Centre for Infectious Disease Genomics and One Health
Blusson Hall, Simon Fraser University, Burnaby
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General Needs Assessment Questionnaire

Version 2.0

Tips for interviewers

- **Before the interview:** Review the project's goals and tailor prompts to the stakeholder's role (collector, analyst, user).
- **During the interview:** Encourage open discussion — focus on how data are collected, structured, and shared.
- **After the interview:** Summarise and extract discrete data concepts, tools, and issues into the Needs Assessment Summary Matrix for comparison across interviews.

Scope and audience

Instructions: Ask the interviewee to describe the main aims of their work or project.

What are the questions your project/initiative is trying to answer (e.g. surveillance, research, monitoring a specific pathogen or target)?

Who are your partners? *Informs data flow, sharing, harmonization needs*

Sampling strategy

Instructions: Capture information on collection devices and methods, sample identifiers, and any relevant data practices that pertain to the sampling event.

What kinds of samples are collected (host, environmental, food, wastewater, etc.) and what is the sampling frequency and duration?

Are you using any previously collected samples? *Speaks to purpose of sampling/sample bias, as well as data reuse*

What contextual data is being collected alongside the samples (e.g. hosts demographics, physico-chemical measurements, weather, location, proximal location, presampling activities, collection method, collection device etc)

Is there a sample plan? Is the sample plan, experimental design, or any other material accessible?

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Specimen processing

Instructions: Capture information related to specimen processing

Are the samples subjected to any special processing before sequencing (e.g. filtering, enrichment, culturing, etc)?

If samples are cultured, what kinds of media and conditions are being used?

Specimen receipt and storage

Instructions: Capture information related to receiving of the specimen including condition and environmental measurements, as well as storage. If samples move between institutions, note how information is transferred and whether receipt or integrity data are recorded.

How are samples stored and for how long (e.g. temperature, duration, location tracking)? *Speaks to cold chain process and comparability.*

Are there receipt processes (e.g., documentation, quality checks, chain-of-custody)?

Library preparation

What are the primary sequencing assays (e.g WGS, WRS, amplicon etc)?

What library preparation or enrichment methods are applied?

Are you using commercial library kits or in-house developed methods?

What are your controls? *Speaks to tracking endogenous controls, replicates, synthetic constructs/data*

Sequencing and Bioinformatics

Instructions: Capture any information relating to the sequencing event, including processes, instruments, result types (e.g., consensus sequences, AMR detection, lineage assignment).

What sequencing instruments are being used?

What bioinformatics tools, pipelines and reference databases are being used? Are there any community workflows or tailored scripts?

How is quality control done and recorded?

Data Management

Instructions: Capture information on how data are recorded, organised, and transferred. Ask about systems or tools used for managing data and how these integrate with collaborators' workflows. Probe for limitations or pain points in data access, structure, and sharing.

How is the contextual data being captured (e.g. spreadsheets, LIMS, RedCap etc)?

Are any data standards being used to structure the data? If not, would there be an interest in using a standard?

Where is the data being stored (e.g locally, public repositories, network databases)?

What are the data sharing workflows - where does it need to go, how does it get there? Are there any restrictions?

During data flow, will the data need to be transformed?

Are there any governance, policy or privacy challenges?

Is there a plan to share the data publicly? If no, why?

Associated Data Types

Instructions: Explore whether other types of analyses or measurements accompany the main sequencing or contextual data. Examples may include clinical data, biochemical assays, environmental measurements, or laboratory testing results. Identify which of these should be linked to or referenced in the data specification (e.g. indicating availability of AMR data, qPCR results, or phenotypic assays).

Are there any other data types or characterizations available for the samples or sequences that were not previously mentioned as contextual data?

Which of these would be useful to indicate availability alongside the sequencing data?

Future Work (anticipating future needs)

Instructions: Encourage the interviewee to reflect on upcoming projects, changing technologies, or unmet needs. Ask what additional data types, tools, or systems they anticipate using, and what current pain points they would like to resolve. This section helps identify emerging requirements for interoperability and standardization.

What data types would you want to collect/foresee integrating in the future?

What are your main contextual data challenges?

What would be on your contextual data wishlist?

Appendix A: Document Revision History

Version	Date	Writer	Description of Change
1.0	March 2025	Emma Griffiths	Initial draft
2.0	17th October 2025	Charlie Barclay	Added additional context in the form of instructions, restructured for clarity and added specimen receipt section