TN Department of Health

Visualization and Communication

Whole Genome Sequencing
Live Learning Series - Session 3

July 2, 2025

Introduction

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Learning Objectives

Data Viz	Evaluate impact vs. investment of routine use of data visualization tools
	Recognize how data visualization can support cluster/outbreak investigations
Communicating WGS Results	Use and interpret standard phrasing for communicating WGS results
	Summarize complex laboratory testing and genetic comparisons during outbreak investigations for a general audience
PulseNet 2.0	List the requirements to obtain access to PulseNet 2.0

Cluster/WGS
Data Visualization

WGS/Cluster Data Visualization Value

Easily identify similarities and differences

Track processes efficiently

Describe trends and gaps

Impact vs. Investment

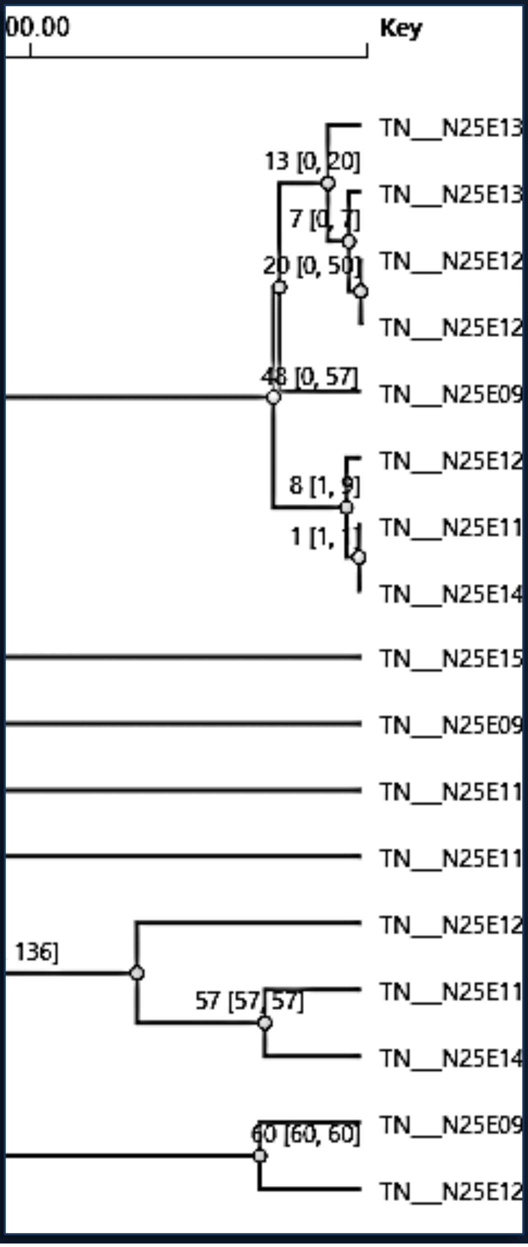
Impact

- Clear communication with partners
- Reduced time and manual processes
- Simplifies monitoring and evaluation

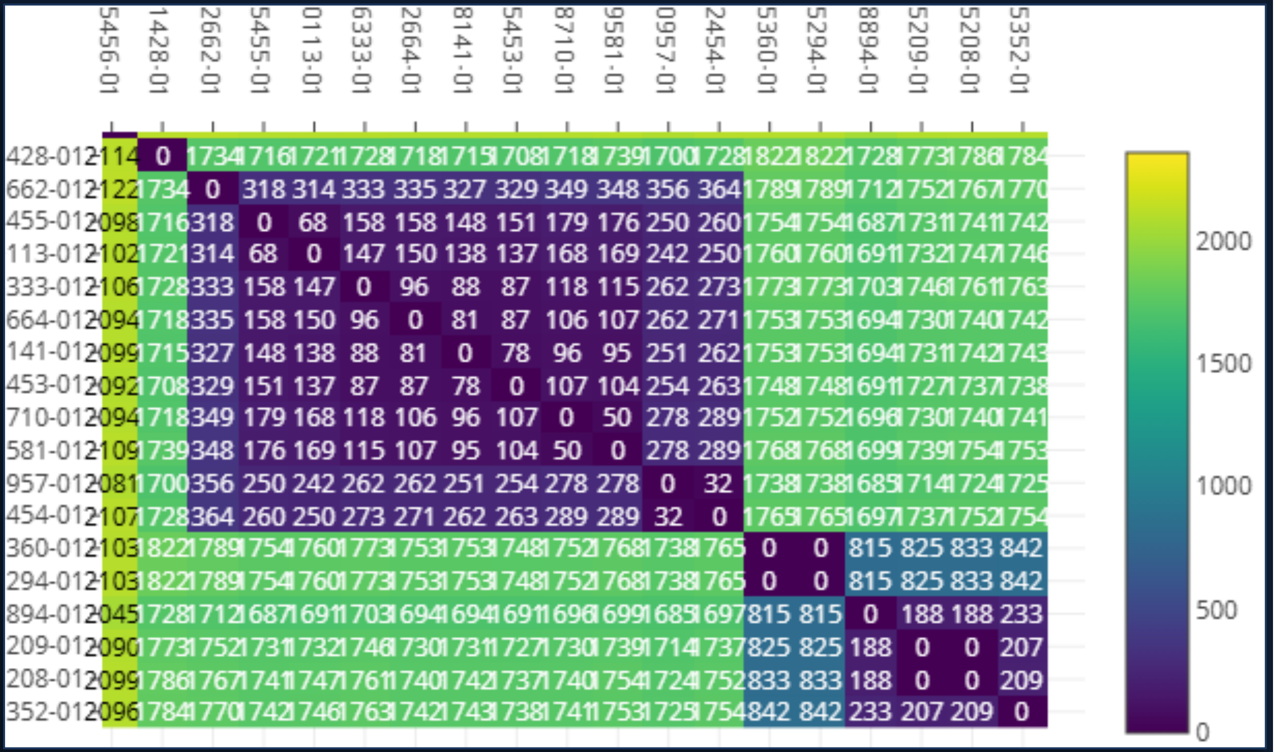
Investment

- Agency buy-in and license cost
- Time to build sufficient expertise
- Building end user data literacy and technical skill

Example #1: Dendrograms and Matrices

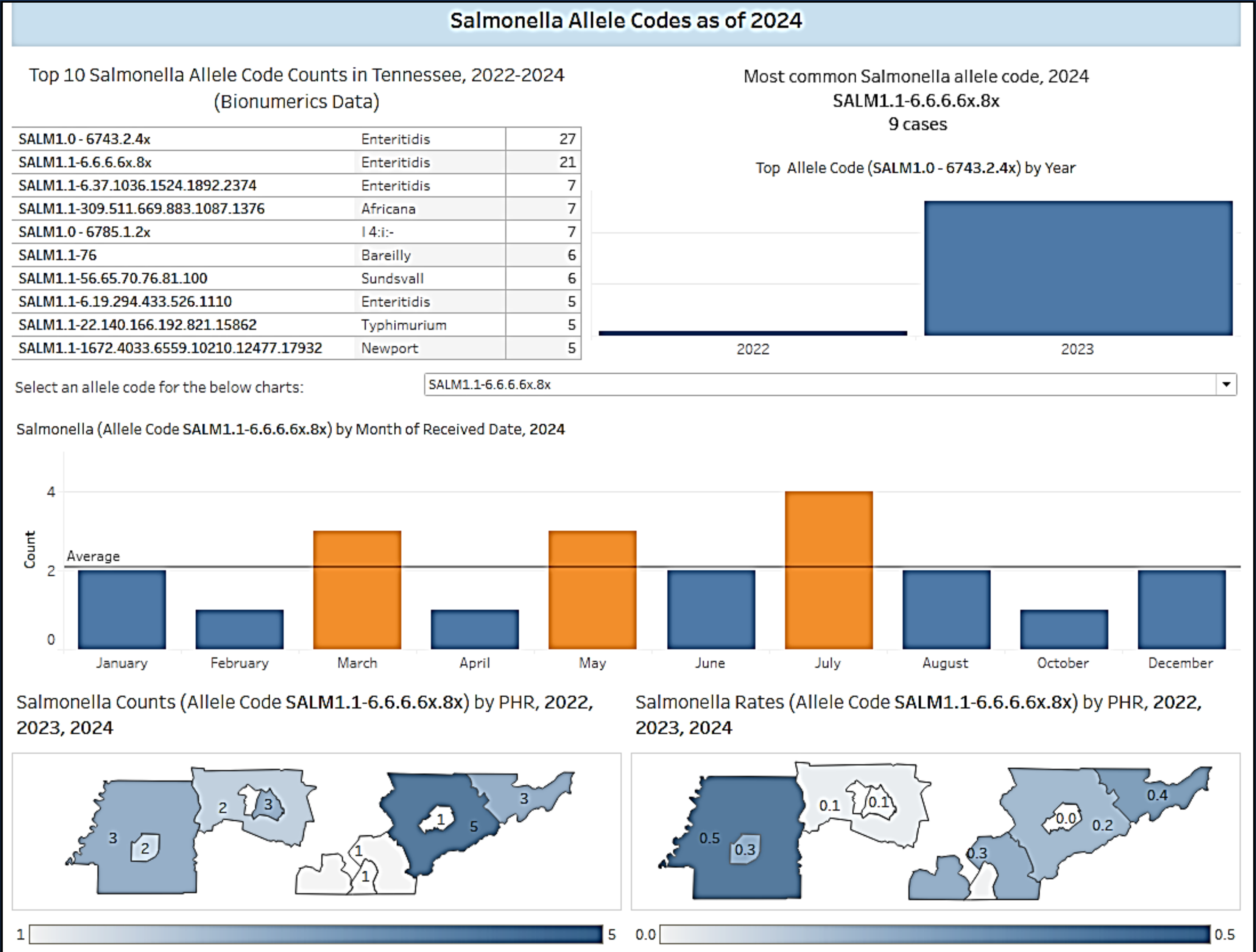


Created from PulseNet 2.0



	5456-01	1428-01	2662-01	5455-01	0113-01	6333-01	2664-01	8141-01	5453-01	8710-01	9581-01	0957-01	2454-01	5360-01	5294-01	8894-01	5209-01	5208-01	5352-01
428-01	2114	0	1734	1716	1721	1728	1718	1715	1708	1718	1739	1700	1728	1822	1822	1728	1773	1786	1784
662-01	2122	1734	0	318	314	333	335	327	329	349	348	356	364	1789	1789	1712	1752	1767	1770
455-01	2098	1716	318	0	68	158	158	148	151	179	176	250	260	1754	1754	1687	1731	1741	1742
113-01	2102	1721	314	68	0	147	150	138	137	168	169	242	250	1760	1760	1691	1732	1747	1746
333-01	2106	1728	333	158	147	0	96	88	87	118	115	262	273	1773	1773	1703	1746	1761	1763
664-01	2094	1718	335	158	150	96	0	81	87	106	107	262	271	1753	1753	1694	1730	1740	1742
141-01	2099	1715	327	148	138	88	81	0	78	96	95	251	262	1753	1753	1694	1731	1742	1743
453-01	2092	1708	329	151	137	87	87	78	0	107	104	254	263	1748	1748	1691	1727	1737	1738
710-01	2094	1718	349	179	168	118	106	96	107	0	50	278	289	1752	1752	1696	1730	1740	1741
581-01	2109	1739	348	176	169	115	107	95	104	50	0	278	289	1768	1768	1699	1739	1754	1753
957-01	2081	1700	356	250	242	262	262	251	254	278	278	0	32	1738	1738	1685	1714	1724	1725
454-01	2107	1728	364	260	250	273	271	262	263	289	289	32	0	1765	1765	1697	1737	1752	1754
360-01	2103	1822	1789	1754	1760	1773	1753	1753	1748	1752	1768	1738	1765	0	0	815	825	833	842
294-01	2103	1822	1789	1754	1760	1773	1753	1753	1748	1752	1768	1738	1765	0	0	815	825	833	842
894-01	2045	1728	1712	1687	1691	1703	1694	1694	1691	1696	1699	1685	1697	815	815	0	188	188	233
209-01	2090	1773	1752	1731	1732	1746	1730	1731	1727	1730	1739	1714	1737	825	825	188	0	0	207
208-01	2099	1786	1767	1741	1747	1761	1740	1742	1737	1740	1754	1724	1752	833	833	188	0	0	209
352-01	2096	1784	1770	1742	1746	1763	1742	1743	1738	1741	1753	1725	1754	842	842	233	207	209	0

Example #2: Allele Code Dashboard



Salmonella Allele Codes as of 2024

Top 10 Salmonella Allele Code Counts in Tennessee, 2022-2024 (Bionumerics Data)

SALM1.0 - 6743.2.4x	Enteritidis	27
SALM1.1-6.6.6.6x.8x	Enteritidis	21
SALM1.1-6.37.1036.1524.1892.2374	Enteritidis	7
SALM1.1-309.511.669.883.1087.1376	Africana	7
SALM1.0 - 6785.1.2x	I 4:i:-	7
SALM1.1-76	Bareilly	6
SALM1.1-56.65.70.76.81.100	Sundsvall	6
SALM1.1-6.19.294.433.526.1110	Enteritidis	5
SALM1.1-22.140.166.192.821.15862	Typhimurium	5
SALM1.1-1672.4033.6559.10210.12477.17932	Newport	5

Most common Salmonella allele code, 2024
SALM1.1-6.6.6.6x.8x
9 cases

Top Allele Code (**SALM1.0 - 6743.2.4x**) by Year

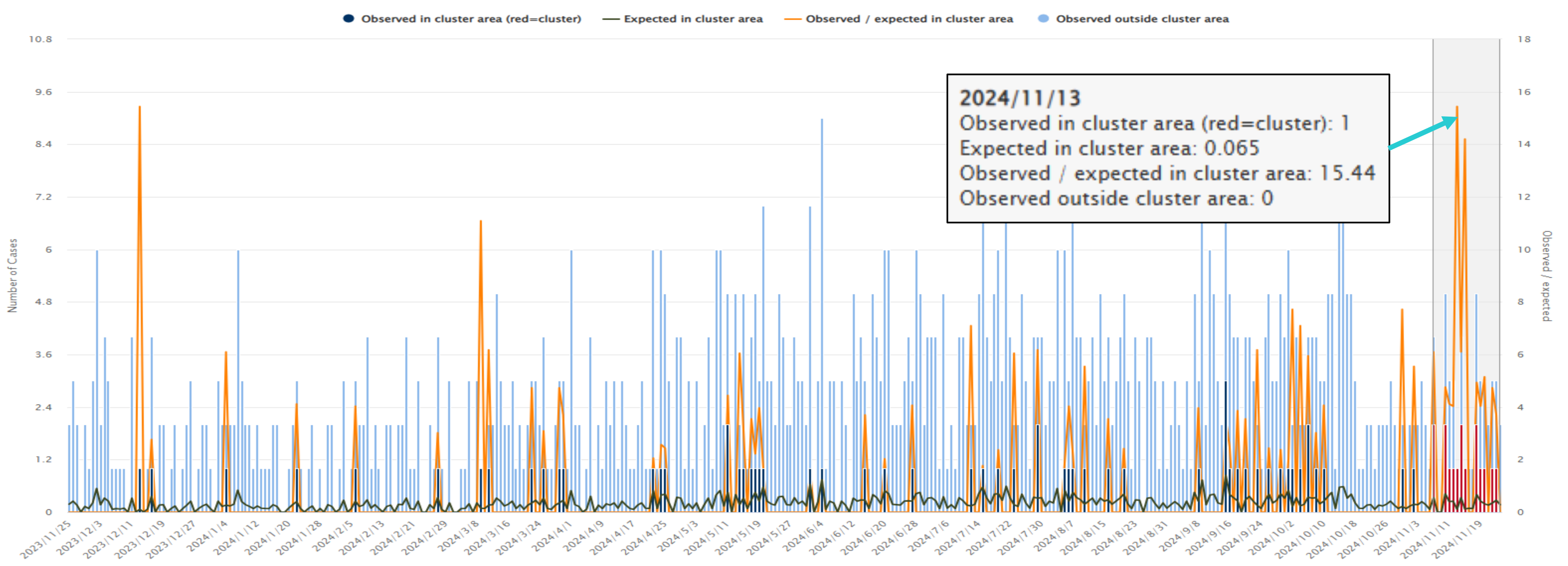
Select an allele code for the below charts: SALM1.1-6.6.6.6x.8x ▾

Salmonella (Allele Code **SALM1.1-6.6.6.6x.8x**) by Month of Received Date, 2024

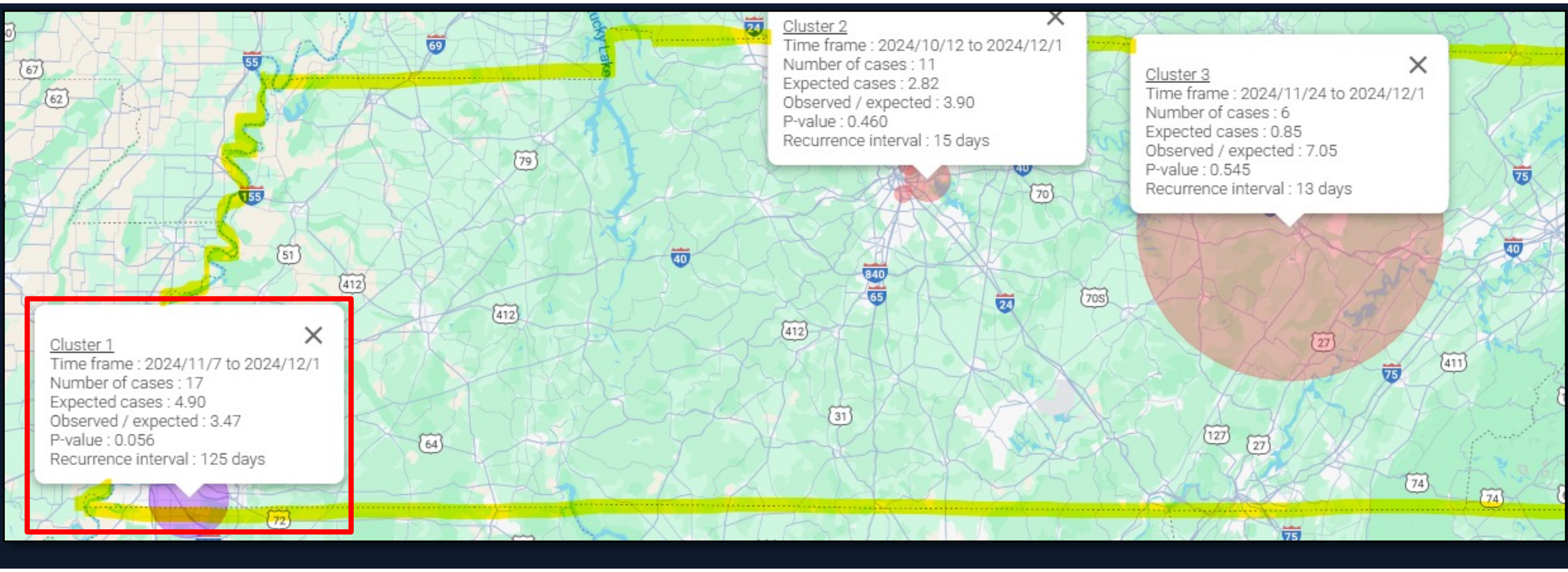
Salmonella Counts (Allele Code **SALM1.1-6.6.6.6x.8x**) by PHR, **2022, 2023, 2024**

Salmonella Rates (Allele Code **SALM1.1-6.6.6.6x.8x**) by PHR, **2022, 2023, 2024**

Example #3: SatScan



2024/11/13
Observed in cluster area (red=cluster): 1
Expected in cluster area: 0.065
Observed / expected in cluster area: 15.44
Observed outside cluster area: 0



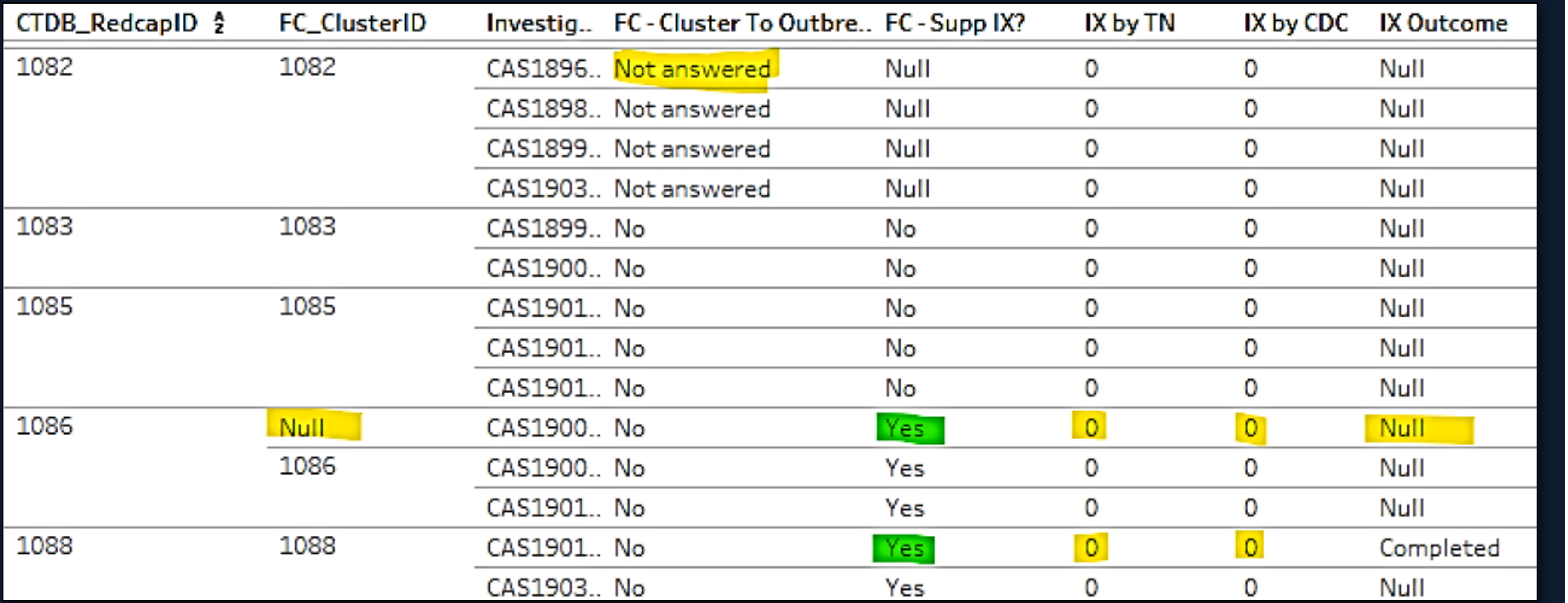
Cluster 2
Time frame : 2024/10/12 to 2024/12/1
Number of cases : 11
Expected cases : 2.82
Observed / expected : 3.90
P-value : 0.460
Recurrence interval : 15 days

Cluster 3
Time frame : 2024/11/24 to 2024/12/1
Number of cases : 6
Expected cases : 0.85
Observed / expected : 7.05
P-value : 0.545
Recurrence interval : 13 days

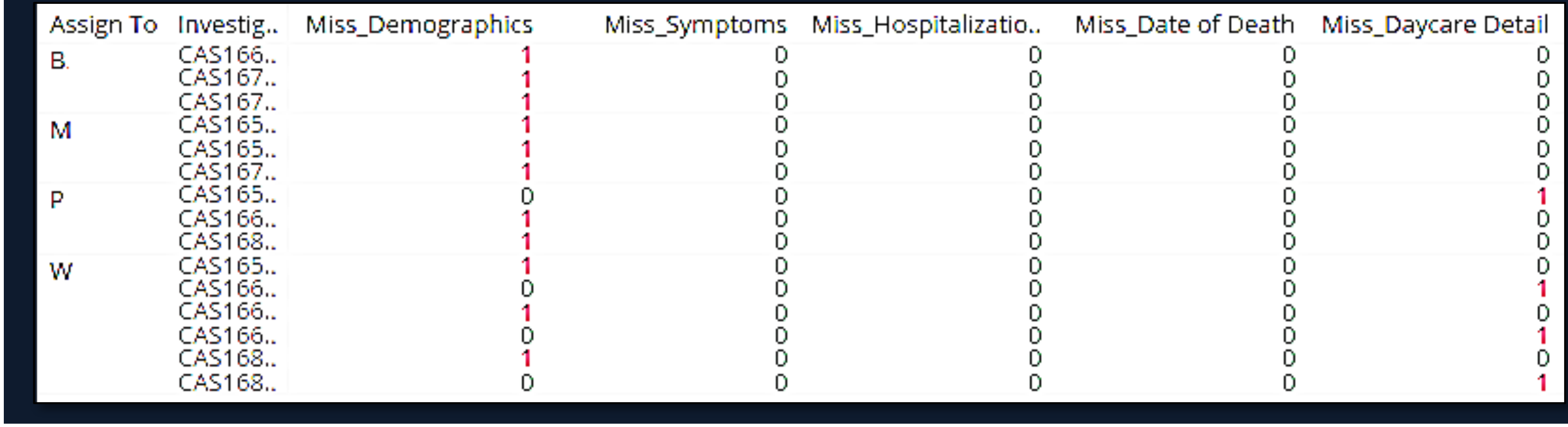
Cluster 1
Time frame : 2024/11/7 to 2024/12/1
Number of cases : 17
Expected cases : 4.90
Observed / expected : 3.47
P-value : 0.056
Recurrence interval : 125 days

Example #4: Closeout Dashboard

Cluster Investigations with Incomplete Individual Case Records



CTDB_RedcapID	FC_ClusterID	Investig..	FC - Cluster To Outbre..	FC - Supp IX?	IX by TN	IX by CDC	IX Outcome
1082	1082	CAS1896..	Not answered	Null	0	0	Null
		CAS1898..	Not answered	Null	0	0	Null
		CAS1899..	Not answered	Null	0	0	Null
		CAS1903..	Not answered	Null	0	0	Null
1083	1083	CAS1899..	No	No	0	0	Null
		CAS1900..	No	No	0	0	Null
1085	1085	CAS1901..	No	No	0	0	Null
		CAS1901..	No	No	0	0	Null
		CAS1901..	No	No	0	0	Null
1086	Null	CAS1900..	No	Yes	0	0	Null
	1086	CAS1900..	No	Yes	0	0	Null
		CAS1901..	No	Yes	0	0	Null
1088	1088	CAS1901..	No	Yes	0	0	Completed
		CAS1903..	No	Yes	0	0	Null



Assign To	Investig..	Miss_Demographics	Miss_Symptoms	Miss_Hospitalizatio..	Miss_Date of Death	Miss_Daycare Detail
B.	CAS166..	1	0	0	0	0
	CAS167..	1	0	0	0	0
	CAS167..	1	0	0	0	0
M	CAS165..	1	0	0	0	0
	CAS165..	1	0	0	0	0
	CAS167..	1	0	0	0	0
P	CAS165..	0	0	0	0	1
	CAS166..	1	0	0	0	0
	CAS168..	1	0	0	0	0
W	CAS165..	1	0	0	0	0
	CAS166..	0	0	0	0	1
	CAS166..	1	0	0	0	0
	CAS166..	0	0	0	0	1
	CAS168..	1	0	0	0	0
	CAS168..	0	0	0	0	1

Interviews with Missing Data

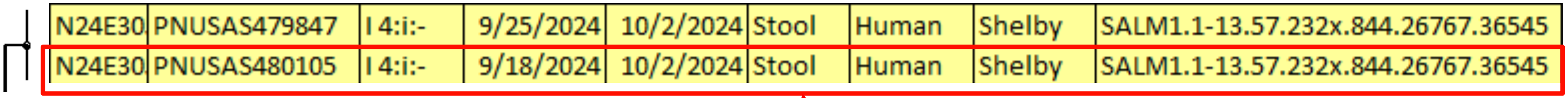
Knowledge Check

Which of the following is NOT a challenge in Cluster/WGS Data Visualization?

A. Ability for users to access visualizations
B. Rapidly detecting commonalities
C. Software security and cost
D. Interpreting the data accurately

Salmonella I 4:i- Outbreak Example

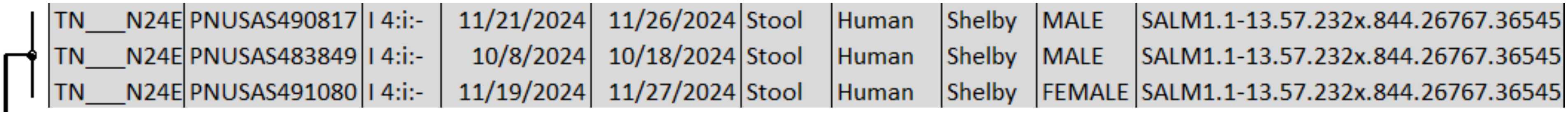
October 15, 2024 Cluster Dendrogram – First Identification



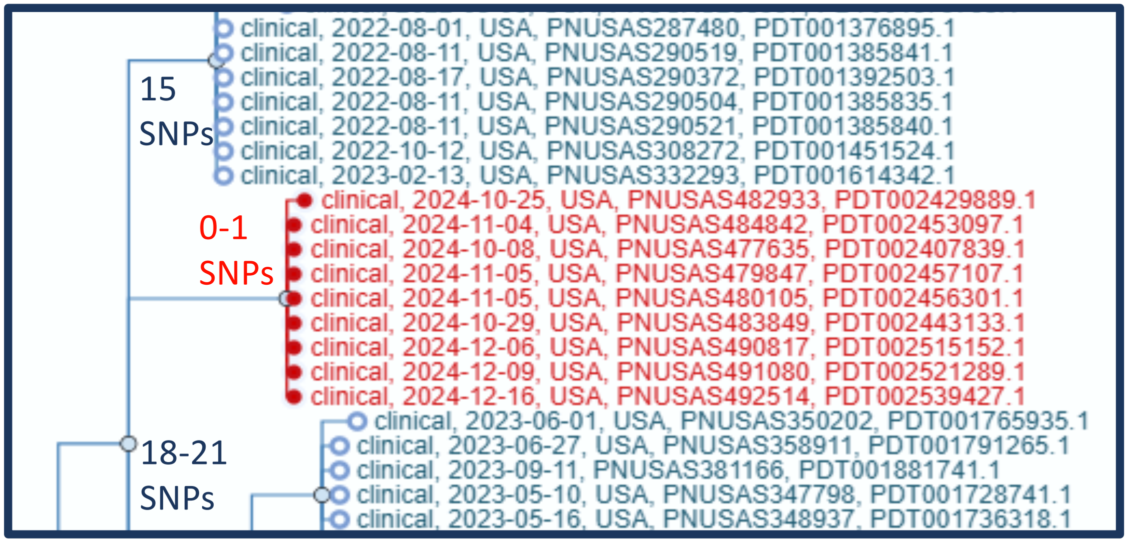
N24E30	PNUSAS479847	I 4:i:-	9/25/2024	10/2/2024	Stool	Human	Shelby	SALM1.1-13.57.232x.844.26767.36545
N24E30	PNUSAS480105	I 4:i:-	9/18/2024	10/2/2024	Stool	Human	Shelby	SALM1.1-13.57.232x.844.26767.36545

Initially lost to follow up; cluster closed

December 10, 2024 Cluster Dendrogram – Reopened with new cases; checked NCBI/SEDRIC

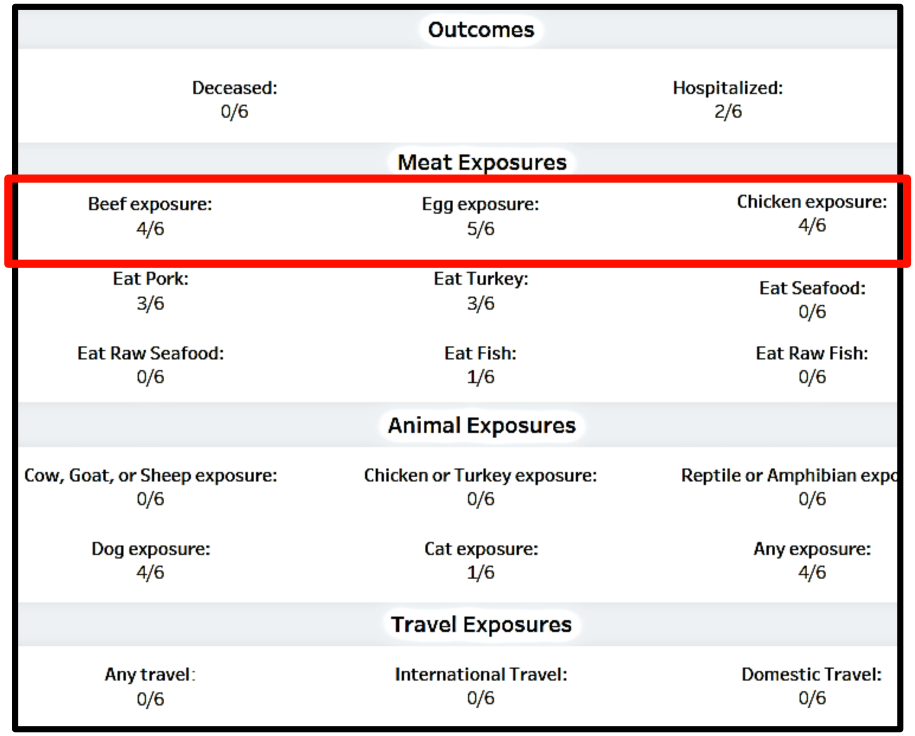


TN___N24E	PNUSAS490817	I 4:i:-	11/21/2024	11/26/2024	Stool	Human	Shelby	MALE	SALM1.1-13.57.232x.844.26767.36545
TN___N24E	PNUSAS483849	I 4:i:-	10/8/2024	10/18/2024	Stool	Human	Shelby	MALE	SALM1.1-13.57.232x.844.26767.36545
TN___N24E	PNUSAS491080	I 4:i:-	11/19/2024	11/27/2024	Stool	Human	Shelby	FEMALE	SALM1.1-13.57.232x.844.26767.36545



clinical, 2022-08-01, USA, PNUSAS287480, PDT001376895.1
clinical, 2022-08-11, USA, PNUSAS290519, PDT001385841.1
clinical, 2022-08-17, USA, PNUSAS290372, PDT001392503.1
clinical, 2022-08-11, USA, PNUSAS290504, PDT001385835.1
clinical, 2022-08-11, USA, PNUSAS290521, PDT001385840.1
clinical, 2022-10-12, USA, PNUSAS308272, PDT001451524.1
clinical, 2023-02-13, USA, PNUSAS332293, PDT001614342.1
clinical, 2024-10-25, USA, PNUSAS482933, PDT002429889.1
clinical, 2024-11-04, USA, PNUSAS484842, PDT002453097.1
clinical, 2024-10-08, USA, PNUSAS477635, PDT002407839.1
clinical, 2024-11-05, USA, PNUSAS479847, PDT002457107.1
clinical, 2024-11-05, USA, PNUSAS480105, PDT002456301.1
clinical, 2024-10-29, USA, PNUSAS483849, PDT002443133.1
clinical, 2024-12-06, USA, PNUSAS490817, PDT002515152.1
clinical, 2024-12-09, USA, PNUSAS491080, PDT002521289.1
clinical, 2024-12-16, USA, PNUSAS492514, PDT002539427.1
clinical, 2023-06-01, USA, PNUSAS350202, PDT001765935.1
clinical, 2023-06-27, USA, PNUSAS358911, PDT001791265.1
clinical, 2023-09-11, PNUSAS381166, PDT001881741.1
clinical, 2023-05-10, USA, PNUSAS347798, PDT001728741.1
clinical, 2023-05-16, USA, PNUSAS348937, PDT001736318.1

Exposure Review – Tableau Dashboard



Outcomes

Deceased: 0/6
Hospitalized: 2/6

Meat Exposures

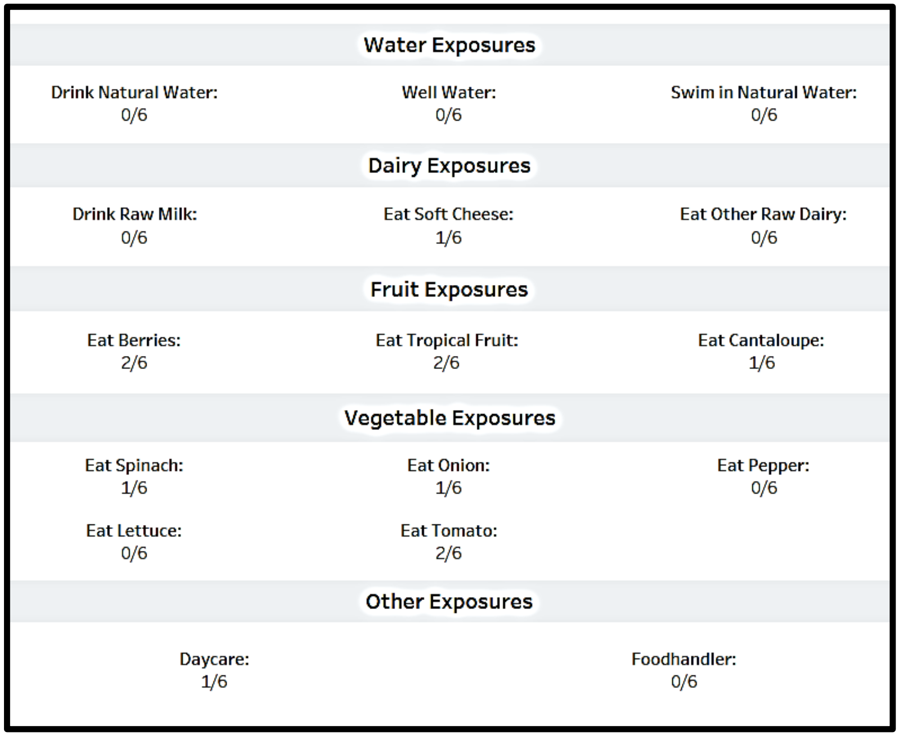
Beef exposure: 4/6
Egg exposure: 5/6
Chicken exposure: 4/6
Eat Pork: 3/6
Eat Turkey: 3/6
Eat Seafood: 0/6
Eat Raw Seafood: 0/6
Eat Fish: 1/6
Eat Raw Fish: 0/6

Animal Exposures

Cow, Goat, or Sheep exposure: 0/6
Chicken or Turkey exposure: 0/6
Reptile or Amphibian expo 0/6
Dog exposure: 4/6
Cat exposure: 1/6
Any exposure: 4/6

Travel Exposures

Any travel: 0/6
International Travel: 0/6
Domestic Travel: 0/6



Water Exposures

Drink Natural Water: 0/6
Well Water: 0/6
Swim in Natural Water: 0/6

Dairy Exposures

Drink Raw Milk: 0/6
Eat Soft Cheese: 1/6
Eat Other Raw Dairy: 0/6

Fruit Exposures

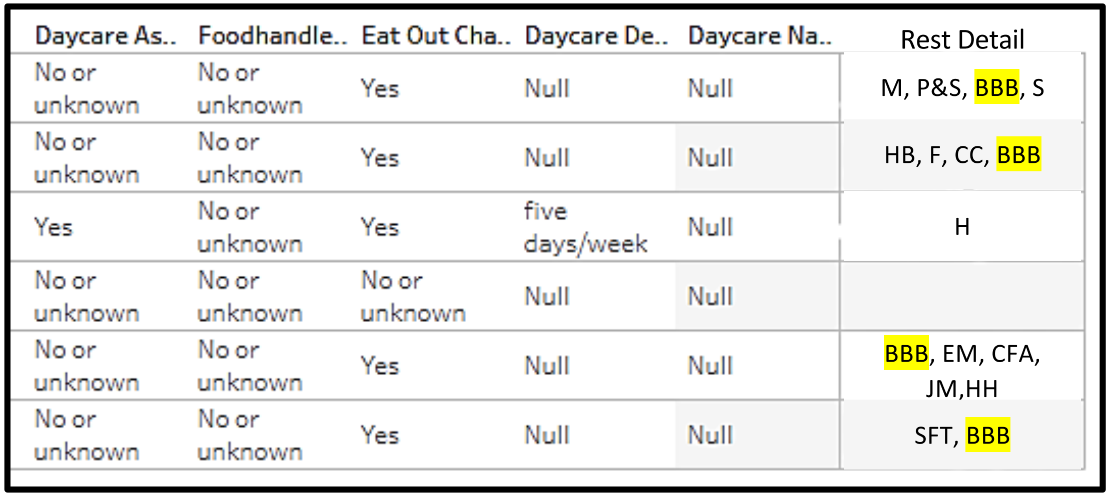
Eat Berries: 2/6
Eat Tropical Fruit: 2/6
Eat Cantaloupe: 1/6

Vegetable Exposures

Eat Spinach: 1/6
Eat Onion: 1/6
Eat Pepper: 0/6
Eat Lettuce: 0/6
Eat Tomato: 2/6

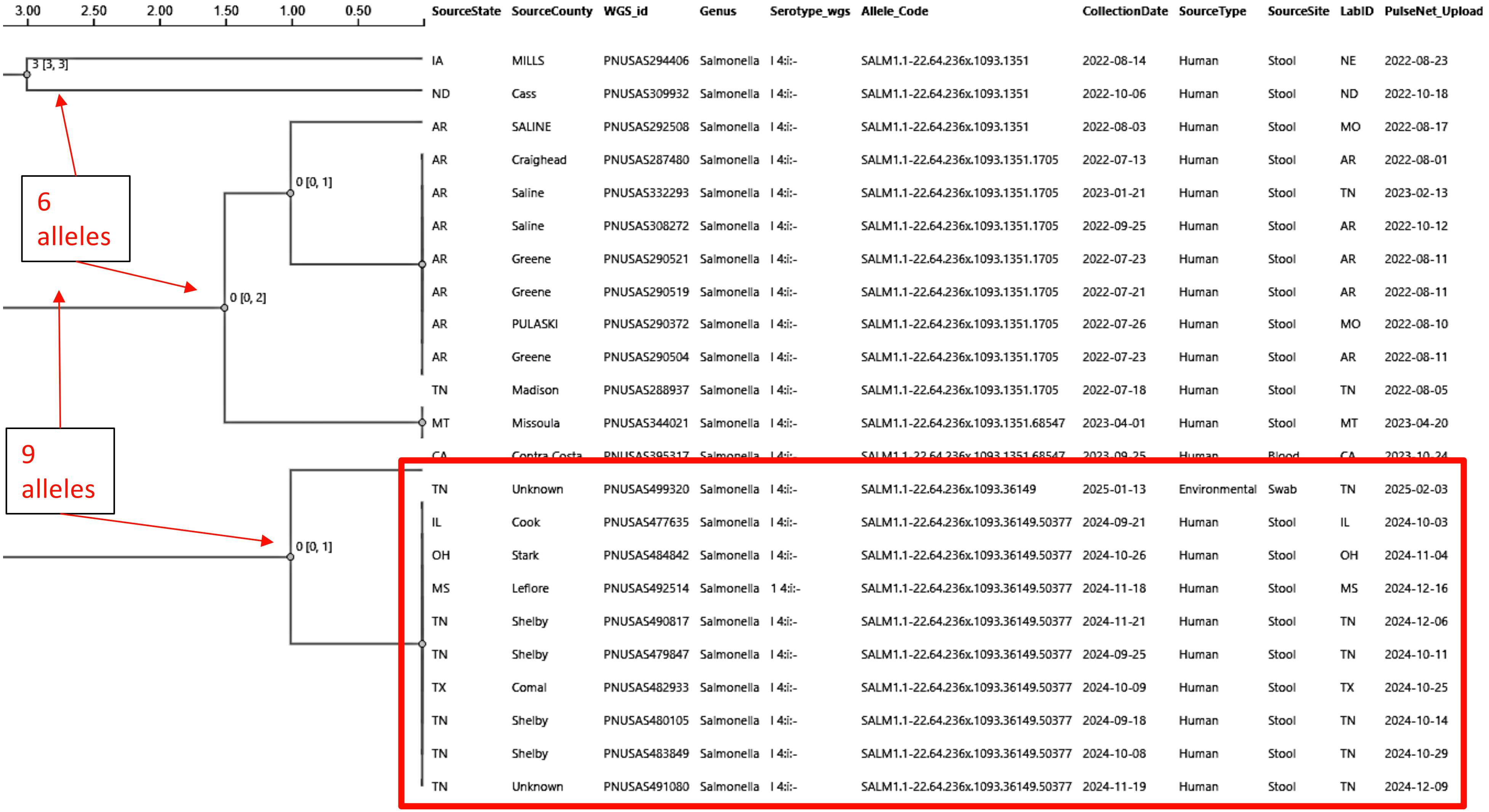
Other Exposures

Daycare: 1/6
Foodhandler: 0/6



Daycare As..	Foodhandle..	Eat Out Cha..	Daycare De..	Daycare Na..	Rest Detail
No or unknown	No or unknown	Yes	Null	Null	M, P&S, BBB, S
No or unknown	No or unknown	Yes	Null	Null	HB, F, CC, BBB
Yes	No or unknown	Yes	five days/week	Null	H
No or unknown	No or unknown	No or unknown	Null	Null	
No or unknown	No or unknown	Yes	Null	Null	BBB, EM, CFA, JM,HH
No or unknown	No or unknown	Yes	Null	Null	SFT, BBB

Final Dendrogram

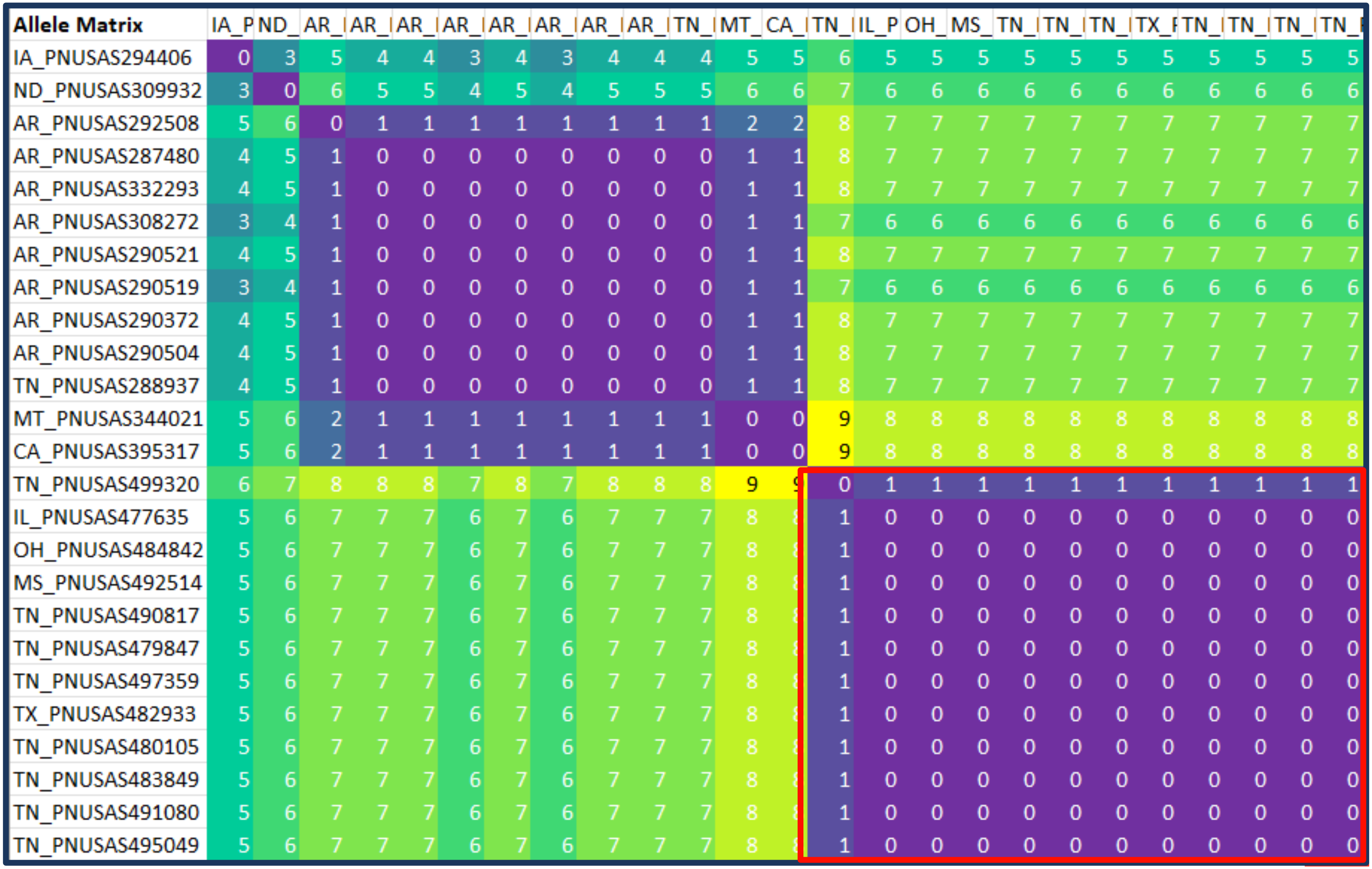


6 alleles

9 alleles

SourceState	SourceCounty	WGS_id	Genus	Serotype_wgs	Allele_Code	CollectionDate	SourceType	SourceSite	LabID	PulseNet_Upload
IA	MILLS	PNUSAS294406	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351	2022-08-14	Human	Stool	NE	2022-08-23
ND	Cass	PNUSAS309932	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351	2022-10-06	Human	Stool	ND	2022-10-18
AR	SALINE	PNUSAS292508	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351	2022-08-03	Human	Stool	MO	2022-08-17
AR	Craighead	PNUSAS287480	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-07-13	Human	Stool	AR	2022-08-01
AR	Saline	PNUSAS332293	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2023-01-21	Human	Stool	TN	2023-02-13
AR	Saline	PNUSAS308272	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-09-25	Human	Stool	AR	2022-10-12
AR	Greene	PNUSAS290521	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-07-23	Human	Stool	AR	2022-08-11
AR	Greene	PNUSAS290519	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-07-21	Human	Stool	AR	2022-08-11
AR	PULASKI	PNUSAS290372	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-07-26	Human	Stool	MO	2022-08-10
AR	Greene	PNUSAS290504	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-07-23	Human	Stool	AR	2022-08-11
TN	Madison	PNUSAS288937	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.1705	2022-07-18	Human	Stool	TN	2022-08-05
MT	Missoula	PNUSAS344021	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.68547	2023-04-01	Human	Stool	MT	2023-04-20
CA	Contra Costa	PNUSAS395317	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.1351.68547	2023-09-25	Human	Blood	CA	2023-10-24
TN	Unknown	PNUSAS499320	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149	2025-01-13	Environmental	Swab	TN	2025-02-03
IL	Cook	PNUSAS477635	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-09-21	Human	Stool	IL	2024-10-03
OH	Stark	PNUSAS484842	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-10-26	Human	Stool	OH	2024-11-04
MS	Leflore	PNUSAS492514	Salmonella	1 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-11-18	Human	Stool	MS	2024-12-16
TN	Shelby	PNUSAS490817	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-11-21	Human	Stool	TN	2024-12-06
TN	Shelby	PNUSAS479847	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-09-25	Human	Stool	TN	2024-10-11
TX	Comal	PNUSAS482933	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-10-09	Human	Stool	TX	2024-10-25
TN	Shelby	PNUSAS480105	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-09-18	Human	Stool	TN	2024-10-14
TN	Shelby	PNUSAS483849	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-10-08	Human	Stool	TN	2024-10-29
TN	Unknown	PNUSAS491080	Salmonella	I 4:i:-	SALM1.1-22.64.236x.1093.36149.50377	2024-11-19	Human	Stool	TN	2024-12-09

Final Matrix



Allele Matrix	IA_P	ND_	AR_	AR_	AR_	AR_	AR_	AR_	AR_	AR_	TN_	MT_	CA_	TN_	IL_P	OH_	MS_	TN_	TN_	TN_	TX_	TN_	TN_	TN_	TN_
IA_PNUSAS294406	0	3	5	4	4	3	4	3	4	4	4	5	5	6	5	5	5	5	5	5	5	5	5	5	5
ND_PNUSAS309932	3	0	6	5	5	4	5	4	5	5	5	6	6	7	6	6	6	6	6	6	6	6	6	6	6
AR_PNUSAS292508	5	6	0	1	1	1	1	1	1	1	1	2	2	8	7	7	7	7	7	7	7	7	7	7	7
AR_PNUSAS287480	4	5	1	0	0	0	0	0	0	0	0	1	1	8	7	7	7	7	7	7	7	7	7	7	7
AR_PNUSAS332293	4	5	1	0	0	0	0	0	0	0	0	1	1	8	7	7	7	7	7	7	7	7	7	7	7
AR_PNUSAS308272	3	4	1	0	0	0	0	0	0	0	0	1	1	7	6	6	6	6	6	6	6	6	6	6	6
AR_PNUSAS290521	4	5	1	0	0	0	0	0	0	0	0	1	1	8	7	7	7	7	7	7	7	7	7	7	7
AR_PNUSAS290519	3	4	1	0	0	0	0	0	0	0	0	1	1	7	6	6	6	6	6	6	6	6	6	6	6
AR_PNUSAS290372	4	5	1	0	0	0	0	0	0	0	0	1	1	8	7	7	7	7	7	7	7	7	7	7	7
AR_PNUSAS290504	4	5	1	0	0	0	0	0	0	0	0	1	1	8	7	7	7	7	7	7	7	7	7	7	7
TN_PNUSAS288937	4	5	1	0	0	0	0	0	0	0	0	1	1	8	7	7	7	7	7	7	7	7	7	7	7
MT_PNUSAS344021	5	6	2	1	1	1	1	1	1	1	1	0	0	9	8	8	8	8	8	8	8	8	8	8	8
CA_PNUSAS395317	5	6	2	1	1	1	1	1	1	1	1	0	0	9	8	8	8	8	8	8	8	8	8	8	8
TN_PNUSAS499320	6	7	8	8	8	7	8	7	8	8	8	9	9	0	1	1	1	1	1	1	1	1	1	1	1
IL_PNUSAS477635	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
OH_PNUSAS484842	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
MS_PNUSAS492514	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS490817	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS479847	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS497359	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TX_PNUSAS482933	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS480105	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS483849	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS491080	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0
TN_PNUSAS495049	5	6	7	7	7	6	7	6	7	7	7	8	8	1	0	0	0	0	0	0	0	0	0	0	0

PulseNet 2.0

Benefits of Using PN2.0

- When compared to SEDRIC, PN2.0 can:
  - Create dendrograms and matrices to visualize clusters more clearly
  - Show all isolates and clusters at once
  - Find *Shigella* clusters and *Campylobacter* clusters other than *jejuni*
  - Immediately show when a new isolate is added to a cluster
- Epi access can allow for workload-sharing and streamline synthesis with epi/clinical data
- Internally consistent review by Epis can help:
  - Determine when epi data supports expanding the time range
  - Weed out household clusters
  - Track clusters that may close and reopen frequently

Steps to Access PN2.0 for Epidemiologists

Request Access

- Ask a laboratorian to email pulsenet@cdc.gov
- Request Read Only Certification

Complete Agreements

- Need SAMS access
- Need PulseNet Sharepoint Access
- Data Use Agreement

Pass Quiz

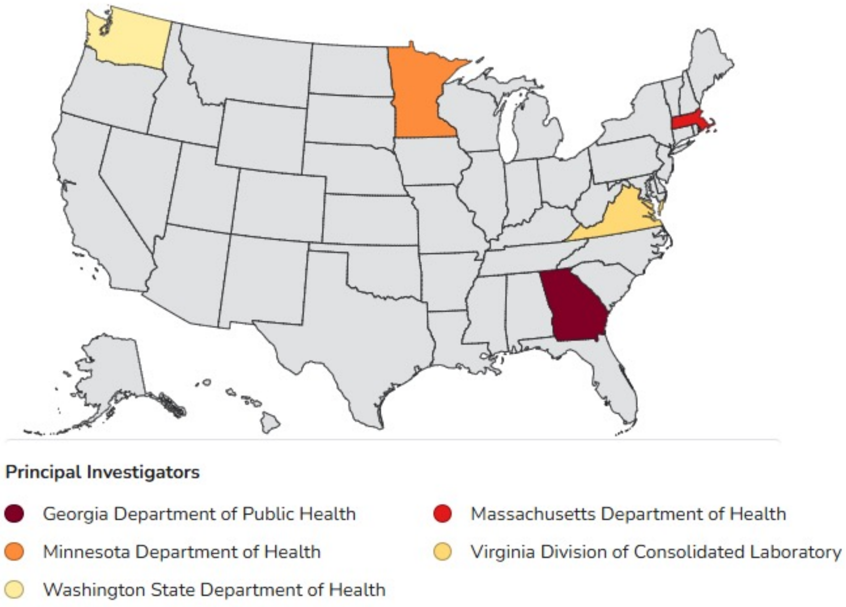
- Review user guide and practice in test environment
- Complete open book quiz

Consult SPHL

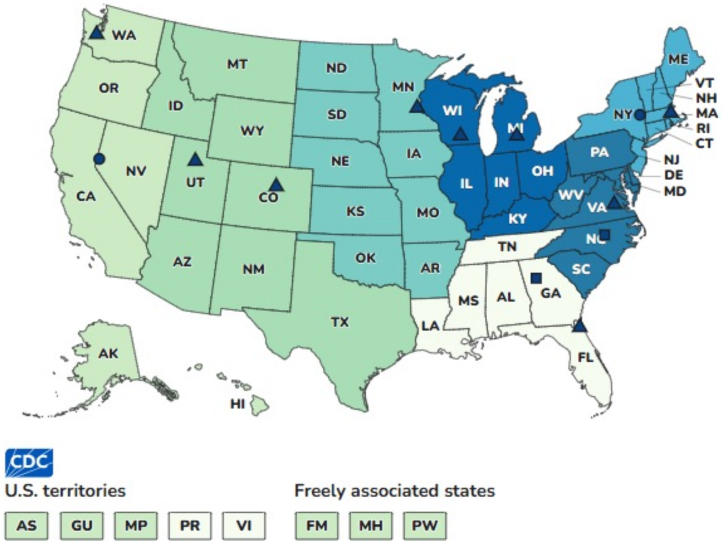
- Laboratorians can train on current process
- Can create new or share existing views

Other AMD Resources

Pathogen Genomics Centers of Excellence



Bioinformatics Regional Resource Centers (BRRs)



Knowledge Check

Epis must have SAMS access <u>and</u> pay for a software license to access PulseNet 2.0

A. TRUE

B. FALSE

Communicating Results

Communicating WGS Results

Discussion:

What communication challenges have you faced around genetic results during outbreak investigations?

Common Challenges with Communication

Scientific jargon

Delay in or lack of lab results

Different access to data/PHI

Interpreting Uncertainty

Potential Solutions

Scientific jargon

Delay in or lack of lab results

Different access to data/PHI

Interpreting Uncertainty

Challenge Scenario #1

Sequence data suggests relatedness, but Epi/EH data is missing or does not align

- Cases in animal contact outbreaks with clinical isolates matching environmental isolates, but cases do not report exposures to these sources
- Stealth ingredient implicated but not identified
- Complaint EH investigation finds violations unrelated to likely transmission of the implicated pathogen

Knowledge Check

WGS Links with No/Unsupportive Epi/EH Data

Which of the following would best help address this challenge?

A. Plain language description of why highly related sequencing data alone is a reliable link

B. Describing all the reasons epi and/or EH data could be biased or unreliable

C. Communicating next steps that could address these challenges

D. A and C

E. All of the above

Challenge Scenario #2

No/unclear genetic relatedness with clinical or environmental samples, but linked to a source due to epidemiological information

- Cyclosporiasis cases linked to a common ingredient or restaurant

- *Salmonella* outbreak cases reporting the same Mexican-styled restaurant but different serotypes, no environmental samples to link clinical samples

- Wide allele range due to length of outbreak or setting/transmission mode

- Environmental/food sample testing is negative

Knowledge Check

No/Unclear WGS Linkage

Which of the following could help address this communication challenge?

A. Describing in concise, plain language how EH and Epi data supports the hypothesis and can "rule out" other sources
B. Explaining why specimens may cluster more loosely or not at all for some serotypes or transmission modes than others
C. Blame lack of cooperation from ill people or facility for lack of good lab data

Developing Standard Language/Comms

- Plain Language Interpretation of WGS
  - Less detail:
    - *"Through lab testing known as whole genome sequencing, we compared the type of Salmonella bacteria that each case had and found they were highly genetically related to each other. This means it is very likely these infections came from the same source."*
  - For the more curious:
    - *"Whole genome sequencing lets us compare all of the Salmonella DNA between cases. As Salmonella bacteria replicate, they can acquire mutations to their DNA. If we have two Salmonella DNA sequences that are exactly identical to each other, the bacteria likely had less time to replicate and mutate as they infected people and made them sick. If they had less time to mutate, it's very likely the bacteria that made people sick came from the same source."*
- Use available resources for standard language
  - CDC/FDA Outbreak Notices
  - Previous press releases (or work with Comms team to develop language)
- Expectation Setting
- Know Your Audience

Salmonella I 4:i- Outbreak Example Wrap-Up

- Weekly written situation reports with updated dendrograms/interpretations shared with investigators
- Shared understanding and language established within the outbreak team on outbreak calls/communications
- Communication with restaurant ownership done with local points of contact, including their routine inspector
- Developed a final written report including clear interpretation of results in the discussion

Final Report Language

> *"Ten clinical specimens and sixteen environmental samples were collected during this outbreak. All clinical specimens were culture positive for* Salmonella *I 4:i- and genetically indistinguishable by whole genome sequencing. Of the sixteen environmental samples collected from the restaurant, one was positive for* Salmonella *I 4:i:- and genetically matched the clinical samples, i.e., the outbreak strain causing human illnesses."*

Questions?