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

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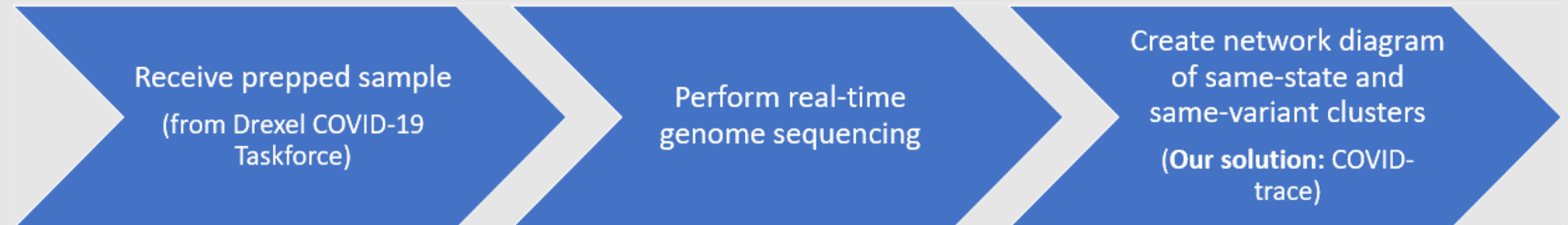*Arun Balaji*
Abbey Crider
Matthew Falcione
Sofia Tanvir

Advisor
Dr. Will Dampier

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
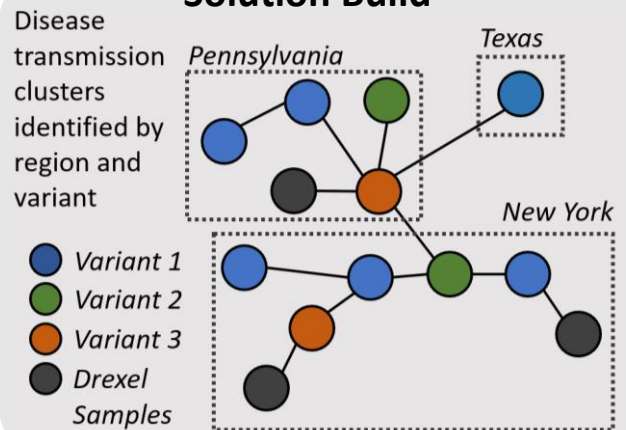
Design Inputs

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 Design

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

Solution Build

Disease transmission clusters identified by region and variant

Pennsylvania — Texas — New York

Legend:
- Variant 1
- Variant 2
- Variant 3
- Drexel Samples

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