

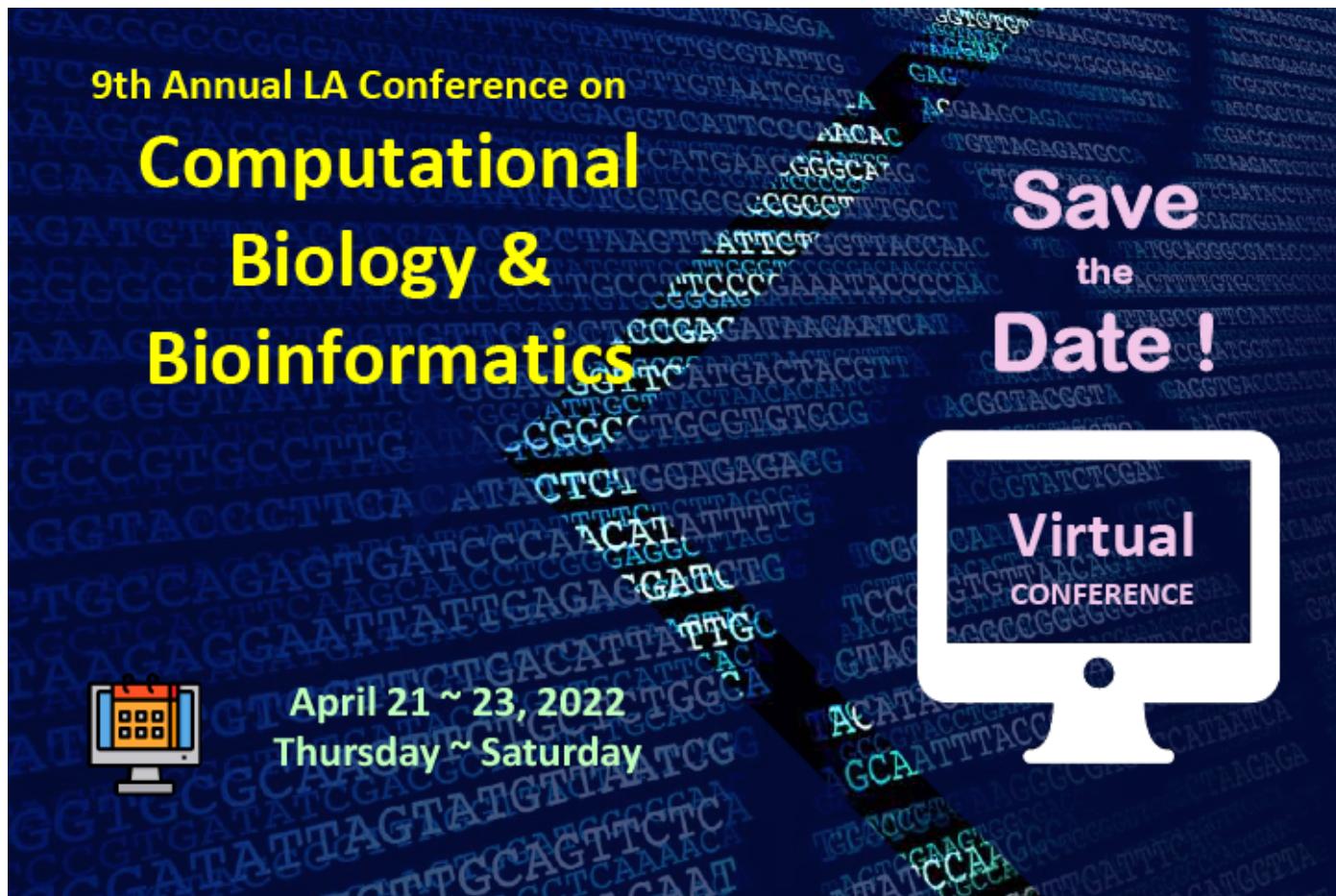
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News, Opportunities and Deadlines for Feb. 2022

Save the Date!

2022 9th Annual LA Conference on Computational Biology & Bioinformatics

We are pleased to invite you on April 21-23, 2022 to the
[9th Annual Louisiana Conference on Computational Biology and Bioinformatics](#)

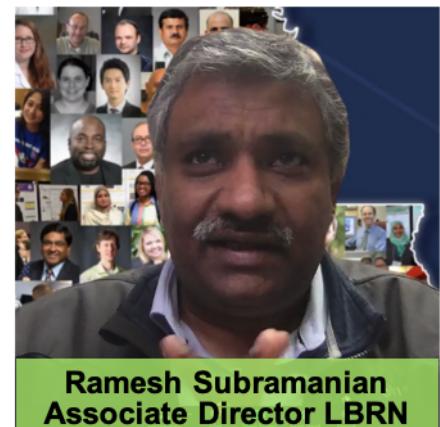
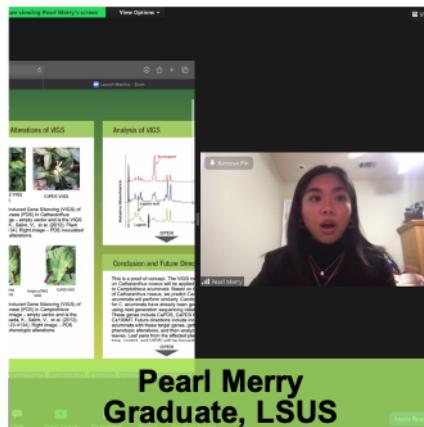
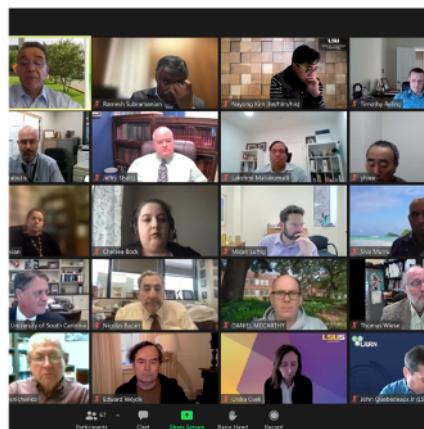


Further details will be announced soon on the LBRN website:
<https://lbrn.lsu.edu/conference-on-biology-and-bioinformatics.html>.

Report : 20th LBRN Annual Virtual Meeting



The [20th LBRN Annual Meeting](#) was held in a completely virtual format on January 28-29, 2022. We had a record number of meeting registrations of 194 and record number of 58 submitted posters from our Project PI's, Graduate, and Undergraduate students from our partner and outreach campuses that are part of the LBRN system throughout the state of Louisiana. Below is a sample of the event and images we screen captured. We hope those who participated benefited and appreciated that we were able to hold this in a virtual format considering the pandemic at this time.





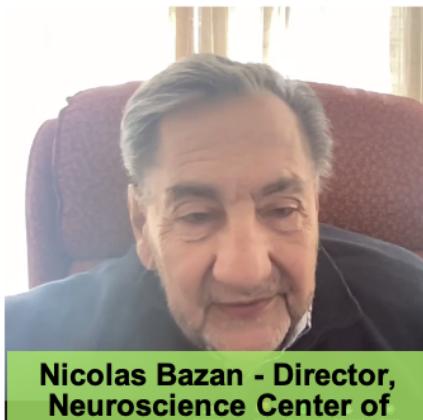
Oliver Garden
Dean, LSU Vet



Tuajuanda Jordan
President, SMCM



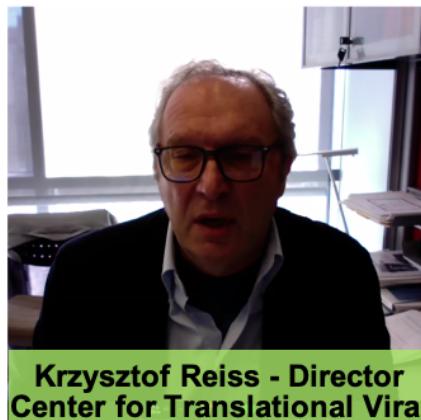
**Matt Lee - Interim Executive
Vice President/Provost**



**Nicolas Bazan - Director,
Neuroscience Center of
Excellence**



**LBRN External Advisory
Committee Meeting**



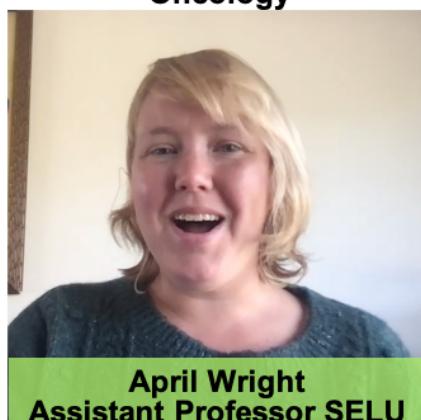
**Krzysztof Reiss - Director
Center for Translational Viral
Oncology**



Alexis White
LBRN Grant Administrator



Urska Cvek
Professor LSUS



April Wright
Assistant Professor SELU

Keynote & Invited Speakers

- **Nicolas Bazan, M.D., Ph.D**

Louisiana State University Health New Orleans

Boyd Professor and Ernest C. and Ivette C. Villere Chair for the Study of Retinal Degenerations at Louisiana State University Health New Orleans

- **Charles Irvin, Ph.D**

University of Vermont Burlington

Professor of Medicine, Pulmonary Medicine Associate Dean for Faculty Affairs, Director, Vermont Lung Center

- **Krzysztof Reiss, Ph.D**

Louisiana State University Health New Orleans Cancer Center

Professor in the Department Interdisciplinary Oncology, Director of the Neurological Cancer Research Program

Oral Presentations

Fifteen academic oral presentations were presented by participants from eight different LBRN campuses, our invited speakers, updates from our LBRN Project PI's and the research done by our summer program graduate students.

Poster Presentations

Participants from 10 different LBRN campuses and high schools exhibited a total of 58 posters through a virtual platform, which was especially possible for presentations, conversations and Q&A through 29 Zoom breakout rooms each into 2 one hour sessions. You can explore and search these posters and contact the authors through the iPosterSession platform we utilized for our meeting: https://lbrn2022am-lsu.ipostersessions.com/Default.aspx?s=lbrn_2022_gallery

LBRN 20th Annual Meeting Poster and Presentation Award Winners

- **Faculty / PI Poster award winners (tied)**

Matthew Hayes – XULA "Complex Germline Structural Variant Discovery Via Discordant Cluster Normalization"

Joseph Chaney – XULA "Applying the Brakes: Understanding the Role of the Conformational Changes in the Kinesin-5 on Processivity and Inhibition"

<https://ibm2022am-lsu.ipostersessions.com/default.aspx?s=92-FA-5B-80-D0-B4-75-12-39-BD-5C-4F-C0-EF-E3-D7&guestview=true>

Complex Germline Structural Variant Discovery Via Discordant Cluster Normalization
 Matthew Hayes, Ph.D.* Derrick Mullins*, Angela Nguyen*
 * Xavier University of Louisiana Department of Physics and Computer Science, ~ Xavier University of Louisiana Department of Biology

Introduction
 disease onset. Simple structural variants (SVs) can be found algorithmically using short reference genome alignments. However, variants with three or more breakpoints are more challenging to detect algorithmically. This study presents a CleanBreak algorithm that can identify complex structural variants (CSVs) with three or more breakpoints compared to SVelter, a state-of-the-art program for SV detection. CleanBreak generally outperformed it in sensitivity and computational running time. Future development will focus on extending the

Methods
 Fig. 4. Discord normalization.
 Deletion normalization
 – Four rules:
 1) (D1) Move left boundary to previous interval boundary
 2) (D2) Move right boundary to previous interval boundary
 OPEN

Discussion
 • Loss of sensitivity in sim data
 – Variants in low-complexity regions
 • Del-dup-inv case
 – CleanBreak only predicts one variant per interval
 • Must extend to account for multiple variants per interval
 OPEN

Conclusion
 • Continue at detecting certain kinds of variants, the following issues will be addressed this year:
 • Extend CleanBreak to detect interchromosomal variants
 • Extend to allow multiple variants per interval to be considered
 • Read depth correction must be

Complex Structural Variants
 Fig. 1 CSVs present with those or more breakpoints and are created from adjacent simple structural variants.

Reference
 A B C D
 Del-dup A C C D
 Del-inv A C D
 OPEN

Results

Algorithm	SV Type	Del-Dup	Del-Inv	Del-Dup-Inv
CleanBreak	Del	0.81 /0.99	0.74 /0.90	0.380/0.38
	Inv	—	—	0.260 / 0.96
	Tand. dup.	0.73 /0.97	—	—
SVelter	Del	0.70/0.99	0.66/0.98	0.480/0.96
	Inv	—	0.48/0.97	0.33/0.95
	Tand. dup.	0.54 /0.98	—	0.30/0.82

Acknowledgements
 This work was partially funded by the National Science Foundation Research Initiation Award, grant number HRD-1901283, and start-up funding from the Louisiana Cancer Research Consortium.

DISCLOSURES **CONTACT AUTHOR** **GET IPOSTER**



<https://ibm2022am-lsu.ipostersessions.com/?s=21-A2-B3-00-09-E0-43-4F-A6-44-69-E5-B5-B5-E8-5B>

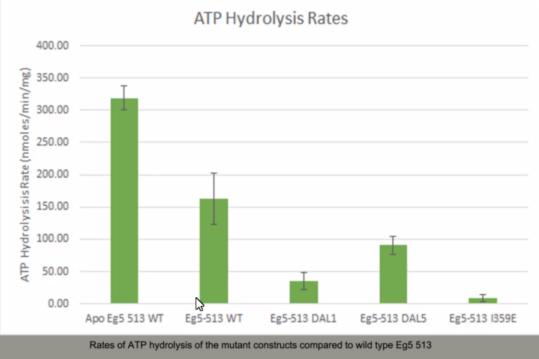
Applying the Bra
 Amaya Sanders1, Tham...

Abstract
 Human Kinesin-5 (Eg5), an antitumor drug target, is of the bipolar spindle during mitosis. Its promise as a drug comes from the fact that they are involved only in metaphase. Some of the leading cancer drugs, however, this kinesin is involved in other processes. For example, if crystal structures of Kinesin-5 reveals the additional central β-sheet is found in one head and absent in the monomerized structural asymmetry between the two regulatory mechanisms involving the terminal Neck.

Background
 Aim 1: Insert DAs into the NL then compare the NL with wild-type NL.
 Aim 2: Mutate the linker region to reduce the activity of the kinesin-5.
 Aim 3: Explore the effect of mutations and insertions to compare the full-length kinesin-5.

Results and Future Direction

ATP Hydrolysis Rates



Construct	ATP Hydrolysis Rate (nmoles/min/mg)
Apo Eg5 513 WT	~320
Eg5-513 WT	~160
Eg5-513 DAL1	~40
Eg5-513 DAL5	~90
Eg5-513 I359E	~10

• Test effects on ATP hydrolysis rates and motility versus wild-type
 • Explore other mutations created using method 2
 • Pursue 3-dimensional structure of Human Kinesin-5 and mutant dimers bound to an inhibitor to give greater detail importance of the neck-linker conformation
 • Comparing the canonical structure of Kinesin-1 to Kinesin-5

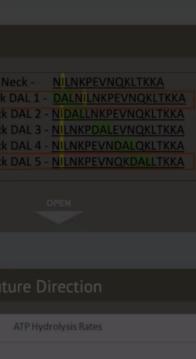
Processivity and Future Direction

Neck - NILNKPEVNQKLTKKA
DAL 1 - DALNLNKPEVNQKLTKKA
DAL 2 - NIDALNLNKPEVNQKLTKKA
DAL 3 - NILNKPALEVNQKLTKKA
DAL 4 - NILNKPEVNDALQKLTKKA
DAL 5 - NILNKPEVNQKDALLTKKA

OPEN

Future Direction

ATP Hydrolysis Rates



Construct	ATP Hydrolysis Rate (nmoles/min/mg)
WT	~320
I359E	~10

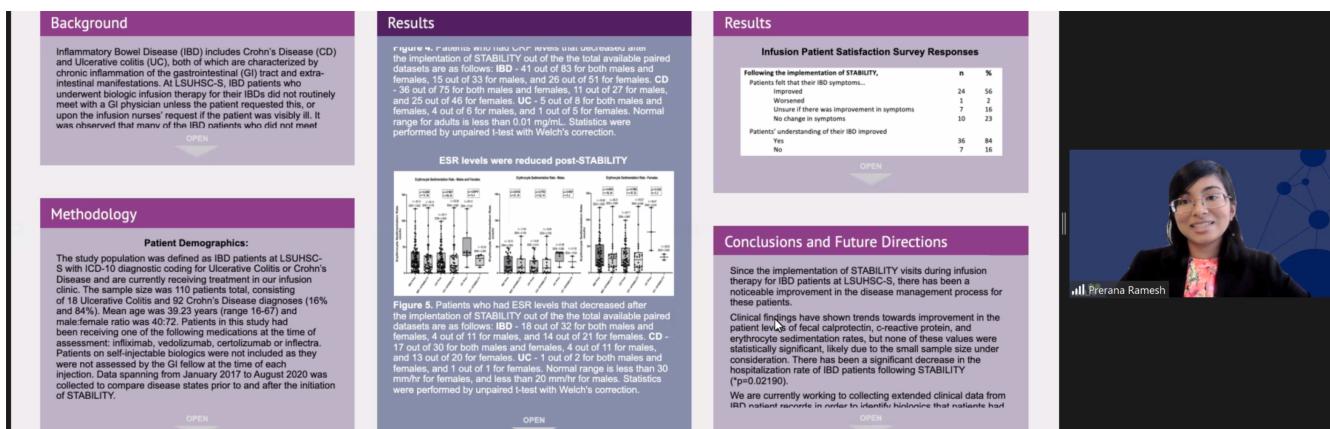
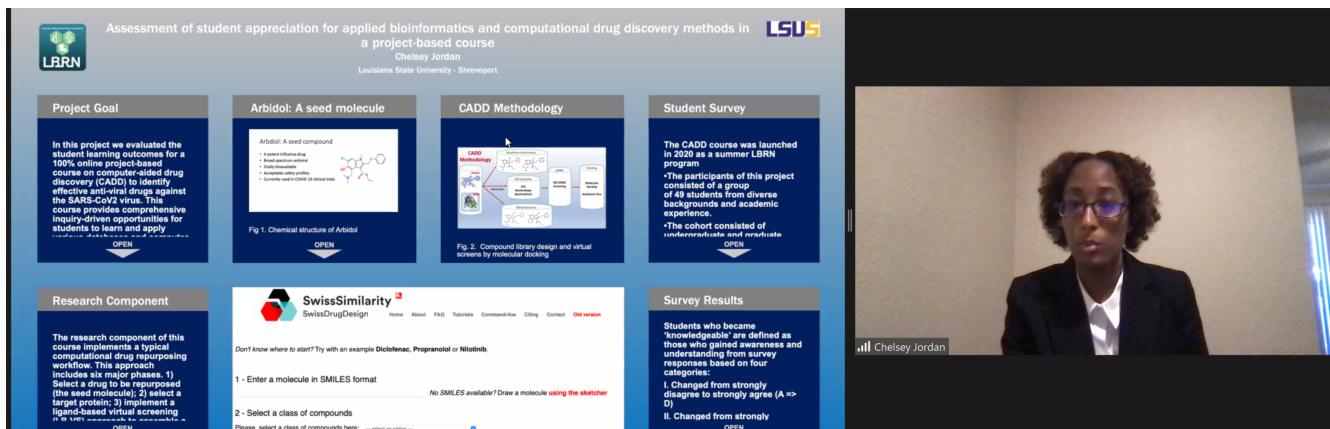
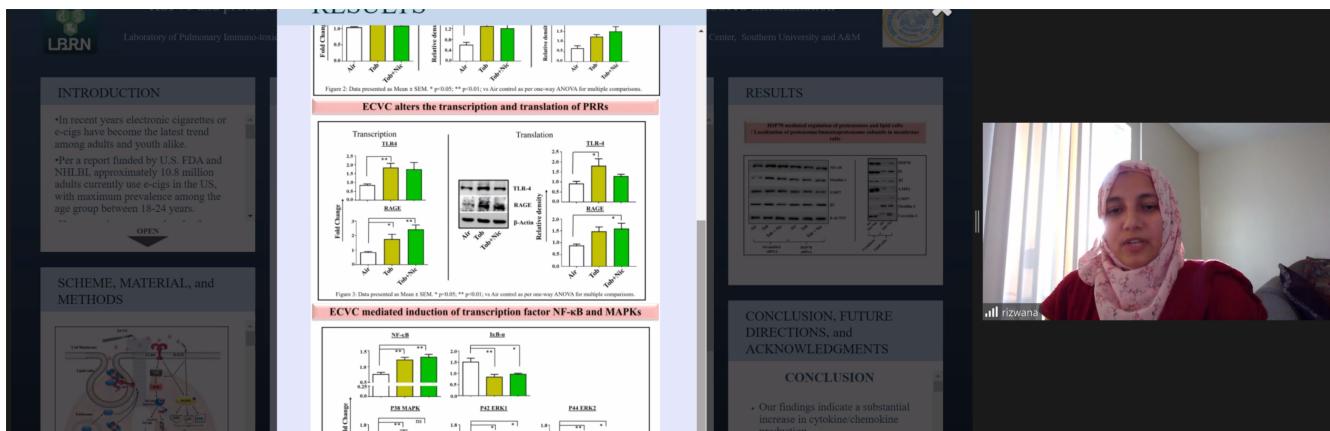


- Graduate Poster award winners (tied for first)

Rizwana Begum – SUBR Tied for 1st Place "HSP70 and proteasomes coalesce in lipid rafts to regulate E-cigarette Vapor condensate induced inflammation"

Chelsey Jordan – LSUS Tied for 1st Place "Assessment of student appreciation for applied bioinformatics and computational drug discovery methods in a project-based course"

Prerana Ramesh – LSUHS 2nd Place "Improving Patient Outcomes for Inflammatory Bowel Disease through Physician Interactions during Infusion Treatment : Symptomatic Review of Biologic Therapy in IBD (STABILITY)"

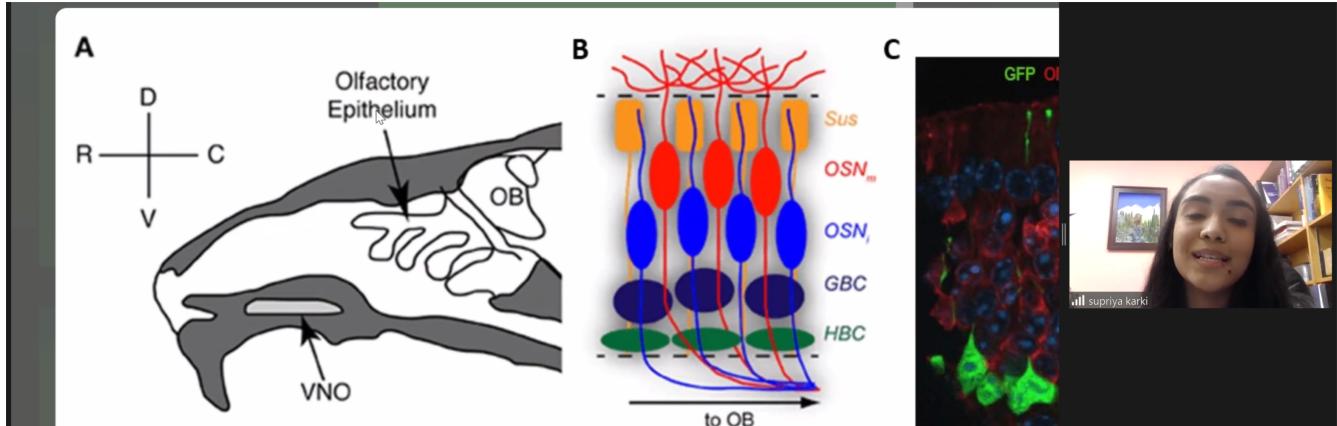


- Undergraduate Poster award winners (tied for second)

Supriya Karki – LSUS 1st Place "Developmental Stages of Olfactory Sensory Neurons in Neonatal Life vs. Adulthood"

Kalani Myles – LSUS Tied for 2nd Place "Computer-aided drug discovery for COVID-19 using virtual screening and molecular docking"

Bryan Strong – ULM Tied for 2nd Place "Translation initiation factors from early-branching eukaryote Giardia lamblia can form multifactor complex in the absence of 40S ribosome in vitro"



Computer-aided drug discovery for COVID-19 using virtual screening and molecular docking

Kalani Myles and Elahe Mahdavian
Louisiana State University - Shreveport

Introduction
The COVID-19 pandemic has negatively affected human health all over the world. This virus, known as SARS-CoV-2, is spreading rapidly and cases are constantly rising every day. People who have contracted the virus have experienced cold-like symptoms or are asymptomatic. Since the pandemic began, over

Novel SARS-CoV-2 Virion
The COVID-19 virus currently has no way of preventing viral entry into the host cell. The virus can enter the host cell and bind to the SPIKE-ACE-2 receptor with no preventative measures. If we create a possible effective drug to treat COVID-19, then the virus would have no way of entering the host cell and would not be able to

Why Drug Repurposing?
• Computer-aided drug discovery (CADD) has expedited drug development for COVID-19.
• Special emphasis has also been placed on repurposing other anti-viral drugs to reduce the time and cost of drug development. CADD-Repurposing
• The existing drug has established safety profile thorough the clinical

Hypothesis
Arbidol and certain analogs will bind to spike-ACE-2 interface, disrupt the CoV-2 –specific viral-host recognition/interactions and thus inhibit a key molecular event needed for viral attachment to the host, a crucial step in the viral infectivity mechanism.

Translation initiation factors from early-branching eukaryote *Giardia lamblia* can form multifactor complex in the absence of 40S ribosome in vitro

Bryan Strong, Zachary Wiggins, Francis Kwarteng, Zachary Shaw, Breanna Gottschalk, Srinivas Garlapati
University of Louisiana at Monroe

Introduction
Initiation complexes are recruited to the initiation codon without a prior scanning mechanism in Giardia lamblia due to the short 5' UTRs (2). However, Giardia cells are known to scan for start sites. This is necessary for the scanning process (2). To determine whether the lack of a scanning mechanism is due to the lack of protein-protein interactions between initiation factors eIF1, eIF2, eIF3, and eIF5, GST pull-down assays were performed. These assays were used to not only determine interactions between these factors but also to detect MPG formation.

Results
same protocol as before; however, this time all initiation factors were expressed together with and without the presence of GlcIF28. Figure 3 shows the results of these assays.

Discussion
From our results, we can see that there are significant interactions between all four initiation factors in the multifactor complex (MFC). Initiation factors GlcIF1, GlcIF3CN, and GlcIF5 interact with each other, while GlcIF28 interacts with GlcIF1 and GlcIF5 outside the complex, but not with GlcIFCN. However, GlcIF28 does not interact with the rest of the complex present. This disproves our hypothesis that the lack of a scanning mechanism in Giardia is due to the lack of protein interactions in the MFC. To examine other possibilities for the lack of scanning mechanism, our lab is currently performing GST pull-down assays to determine if

Conclusion
We have discussed a few of the differences in the translation initiation machinery and process between Giardia lamblia and higher eukaryotes. While we were unable to determine protein-protein interactions in the Giardia multifactor complex, we were able to show that the lack of scanning does not occur in Giardia translation initiation. Furthermore, we believe that the MFC initiation multifactor complex could possibly include purifying the 40S ribosome subunit to determine if the lack of a scanning mechanism is due to the lack of a 40S ribosome.

Methods
Giardia initiation factors eIF1, eIF28, eIF3CN, and eIF5 were expressed and purified in E. coli. They were then purified with Glutathione S-Transferase (GST) tag specific for each protein. A GST protein was also purified to function as our control.

Translation initiation in Mammals


Translation initiation in Giardia lamblia


Acknowledgements
Research reported in this poster 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 P20 GM103424-20.

Bryan Strong

- High School Poster award winners

Raj Letchuman – Caddo Parish Magnet High School 1st Place "Identifying Promising Drug Candidates Against SARS-CoV-2 Using Computational Drug Repurposing Methodology"

Devika Dua – Cedar Creek School 2nd Place "Investigating Key COVID-19 Questions by Using Natural Language Processing on Scientific Publications"

CADR Methodology

Computer-Aided Drug Repurposing Methodology

Find Similar Compounds:
Similar molecules tend to have similar biological activity and binding partners.
Over 14 million compounds were screened across three distinct compound libraries using an electrospray screening method. The top 30 analogs with a similarity threshold >0.85 were chosen for molecular docking.

Identify Drug Characteristics:
Ensure that the drug reaches the site of action at the therapeutic dosage.
ADMET properties of the 30 analogs were analyzed and documented.

Evaluate Compound's Binding Affinities:
How well do the analogs bind to the protein target? How stable is the binding position?

Conclusions

In applying the CADR methodology and structure and ligand-based approaches to drug repurposing, we have identified 30 analogs as having promising antiviral activities towards SARS-CoV-2. Analogs 4, 12, and 18 exhibited IC₅₀ values of 7.2, 7.5, and 7.2 nM, respectively. These analogs also exhibited sufficient drug-like properties to make them viable drug candidates for further experimentation. Analogs 4, 12, and 18 exhibited high binding affinities to the SARS-CoV-2 main protease enzyme of the novel coronavirus.

Abstract **References** **Contact Author** **Get Poster**

Raj Letchuman
Ram Samudrala

Investigating Key COVID-19 Questions by Using Natural Language Processing on Scientific Publications

Devika Dua, Dr. Norman John Mapes
Cedar Creek School, Louisiana Tech University

Introduction

able to perform text-to-text tasks. Transformers can overcome the limitations of other sequence-to-sequence models, such as Convolutional Neural Networks and Recurrent Neural Networks. From the perspective of NLP, this model can extract information through many published journals both quickly and accurately, researchers can benefit from this model. This model also claims to be the most efficacious model on more than twenty well-established NLP tasks. This project employs the T5 model to narrow down the search space.

Dataset and Preprocessing

Currently, I am using journals from JSTOR, PubMed, and Google Scholar to extract COVID-19 related information. I have extracted 180,000 abstracts from the JSTOR dataset under different keys [2]. After reviewing multiple publications, we determined that the data was incomplete and inconsistent. To achieve efficient analysis, we focused on the abstracts of those publications. At first, we removed the abstracts with duplicated abstracts and the ones with missing data. Additionally, we narrowed the abstracts by removing the ones that did not contain them ("covid", "covid-2", "cov2", and "ncov"). After the preprocessing stage, we had 180,000 journal abstracts, removed from initially

Methodology

sample question.

Input question: What is the range of incubation period of COVID-19 in humans?
Input answer: Incubation period is 14 days in humans.
Return: 14 days

Then, we classified abstracts based on question-related phrases using a string-matching algorithm. For the question related to the incubation period of COVID-19, the phrases used were "incubation period", "contagious period". String matching finds patterns in the designated text that match the words or phrases in the question.

Finally, we developed a ranking approach using the concept of multiple-choice answers for extracting the best answer from the process of ranking. This project's full code, including that of this ranking approach, is available online and can be accessed through reference [11].

Results

Below, we present the P-values calculated for each argument, as demonstrated in the table below. Based on the analysis of the derived p-values, no comparison of two different results (e.g., our results vs. GA Tech CORD-19) agreed.

	P-value	Inference
Our results vs. GA Tech CORD-19	0.0008	Very statistically significant
Our results vs. CDC	0.0002	Extremely statistically significant
GA Tech CORD-19 vs. CDC	0.0006	Statistically significant

From the two confusion matrices, we calculate the precision, recall, and F1 scores of our model vs. GA Tech CORD-19%. The higher precision of our model relates to the low false-positive rate, and the higher F1 score of our model relates to its higher accuracy.

	Our results	GA Tech CORD-19% results
Precision	0.8	.87
Recall	1.0	1.0
F1 score	0.9	.93

Special Populations & Second Question Analysis

Based on the P-values collected from the T-Tests performed upon our results, those of GA Tech CORD-19, and that of CDC, we inferred that there is a difference between our populations, as presented in the table below. The difference between our values with those of GA Tech CORD-19 is due to differently sorted data due to our algorithm and transformer's ability to analyze complex language.

	Our results	Special Populations
6 days	Taiwan, N/A	
20 days	Hospitalized patients in Wuhan, China	

Conclusion & Future Work

can create a searching tool similar to Google can implement our model and a wide variety of disease/condition-related data to help medical professionals relate to clinicians, physicians, and other medical professionals as well.

A potential application of our model is self-verifying the answers extracted from the model as true/false (for the confusion matrices). In future work, we'll collaborate with medical professionals to gain insights on medical professionals' medical insights.

Choose a different breakout room

Devika

- Oral Presentation Award Winner

Eric Clifford – Graduate talks winner LSUS "Drug Screen Trends in Emergency Rooms Among Childbearing-Aged Females"

- Full project talk Winners (tied)

Kyle Piller – Tied for 1st Place SELU "Life in the fast lane: Testing for congruence among transcriptomic signatures"

Vonny Salim – Tied for 1st Place LSUS "Elucidation of Plant-Derived Drug Biosynthetic Pathways"

Drug Screen Trends Among Childbearing-Aged Females

Eric Clifford¹, Phillip C.S.R. Kilgore¹, Urska Cvek¹, Marjan Trutschl¹, Nadejda Korneeva², Steven A. Conrad³, Thomas Arnold⁴

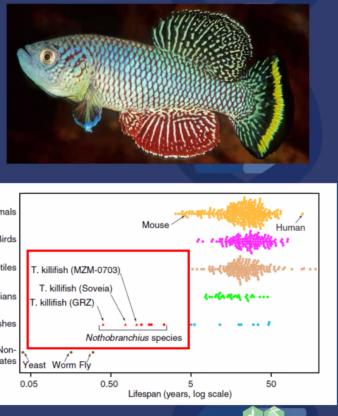
¹ Laboratory for Advanced Biomedical Informatics, Department of Computer Science, Louisiana State University Shreveport, Shreveport, LA 71135
² Department of Internal Medicine, Feist-Weiller Cancer Center, Louisiana State University Health Sciences Center, Shreveport, Shreveport, LA 71130
³ Department of Medicine, Department of Emergency Medicine, Department of Pediatrics, and Department of Anesthesiology, Louisiana State University Health Sciences Center Shreveport, LA 71130
⁴ Department of Emergency Medicine, Louisiana State University Health Sciences Center Shreveport, LA 71130



Eric Clifford

Why is it a model?

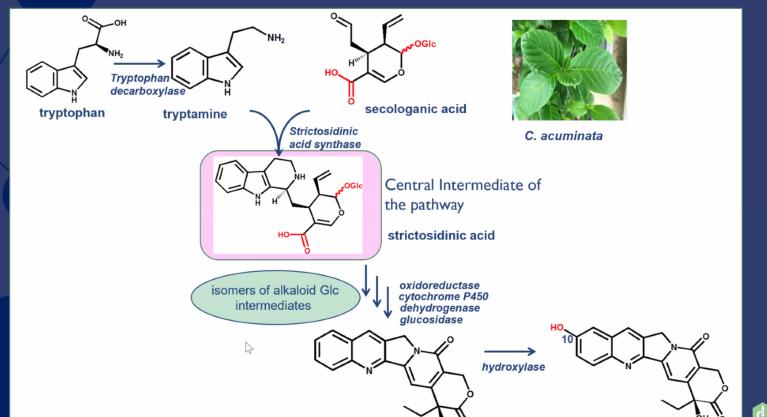
- Complete its entire life-cycle between 10 and 31 weeks
 - Life-span variation among populations (different strains)
- GRZ strain (shortest)
 - Gona-Re-Zhou National Park of Zimbabwe



The graph shows lifespan in years on a log scale from 0.05 to 50. Species are listed on the left: Mammals, Birds, Reptiles, Amphibians, Fishes, Non-vertebrates. A red box highlights three killifish strains: T. killifish (MZM-0703), T. killifish (Sovia), and T. killifish (GRZ). Other species shown include Mouse, Human, Yeast, Worm Fly, and Nothobranchius species.



Kyle Piller



The diagram illustrates the biosynthetic pathway of alkaloids in *C. acuminata*. It starts with tryptophan, which is converted to tryptamine by tryptophan decarboxylase. Tryptamine is then converted to secologanic acid by strictosidinic acid synthase. The central intermediate of the pathway is strictosidinic acid. This intermediate can be converted into various isomers of alkaloid Glc intermediates or further modified by oxidoreductase, cytochrome P450, dehydrogenase, and glucosidase to form other alkaloids. Finally, hydroxylase converts one of these intermediates into a hydroxylated product.



Vonny Salim

The award list and any links to relevant posters is available here: <https://lbrn.lsu.edu/highlights/2022-01-31-LBRN-AM-Awards.html>

Online

All the major parts of the meeting are available to re-watch here: <https://lbrn.lsu.edu/annual-meetings-2022.html#eventMediaLink>



LSU HPC Training



Our next HPC training will be held on Wednesday, February 16 at 9:00 AM. Due to concern about the COVID-19 pandemic, all training sessions are Zoom online events from 9:00AM to 11:00AM. The sessions will be recorded for later review.

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

- **Wednesday, February 16, 2022: Version Control with Git**

Version control system is used for tracking changes in computer files and coordinating work on those files among multiple people. It is primarily used for source code management in software development and also used to keep track of changes in any set of files. This tutorial gives an introduction to the Git version control software and will cover the following topics:

- Basic Git usage: create, manage and track changes in git repository
- Working with Git branch
- Remote repository

Prerequisites:

A laptop/desktop with Git installed, OR

LONI or LSU HPC account to access the Git installed on cluster.

Next HPC training:

- **Wednesday, February 23, 2022: Introduction to Python**

Python is a high-level programming language, easy to learn yet extremely powerful. This training will provide an introduction to programming in Python. The subjects include basic Python syntax, Python classes used in object-oriented programming. Basic Python modules for scientific computing and plotting will also be introduced. During the training, simple Python programs will be provided for demonstration.

Prerequisites:

Basic understanding of a programming language is assumed but not required.

Please visit <http://www.hpc.lsu.edu/training/tutorials.php> for more details and register using the link provided. Users 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>.

NRMN : Upcoming Webinar



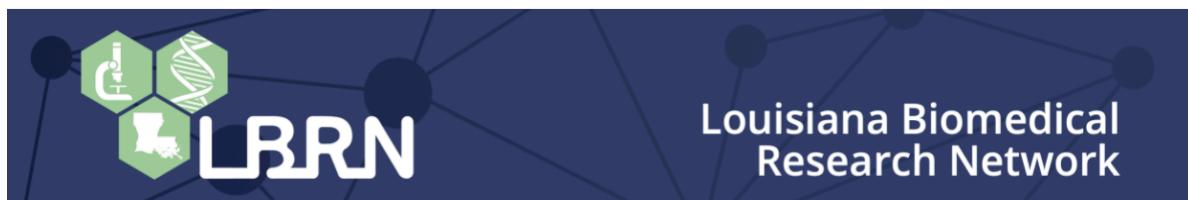
We are excited to announce that we will be hosting a new webinar in our Black History Month webinar series with Drs. Antentor Hinton, Tam'ra-Kay Francis, Zer Vue, Brittany Taylor and Arnaldo Diaz Vazquez!

In this webinar, our speakers will be discussing allyship and the benefits and impact it can provide for black scientists.

Join us on February 24 at 11am CST for an important discussion about the importance of allyship for black STEMM professionals.



LBRN "Core Bucks"



The BBC Core and MCBR Core offer researchers the opportunity to earn “Core Bucks” to support faculty and students upto \$1500. Requests for Core Bucks from Member Institutions must be initiated through the respective Core Contact on campus.



- The Bioinformatics, Biostatistics, and Computational Biology Core (BBC Core)

The BBC Core serves to train and support project investigators and their teams across Louisiana. It works to enable Louisiana Biomedical Research Network project PIs and their teams to employ Louisiana cyberinfrastructure (especially high performance computing), and to provide bioinformatics services, training, and educational support.

The core provides bioinformatics training, conducts workshops, and provides bioinformatics analysis services. The core also provides access to the IBM Delta Cluster and has a dedicated BBC allocation for the high performance computing resources at LSU. The BBC Core maintains software licenses and access to Ingenuity Pathway Analysis (IPA), Partek Flow, DNASTAR, and Ion Torrent analysis software. In addition, several open source tools for bioinformatics such as bowtie, tophat, cufflinks, samtools, GATK, QIIME, DADA2, Phyloseq, etc. are installed and maintained.

Some examples of standard bioinformatics workflows that can be supported through core bucks requests:

- Gene Pathway Analysis
- RNA-Sequencing Processing and Analysis
- 16S rRNA Microbial Community Analysis
- ITS2 Fungal Community Analysis

Other workflows can be developed or adapted from existing software on an as needed basis.

For more information, see: <https://lbrn.lsu.edu/cores.html#corebucks>



- The Molecular and Cell Biology Resources Core (MCBR Core)

MCBR Core Services include both one-on-one training for faculty and students as well as workshops on

topics like bioinformatics and protein purification.

Sample services:

1. Molecular Biology Reagent Equipment and Services

- GeneLab provides conventional and next generation nucleic acid sequencing (NGS), and recombinant DNA Service. NGS equipment includes Torrent PGM, Ion Proton etc
- NGS Services provides a reliable connection between NGS experiments and the analysis of NGS data

2. Protein Production, Purification and Characterization Laboratory

- Protein Purification and Characterization includes semi automated Bio-rad profinia affinity chromatography system, AKTA Explorer FPLC system, and HPLC and ultracentrifugation equipment
- Peptide Synthesis and purification
- Protein-protein interactions are investigated using primarily Surface Plasmon Resonance (SPR) implemented on Biacore and ForteBio SPR equipment. Additional physicochemical characterization of protein-protein interactions is available through collaborations with the LSU Department of Chemistry.
- Gene-to-Protein-to-Antibody Services – you provide the gene, we return an antibody

3. Molecular Immunopathology Laboratory Services

- Pathology Services including necropsy procedures, gross and histopathological examinations and interpretation of immunohistochemistry and special stains performed by veterinarians and histology specialists
- Flow Cytometry and immunophenotyping Services
- Multiplex/Luminex complements immunophenotyping services for rapid and standardized analysis of soluble factors e.g., lymphokines, using bead based array technology.
- Microscopy – contains transmission and scanning electron microscopes, a laser dissection microscope, a Leica TCS SP2 for 3D fluorescence microscope, and a high-throughput digital slide-scanner.

For more information, see: <https://lbrn.lsu.edu/cores.html#corebucks>

Coronavirus (COVID-19) Information

Information from CDC: <https://www.cdc.gov/coronavirus/2019-ncov/index.html>

Self-Testing At Home or Anywhere

What is a Self-Test or At-Home Test?

Self-tests for COVID-19 give rapid results and **can be taken anywhere**, regardless of your vaccination status or whether or not you have symptoms.

- They detect **current** infection and are sometimes also called “home tests,” “at-home tests,” or “over-the-counter (OTC) tests.”
- They give your **result in a few minutes** and are different from laboratory-based tests that may take days to return your result.
- Self-tests along with vaccination, wearing a well-fitted mask, and physical distancing, help protect you and others by reducing the chances of spreading COVID-19.
- Self-tests **do not** detect antibodies which would suggest a previous infection and they do not measure your level of immunity.

When To Take an At-Home COVID-19 Test

Test Yourself If...	Timing
You have any COVID-19 symptoms	Immediately
You were exposed to someone with COVID-19	<p>At least 5 days after your exposure</p> <p>If you test negative for COVID-19, consider testing again 1 to 2 days after your first test</p>
You are going to an indoor event or a gathering	<p>Immediately before the gathering, or as close to the time of the event as possible</p> <p>This is especially important before gathering with individuals at risk of severe disease, older adults, those who are immunocompromised, or people who are not up to date on their COVID-19 vaccines, including children who cannot get vaccinated yet.</p>

Learn what to do if you [test positive](#) or [test negative](#).

How to Get an At-Home COVID-19 Test

- **Order free tests** at [COVIDtests.govexternal icon](#). Free tests are also available through [local health departments](#).
- **Buy tests** online or in pharmacies and retail stores. Private health insurance may reimburse the cost of purchasing self-tests. Visit [FDA's websiteexternal icon](#) for a list of authorized tests.
- If you're not able to obtain a self-test when you need it, you might also **visit a community testing site, or call your local health department** for more options.

How to Use an At-Home COVID-19 Test

Read the complete manufacturer's instructions for use before using the test.

- To use an at-home test, you will collect a nasal specimen and then test that specimen.
- If you do not follow the manufacturer's instructions, your test result may be incorrect.

- Wash your hands before and after you collect a nasal specimen for your test.

-

What Your Test Results Mean



IF YOUR TEST IS

Positive

- The test detected the virus and **you have an infection**.
- Stay home for at least 5 days and isolate from others in your home.
- Tell your close contacts.
- Wear a well-fitted mask when around others. If available, a N95 or KN95 respirator is recommended.
- Watch for symptoms. If you have any emergency warning signs, seek emergency care immediately.
- Tell your healthcare provider. Contact them as soon as possible if:
 - Your symptoms get worse.
 - You are more likely to get very sick because you are an older adult or have an underlying medical condition. Possible treatment may be available for you.
 - You have questions about your isolation.



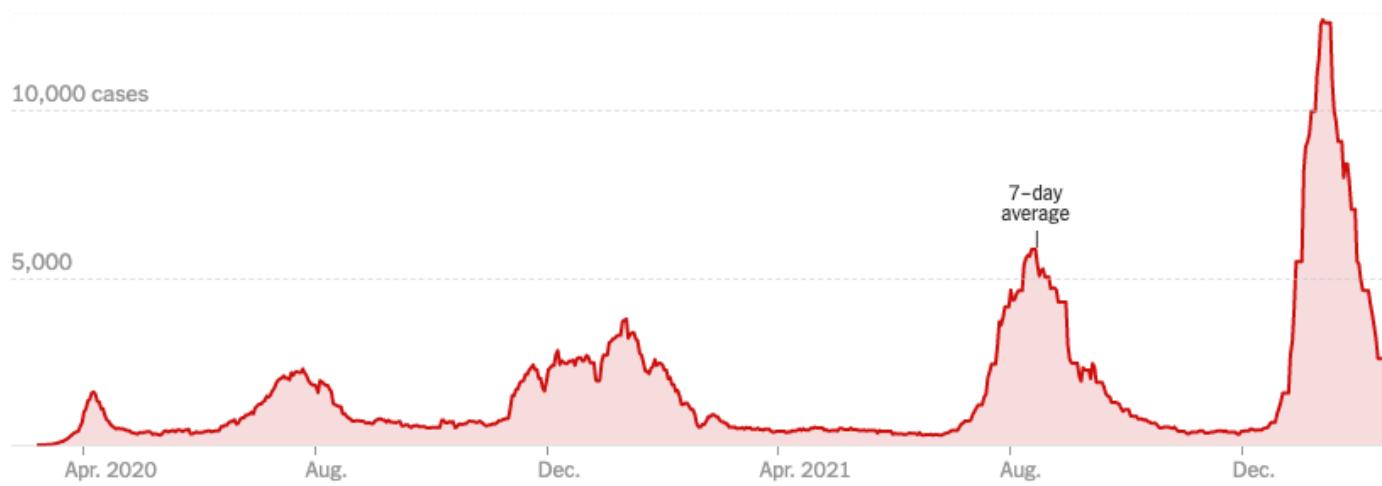
IF YOUR TEST IS

Negative

- The test did not detect the virus, **but doesn't rule out an infection**.
- Some self-tests are designed to be used in a series (also known as serial testing). Consider repeating the test 24 to 48 hours later. Multiple negative tests increases the confidence that you are not infected with the virus that causes COVID-19.

COVID-19 in Louisiana

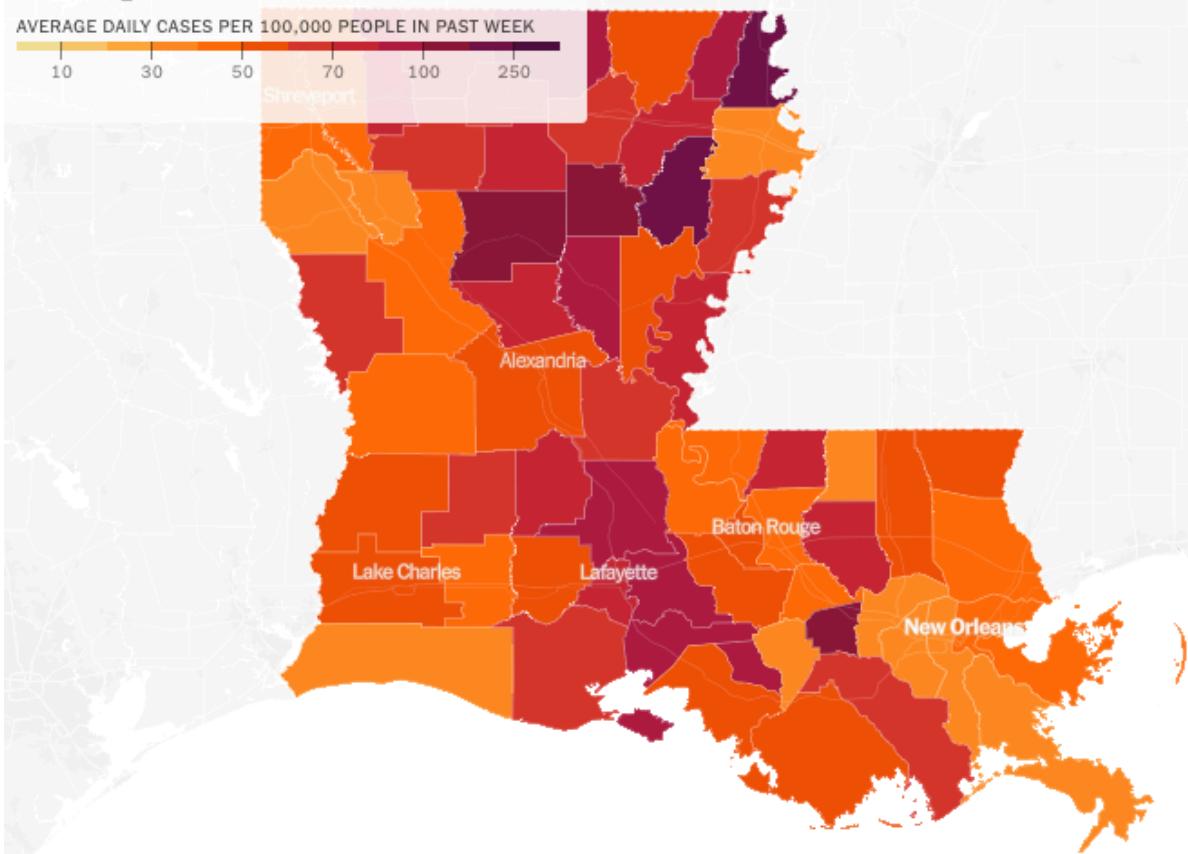
Information from New York Times: <https://www.nytimes.com/interactive/2021/us/louisiana-covid-cases.html>



Hot spots

AVERAGE DAILY CASES PER 100,000 PEOPLE IN PAST WEEK

10 30 50 70 100 250



NIH Extramural Nexus

- **New NIH Administrative Supplements Available to Support Diversity Mentorship**

Qualified investigators can now submit proposals in response to the Chief Officer for Scientific Workforce Diversity (COSWD)-led [Notice of Special Interest \(NOSI\) NOT-OD-22-057: Administrative Supplements to Recognize Excellence in Diversity, Equity, Inclusion, and Accessibility \(DEIA\) Mentorship](#). Proposals are due by April 7, 2022.

Mentorship is a critical part of recruiting and retaining an inclusive scientific workforce. Evidence suggests [mentorship helps foster scientific identity](#) and [career progression](#) in science, technology, engineering, mathematics, and medicine (STEMM) disciplines. For example, research shows that grant-writing mentorship for early-career biomedical investigators from underrepresented groups [can foster increased publication productivity](#), a key contributor to scientific career advancement.

Based on this evidence, [one goal of my office](#) is to support and amplify the impact of programs that develop scientific talent through training and mentorship. Thus, this new NOSI is part of our commitment to enhancing mentorship within NIH-supported research, with an emphasis on scientists from underrepresented groups.

The [participating NIH Institutes and Centers](#) will supplement the existing awards of scientists who have demonstrated a commitment to exceptional training and mentorship, especially to individuals from groups identified as [underrepresented in the biomedical sciences](#).

Supplements are available for various grant types, including career development, training, cooperative, and Research Project Grants (R01). They will provide up to \$250,000 in [direct costs](#), not to exceed the direct costs of the parent award. Investigators may use the funds to perform additional research within the parent grant's scope, develop curricula or training activities to strengthen mentor training, or help foster the research career development of additional students, post-doctorates, or other trainees.

The NIH [has an array of mentorship initiatives and resources](#), and I am excited about this addition to the agency's offerings. I encourage all eligible investigators to take advantage of this opportunity to be recognized for outstanding mentoring, and for promoting inclusive excellence.

- **All About Grants Podcast – How to Find Help**

Have questions about funding opportunities, developing an application, or managing a grant award? Unsure to whom you should reach out for help? Check out this [NIH All About Grants](#) podcast to get a refresher on the ins and outs of what to do when seeking assistance from NIH extramural staff ([MP3 / Transcript](#)). Sheri Cummins, with the NIH Office of Extramural Research's communications group, explains where to find answers to many [frequently asked questions](#) and other information online, deciphering program, review, and grants administrative [staff roles at NIH](#), when to reach out and when not to, and much more.

“...[I have] asked: Have you ever wanted to reach out to NIH but decided not to and why? And I was floored to see how many people said fear. Fear of looking stupid or uninformed, feeling that their questions were somehow unworthy of NIH attention...It’s literally our job to help. We all want the same thing...to advance our scientific understanding and ultimately improve the nation’s health...the pandemic has shown us all how truly vital that NIH mission is for everyone and we really just need to help each other to get there.” – Sheri Cummins

Please also visit our [Help page](#) for more information.

- Feedback Sought on the NIH-Wide Strategic Plan Framework for Diversity, Equity, Inclusion, and Accessibility**

We are pleased to announce that the framework for the NIH-Wide Diversity, Equity, Inclusion, and Accessibility (DEIA) Strategic Plan was released earlier this week ([NOT-OD-22-061](#)). Your input on the framework as the plan is developed is encouraged. Feedback will help us ensure that DEIA principles continue to be embraced and integrated across NIH going forward.

We strongly believe that an inclusive and diverse pool of highly talented individuals is key for the country to remain a global leader in scientific discovery and innovation (see [these posts for more](#)). This means we must actively consider factors that address DEIA principles and appropriately embed them within NIH and the wider scientific community. Embracing this DEIA vision will enhance our ability to drive biomedical innovation and serve an increasingly diverse US population.

The NIH-Wide DEIA Strategic Plan strives to clearly communicate our DEIA vision. It will align with the [NIH-Wide Strategic Plan](#) released last year, and encompass our ongoing initiative to address [structural racism in biomedical research](#) as well as build on the wider [federal effort](#) to expand DEIA across the workforce.

The scope of the plan covers accomplishments, needs, opportunities, and challenges related to DEIA within the NIH workforce, its structure and culture, and our supported research. The main objectives are to:

- Implement organizational practices to center and prioritize DEIA in the workforce
- Grow and sustain DEIA through structural and cultural change
- Advance DEIA through research

What are the potential benefits or drawbacks to this framework? Are there priority areas missing? Which best practices and policies are likely to foster positive culture change? What barriers stand in the way? How should DEIA be defined for the purposes of this effort? What metrics measure progress?

We welcome your comments and feedback on the framework. Please send them [electronically](#) by April 3, 2022.

• Gearing Up for 2023: Implementing the NIH Data Management and Sharing Policy

Guest post by Dr. Lyric Jorgenson, Acting Associate Director for Science Policy and Acting Director of the NIH Office of Science Policy, originally released on the [Under the Poliscope blog](#).

Frequent readers of this blog will remember that back in October 2020, NIH issued its [Data Management and Sharing \(DMS\) Policy](#) to further our commitment to making the research we fund available to the public. Our strategic decision to make the effective date for the Policy approximately two years later led some to ask NIH “why wait so long?” while others asked “why not give us more time?” Fortunately, the answer to both these questions is the same. Our goal is to lead a [cultural shift](#) that makes data sharing the norm. The degree of that shift, for some, may vary. For example, many data sharing policies are already in place and researchers currently sharing data will likely not need to significantly alter their approach. But prospective planning for how to share data (i.e., developing plans, requesting NIH funds) may be new for some. As such, it seemed reasonable that two years was the right balance of time to lay the groundwork for implementation. Today I am excited to provide an update on what NIH is doing to make our data management and sharing efforts a success on the one-year mark prior to the Policy’s effective date.

Since the Policy’s release, NIH has continued its approach of meeting and seeking feedback from its stakeholders. For example, in April 2021, NIH supported a two-day National Academies [workshop](#) to share strategies for successful data management and sharing and identify areas of additional need for seamless policy implementation. Thanks to the success of this workshop, we were able to continue engaging the public on multiple related resources and issues, such as [consent for data sharing](#), [harmonizing the NIH Genomic Data Sharing Policy](#) with the DMS Policy, and the [discoverability of our data resources](#). We also have been partnering with our colleagues in the NIH Office of Extramural Research to provide implementation updates at extramural-focused meetings such as last year’s [Virtual Seminar](#).

As you may recall, when the DMS Policy was released, we asked the community what other types of information would be of value to help with implementation. Based on the feedback we received, we are releasing additional resources today and have plans for continuing to release more throughout 2022.

Today, NIH is:

- Publishing a new set of [FAQs](#) that respond to questions we have heard since the release of the DMS Policy. We plan to update these FAQs throughout the year, as necessary
- Issuing a request for public comments on draft [Supplemental Information to the NIH Policy for Data Management and Sharing: Responsible Management and Sharing of American Indian/ Alaska Native Participant Data](#) to continue our partnership with Tribal communities by promoting responsible management and sharing of AI/AN participant data

Over the course of 2022, you can expect to hear more from us regarding resources, including:

- Helpful tips for developing budgets in Plans describing data management and sharing
- Updated information on principles for protecting research participant privacy and de-identification to help guide sharing of research participant data
- Educational resources including webinars and potentially sample Plans
- Plans for further harmonizing NIH's data management and sharing expectations, particularly with reducing duplicative plan submissions

In addition to the above, during 2022 NIH will also continue providing supplemental funding for grantees to:

- Improve the FAIR and Artificial Intelligence/Machine Learning-Readiness of their NIH-Supported Data
- Align existing data repositories with FAIR and TRUST principles and evaluate usage, utility, and impact

This is definitely an exciting year for NIH, and we look forward to continuing our engagement with the stakeholder community throughout 2022. Make sure to stay tuned –there is plenty more to come as we work together to accelerate scientific discovery through effective data management and sharing.

- **Extending Existing Guidance for Preparing Applications During COVID-19**

For Spring 2022 due dates, NIH recently [extended the guidance](#) that while grant applications should not include contingency or recovery plans for problems resulting from the COVID-19 pandemic, investigators may address effects due to the pandemic on productivity or other scoreable issues in the personal statement of the biosketch. Reviewers will be instructed to take these pandemic-related circumstances into account when assessing applicants' productivity and other score-driving factors. If needed, NIH staff will request and assess plans to resolve specific problems arising from the COVID-19 pandemic prior to funding.

NIH also [extended the special exception for post-submission material](#) to applications submitted for the August/October 2022 Council rounds. For applications submitted for the August/October 2022 Council rounds (beginning with applications submitted for the January 25, 2022 due date), the NIH, AHRQ, and NIOSH will accept a one-page update with preliminary data as post-submission materials for applications submitted under all activity codes, ONLY if the Funding Opportunity Announcement (FOA) used for submission allowed preliminary data in the application. One page of preliminary data will be accepted for single component applications or for each component of a multi-component application.

The deadline for submitting all post-submission materials, including preliminary data, will be 30 days before the study section meeting, unless specified otherwise in the FOA. Because applications for

emergency competitive revisions and urgent competitive revisions undergo expedited review, post-submission materials will not be accepted for those applications.

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 2021/2022.

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 GM103424-20.

- 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 P20GM103424-20.

- 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 (2P20GM103424-20) an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health.

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