News, Opportunities and Deadlines for Nov. 2021

Happy Thanksgiving LBRN!

LBRN PI Dr. Gus K. Kousoulas named 2020 NAI Fellows

The NAI Fellows Program highlights academic inventors who have demonstrated a spirit of innovation in creating or facilitating outstanding inventions that have made a tangible impact on the quality of life, economic development, and the welfare of society. Election to NAI Fellow is the

highest professional distinction accorded solely to academic inventors. To date, NAI Fellows hold more than 42,700 issued U.S. patents, which have generated over 13,000 licensed technologies and companies, and created more than 36 million jobs. In addition, over $2.2 trillion in revenue has been generated based on NAI Fellow discoveries.

The 2020 Fellow class represents 115 research universities and governmental and non-profit research institutes worldwide. They collectively hold over 4,700 issued U.S. patents. Among the 2020 Fellows are recipients of the National Academies of Sciences, Engineering, and Medicine, American Academy of Arts & Sciences and Nobel Prize, as well as other honors and distinctions. Their collective body of research covers a range of scientific disciplines including biomedical engineering, computer engineering, materials science, and physics.

The complete list of NAI Fellows is available on the NAI website.

About the National Academy of Inventors

The National Academy of Inventors is a member organization comprising U.S. and international universities, and governmental and non-profit research institutes, with over 4,000 individual inventor members and Fellows spanning more than 250 institutions worldwide. It was founded in 2010 to recognize and encourage inventors with patents issued from the United States Patent and Trademark Office (USPTO), enhance the visibility of academic technology and innovation, encourage the disclosure of intellectual property, educate and mentor innovative students, and translate the inventions of its members to benefit society. The NAI has a close collaborative

relationship with the USPTO and is one of three honorific organizations, along with the National Medals and National Inventors Hall of Fame, working closely with the USPTO on many discovery and innovation support initiatives. The NAI publishes the multidisciplinary journal, *Technology and Innovation*. www.academyofinventors.org

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Save the Date
20th LBRN Annual Meeting

Save the Date: January 28-29, 2022 for the 20th LBRN Annual Meeting

--- === VIRTUAL CONFERENCE === ---

Mark your calendars!

January 2022

Wk	Sun	Mon	Tue	Wed	Thu	Fri	Sat
52							1
1	2	3	4	5	6	7	8
2	9	10	11	12	13	14	15
3	16	17	18	19	20	21	22
4	23	24	25	26	27	28	29
5	30	31					

Reports : 2021 Southeast Regional IDeA Conference

The conference was dedicated to discussions about the latest progress in biomedical research around the region as well as important challenges being addressed through NIH funding appropriated under the IDeA program. Concurrent sessions throughout the day covered topics of *Community Engagement and Health Disparities, MultiOmic Research Approaches, Bioinformatics and Data Science, Collaborative Research in IDeA states, Neuroscience, and Clinical Research*, highlighted with a Plenary Speaker presentation and Poster Sessions.

Keynote Speakers addressed topics on Entrepreneurship in the South Eastern Region. In addition, speakers from the NIH presented important topics related to funding, including *Data Science* and an *R15 Program Update*.

Louisiana INBRE Participants

Dr. Urska, LSU Shreveport LBRN PI and PUI Liaison, was an invited speaker giving a talk on drug abuse in Louisiana

Philip Kilgore, LSU Shreveport, LBRN awarded Best In Person Poster: *"Racial Disparities in COVID-19 Symptoms"*

Racial Disparities in COVID-19 Symptoms

P.C.S.R. Kilgore[1], D. Janese[2], J. Jones[2], K. Addison[2], R. Kessler[2], R. Waesche[2], M. Edens[2], A.P. Cornelius[2], M. Trutschl[1], U. Cvek[1]

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[2] Department of Emergency Medicine, Louisiana State University Health Sciences Center, Shreveport, Shreveport, LA 71130

:: Abstract

Since the onset of the COVID-19 pandemic, the question of racial differences has been at the forefront of prognostic thought in determination of high-risk groups. We identified a total of 410 unique Medical Record Numbers (MRNs) in a retrospective data collection of patients in the Ochsner LSU Health System (LSUH) in Shreveport and Monroe, Louisiana. Data was collected from a mix of rapid and regular PCR nasal swabs collected at the two locations from 4/1/2020 to 4/30/2020. Data collected included symptoms, race, ethnicity, occupation, gender and age. to determine if there was a statistical difference in presenting symptoms based on race.

Black/African American patients were the most represented race (74%) with COVID-19 and most patients were non-Hispanic (70.15%) with a female predominance amongst all races. Gender was evaluated as a covariable, which demonstrated a slight female predominance in symptoms, with females representing 58.73%, and males representing 41.27% of the African American cohort. Fever was frequently accompanying cough, shortness of breath, headache, arthralgias/myalgias, non-Hispanic ethnicity, and male sex. In the grouped data, the top 10 rules predicted either shortness of breath or fever with COVID-19, and five of the rules were associated with African American race. Caucasian and African American patients had similar rates of anosmia.

While evaluating the racial distribution of COVID-19 as it pertained to symptoms, gender, and occupation, African American patients were statistically more affected by COVID-19 in Northern Louisiana, which was not observed in Southern Louisiana.

:: Introduction

SARS-CoV-2 infection is the cause of severe acute respiratory syndrome, commonly known as COVID-19. COVID-19 has a poor prognosis and has been associated with approximately 4.9 million deaths worldwide since December 2019, with the global number of cases exceeding 242 million [1]. The COVID-19 pandemic has been known to affect the African American/Black (AA) community in the United States disproportionately since its beginnings [2].

Shreveport, LA represents a unique opportunity to study outcomes of COVID-19 in the AA population because its population is majority AA. AA individuals represent 13.4% of the United States population as of 2019; however, the AA population makes up an estimated 57.1% of inhabitants in Shreveport as of 2019 [3]. Additionally, Shreveport serves as a large catchment area which includes the for the surrounding region (known as the Ark-La-Tex), with Ochsner Shreveport being LERN Region 7's sole Level I Trauma Center [4].

We obtained de-identified data from COVID-positive patients arriving to the Ochsner facility in April of 2020. Additionally, we assessed the prevalence of both common COVID-19 symptoms (such as cough or anosmia) and other symptoms that are thought to be atypical (such are cardiac or GI events). Our primary goal was to determine a) if racial disparities manifested themselves in the Shreveport population, and if so, b) the nature of those disparities. We also look at how race relates to discharge disposition and admission status. Our study excluded pregnant women, prisoners, and pediatric patients.

Race	Count	Percent	Mean Age	% Female	% Male	% Hispanic	% Not Hispanic
AI	10	2.46	32.30	80.00	20.00	60.00	30.00
AS	4	0.97	45.25	25.00	75.00	0.00	75.00
AA	306	74.27	43.86	62.75	36.93	0.33	69.28
CC	79	19.17	47.46	45.57	54.43	1.27	84.81

Table 1. Distribution by race and gender, for AI=American Indian/Native American, AS = Asian, AA = African American/Black, and CC = Caucasian/White. Nearly 75% of the patient population was AA and nearly 2/3rds female. Note that only 399 patients have race data available, and not all percentages add up to 100%.

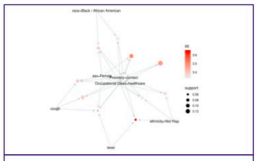

Figure 1. arulesViz visualization for top 10 association rules for the refactored input set. Race, ethnicity, gender, occupation class, and proximity were frequently associated with the association rules that were mined for the data.

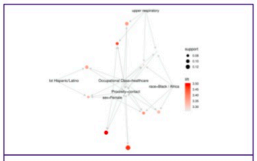

Figure 2. arulesViz visualization for top 10 association rules for the collapsed input set. A variety of features are associated. Race, ethnicity, gender, occupation class, and proximity were frequently associated with the association rules that were mined for the data.

:: Methods

We received data for 2,484 encounters (visits) for 453 de-identified patients; 7 patients fell within our exclusion criteria and were removed. We also removed records with obviously erroneous values (for instance, BMI well in excess of the largest ever recorded) when they were irreconcilable with other data, resulting in 1,961 encounters over 412 patients. Race was defined for 399 of these patients.

Hypothesis testing was performed on the basis of a) domain and b) normality of the dependent variable (if numeric). For non-numeric data, we used the X^2 test. Numeric variables were first tested for normality using Shapiro-Wilk's normality test for $p > \alpha = 0.1$. This limit is standard practice with Shapiro-Wilk because the null hypothesis is that the distribution is normal and a larger α value indicates a greater caution towards accepting normality. For normal data, we used either Student's *t*-test for a binary independent variable, or One-way Analysis of Variance (ANOVA) for others. For non-normal data, we used the Wilcoxon rank sum test and Kruskal-Wallis respectively. For all hypothesis testing, we rejected the null hypothesis when $p <= \alpha = 0.05$.

We considered the data set in two forms: *refactored* (where atypical symptoms were broken into granular categories) and *collapsed*, where collapsed data was grouped into GI, cardiovascular and upper respiratory symptoms. We performed association rule mining (ARM) using the "arules" package for R [5]. Association rules are directional rules that suggest that if one attribute is present (the antecedent), other specific attributes (the subsequent) can also be expected to be present. We visualized the rules using the "arulesViz" package for R and selected rules which had a lift >= 1.

Count of...	*p*	AA	CC	Δ
*Typical Symptoms**	0.033	2.92 ± 2.07	2.37 ± 2.01	0.56
Refactored Symptoms	0.589	0.43 ± 0.77	0.47 ± 0.75	-0.04
*Collapsed Symptoms**	0.026	1.04 ± 0.77	0.82 ± 0.84	0.21

Table 2. Hypothesis testing for a number of typical, refactored, and collapsed symptoms. "*" denotes a statistically significant difference in the number of such symptoms. Typical and collapsed symptoms were found to be significantly different between AA and CC.

Symptom	% of AA	% of CC	Δ%	Symptom	% of AA	% of CC	Δ%
*Shortness of breath**	39.22	11.52	17.70	*Weakness*	10.78	8.86	1.92
*Cough**	66.34	54.43	11.91	*Rash*	0.33	0.00	0.33
Arthralgias or myalgias	26.47	16.46	10.01	*Nausea*	11.44	11.39	0.05
Agnosia	7.52	1.27	6.25	*Hypoxemia*	1.31	1.27	0.04
Coryza	11.76	6.33	5.44	*Dizziness*	1.96	2.53	-0.57
Headache	18.95	13.92	5.03	*Dyspnoea*	2.94	3.80	-0.86
Anosmia	8.17	5.06	3.11	*Fever*	46.41	48.10	-1.70
Hypotension	6.21	3.80	2.41	*Diarrhea*	12.75	15.19	-2.44
Sore throat	13.40	11.39	2.01	*Altered mental status*	6.54	11.39	-4.86

Table 3. Comparison of "typical" symptoms measured in COVID-19 patients. The Δ% column depicts the relative difference between the AA and CC cohorts. Occurrence of shortness of breath, cough, and arthralgias or myalgias were at least 10% greater in the AA than in the CC population. Only shortness of breath was significantly different (p=0.005).

:: Results

74.27% of patients in our data set were AA (Table 1), of which about 63% were female and 37% were male; the vast majority (84.81%) were non-Hispanic. We also captured data for Asian Americans (AS) and American Indian/Alaskan Natives (AI), but because of the relatively small size of these cohorts, they are not considered for subsequent processing. The AA cohort was statistically significantly different in both, the number of typical symptoms, and the number of collapsed, atypical symptoms, in both cases having greater incidence (Table 2).

Concerning the typical symptoms of COVID-19, the AA population had a greater relative incidence of shortness of breath, cough, and either arthralgias or myalgias (Table 3); of this, only shortness of breath was statistically significantly different. When we look at the collapsed atypical symptoms, only upper respiratory symptoms were statistically significantly different (Table 4).

Our ARM analysis showed that the most frequent association rules involved race, ethnicity, gender, occupational class, and proximity (Figures 1 and 2). We mined 124 rules which had a lift of at least 1. Lift is a measure of the performance of a targeting model (association rule) at predicting or classifying cases as having an enhanced response (with respect to the population as a whole), measured against a random choice targeting model. The top 5 mined rules included:

1. {Sex = Female, Occupational Class = Healthcare} → {Proximity = Contact} (lift = 3.504)
2. {Occupational Class = Healthcare} → {Proximity = Contact} (lift = 3.474)
3. {Sex = Female, upper respiratory, Occupational Class = healthcare} → {Proximity = contact} (lift = 3.466)
4. {Sex = Female, Race = AA, Occupational Class = healthcare} => {Proximity = contact} (lift = 3.381)
5. {upper respiratory, Occupational Class = healthcare} => {Proximity = contact} (lift = 3.751)

Rule 10 was also instructive: {race = AA, upper respiratory, Occupational Class = healthcare} => {Proximity = contact} (lift = 3.262).

Value	% of AA	% of CC	Δ%
GI symptoms	23.86	26.58	-2.73
Cardiovascular	12.75	7.59	5.15
*Upper respiratory**	66.99	48.10	18.89

Table 4. Comparison of collapsed or grouped "atypical" symptoms measured in COVID-19 patients. The Δ% column depicts relative difference between the AA and CC cohorts. Only upper respiratory symptoms had a greater than 10% relative difference and it was also significantly different (p=0.002).

:: Discussion and Conclusions

Our analysis shows that the AA and CC cohorts respond differently to COVID-19 infection, at least in the period of April 2020. AA cohort was more prone to upper respiratory symptoms than the CC cohort (including shortness of breath). During this interval, the α variant of SARS-CoV-2 was the only variant known to exist. As several variants have been identified since this point, it is not known whether or not the symptoms associated with these variants show a similar disparity. These results not only confirm previous findings of disparity [2] but also provide more clarity to the medical impact of this disparity.

Due to the population distribution in Shreveport, insufficient data was available for the study of the AI and AS populations. Our data trend towards disparity in the AI population, but low sample size suggests reduced statistical power and we have left this to a future study.

Our ARM analysis strongly implied that female AA healthcare workers were likely to have contact proximity with COVID-19 infected individuals, and that they were associated with upper respiratory symptoms. The top 10 association rules predicted contact proximity and this fact in isolation is not particularly interesting as it is a function of their job; however, they also included instances where upper respiratory symptoms were part of the antecedent, possibly indicating the female healthcare workers may be at greater risk of symptomatic infection than their male counterparts. This should be studied further before any conclusions can be made.

:: Acknowledgment

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.

:: References

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LBRN at SuperComputing 2021

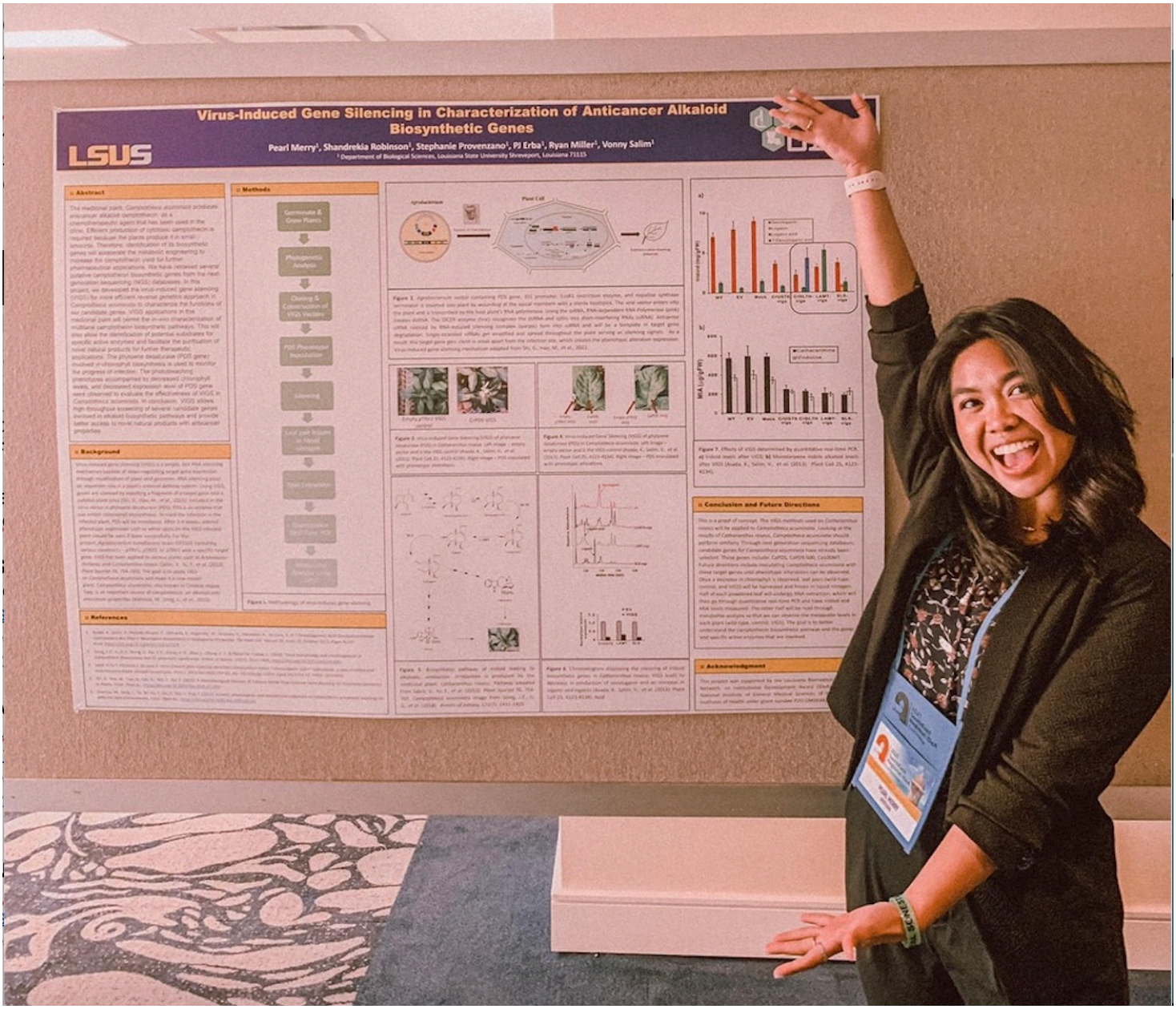
LBRN regularly attends the The International Conference for High Performance Computing, Networking, Storage, and Analysis. Last year it was 100% Virtual, this year it came back as a hybrid attendance in-person and virtual conference. LSU Center for Computation and Technology and LSU High Performance Computing were also represented at the conference.

Some of the talks our LBRN Computer Manager, John Quebedeaux, attended in St. Louis at the Conference Nov 14-19th: "Bioinformatics, HPC and AI: Convergence, Perspectives and the Future for Biomedical Applications", "High-Performance Statistical Computing: Building a Statistics Community within Supercomputing", and "Consumption and Distribution of Data Sets in the Cloud."

Any questions or information, please be sure to reach out to John Quebedeaux regarding the conference.

LBRN Achievement

Pearl Merry with her poster at the SouthEast Regional IDeA meeting, LSU Shreveport graduate student and LBRN student researcher, crowned Miss City of Lights 2022 and headed to Miss Louisiana Pageant:



She is currently enrolled in the Master of Business Administration program concentrating in Marketing while conducting medicinal plant research in the LSU Shreveport Cyber Collaboratory with Assistant Professor of Biological Sciences, Dr. Vonny Salim, an existing LBRN Full Project PI.

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

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Coronavirus (COVID-19) Information

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

Who Is Eligible for a COVID-19 Vaccine Booster Shot?

What You Need to Know

COVID-19 Vaccine booster shots are available for the following Pfizer-BioNTech vaccine recipients who completed their initial series at least 6 months ago and are:

- 65 years and older
- Age 18+ who live in long-term care settings
- Age 18+ who have underlying medical conditions

- Age 18+ who work and live in high-risk settings

Data Supporting Need for a Booster Shot

Studies show that after getting vaccinated against COVID-19, **protection against the virus may decrease** over time and be less able to protect against the Delta variant. Although COVID-19 vaccination for adults aged 65 years and older remains effective in preventing severe disease, recent data pdf icon[4.7 MB, 88 pages] suggest vaccination is less effective at preventing infection or milder illness with symptoms. Emerging evidence also shows that among healthcare and other frontline workers, vaccine effectiveness against COVID-19 infections is decreasing over time. This lower effectiveness is likely due to the combination of decreasing protection as time passes since getting vaccinated (e.g., waning immunity) as well as the greater infectiousness of the Delta variant.

Data from a small clinical trial show that a Pfizer-BioNTech **booster shot increased the immune response** in trial participants who finished their primary series 6 months earlier. With an increased immune response, people should have improved protection against COVID-19, including the Delta variant.

Booster Shots Are Only Available for Some Pfizer-BioNTech Vaccine Recipients

Employees and residents at increased risk for COVID-19 exposure and transmission

People aged 18–64 years at increased risk for COVID-19 exposure and transmission because of occupational or institutional setting **may get a booster shot of Pfizer-BioNTech vaccine based on their individual benefits and risks.** Adults aged 18–64 years who work or reside in certain settings (e.g., health care, schools, correctional facilities, homeless shelters) may be at increased risk of being exposed to COVID-19, which could be spreading where they work or reside. Since that risk can vary across settings and based on how much COVID-19 is spreading in a community, people aged 18–64 years who are at increased risk for COVID-19 exposure and transmission because of occupational or institutional setting may get a booster shot after considering their individual risks and benefits. This recommendation may change in the future as more data become available.

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

National Institutes of Health
Office of Extramural Research

- **Registration is open for "Achieving Equity in Faculty – Pros and Cons of Cohort Recruitment," being held on Wednesday, December 8, from 1:00–2:00 p.m. ET.**

The NIH Chief Officer for Scientific Workforce Diversity (COSWD) Office is hosting a seminar and virtual forum on faculty cohort recruitment programs and other evidence-based strategies as tools to foster diversity. The first event will be on December 8, while the second will be in February 2022 (date TBD). Both events are open to NIH staff and the public.

During this third seminar in our ongoing NIH Scientific Workforce Diversity Seminar Series (SWDSS), I will moderate a discussion on the science behind faculty cohort recruitment and how such programs promote diversity, equity, inclusion, and accessibility (DEIA) in science and medicine.

The following scholars will join me for the discussion:

- David A. Acosta, M.D., Chief Diversity and Inclusion Officer, Association of American Medical Colleges (AAMC)
- Sibby Anderson-Thompkins, Ph.D., Vice Provost for Diversity, Equity, and Inclusion, University of the South
- Michelle M. Camacho, Ph.D., Professor of Sociology, University of San Diego
- Carla Freeman, Ph.D., Goodrich C. White Professor of Women's, Gender, and Sexuality Studies and Executive Associate Dean, Emory College of Arts and Sciences, Emory University

Virtual Forum: Fostering Cohort Recruitment

The December 8 seminar is a precursor to an intensive two half-day event—Fostering Cohort Recruitment (FCR) Virtual Forum—scheduled for February 2022. Hosted by the COSWD Office, the forum will introduce attendees to faculty cohort programs that have successfully enhanced diversity both within and outside of the NIH and delve deeper into the science behind why these programs are successful.

The FCR will include presentations, break-out discussion groups, and report-out sessions; the event will be especially relevant for those implementing or considering faculty cohort recruitment

activities. The FCR is free, and registration will open in early 2022.

• Enhanced Checks for Compliance with Clinical Trial Registration and Reporting in RPPR

Enhanced checks on non-compliance with clinical trial registration and reporting came into effect in eRA's Human Subjects System on October 1 that could delay your RPPR submission if you are late on either front (see details in eRA news item).

Remember that all NIH-funded clinical trials are expected to register and submit results information to Clinicaltrials.gov, as per the "NIH Policy on Dissemination of NIH-Funded Clinical Trial Information."

These new checks will now result in an error for grant recipients upon submission of a Research Performance Progress Report (RPPR) when clinical trial registration (required 21 days after enrollment of first participant) and/or results reporting (required 12 months after trial actual primary completion date) is overdue.

- Currently, grant recipients receive a warning if they are not in compliance with clinical trial registration at 21 days after the enrollment of the first participant. They will also now see a new error if they are more than 30 days past this date.
- Similarly, the current warning for results reporting will change to an error; grant recipients will now receive an error when results are overdue by more than 12 months after the trial's actual primary completion date.

The clinical trial registration error for RPPR submission or red bar to award will be resolved when:

- the recipient completes the required registration and provides the NCT# (Clinicaltrials.gov identifier) on the Human Subjects Clinical Trial Information (HSCT) form, or by
- providing the ClinicalTrials.gov registration receipt that is received upon submission of the trial registration information to ClinicalTrials.gov. The receipt must be uploaded in other attachments section of the HSCT form (Section 5.1) as a PDF document. The file name must be CTgov_Registration_Receipt.pdf.

The results reporting error or award bar will be resolved when:

- results are submitted in Clinicaltrials.gov, or by
- the ClinicalTrials.gov submission receipt for a (1) Good Cause Extension request or (2) Certification of Delayed Submission of Results Information from ClinicalTrials.gov has been

provided. The receipt must be uploaded in the other attachments section of the HSCT form (Section 5.1) as a PDF document. The file name must be CTgov_Registration_Receipt.pdf.

Note: Please see the NIH guide notice NOT-OD-22-008 for additional details.

Animal Welfare Assurance Annual Reports to OLAW Due by December 1, 2021

Recipient institutions with an Animal Welfare Assurance must submit their Annual Reports to the NIH Office of Laboratory Animal Welfare by December 1, 2021 (NOT-OD-22-002). These reports cover the October 1, 2020, through September 30, 2021, reporting period, as required by the Public Health Service Policy on Humane Care and Use of Laboratory Animals.

The following information must be reported:

- Changes in the institution's AAALAC International accreditation status, animal care and use program, Institutional Official, and/or Institutional Animal Care and Use Committee (IACUC) membership
- Dates for the program and facility IACUC Semiannual evaluations
- Any IAUC member minority view

You can download the Annual Report Form, and watch this webinar for more on the updated annual reporting period (NOT-OD-20-109).

Long-Term Trends in the Age of Principal Investigators Supported for the First Time on NIH R01-Equivalent Awards

The R01 (or R01-equivalent) grant has traditionally been a critical component to the launch of one's research career. A number of academic leaders have described and expressed concerns about the age at which scientists are first supported on an R01 award ("age at first R01"). The biomedical research workforce is aging over the past several decades due to demographic trends and the end of mandatory retirement in academia. Difficulties faced by early-career investigators may include prolonged training, advantages of incumbency, and cost-shifting to universities.

We have heard these concerns too, and recognize the potential impact on the future biomedical workforce. That is one of the reasons why, in the late 2000's, we implemented an Early-Stage

Investigator policy And, after considering recommendations from the Advisory Committee to the Director (ACD) and the National Academies of Sciences, NIH has over the past few years implemented its Next Generation Researchers' Initiative. NIH is funding record numbers of early stage investigators. We recently published data showing that long-term career stage trends may have stabilized.

Here we present data from fiscal years 1995 to 2020 on age at first R01-equivalent grant. Tables 1 and 2 and Figure 1 show secular trends for age distributions according to gender. There are no differences between men and women. While age has been continuously increasing, the rate of increase has slowed over the last 10 years.

Table 1: Age at receiving support on a first NIH R01 award for Principal Investigators self-identifying as men according fiscal year.

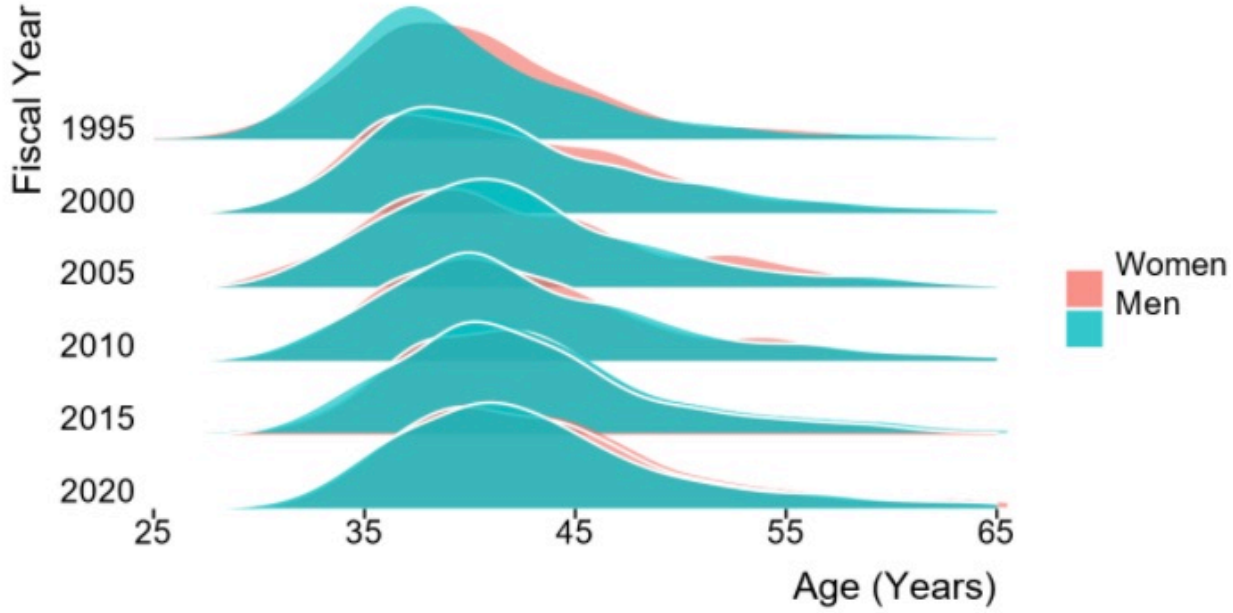
Fiscal Year	Number	Mean	Median	10th Percentile	25th Percentile	75th Percentile	90th Percentile
1995	897	40	38	33	36	43	47
2000	1027	42	41	35	37	46	52
2005	933	42	41	35	38	46	51
2010	1259	43	41	35	38	47	53
2015	1032	43	42	35	38	46	52
2020	1342	44	42	36	39	47	54

Table 2: Age at receiving support on a first NIH R01 award for Principal Investigators self-identifying as women according to fiscal year.

Fiscal Year	Number	Mean	Median	10th Percentile	25th Percentile	75th Percentile	90th Percentile
1995	376	40	39	34	36	43	47
2000	411	42	41	34	37	46	50
2005	404	42	41	34	37	46	53
2010	655	43	42	35	38	46	54
2015	522	43	42	36	38	46	52
2020	1003	44	42	36	39	47	53

Figure 1: Gender-based distributions by fiscal year of age of Principal Investigators receiving

support on NIH R01 award for the first time.



... to see more details

- ## Replace eRA Commons Password with Passphrase, Starting Sometime in November

While eRA has been transitioning users of eRA Commons, Commons Mobile, ASSIST and IAR to two-factor authentication using either Login.gov or an InCommon Federated Account that supports NIH's two-factor authentication standards, users will still need to maintain their eRA Commons username and password for the time being.

So eRA account credential maintenance will continue, at least for now, but not to worry, gone are the days of having to continually change your password every 120 days. NIH is moving from passwords to passphrases — a set of random words or a sentence at least 15 characters long — effective sometime in November (date to be confirmed). Passphrases will only need to be updated annually.

This change is part of a new NIH password policy designed to make passwords easy for users to remember but hard for others to guess. The new policy aims to improve user experience and enhance cybersecurity.

Once this new change is in effect, Commons users will be prompted to change their password to a passphrase when trying user credentials with an expired or forgotten password. Users are advised to avoid words that can be easily guessed, such as family names.

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.*

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.