Team 3 – Source Tracking of COVID-19 Infection by Rapid Sequencing

**Need:**
- 160M COVID-19 cases worldwide
- Highly contagious variants of COVID-19
- Aid contact-tracing efforts
- Support Drexel COVID Task Force to monitor the spread on campus

**Objective:** Design a process to **visualize the relationship between COVID-19 sequences** to distinguish between community spread and novel traveler spread and identify varying strains of the virus to help guide contact tracing

**Solution Design**
1. Receive prepped sample (from Drexel COVID-19 Taskforce)
2. Perform real-time genome sequencing
3. Create network diagram of same-state and same-variant clusters (Our solution: COVID-trace)

**Design Inputs**
1. Software must be able to achieve **accuracy ≥ 90%**
   - Sample variant must be accurately identified
   - Sample US state must be accurately identified
2. Time to complete full analysis must be **less than 7 days**
   - Sequencing must be completed in less than 24 hours
   - Network Diagram/Covariant analysis must be completed in less than 24 hours

**Solution Build**
- Disease transmission clusters identified by region and variant
- Pennsylvania
- Texas
- New York

**Testing Results**
- Our sequencing was **99.98%** accurate compared to the gold standard
- Correctly identified a sample’s variant with **100%** accuracy
- Time per full analysis: **< 25 hours**

**Future**
- First time sequencing has been done on a COVID sample within Drexel
- Help understand transmissibility and infectivity of COVID-19
- Can be adapted and applied to future pandemics

**Team Members**
- Arun Balaji
- Abbey Crider
- Matthew Falcione
- Sofia Tanvir

**Advisor**
- Dr. Will Dampier