- January 14 – The role of mentoring in promoting DEI in STEM education and research
- January 21 – How to be an effective mentor for Underrepresented STEM trainees
- January 28 – Candid Conversations: Awfulizing & Musturbation during Mentoring
- Register in advance here.
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Funding for Research Training

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ASH Minority Recruitment Initiative:
The ASH Minority Recruitment Initiative (MRI) was created in 2003 to increase the participation of underrepresented minorities training in hematology-related fields and to increase the number of minority hematologists with academic and research

appointments.

Additional Opportunities housed on NRMN found **HERE**.

NIH Extramural Nexus (NIH/OD)

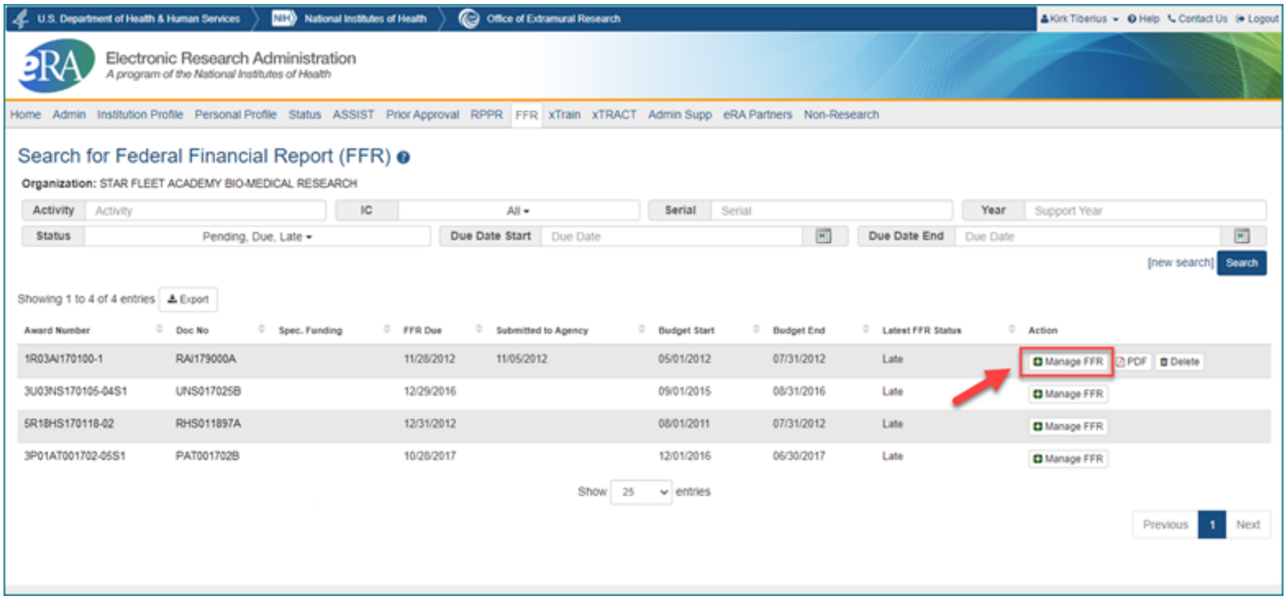
NIH National Institutes of Health
Office of Extramural Research

- ### Federal Financial Report (FFR) Required to be Submitted in the Payment Management System, Effective January 1, 2021

Recipients will be required to submit the SF-425 Federal Financial Report, a statement of expenditures associated with their award, to the Payment Management System (PMS) instead of eRA Commons, effective January 1, 2021 (see NIH Guide Notice NOT-OD-20-127).

The change in submission requirement is part of an HHS initiative to consolidate FFR reporting from all the HHS Operating Divisions into PMS.

To make it seamless for recipients, clicking on the new Manage FFR button next to a particular grant on the *Search for Federal Financial Report (FFR)* screen in eRA Commons will take the recipient directly to PMS, where the recipient will log in and be taken straight to the *Federal Financial Report — Details* screen for that grant in PMS. While the interface will appear new to the recipients, the questions remain the same. Once the form is completed in PMS, the recipient will submit it to the agency. Recipients will still be able to see the status of their submission in the eRA Commons/FFR module.



Search for Federal Financial Report (FFR)

Organization: STAR FLEET ACADEMY BIO-MEDICAL RESEARCH

Activity Activity
IC All
Serial Serial
Year Support Year
Status Pending, Due, Late
Due Date Start Due Date
Due Date End Due Date

Showing 1 to 4 of 4 entries

Award Number	Doc No	Spec. Funding	FFR Due	Submitted to Agency	Budget Start	Budget End	Latest FFR Status	Action
1R03AI170100-1	RAI179000A		11/28/2012	11/05/2012	05/01/2012	07/31/2012	Late	Manage FFR PDF Delete
3U03NS170105-04S1	UNS017025B		12/29/2016		09/01/2015	08/31/2016	Late	Manage FFR
5R18HS170118-02	RHS011897A		12/31/2012		08/01/2011	07/31/2012	Late	Manage FFR
3P01AT001702-05S1	PAT001702B		10/28/2017		12/01/2016	06/30/2017	Late	Manage FFR

Show 25 entries

Note that recipients should register with PMS and obtain log in credentials prior to submitting an FFR. Recipient organizations should be familiar with PMS as they use the tool to draw down grant funds. Also note that recipients who have FFRs in the eRA Commons/FFR module that are a work-in-progress as of Jan. 1, 2021, will need to start over in PMS.

The change to FFR submission requirements does not affect the timeline. Therefore, FFR due dates, as outlined in the NIH Grants Policy Statement, 8.4.1.5.2 and 8.6.1, remain unchanged. FFRs that are submitted *prior to* January 1, 2021 will use the FFR module in eRA Commons.

A second guide notice will be issued soon. Training sessions offered by PMS for recipients will be posted at this link as they become available: https://pms.psc.gov/training/gr-ffr-training.html

eRA Will Require the Use of Login.gov to Access eRA Commons, ASSIST, IAR and Commons Mobile in 2021

Users will be required to use two-factor authentication (2FA) through login.gov to access eRA Commons, ASSIST, Internet Assisted Review (IAR), and Commons Mobile by September 15, 2021. This secure 2FA allows users to log in to four different grants systems (eRA, Grants.gov, GrantSolutions.gov and Payment

Management System) using the same login.gov credentials.

We first shared information about eRA initiating the use of 2FA as part of HHS' Reinvent Grants Management Initiative in April 2020.

eRA is first phasing in the requirement for reviewers using IAR. The new requirement started being phased in December 14, 2020, for reviewers, meeting by meeting, effective for review meetings February 1, 2021 and beyond. As reviewers are enabled for meetings, their accounts will be transitioned to require login.gov to access IAR.

All users of eRA Commons, ASSIST, IAR and Commons Mobile are encouraged to switch to 2FA through login.gov now, before the mandatory deadline of September 2021.

For more information on making 2FA a requirement, please see Guide Notice NOT-OD-21-040.

Resources

- Web page: Two-Factor Authentication: Accessing eRA Modules via login.gov
- Two-factor authentication video tutorials:
  - Two-Factor Authentication: Accessing eRA Modules via login.gov
  - What to Do If You Already Have a login.gov Account
  - What to Do If You Want to Switch to a Different login.gov Account
- One-page flyer
- Two-Factor Authentication FAQs
- eRA Commons Online Help
- ASSIST Online Help

Help

- If users run into issues with login.gov or associating your login.gov account with their eRA account, they contact the eRA Service Desk at https://grants.nih.gov/support/index.html .
- Users can also refer to login.gov for additional help at https://www.login.gov/help/

New OLAW Webinar: Developments in FOIA in the Context of Animal Research

The NIH Office of Laboratory Animal Welfare released a new 30-minute webinar **discussing how Freedom of Information Act (FOIA) requests related to animal welfare compliance are handled. You can listen to an engaging discussion between** OLAW Deputy Director, Dr. Axel Wolff, and NIH FOIA Program Officer, Mr. Gorka Garcia-Malene on:

- Reviewing and fulfilling FOIA requests at NIH
- Applying FOIA Exemptions
- Recent trends in FOIA requests related to animal activities and the implications for your institution
- Meeting OLAW reporting requirements without submitting additional, unnecessary information

"All About Grants" Podcast – Alternatives to Animals

Your experimental designs are coming into focus. Sample sizes…power analyses…and treatment conditions, oh my! And, all throughout, perhaps laboratory animals are needed. But, are they? Can you actually replace them and still rigorously test the hypothesis? If not, maybe the protocol can be refined in such a way to reduce their overall numbers, while still ensuring their humane care and use?

Considering alternatives to animals in your application is the topic of our next NIH All About Grants podcast. Drs. Neera Gopee with the NIH Office of Laboratory Animal Welfare and Christine Livingston with the National Center for Advancing Translational Sciences join us for this conversation (MP3 / Transcript). We will go into the 3Rs (replace, refine, and reduce), helpful resources for relevant policies, what's needed for the vertebrate animal section, role for IACUCs and peer review, as well as organoids, *in silico* models, and other alternatives…oh my again!

On a related note, keep an eye out for recommendations coming from the Advisory Committee to the NIH Director working group on Enhancing Rigor, Transparency, and Translatability in Animal Research this December. Part of their charge is validating alternative models to animal research as well as considering benefits and burdens of registering animal studies. Their recommendations will also encompass public feedback in response to a Request for Information (NOT-OD-20-130) released this summer (see this NIH Open Mike blog post for more).

NIH Releases New Policy for Data Management and Sharing

Guest post by Carrie Wolinetz, Ph.D., NIH Associate Director for Science Policy, originally released on the Under the Poliscope blog

Today, nearly twenty years after the publication of the Final NIH Statement on Sharing Research Data in 2003, we have released a Final NIH Policy for Data Management and Sharing. This represents the agency's continued commitment to share and make broadly available the results of publicly funded biomedical research. We hope it will be a critical step in moving towards a culture change, in which data management and sharing is seen as integral to the conduct of research. Responsible data management and sharing is good for science; it maximizes availability of data to the best and brightest minds, underlies reproducibility, honors the participation of human participants by ensuring their data is both protected and fully utilized, and provides an element of transparency to ensure public trust and accountability.

This policy has been years in the making and has benefited enormously from feedback and input from stakeholders throughout the process. We are grateful to all those who took the time to comment on Request for Information, the Draft policy, or to participate in workshops or Tribal consultations. That thoughtful feedback has helped shape the Final policy, which we believe strikes a balance between reasonable expectations for data sharing and flexibility to allow for a diversity of data types and circumstances. How we incorporated public comments and decision points that led to the Final policy are detailed in the Preamble to the DMS policy.

The Final policy applies to all research funded or conducted by NIH that results in the generation of scientific data. The Final Policy has two main requirements (1) the submission of a Data Management and Sharing Plan (Plan); and (2) compliance with the approved Plan. We are asking for Plans at the time of submission of the application, because we believe planning and budgeting for data management and sharing needs to occur hand in hand with planning the research itself. NIH recognizes that science evolves throughout the research process, which is why we have built in the ability to update DMS Plans, but at the end of the day, we are expecting investigators and institutions to be accountable to the Plans they have laid out for themselves.

I strongly suspect we will hear both from those who think we should have gone farther and required that all data resulting from NIH-funded research be shared, regardless of extenuating factors, and those who think we have gone too far in requiring all applicants to develop a Plan. Which perhaps means we've gotten it just right! For some investigators and disciplines, who have been at the forefront of data sharing, this will be very familiar; for others, this will be new territory. Anticipating that variation in readiness, and in recognition of the cultural change we are trying to seed, there is a two-year implementation period. This time will be spent developing the information, support, and tools that the biomedical enterprise will need to comply with this new policy. NIH has already provided additional supplementary information – on (1) elements of a data management and sharing plan; (2) allowable costs; and (3) selecting a data repository – in concert with the policy release.

As NIH Director Francis Collins notes in his Director's Statement today, the novel coronavirus pandemic has highlighted the importance of making research data broadly accessible. But even as the world struggles with this acute global crisis, it is important to note that we are at an extraordinary time in biomedical science, where new technologies, data science, and understanding of fundamental biology are converging to accelerate the pace of discovery and medical advancement. The Final NIH Policy for Data Management and Sharing builds on those exciting opportunities, and we look forward to working with our stakeholders to fulfill its vision.

The National Association of IDeA Principal Investigators

NAIPI

NATIONAL ASSOCIATION OF
IDEA PRINCIPAL INVESTIGATORS

The National Association of IDeA Principal Investigators (NAIPI) is the collective voice of all of us in the IDeA community.

Dr. Gus K. Kousoulas, the LBRN PI, will serve NAIPI as a president for 3 years.

NAIPI aims to protect and promote the IDeA programs. It fosters interactions, promotes resource sharing, enhances the national visibility of the INBREs, COBREs, and CTRs, develops consensus on priorities, identifies and disseminates best practices, identifies opportunities and develops strategies.

NAIPI's mission is to protect and promote the INBRE, COBRE, and CTR programs within the IDeA states. NAIPI provides leadership and communication across the IDeA community. As a Principal Investigator, Project Coordinator, Project Investigator, or Project Leader on an NIH IDeA award or an award co-funded by IDeA, you are a member of NAIPI.

The NAIPI represents you and the interest of your state in biomedical research education and infrastructure building. Our goals are to become stronger by:

- Sharing best practices
- Connecting researchers to facilities, collaborations, and colleagues
- Collecting and highlighting our IDeA successes
- Developing a consensus on priorities important to the IDeA community
- Identifying opportunities within the IDeA community

In addition to NAIPI members, this site helps the lay public, state and federal legislators, higher education administrators, and business communities learn about health-related research and education in their state, region, and across the nation.

Nationwide Voucher Program

IDeA National Resource for Quantitative Proteomics

Purpose: The IDeA National Resource for Quantitative Proteomics provides subsidized access to sophisticated proteomics services for investigators performing biomedical research within the mission of NIGMS (http://idearesourceproteomics.org/). In addition to providing cost effective access to a variety of proteomics services, the resource supports a competitive voucher program that provides fully subsidized access at no cost to the user. The goal of the voucher program is to provide pilot scale data to investigators that will create new hypotheses, support publications, and support on-going research studies within the mission of NIGMS. This voucher program supports discovery proteomics workflows limited to 10 sample Tandem Mass Tag (TMT) or 20 sample data independent acquisition (DIA) quantitative proteomic platforms. For example, a 10-plex TMT could be 5 biological replicates of a control verses 5 biological replicates of a treated cell line, while a 20 sample DIA could be 10 control vs 10 experimental tissue/plasma samples. Interested applicants may contact the resource prior to applying to discuss the proposed sample analysis and determine eligibility for the voucher program.

Voucher application due dates: 5:00pm on October 15, February 15, June 15. Earliest start date: November 1, March 1, July 1. Anticipated number of awards: 100

annually

Award budget: Fee-free voucher for 10-plex TMT (>7,000 proteins) or 20 sample DIA Award Period: Samples must be submitted within 4 months from award date

Eligibility: One awarded voucher per laboratory Principal Investigator per year. Priority will be given to researchers funded by NIGMS, funded through the NIGMS-IDeA Program, and early-stage/new investigators working within the mission of NIGMS. Only one submission per laboratory Principal Investigator per due date.

Pre-submission consultation: Interested applicants may contact the resource at IDeAproteomics@uams.edu to discuss the proposed sample analysis and determine voucher eligibility.

Content and form of application submission: Applications are limited to 2 pages (11pt font, single spaced, 0.5 inch margins) and should include the following sections: Project Overview (outlining the specific research question), Preliminary Studies (providing example data to support the proposed proteomics analysis), Quality Control Data (provide evidence of sample quality such as a gel image, verification of 50 micrograms of protein or 25 microliters of plasma/serum, and details on sample homogenization including buffer components), and Data Utilization (discussing how the proteomics data will be used to support work within the scope of NIGMS). An optional pre-submission consultation may be used to determine whether TMT or DIA proteomics would be most appropriate for the study. Applications are to be submitted as a PDF file at https://is.gd/IDeAVoucher.

Other documents for submission: Principal Investigator NIH Biosketch and NIH Other Support documents.

Other requirements: For eligibility, recipients will be required to participate in pre- and post-award surveys.

Contacts: For general questions, contact IDeAproteomics@uams.edu. For administrative questions, contact Ms. Sonet Weed (SWeed@uams.edu)

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. Please contact your LBRN Steering Committee Member.

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 2020/2021.

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.

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 (*2P20GM103424-19) *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.
