



How WGS/NGS is reshaping the future of Food Safety

Eric L. Stevens, Phd
Hygiena

Vertical Segment Manager - Food

October 21, 2025

- **Where are we now**
 - Landscape of Public Health Agencies/Industry/Academia
 - When traditional methods vs WGS/NGS
- **What does the future look like (or is it already here?)**
 - Risk
 - RCA
 - Metagenomics
- **How are we going to get there?**
 - Words of Caution
- **General Summary**

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General Interest

Use of Whole Genome Sequencing by the Federal Interagency Collaboration for Genomics for Food and Feed Safety in the United States

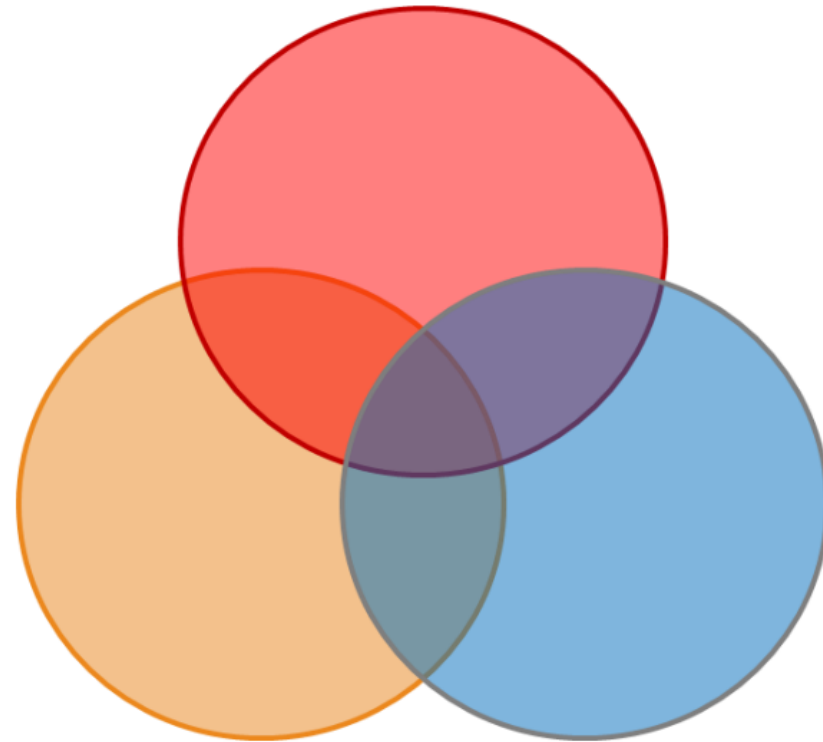
ERIC L. STEVENS¹<https://orcid.org/0000-0001-6044-7611>,^{1*}† **HEATHER A. CARLETON**,²† **JENNIFER BEAL**,¹† **GLENN E. TILLMAN**,³ **REBECCA L. LINDSEY**,² **A. C. LAUER**,² **ARTHUR PIGHTLING**,¹ **KAREN G. JARVIS**,¹ **ANDREA OTTESEN**,¹ **PADMINI RAMACHANDRAN**,¹ **LESLIE HINTZ**,¹ **LEE S. KATZ**,² **JASON P. FOLSTER**,² **JEAN M. WHICHARD**,² **EIJA TREES**,² **RUTH E. TIMME**,¹ **PATRICK McDERMOTT**,⁴ **BEVERLY WOLPERT**,¹ **MICHAEL BAZACO**,¹ **SHAOHUA ZHAO**,⁴ **SABINA LINDLEY**,¹ **BEAU B. BRUCE**,² **PATRICIA M. GRIFFIN**,² **ERIC BROWN**,¹ **MARC ALLARD**,¹ **SANDRA TALLENT**,¹ **KARI IRVIN**,¹ **MARIA HOFFMANN**,¹ **MATT WISE**,² **ROBERT TAUXE**,² **PETER GERNER-SMIDT**,² **MUSTAFA SIMMONS**,³ **BONNIE KISSLER**,³ **STEPHANIE DEFIBAUGH-CHAVEZ**,³ **WILLIAM KLIMKE**,⁵ **RICHA AGARWALA**,⁵ **JAMES LINDSAY**,⁶ **KIMBERLY COOK**,⁶ **SUELEE ROBBE AUSTERMAN**,⁷ **DAVID GOLDMAN**,³ **SHERRI McGARRY**,² **KIS ROBERTSON HALE**,³ **UDAY DESSAI**,³ **STEVEN M. MUSSER**,¹ AND **CHRIS BRADEN**²

¹U.S. Food and Drug Administration, Center for Food Safety and Applied Nutrition, College Park, Maryland 20740; ²Centers for Disease Control and Prevention, Division of Foodborne, Waterborne and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, Atlanta, Georgia 30329; ³U.S. Department of Agriculture, Food Safety and Inspection Service, Washington, DC 20250; ⁴U.S. Food and Drug Administration, Center for Veterinary Medicine, Laurel, Maryland 20708; ⁵National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Maryland 20894; ⁶U.S. Department of Agriculture, Agricultural Research Service, Beltsville, Maryland 20705; and ⁷U.S. Department of Agriculture, Animal and Plant Health Inspection Service, Ames, Iowa 50010, USA

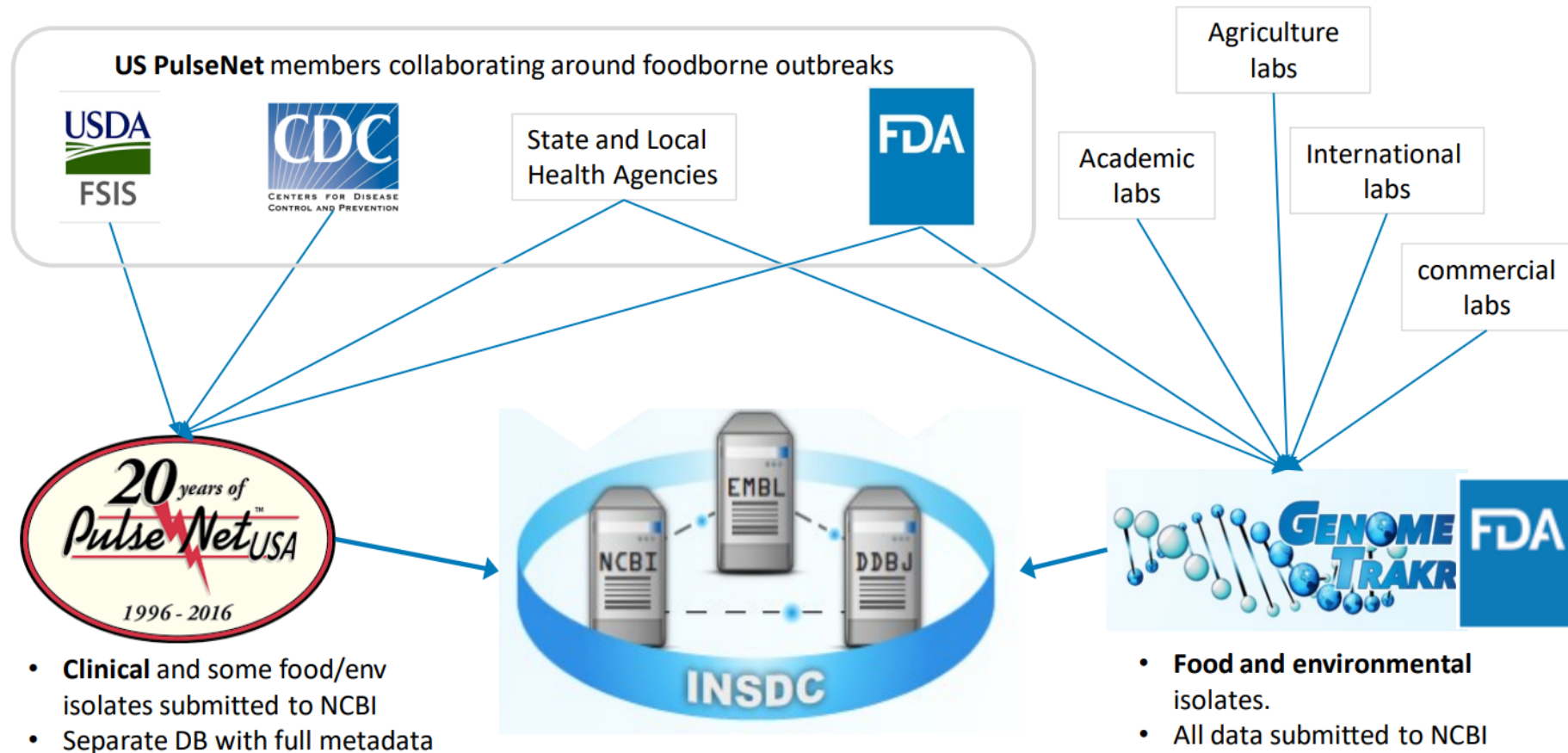
Identifying an Outbreak Vehicle: Lines of Evidence

Three types of evidence used:

- **Epidemiologic**: association between illness and food exposure
- **Traceback**: suspected food item links back to a common source of contamination
- **Microbiologic/laboratory**: pathogen found in the food, farm or facility



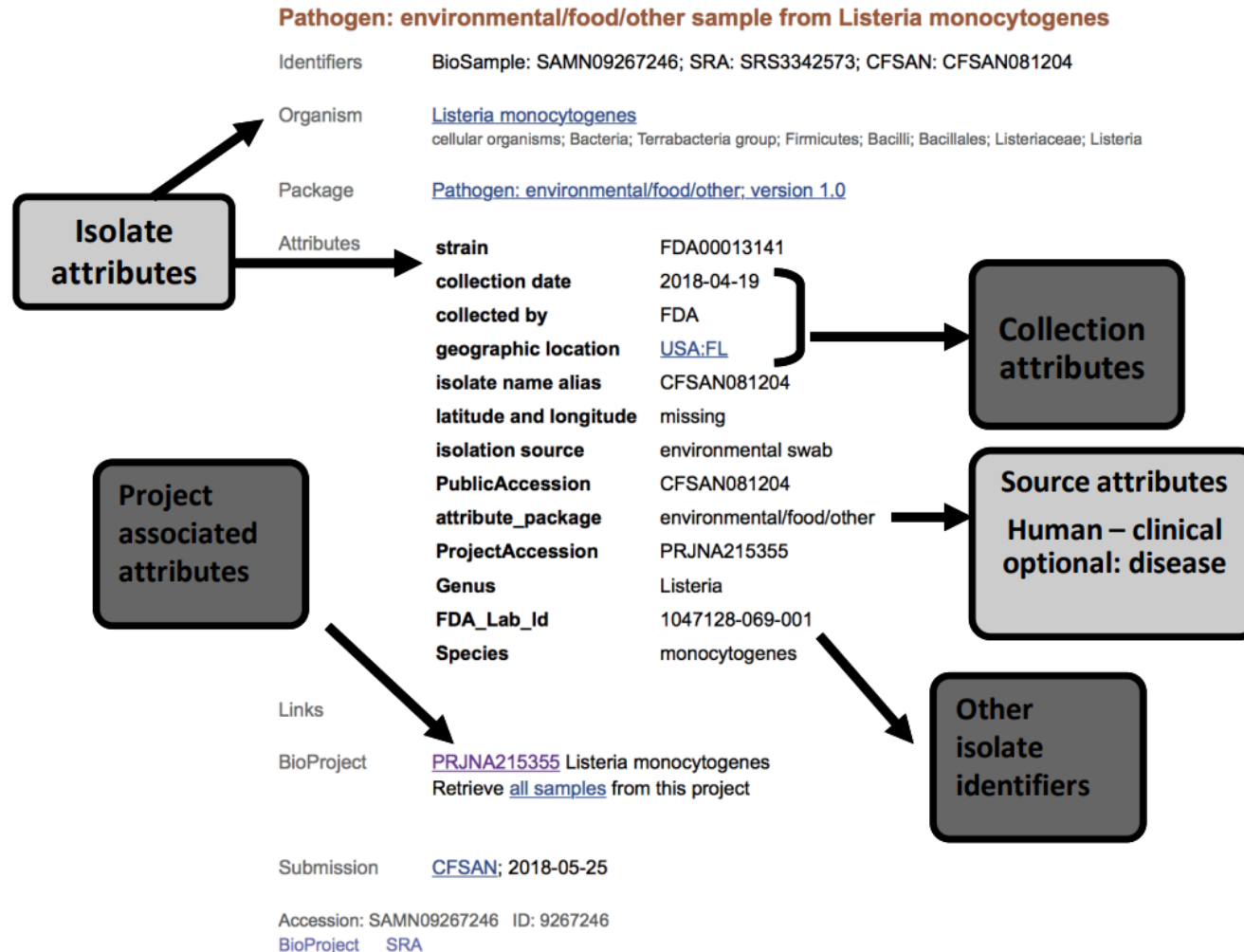
US Surveillance Network



- **NCBI's Pathogen Detection**
- contains ALL WGS data generated from PulseNet and GenomeTrakr labs.
- Public Health England, Argentina, and others.
- Produces daily trees from current SNP clusters

- **Food and environmental** isolates.
- All data submitted to NCBI

NCBI: Not Just Genomes!



- **Data in NCBI Pathogen Detection (minimal metadata)**
 - Sequence
 - Date of collection
 - Geographic location
 - Clinical, food (as specific as possible*), environmental
 - Who uploaded it
- **Data kept Private**
 - Everything else

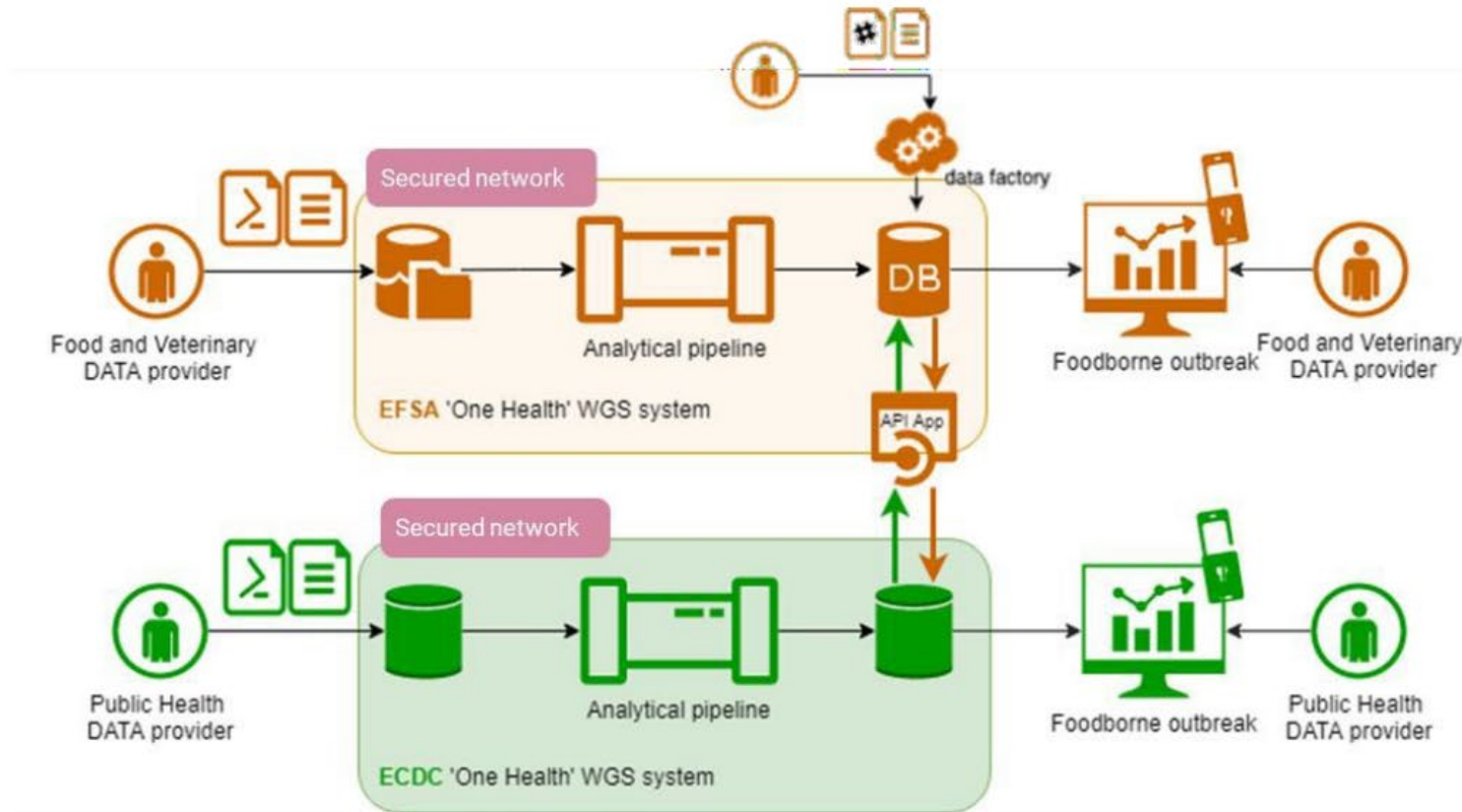




- **Typically, it is the collector***

COMBINATION OF APPROACHES

- **Controlled-Centralized Data Sharing at sector level:** EFSA and ECDC collect data centrally based on their remit
- **Cross-Sectoral Collaboration:** interoperability and comparability of the EFSA and ECDC platforms allow the data exchange for allowing cluster detection and outbreak investigation



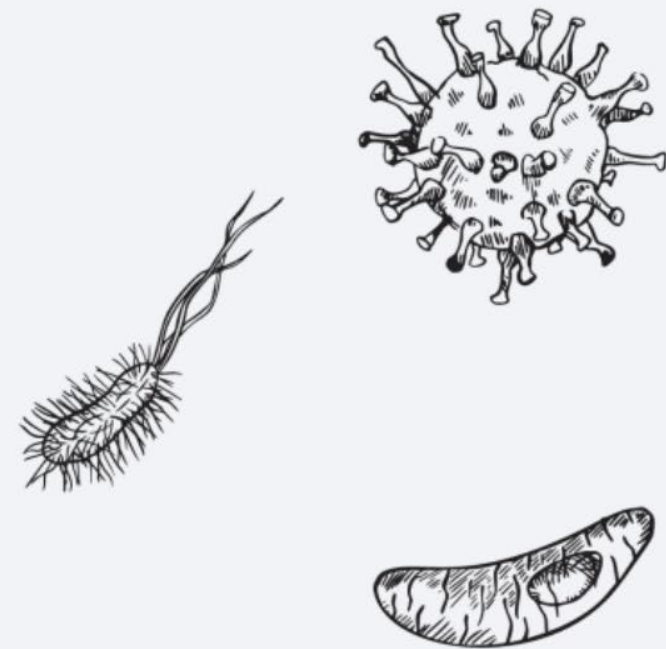
Why PHA4GE

Establish Global Consensus Data Standards >

To Document And Share Best Practices >

To Improve The Availability Of Critical
Bioinformatic Tools And Resources >

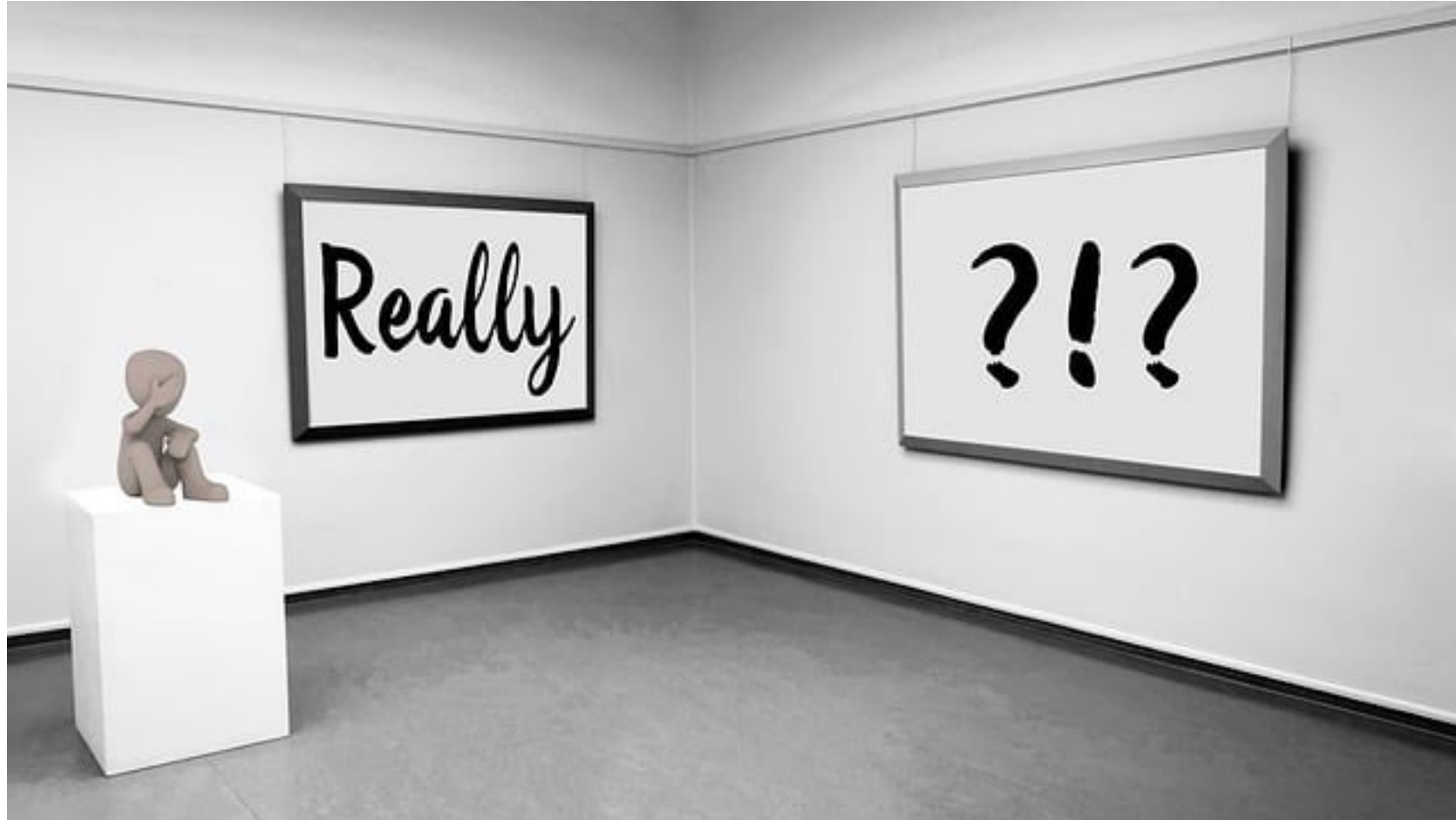
To Advocate For Greater Openness,
Interoperability, Accessibility And Reproducibility
In Public Health Bioinformatics >



Join PHA4GE →

- **It depends***

When Do You Use WGS?



And?



- **FDA/USDA require verifying that equipment/surfaces are cleaned and that microbial risk is controlled**
- **ATP monitoring gives measurable data to support cleaning effectiveness**
 - Same with indicator and index testing
- **PCR monitoring also gives measurable data to support cleaning effectiveness/compliance**
- **Documentation of cleanliness/EMP/testing helps show proactive preventive control**
- **FDA/USDA expect documentation of control measures, sanitation verification, environmental monitoring, corrective actions**

- **Recurring hits in same area or serotype (resident vs transient)**
- **Regulatory/Consumer Pressure**
 - Expectation for RCA when common approaches are inconclusive/exhausted
 - RCA Fatigue
 - When std sanitation/cleaning/RCA keeps failing
- **Supplier Complexity**
 - Cross plant incidence (contamination at multiple plants involves same strain)
- **Not my Pathogen**
- **Research**

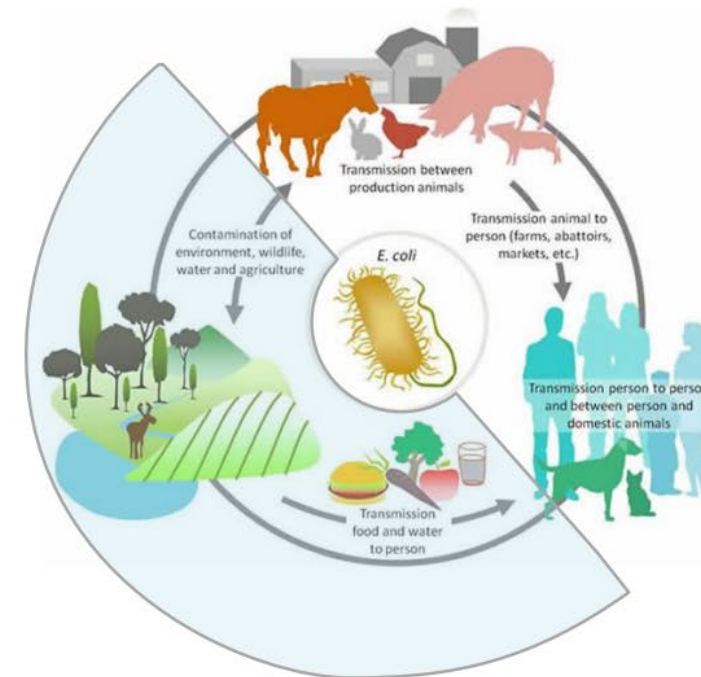
- **Regulatory frameworks recognize the inherent risks of producing food**
- **Want to see tests/data**
 - EXPECT you to find pathogens/problems
 - EXPECT you to work on mitigating/preventing them
- **WANT to see trend analysis**



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 - Words of Caution
- **General Summary**

One Health framework: uniquely important for foodborne pathogens

Pathogen surveillance: need to sample the full lifecycle of these pathogens (humans, animals, environment, water, air, food processing plants, food products)



Openly sharing data enables us to traverse the One Health sphere

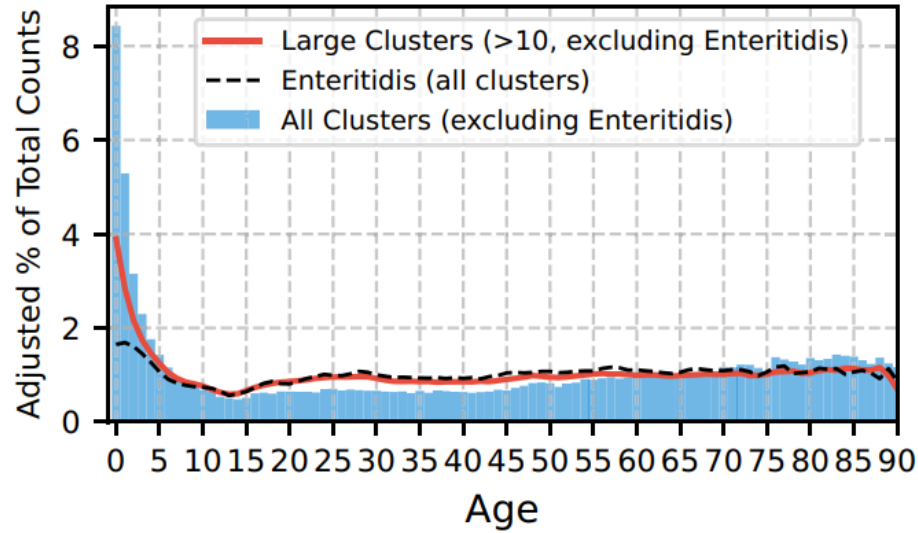
The Global Food Supply



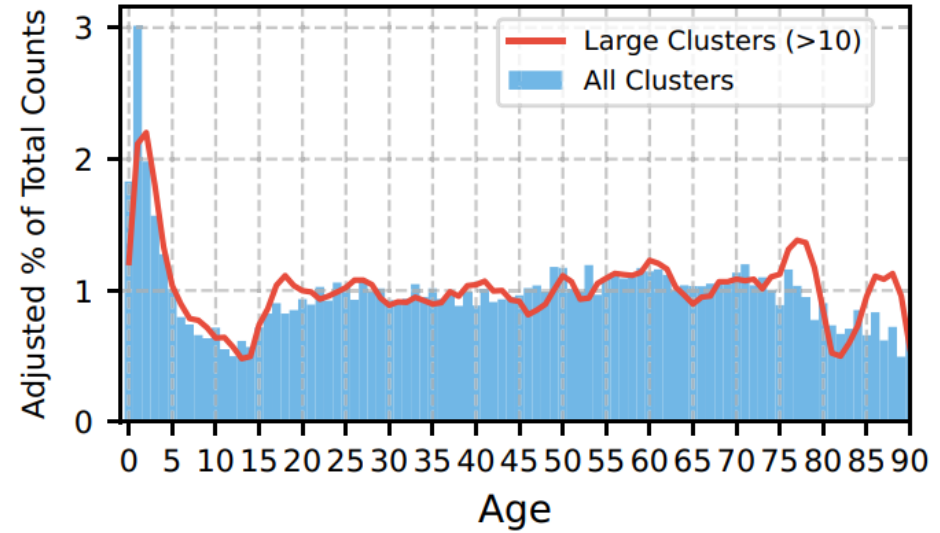
The Future of Risk (baseline)



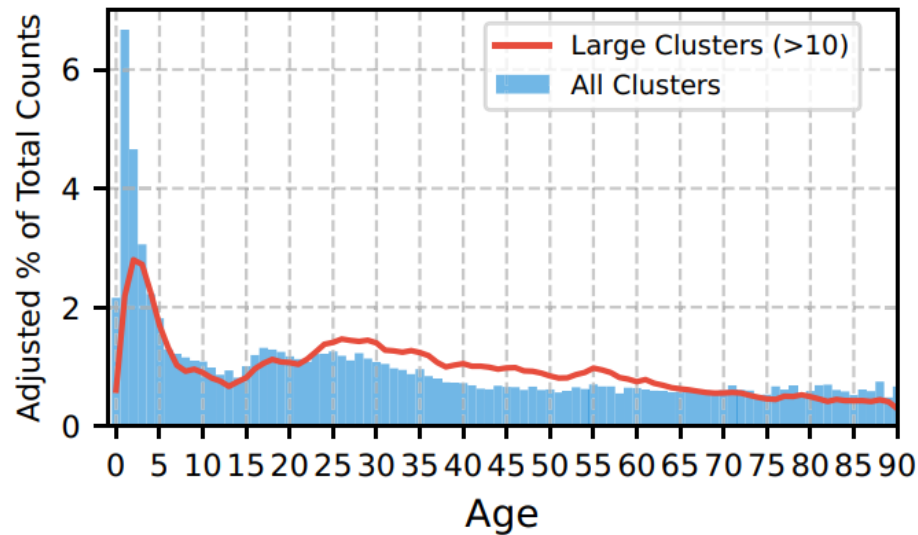
Salmonella



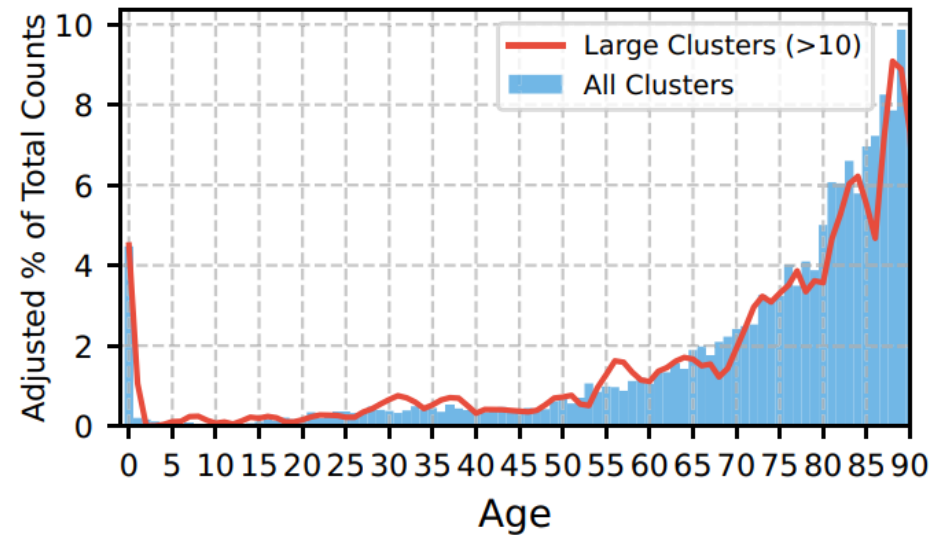
Campylobacter



Escherichia coli



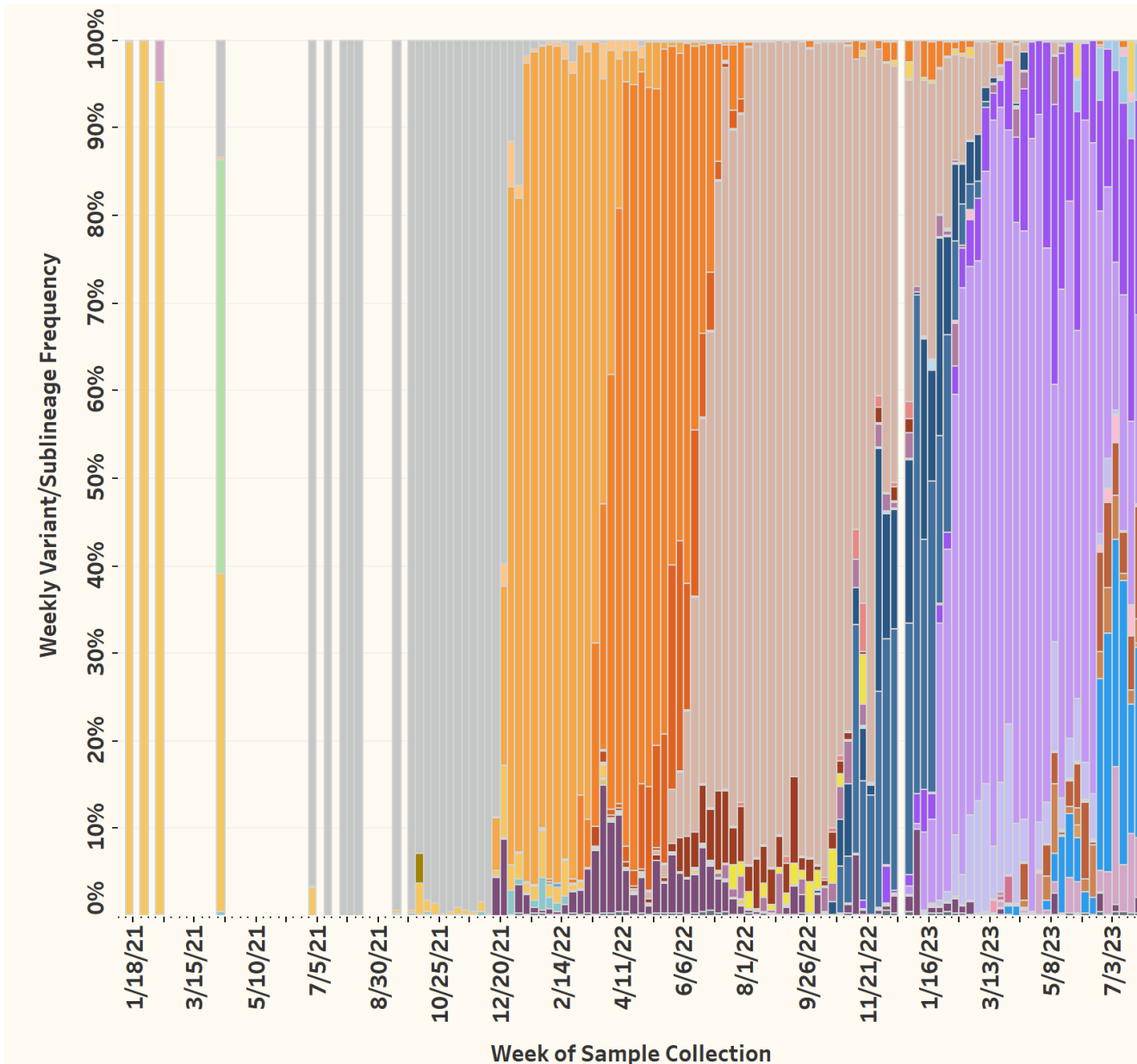
Listeria



- **Pathogenicity**
 - Salmonella serotypes
- **Virulence**
 - STEC, L. Mono
- **Source Attribution**
- **Stratify risk by weighting isolates by virulence or gene content or epi linkage**
- **Stress tolerance, cleaning tolerance, or other survival dynamics within a facility**

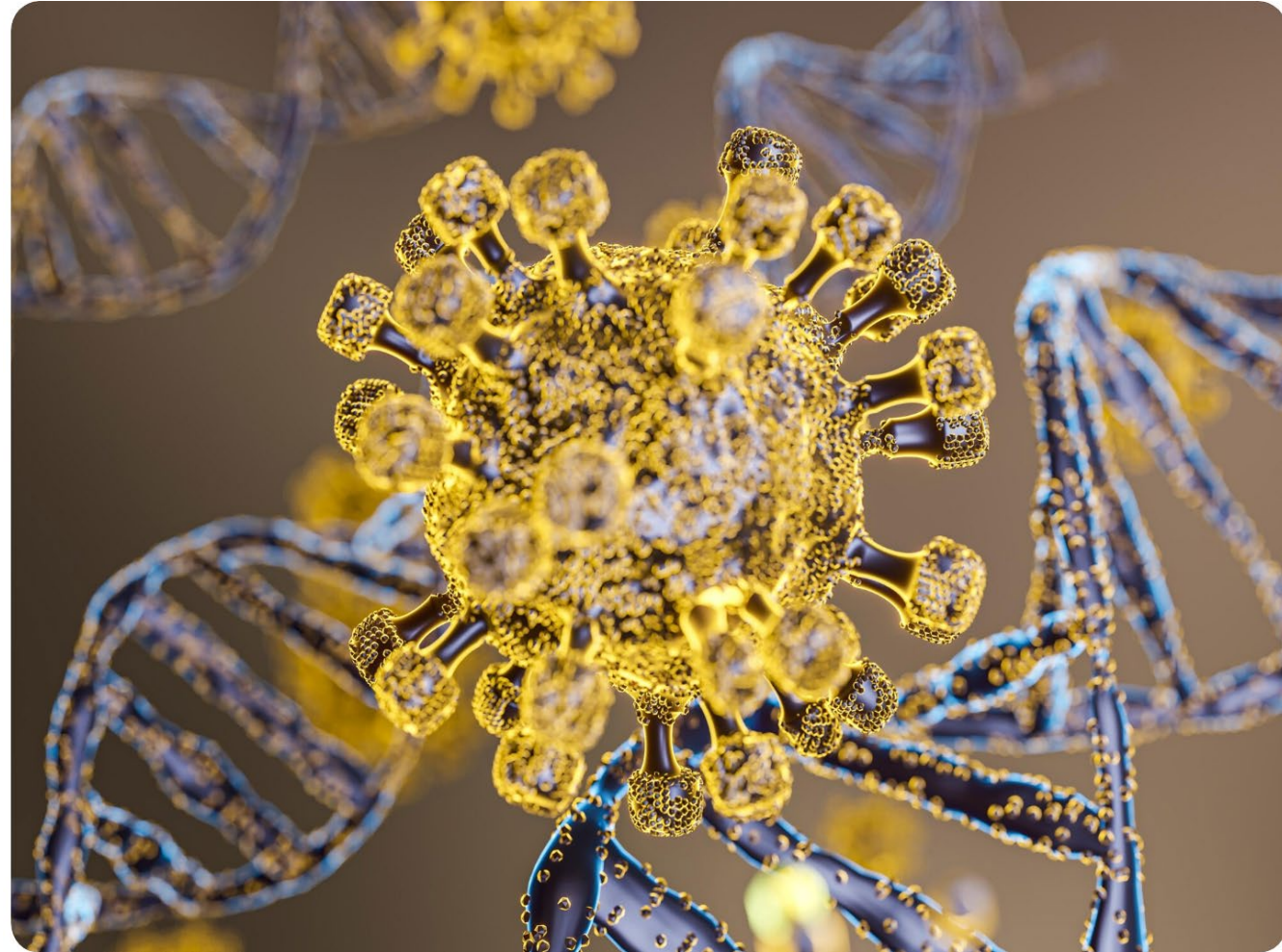


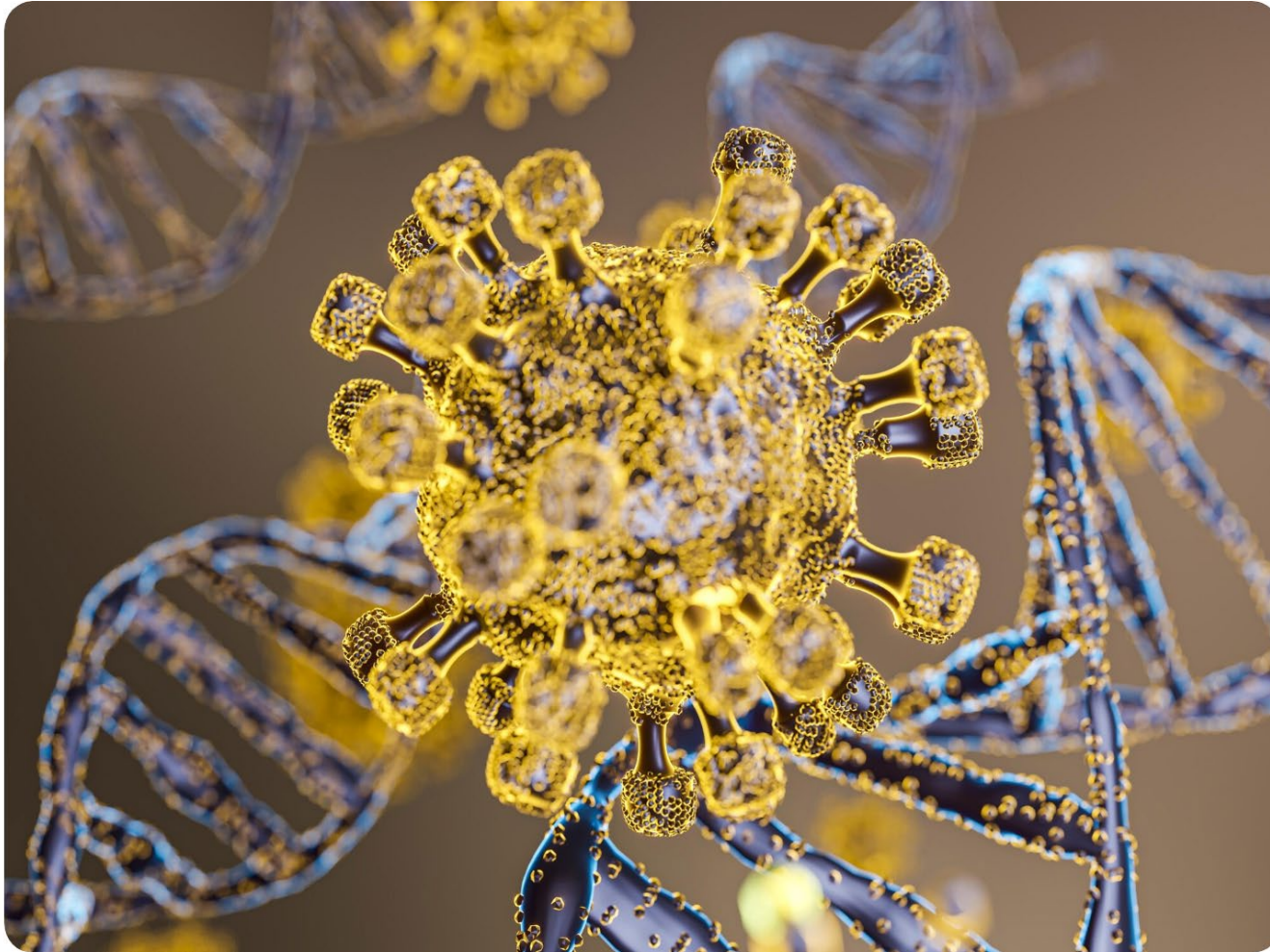
Variation in Real Time



- **What would this look like for pathogens?**
- **For clinicals?**
- **For food/environmental?**
- **Would they agree?**
 - Should they?

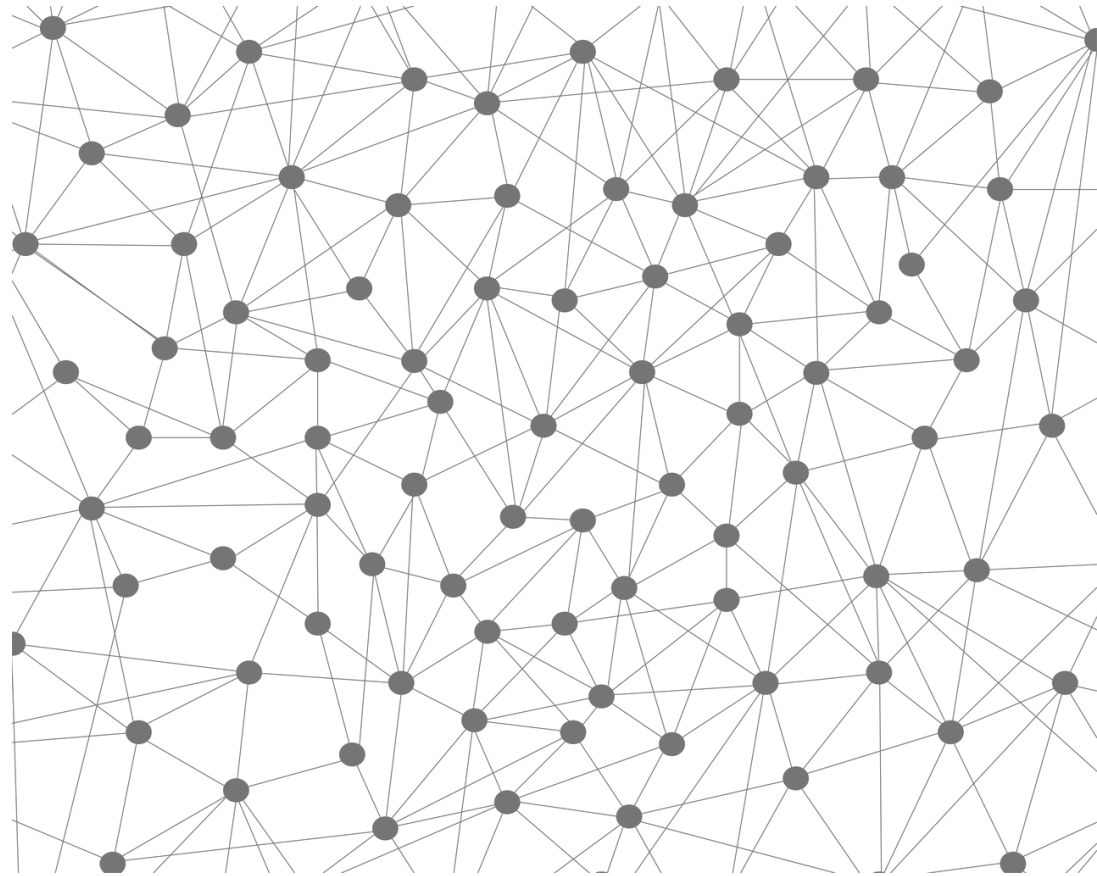
- **Answers:**
 - Who is there?
 - What are they doing?
 - How do they change when something goes wrong?
- **Future Uses?**
 - Characterize microbial ecosystems (drains, conveyors, slicers)
 - Persistent house flora and spoilage/harborage sites
 - Normal vs out of control states?
 - Raw material surveillance





- **Bioinformatic challenges?**
- **Are CIDTs repeatable?**
 - What is the validation going to look like?
 - Regulatory acceptance?
- Go from “**Did I find *Listeria* today?**” to “**Is my microbiome drifting toward *Listeria* risk?**”

(Haven't Even Mentioned AI)



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ROADMAP TO THE FUTURE OF WGS FOR FOOD SAFETY



ROADMAP TO THE FUTURE OF WGS FOR FOOD SAFETY



CFSAN SNP Pipeline 2 (CSP2): a pipeline for fast and accurate SNP distance estimation from bacterial genome assemblies.

Literman R, Gangiredla J, Rand H, Pettengill JB.

PeerJ Comput Sci. 2025 Jul 9;11:e2878. doi: 10.7717/peerj-cs.2878. eCollection 2025.

PMID: 40989335 [Free PMC article.](#)

BACKGROUND: Accurate genetic distance estimation from pathogen whole-genome sequence data is critical for public health surveillance, and with respect to **food safety** it provides crucial information within traceback and outbreak investigations. ...METHODS: To facilit ...

Genomic characterization of vancomycin-resistant enterococci in Norwegian poultry.

Frederiksen RF, Urdahl AM, Slette-meås JS, Granstad S, Simm R, Lagesen K.

PLoS One. 2025 Jun 4;20(6):e0324789. doi: 10.1371/journal.pone.0324789. eCollection 2025.

PMID: 40465609 [Free PMC article.](#)

A total of 30 VRE isolates from the years 2002-2013 were included, 23 from broiler flocks and seven from turkey flocks. **WGS** analyses showed that the isolates were genetically diverse with the number of SNPs ranging from 10 to 2807. ...Overall, the results support that the ...

Advances in whole genome sequencing for foodborne pathogens: implications for clinical infectious disease surveillance and public health.

Gomes E, Araújo D, Nogueira T, Oliveira R, Silva S, Oliveira LVN, Azevedo NF, Almeida C, Castro J.

Front Cell Infect Microbiol. 2025 Apr 28;15:1593219. doi: 10.3389/fcimb.2025.1593219. eCollection 2025.

PMID: 40357405 [Free PMC article.](#) [Review.](#)

This capability enhances outbreak surveillance, source tracing and **risk** assessment, making **WGS** an increasingly integrated component of public health surveillance systems. ...Addressing these barriers is crucial to maximizing the impact of **WGS** on foodborne dis ...

Evaluation of universal preenrichment broth and comparison of rapid molecular methods for the detection of Salmonella from spent sprout irrigation water (SSIW).

Zheng J, Reed E, Maounounen-Laasri A, Deng X, Wang SS, **Ramachandran P**, Ferreira C, Bell R, Brown EW, Hammack TS, Wang H.

Int J Food Microbiol. 2024 Feb 2;411:110527. doi: 10.1016/j.ijfoodmicro.2023.110527. Epub 2023 Dec 14.

PMID: 38118357 [Free article.](#)

Prediction of reduction behavior by heating and strain variability of Campylobacter jejuni using amino acid phylogenetics from whole genome sequencing data.

Abe H, Kawasaki S.

Int J Food Microbiol. 2026 Jan 2;444:111446. doi: 10.1016/j.ijfoodmicro.2025.111446. Epub 2025 Sep 15.

PMID: 40974773

Predicting bacterial behavior and strain variability is essential for quantitative microbial **risk** assessments in **food safety**. The growing availability of whole-genome sequencing (**WGS**) data enables deeper insights into microbial thermotolerance. ...Thes ...

Whole-genome sequencing of soil- and foodborne Bacillus cereus sensu lato indicates no clear association between their virulence repertoire, genomic diversity and food matrix.

Jacobs B, Bogaerts B, Verhaegen M, Vanneste K, De Keersmaecker SCJ, Roosens NHC, Rajkovic A, Mahillon J, Van Nieuwenhuysen T, Van Hoorde K.

Int J Food Microbiol. 2025 Aug 2;439:111266. doi: 10.1016/j.ijfoodmicro.2025.111266. Epub 2025 May 14.

PMID: 40378489 [Free article.](#)

It is unclear whether certain strains have a higher affinity for specific **food** matrices, which can be of interest for **risk** assessment. This study reports the characterization by whole-genome sequencing of 169 B. cereus isolates, isolated from 12 **food** types an ...

Organism Groups

Species	Version	Publication Date*	Latest Isolate Creation Date*	Clusters	New Isolates	New Clinical Isolates	New Environmental Isolates	Total Isolates
Salmonella enterica	PDG000000002.3747	2025-10-20 05:11	2025-10-19 01:41	32,508	95	95	0	786,703
E.coli and Shigella	PDG000000004.5607	2025-10-19 17:39	2025-10-19 01:41	51,817	151	151	0	504,800
Campylobacter jejuni	PDG000000003.2617	2025-10-19 06:27	2025-10-18 23:45	10,029	11	0	11	158,329
Staphylococcus aureus	PDG000000073.1058	2025-10-17 07:32	2025-10-16 15:41	17,788	25	20	0	154,218
Klebsiella pneumoniae	PDG000000012.2209	2025-10-18 05:47	2025-10-17 17:04	12,429	7	7	0	138,653
Streptococcus pneumoniae	PDG000000074.546	2025-10-18 05:20	2025-10-17 03:40	10,887	1	0	0	117,333
Listeria monocytogenes	PDG000000001.4410	2025-10-20 04:31	2025-10-19 21:39	6,479	10	0	10	76,508



- **Incomplete Metadata/bioinformatic support**
- **Lack of foodborne incidence data**
 - We could be flying blind
- **Data Biases**
 - Who is sequencing?
 - What are they sequencing?
 - Is it good data?

- **Don't forget microbiology**



- **AMR**



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- **Metadata = critical**
 - Value of data lies in context
- **Data expertise will only increase**
 - Trend analysis (regardless of WGS/metagenomics)
- **More information will lead to new/rapid diagnostics**
 - Fit for purpose, fit for decision-making, fit for compliance
- **Not all pathogens are equal**
 - Not all strains are equal
- **Machine learning (AI) will have a seat at the table (it should not be at the head)**
- **Start somewhere (at least understand)**



Thank You

October 21, 2025