



Coronavirus Research at the JGI

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- JGI has developed pipelines for identifying and analyzing RNA viruses and is deploying these in an Exabiome-funded project
- JGI is leading the “High-throughput Characterization of Viral-Host Interactions” project
- JGI staff have played key roles in assisting developing IGI’s automated SARS-CoV-2 diagnostics facility that has processed >1000 samples
- With our core capabilities in sequencing and genomics, JGI has proposed and is on several new R&D proposals for the National Virtual Biotechnology Lab e.g. viral mutation analysis, metagenomic analyses, visualization tools
- JGI is providing support for establishing a new lab for COVID-19 research on the hill
- JGI received \$3M for state-of-the-science equipment to support COVID-19 and JGI User Mission research
- IGB staff have raised almost \$6000 for the Food Bank of Contra Costa and Solano

- Key Personnel: Russell Neches, Nikos Kyrpides
- **Exploring ancestral recombination and evolutionary origins of SARS-CoV-2:**

Goal: Develop computational and ML/AI approaches to study the evolutionary and recombination patterns of SARS-CoV-2 to decipher its evolutionary origins.

Approach: Utilize existing tools (e.g., ARGweaver, ClonalOrigin, InferRho) to examine SARS-CoV-2 and relevant outgroup genomes for evidence of recombination

Implications: Recombination takes place in some retroviruses but is not well understood in coronaviridae and may play a role in determining whether the COVID-19 can be effectively controlled with vaccines.

If SARS-CoV-2 strains are able to recombine with one other or with other coronavirus species, a vaccine may only confer seasonal protection.

Progress: Russell been working on automating the cleaning of formatting problems from the data we have been getting from GISAID. A script to do that has been completed and shared with the Exabiome team on Slack.

High-throughput characterization of viral-host interactions

- Key Personnel: Simon Roux (PI), Adam Deutschbauer (Co-PI), Vivek Mutalik (Co-PI)
- Need for high-throughput & high-resolution understanding of virus-host dynamics

3 Goals:

- Fast genome-wide screens for **regulators of virus-host interactions**
- Characterize eco-evolutionary **drivers of resistance mechanisms**
- Obtain **quantitative virus-host networks**

Safety considerations and how they are being addressed

- This project will most likely handle any COVID-19 samples so normal lab safety measures will be employed

