

Overcoming challenges of SARS-CoV-2 genomics data  
harmonization and integration for public health  
surveillance, outbreak investigations and research using the  
PHA4GE SARS-CoV-2 contextual data specification

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Sequencing SARS-CoV-2 genomes has helped track the spread of the virus worldwide.

## Sequence data



## Contextual data



Sample metadata



Lab results



Clinical/Epi data



Methods

**Contextual data** (metadata) used for **surveillance** and **outbreak investigations**:

- **characterize** lineages and clusters
- identify variants with **clinical significance**
- correlate genomics trends with **outcomes, risk factors**
- **inform decision making** for public health responses and **monitor effects of interventions**

# Challenge: How data is encoded impacts how it can be integrated and used for analyses.

Specimen:

Specimen Collected
<input type="checkbox"/> Upper respiratory (e.g., Nasopharyngeal or oropharyngeal swab)
<input type="checkbox"/> Lower respiratory (e.g., sputum, tracheal aspirate, BAL, pleural fluid)

6 - Specimen Type (check all that apply)	
Specimen Collection Date: yyyy / mm / dd (required)	
<input type="checkbox"/> NPS in UTM	<b>If possible:</b>
<input type="checkbox"/> Throat Swab in UTM	<input type="checkbox"/> BAL
<input type="checkbox"/> Other (Specify):	<input type="checkbox"/> Sputum

Patient Setting:

7 - Patient Setting / Type		
<input type="checkbox"/> Assessment Centre	<input type="checkbox"/> Family doctor/clinic	<input type="checkbox"/> Outpatient/ER not admitted
Only if applicable, indicate the group:		
<input type="checkbox"/> Healthcare worker	<input type="checkbox"/> Institution / all group living settings	
<input type="checkbox"/> Inpatient (hospitalized)	<input type="checkbox"/> Confirmation (for use <b>ONLY</b> by a COVID testing lab). Enter your result (NEG/POS/or IND)	
<input type="checkbox"/> Inpatient (ICU/CCU)		
<input type="checkbox"/> First Nations / Inuit		
<input type="checkbox"/> Unhoused / shelter	<input type="checkbox"/> For clearance of disease	
<input type="checkbox"/> ER - to be hospitalized	<input type="checkbox"/> Other (Specify):	
<input type="checkbox"/> Deceased / Autopsy		

<input type="checkbox"/> Acute care facility	<input type="checkbox"/> Long term care facility
<input type="checkbox"/> Group home (community living)	
<input type="checkbox"/> Correctional facility	<input type="checkbox"/> School or daycare
<input type="checkbox"/> Assisted living	<input type="checkbox"/> Independent living
<input type="checkbox"/> Other residential facility type, specify: _____	
<input type="checkbox"/> Shelter	<input type="checkbox"/> Conference

# Getting the right information to the right people is critical during health emergencies.

- Need to share data: **within** organization, with **trusted partners**, with **international** agencies/**public** repositories

<b>isolate</b>	SARS-CoV-2/186197/human/2020/Malaysia
<b>collected by</b>	Universiti Malaya COVID Research group
<b>collection date</b>	14-Mar-2020
<b>geographic location</b>	<a href="#">Malaysia</a>
<b>host</b>	Homo sapiens
<b>host disease</b>	COVID-19
<b>isolation source</b>	Nasopharyngeal/throat swab
<b>latitude and longitude</b>	<a href="#">3.1390 N 101.6869 E</a>

<b>source name</b>	Lung sample from postmortem COVID-19 patient
<b>cell type</b>	Lung Biopsy
<b>strain</b>	NA
<b>subject status</b>	No treatment; >60 years old male COVID-19 deceased patient

Compare these public datasets:

- different **standards**
- different **granularity**
- **free text**
- different **formats**
- different **interpretation**
- **privacy** concerns
- **methods**

Different data structures make information less interoperable and more difficult to integrate.

That means you need to spend more time and resources to clean/re-structure information before you can use it.



# Public Health Alliance for Genomic Epidemiology

Data Structures | Bioinformatic Pipelines and Visualizations | Infrastructure  
Public Repositories | Reference, QC and Validation | Workforce Development  
Data Sharing and Ethics | Users and Applications

<https://www.pha4ge.org>

| <https://www.github.com/pha4ge>

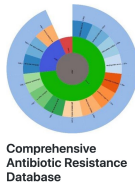
|  @pha4ge

# Data Structures Working Group

- 21 Members (9 countries, 4 continents)

## Goal: develop/promote data standards

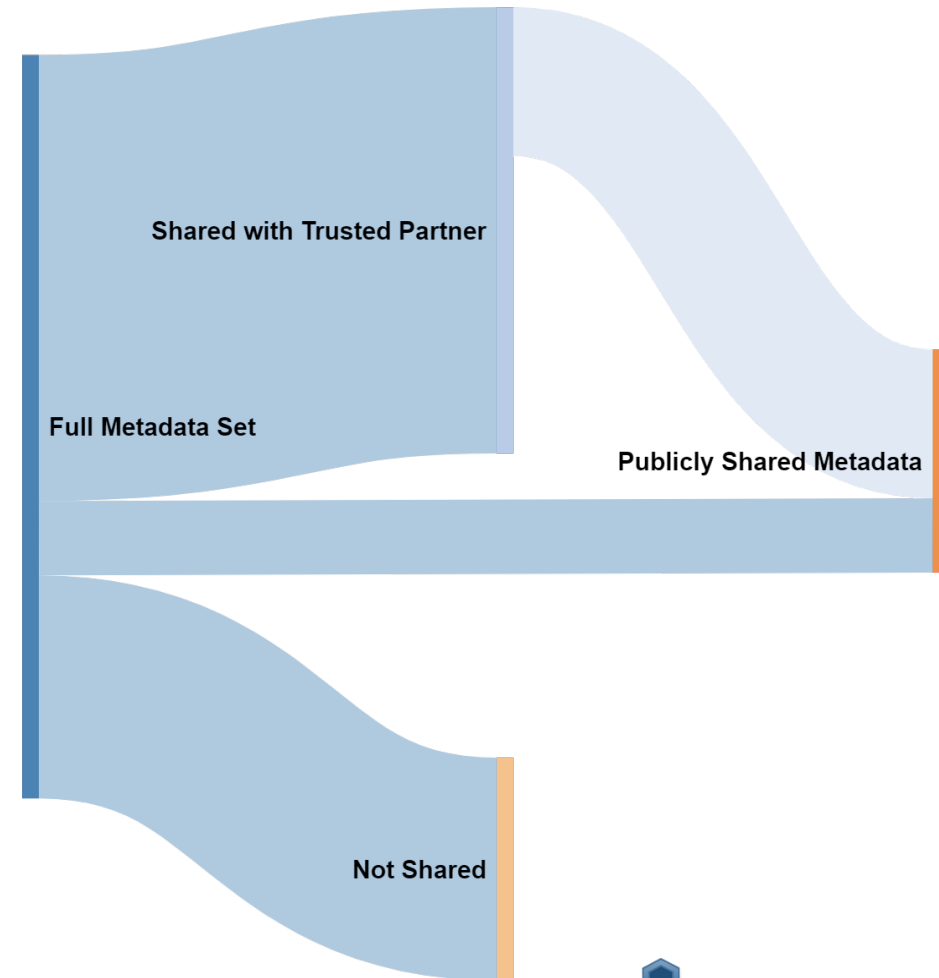
- COG-UK, SPHERES, CanCOGeN, Latin American Genomics Network
- identified need for fit-for-purpose contextual data standard for SARS-CoV-2 genomics



# The SARS-CoV-2 Contextual Data Specification Package

## PHA4GE SARS-CoV-2 Full Specification Content

Repository accession numbers and identifiers  
Sample collection and processing  
Host information  
Host exposure information  
Sequencing methods  
Bioinformatics and quality control metrics  
Pathogen diagnostic testing details  
Provenance and attribution







# Supporting documentation

The screenshot shows the GitHub repository page for 'pha4ge / SARS-CoV-2-Contextual-Data-Specification'. The repository is on the 'master' branch with 1 branch and 3 tags. It has 48 commits. The commit history is as follows:

Commit Message	Commit Hash	Date	Commits
PHA4GE Contextual Data SOP.docx	2c69e91	on Jul 15	48 commits
PHA4GE SARS-CoV-2 Contextual D...			
PHA4GE SARS-CoV-2 EBI assembly...			
PHA4GE SARS-CoV-2 EBI submissi...			
PHA4GE SARS-CoV-2 GISAID Subm...			
PHA4GE SARS-CoV-2 NCBI assemb...			
PHA4GE SARS-CoV-2 NCBI submis...			
PHA4GE SARS-CoV-2 Standardised...			
PHA4GE SOP for populating EBI su...			
PHA4GE SOP for populating NCBI s...			
PHA4GE to Sequence Repository Fi...			
PHA4GE_SARS-CoV-2_Contextual_...			
README.md			

- **SOP:** how to use specification, find new terms, highlight practical/ethical/privacy issues
- **Field mapping to existing standards:** highlight alignment and gaps
- **JSON schema:** machine readable

<https://github.com/pha4ge/SARS-CoV-2-Contextual-Data-Specification>

# Protocols to mobilize harmonized data

The screenshot displays the PHA4GE workspace on the Protocols.io platform. The workspace is titled "Workspaces / PHA4GE / Publications" and features a navigation menu with options like ADMINISTRATION, NEW, UPGRADE, WORKSPACE FOLDER (8), TASKS, EXPORT GROUP PUBLICATIONS, and CONTACT ADMIN. The main content area shows a list of publications under the "Publications" tab, which has 7 items. Two publications are visible, both dated Jul 09, 2020, and associated with the ENA (European Nucleotide Archive) logo. The first publication is titled "SARS-CoV2 EBI assembly submission protocol" and the second is "SOP for populating EBI submission templates (ENA)". Both publications list authors: Nabil-Fareed Alikhan<sup>1</sup>, Emma Griffiths<sup>2</sup>, Ruth Timme<sup>3</sup>, and Duncan MacCannell<sup>4</sup>. The affiliations are: <sup>1</sup>Quadram Institute Bioscience, <sup>2</sup>University of British Columbia, <sup>3</sup>US Food and Drug Administration, and <sup>4</sup>Centers for Disease... Both publications are associated with the "Coronavirus Method Development Community" and "PHA4GE" tags. The contact for both is Nabil-Fareed Alikhan. The first publication has 49 views and the second has 28 views.

- **7 public repository submission protocols (GISAID, NCBI, EMBL-EBI) on **Protocols.io****

<https://www.protocols.io/workspaces/pha4ge>

# Uptake: early adopters



**Welcome to AusTrakka**  
From genomics to public health decisions for Australia

**Combining Genomics & Epidemiological Data**  
Human, Environment or Food Sample  
Genomic and Epidemiological Data

**Promoting Data Sharing Across Public Health Labs**

**Ensuring Better Health Outcomes for Australians**  
More Efficient Public Health Outcomes  
Healthier Australia

The graphic is a white rectangular area with a green shield icon at the top center. It contains three columns of information. The first column has a green header, a green box with icons of a person, a hospital, and a leaf, and a pink box with a DNA helix and a document icon. The second column has a map of Australia with data points. The third column has a blue box with a stethoscope, clipboard, and monitor icon, and an orange box with a group of people icon.

# Want to know more?

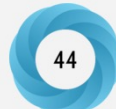
preprints.org > doi: 10.20944/preprints202008.0220.v1

Preprint Article Version 1 **This version is not peer-reviewed**

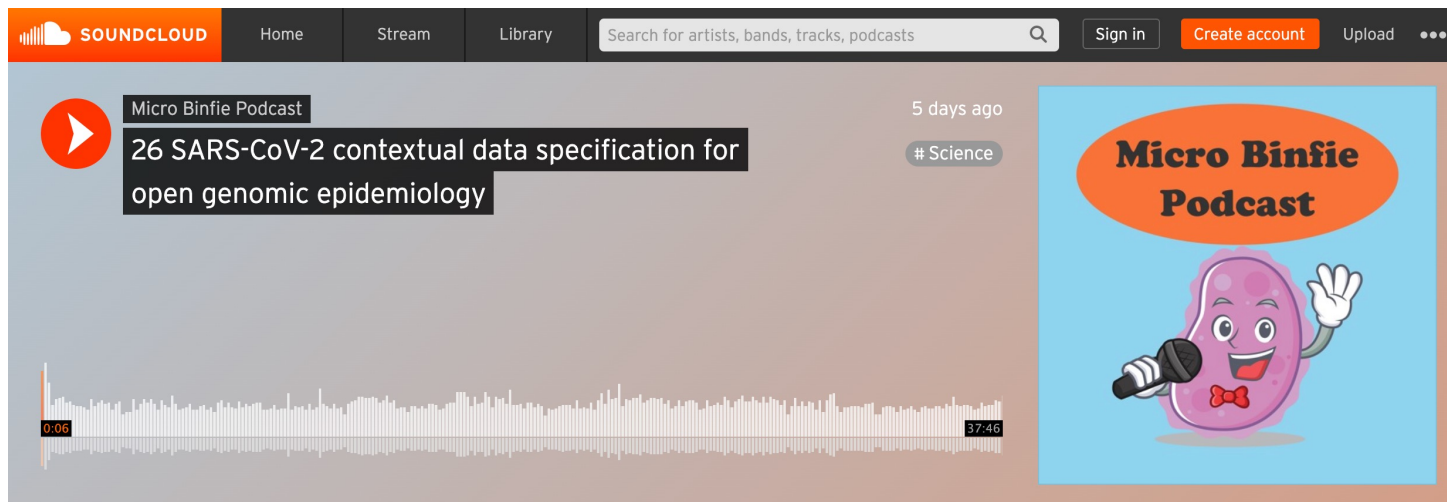
## The PHA4GE SARS-CoV-2 Contextual Data Specification for Open Genomic Epidemiology

Emma J. Griffiths\*, Ruth E. Timme , Andrew J. Page, Nabil-Fareed Alikhan, Dan Fornika, Finlay Maguire, Catarina Inês Mendes, Simon H. Tausch , Allison Black, Thomas R. Connor, Gregory H. Tyson, David M. Aanensen, Brian Alcock, Josefina Campos, Alan Christoffels , Anders Gonçalves da Silva, Emma Hodcroft, William W.L. Hsiao, Lee S. Katz, Samuel M. Nicholls, Paul E. Oluniyi, Idowu B. Olawoye, Amogelang R. Raphenya, Ana Tereza R. Vasconcelos, Adam A. Witney, Duncan R. MacCannell

Version 1 : Received: 7 August 2020 / Approved: 9 August 2020 / Online: 9 August 2020 (15:53:58 CEST)

Views	Downloads
942	152
Comments	
0	44

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Cite



Stay tuned for  
workshops coming  
soon!



# Summary

- contextual data is critical for **interpreting** genomics data/analyses
- specification structures metadata **consistently across labs**
- share with **public** repos, **trusted partners**, use for more **efficient private analyses**
- **future-proof** metadata
  
- success depends on community uptake

Ongoing challenges: trust, equitable data sharing, better understanding of risk, co-ordination, sharing mechanisms

→ **public health genomics ecosystem**

Thank you to  
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### **Data Structures Team**

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**This work would not be possible without  
the contributions and dedication of  
these wonderful people.**

Find us:

<https://www.pha4ge.org>

<https://www.github.com/pha4ge>

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Public Health Alliance for  
Genomic Epidemiology