**USF 2021 Codeathon Team Project Goals Descriptions**

**Team 1 (Side Effects)**

Leads: Anujit Sarkar & Agaz Wani

Members:Ashley Denslow, Ashley Lui, Ji Youn, Yoo, Krishna Sharma, Nicole Avalon, Peter Radulovic, Yibo Dong, Zoe Taylor

(1) Determine significant predictive factors for adverse events of SARS-CoV-2 mRNA based vaccines.

(2) Design a web-based interface with aims:  
a) Provide a predictive tool for medical providers to determine the risk of adverse events to SARS-CoV-2 mRNA vaccination via a machine learning algorithm.

b) Provide a place for visualization of publicly-available data regarding adverse events relating to the SARS-CoV-2 mRNA vaccine.

**Team 2 (Zoo-Cov)**

Leads: Swamy Rakesh Adapa & Thomas Keller

Members: Celine Grace F. Atkinson, William Cromwell, Raúl A. González-Pech, Kyle Koller, Morgan Young

A GUI to identify putative host switches (human to non-human). The basic idea is to look for sequences that are say, bat or mink derived, but are part of the human clade of the phylogeny. Then we could highlight mutations that have occurred since the most recent human sequence.

**Team 3 (Viral Spacetime) - Exploring COVID-19 mutation rate covariates**

Leads: Ryan McMinds & Jesper Madsen

Members: Janelle Donglasan, Samuel Coleman, Omkar Dokur, Jan Dahrendorff, Ann Mathew, Sofia Bhatia

In order to explore the factors that lead to faster pathogen evolution, we plan to link geographic information from sequenced COVID genomes to the degree of divergence from inferred ancestral states, and build a simple tool hosted on GitHub that will correlate arbitrary geographic metadata with these divergence rates.

**Team 4 - Social Cost**

Leads: Jenna Oberstaller & Justin Gibbons

Members: Cameron Parsey, Alyssa Obermayer, Samira Jahangiri, Vyoma Sheth, Teresa Darcey, Justin Swanson

The goal of our project is to address vaccine and resource distribution and disparities as well as vaccine hesitancy by providing the public with pertinent and easily accessible data on COVID-19 cases and risk factors/vulnerability indices, as well as social media-derived sentiment analysis.

**Team 5** - **DECODE human breath microbiomes**

Leads: Rays Jiang & Minh Pham

Members: Andrea Vianello, Sylvia Thiong’o, Ojas Natarajan, John Parkinson, Long Dang, Jinyong Pang, Gloria Ferreir

Goals: We share the air we breathe, especially in a tightly urbanized world with rapid population growth. Average adult human breathe over 10,000 liters air per day. Yet, current monitoring of airborne pathogens is limited. we aim to identify breath microbiomes and viromes by integrating data from human airways, indoor viromes and microbiomes captured from air in urban settings. We will produce the first comprehensive breath virome/microbiome mapping**.** We aim at recognizing the hotspots and dynamic patterns of pathogen emergence from microbiomes and viromes captured in different environments for surveillance and preventions.

**Team 6 - Spatial-Temporal Prediction Models for COVID-19**

Leads: Awtum Brashear, Jing Lin, & Ming Ji

Members: Michelle Grundahl, Santiago Hernandez, Weiliang Cen, Sur\endra Kolli, Siva Allam, Chang Li, Charley

In order to establish a spatially informed COVID-19 model, we plan to (1) automatically pull COVID-19 daily cases and deaths from 1point3acres.com; (2) apply spatial-temporal prediction modeling to generate predictions of future COVID-19 daily cases and deaths; (3) disseminate our model through GitHub, an Online Dashboard and the CDC COVID-19 Forecast website.