

Researchers design COVID-19 knowledge base and risk assessment tool powered by AI

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A sample screenshot of the COVID-19 knowledge base dashboard under development. The screen shows four types of COVID-19 related entities, virus (blue), cell (pink), gene or genome (green), and disease or syndrome (red), and their relationships. All entities are Unified Medical Language System (UMLS) compatible for convenient knowledge sharing. The systems support 75 types of UMLS entities. Credit: Florida Atlantic University

Researchers from Florida Atlantic University's College of Engineering and Computer Science, in collaboration with FAU's Schmidt College of



Medicine, have received a one-year, \$90,000 National Science Foundation (NSF) RAPID project grant to conduct research using social networks and machine learning, facilitated by molecular genetics and viral infection, for COVID-19 modeling and risk evaluation. The project will create a web-based COVID-19 knowledge base, as well as a risk evaluation tool for individuals to assess their infection risk in a dynamic environment.

"COVID-19 is an evolving epidemic and there is little knowledge about its outbreak and spread patterns, or the impact of viral evolution, demography, social behavior, cultural differences, and quarantine policies regarding these outbreaks," said Stella Batalama, Ph.D., dean of FAU's College of Engineering and Computer Science. "As the battle against COVID-19 continues, a deluge of information is being produced. As a result, the dramatic outbreak differences with respect to diverse geographies, regional policies, and cultural groups is raising confusion, contradictions, and inconsistencies in disease outbreak modeling."

The FAU project, "RAPID: COVID-19 Coronavirus Testbed and Knowledge Base Construction and Personalized Risk Evaluation," will address these discrepancies by building a knowledge base of COVID-19 to understand the correlations and roles that different factors play in predicting the spread of the virus. The technology will result in the implementation of appropriate policies to mitigate the effects of the epidemic on <u>public health</u> and society-at-large.

"Academia, news agencies, and governments are continuously publishing advances in the understanding of the virus' clinical pathologies, its genome sequences, and relevant administrative policies and actions taken. In addition, the public also responds to the changing environments through <u>social media sites</u> or other online sources, resulting in real-time social sensing opportunities," said Xingquan (Hill) Zhu, Ph.D., principal investigator (PI) of the grant and a professor in FAU's Department of



Computer and Electrical Engineering and Computer Science. "This is why a knowledge base of COVID-19 using machine learning is so crucial for us to model and understand the spread of COVID-19, and eventually mitigate the negative effects of the virus on public health, society, and the economy."

The technical aims of the FAU project are two-fold. First, researchers will create a knowledge base that includes information for modeling outbreak and mutation of COVID-19, which will serve as a benchmark for better understanding the spread of the virus. The second aim of the project is to develop a multi-source deep neural network-based predictive tool to combine demographics, policies, regional infections, and individual information for risk evaluation.

"The COVID-19 knowledge base uses graph/network to represent entities and their relationships. The entities are fully compatible to the Unified Medical Language System or UMLS standard for convenient knowledge sharing. Supported by the knowledge base, the public will be able to employ information to estimate their infection risk level using social and behavioral information such as their family size, shopping patterns, and dining patterns, as well as local authority policies such as school, restaurant, and movie theater closures and night time curfews," said Zhu. "They also will have access to demographic information such as population age, density and income, as well as health conditions like heart disease incidence, cancer prevalence, and substance misuse. Public health officials and the public-at-large also will be able to access regional virus conditions such as the number of infection cases in the area studied and infection rate."

Co-investigators of the FAU NSF RAPID grant are Michael DeGiorgio, Ph.D., an assistant professor in the Department of Computer and Electrical Engineering and Computer Science; and Massimo Caputi, Ph.D., a professor of biomedical science in FAU's Schmidt College of



Medicine. Caputi has developed novel techniques to study RNA—RNA binding protein interactions, and has made important contributions in the understanding of how cellular proteins modulate the replication of the HIV-1 genome. He has expanded his research through collaborative grants for the development of microfluidic diagnostic devices to detect multiple viral species from blood and other bodily fluids.

Provided by Florida Atlantic University

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