

19 March 2021

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Standards to support Genomic Surveillance

Jack Collins
Frederick National Lab
(sponsored by NCI)

Coronavirus Standards Working Group

What should a Coronavirus Standards Working Group do?



Assure development and availability of standards, controls, interlab testing, knowledge to support successful rollout & scaling of 2019-nCoV testing



Identify and develop critical infrastructure to support...

- confidence in test results
- interoperability
- scale-up
- long-term capacity



Identify best practices that should be institutionalized

Learn what we need to so next time we have a global network in place ready to make standards.

Agenda



Updates



Standards to
support genomic
surveillance

Jack Collins

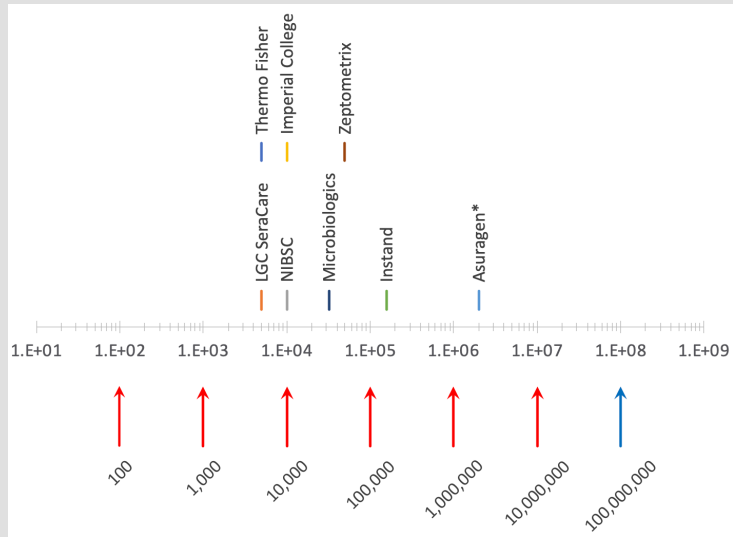
Updates

Viral RNA Standards Harmonization Study

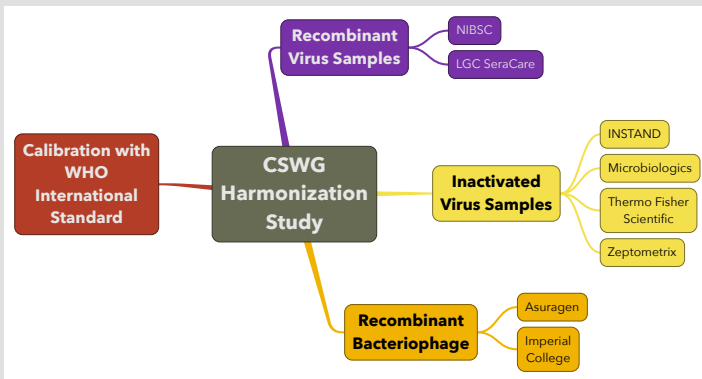
- Zeptomatrix samples found in our freezer
- Zeptomatrix samples shipped, panels now complete
- Panel to Slovenia lost; reshipment on Monday

Serology Standards Harmonization Study

- Neil Almond of NIBSC presenting next week
- Working with May Chu and team at Colorado School of Public Health Anschutz Medical Center on study development
- Coordinating with Ligia Pinto and Troy Kemp of Frederick National Lab (leaders of SeroNet project)



Zeptomatrix sample
now included in panel



Timeline for results

April 9

Jack Collins, FNL

Standards for SARS-CoV-2 Genomic
Surveillance

What can we do to support community to understand & report sequencing data quality?

What can we do to be confident in genomic surveillance?

Shared, widely available genome reference samples	Authoritative Characterization	Open Data	Reference Pipeline	Benchmarking Tool
<ul style="list-style-type: none">• Establish a library of reference samples representing strains of interest• use strain library from BEI	<ul style="list-style-type: none">• Integrate results from multiple sequencing platforms• distinguish between variation and sequencing artifacts	<ul style="list-style-type: none">• Make available raw data from characterization<ul style="list-style-type: none">• multiple technologies• data support methods development	<ul style="list-style-type: none">• Make available full analysis for characterization<ul style="list-style-type: none">• offer prototype analysis pipeline for field use	<ul style="list-style-type: none">• Enable field use of reference samples to evaluate performance of...<ul style="list-style-type: none">• wet lab• dry lab

Deliver technology-agnostic standards for Wet Lab -> Dry Lab -> Public Health

Standards like these enable...

Transparent knowledge of method performance

- labs can know what to expect

Optimization

- labs can balance cost, quality, speed

Interoperability

- data can be shared, aggregated, and compared

Consistency of data in public repositories

- repositories can be of known quality

Public health decision- making

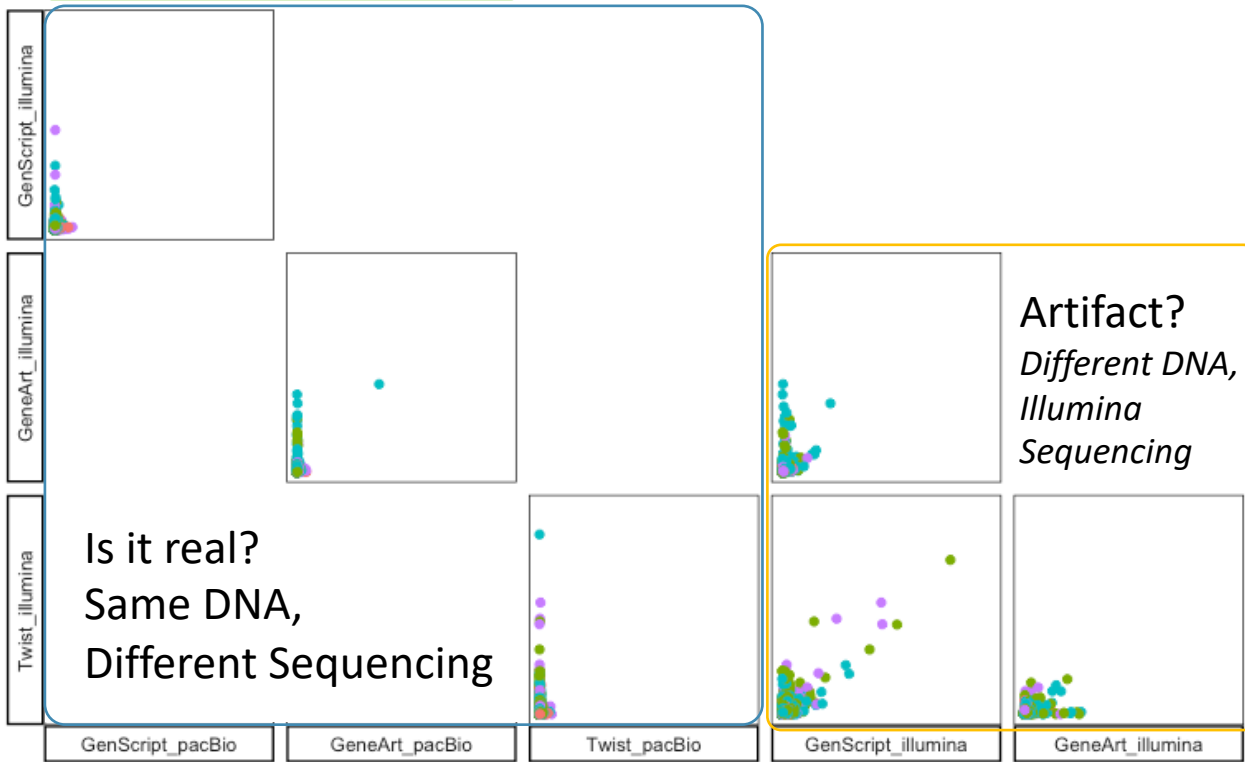
- based on trustworthy objective data

Model for enduring approach for what comes next

- institutionalize exemplar capability



These are SNP frequency correlations.
Graphs all on 2% allele fraction scale.
Represents about 500 kB of sequence.



Homopolymer Size • >3 • Size_1 • Size_2 • Size_3

Sequence on multiple platforms

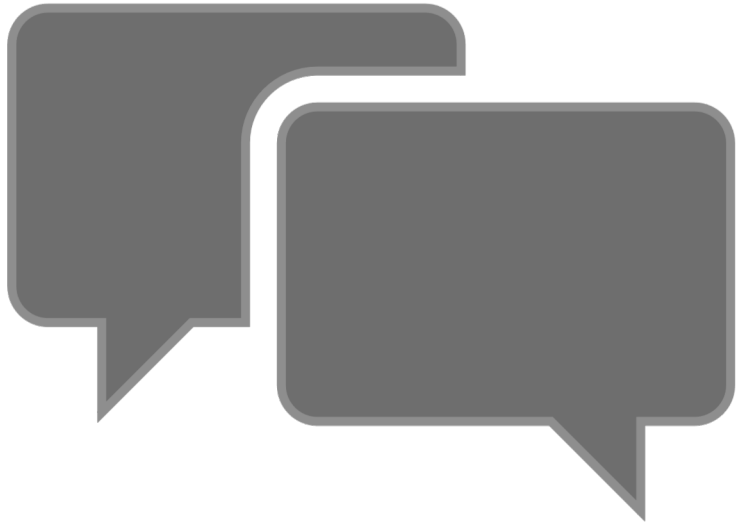
Distinguish between sequencing artifacts and variants in the DNA

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Discussion

