



Bioinformatics Solutions for SARS-CoV-2 Genomic Analysis

Overview of the PHA4GE Guidance Document

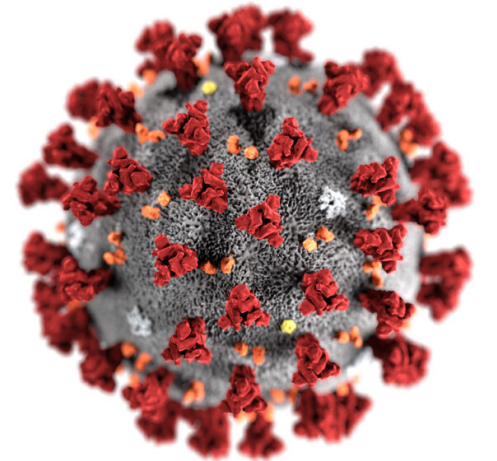
Kevin G. Libuit, MS - PHA4GE Bioinformatics Pipelines and
Visualization Working Group Co-Chair

Guidance Document Overview

Defining the major challenges and highlighting solutions

Genomic analysis of SC2 is an increasingly critical function of public health laboratories around the world

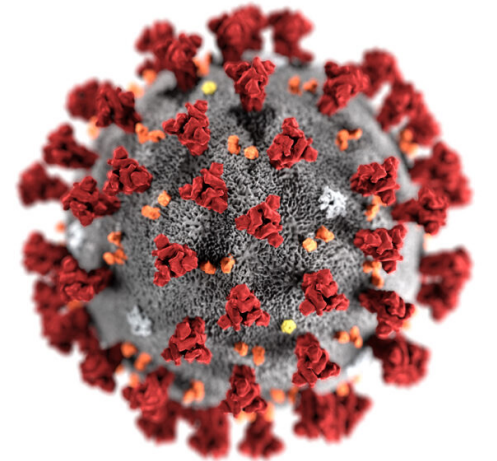
- PHA4GE document aims to assist in the integration of bioinformatics solutions by
 - Categorizing the major challenges
 - Curating resources to address challenge



SC2 Bioinformatics Challenges

Four key challenges for public health laboratories

1. Generating consensus assemblies from PCR tiling NGS data
2. Submitting data to internationally-accessible databases
3. Screening sequenced SC2 samples for variants of concern
4. Performing phylogenetic analysis of SC2 datasets



PHA4GE Guidance Document

Curation of Open Access/Source Solutions

Landing page of reference documents and bioinformatics software that address the four major challenges

- [Published as a public GitHub page](#) to allow for continuous updates and collaborative development

