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Award Abstract #2028728

RAPID: Epidemiological and Phylogenetic Models for Contact-Based Control of COVID-19

NSF Org:	**DMS** **Division Of Mathematical Sciences**
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Program Manager:	Zhilan Feng DMS Division Of Mathematical Sciences MPS Direct For Mathematical & Physical Scien
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Awarded Amount to Date:	$199,009.00
Investigator(s):	Cameron Browne cxb0559@louisiana.edu (Principal Investigator) Hayriye Gulbudak (Co-Principal Investigator)
Sponsor:	University of Louisiana at Lafayette 104 E University Ave Lafayette, LA 70503-2014 (337)482-5811
NSF Program(s):	COVID-19 Research
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ABSTRACT

The current COVID-19 pandemic shows that effective and responsive public health systems are crucial for curbing emergent outbreaks. Increased case detection, contact tracing, and broad quarantine and social distancing measures, have been vital for containing COVID-19 outbreaks. Mathematical modeling and analysis can provide important insights into the efficacy of these ?contact-based? non-pharmaceutical interventions. However, model parameterization requires detailed case data, which is often challenged by inconsistent, unreported and asymptomatic cases. To overcome these difficulties, the researchers will: develop outbreak models of COVID-19 with quarantine, tracing and social distancing and derive new results on final epidemic size and reproduction number under quarantine measures to flatten and shrink the epidemic curve. The researchers will also integrate case and phylogenetic data for an innovative framework that reveals region-specific control and predicts how to best implement contact-based measures for efficiently containing the outbreaks. Results will be communicated with policymakers, along with scientific and public audiences, in order to have a real-time impact on the coronavirus pandemic.

This project will consider compartmental outbreak models of COVID-19 with responsive quarantine, tracing and social

distancing measures. The novel formulation allows for derivation of outbreak size, dependent on contact tracing and broad quarantine intervention parameters. Reproduction number estimates and model fitting of case, tracing and quarantine data will quantify region-specific control characteristics. Sensitivity of epidemic size to combinations of contact tracing and social distancing measures will be assessed to understand viable strategies for flattening and shrinking epidemic curves. Long term scenarios of loosening and tightening of quarantine interventions for sustainable control will be investigated through analysis and simulation of the models. In addition, through interdisciplinary collaboration, the researchers will incorporate multi-region stochastic versions of the epidemiological models with phylodynamic computations of genomic data to improve model projections in the presence of possible unknown chains of transmission and area-specific responsive interventions. A ?forward simulation-backward coalescent? approach will track migration events and produce phylogenetic tree signatures for matching model simulations to phylogenetic data. The overall combined phylodynamic and epidemic model analysis will quantify heterogeneous disease spread and contact-based control efficacy to inform public health authorities.

This award is being funded by the CARES Act supplemental funds allocated to MPS.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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