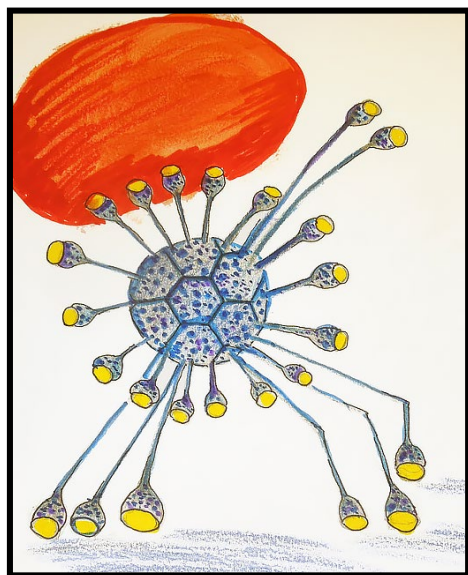


ONE HEALTH Codeathon

February 24-26, 2021 | Virtual Event



Collaborative coding in the time of COVID:

*Harnessing data
sciences against pandemics*

Sponsored by the USF Genomics Program

In partnership with the Global Virus Network

At this NCBI-style Codeathon, we will investigate pandemic initiation, spread, and public health interventions by integrating genomics, clinical data, geoscience, modeling, and social sciences. Projects developed within this event will consider questions such as:

- What host, viral, or environmental factors are predictive of pandemic emergence and spread in different populations?
- How can complex data-sources be integrated to create tools for public health intervention?
- What are the urgently needed 'dream applications' for future pandemic prevention and management?

**An introduction to Codeathons will be given during the USF Genomics Forum
on Tuesday, January 19 from 12:30-1:30 pm**

Register by February 5, 2021
at the [USF Genomics Website](#) or [Click Here](#)



**UNIVERSITY OF
SOUTH FLORIDA**



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Collaborative coding in the time of COVID:

Possible Team Projects:

- **Social Cost** – a tool to register social and emotional cost of pandemics. Pandemics have extracted a health toll not only in human physical health, but also in emotional and social health. A tool to monitor, register and quantify social cost of large epidemics is needed
- **Viral Discovery and Surveillance** – zoonotic viruses have a large reservoir with directly (viral or metagenomic databases) or indirectly (animal or human tissues) related to viruses, which may have been deposited in various databases. A tool of effectively mining through these databases and exploring the hidden viral diversity is needed.
- **Host Genetics** – efficient interrogation of human variants for disease outcomes. The viral infection outcome varies radically in terms of host co-morbidity, age, ethnicity, and other factors including human genetic variation.
- **Nonhuman Host Susceptibility** – prediction of selection pressures on other mammalian hosts and potential disease evolution. In the wake of Denmark's experience with the so-called "Cluster 5" of SARS-CoV-2 in mink farms, it is of interest and in the theme of One Health to evaluate potential reverse zoonotic disease transmission.
- **Genetic Evolution of Human Pathogens** – many RNA viruses are important human pathogens. RNA viruses generally have high mutation rates because of the lack of proofreading ability of their RNA polymerases. This mutation can also affect the protective efficacy of vaccines. Bioinformatics can be utilized to monitor genetic evolution of emerging and existing human RNA viruses.
- **Virus and Human Interactions** – explore the relationship between human virome and respiratory diseases. Human airways are colonized by many viruses not only causing acute symptomatic infections, but also without causing clinical symptoms. It will be necessary to define the virome in the human respiratory tract and to evaluate the effects of viral infections on the dynamics of lung diseases.
- **Microbiome and Infections Diseases** – introduce how the microbiome can impact the susceptibility to and severity of infectious diseases. What technologies can be applied and what are the available platforms of bioinformatics for infections diseases?
- **Respiratory Microbiome** – interrogate and explore air-borne microbiome diversities. There are myriads of microbes circulating in the air globally, including hundreds of respiratory viruses that occupy indoor spaces and public transportations.
- **Sewage Microbiome Mining** – mining and searching for potential pathogens. Many human viruses, including SARS-CoV-2, are able to replicate in the gastrointestinal track epithelial, and occur in human sewage systems. Efficient tools of monitoring the system and detecting potential pathogens can be used as part of urban health surveillance.

Other project ideas are welcome and can be submitted in the registration form.

We are still looking for Team Leads! If you are interested include this in your registration