

Using Aggregated Diagnostic Data in Swine Disease Surveillance and Monitoring

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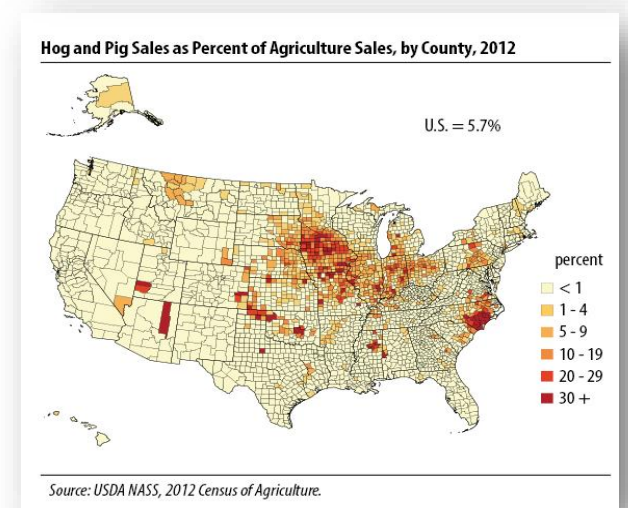
Surveillance vs Monitoring

- While often used interchangeably, there is a difference in intent:
 - **Surveillance** intends to detect a pathogen if present
 - Often attempts to prove a negative
 - May be used to assess geographic distribution
 - Can be done periodically
 - Is generally 'actionable' if positive
 - *Examples:*
 - *Sick pig surveillance for ASF/CSF*
 - *Processing fluids for PRRSV in a negative herd*
 - **Monitoring** aims to detect temporal changes or trends
 - Can be pathogen detection or disease expression
 - Typically a process evaluation
 - Is generally performed continually
 - *Examples:*
 - *M. hyopneumoniae ELISA in a negative herd*
 - *Processing fluids for PRRSV in unstable herd*



Surveillance Sampling

- What is your specific goal?
 - Confidence can be considered at various levels:
 - Animal
 - Confidence relates solely to test characteristics (DSe, DSp)
 - Round
 - Where multiple animals are tested around the same time by the same method
 - Expected prevalence impacts sampling and confidence
 - Herd
 - One related unit of animals with a geographical area
 - Rounds of testing over time add to confidence
 - Zone
 - All herds within a geographical area (county, state, region, etc.)
 - Type & amount of testing is dependent upon use case



Surveillance Sampling

- How Many Samples Do I Need?
 - Classic Statistical Tables (Cannon and Roe, 1982)
 - Simple random sampling
 - Assumes perfect tests, homogeneous distribution, binomial distribution
 - Truly random, not just easiest pigs to catch
 - Best for point in time analysis (confirming regional status)
 - May require many samples to achieve desired confidence in a negative
 - Accumulated Temporal Data (Rotolo et al. 2017)
 - Fixed spatial sampling
 - Collect the same location repeatedly [same pen(s) every time]
 - Best for individual herd surveillance
 - Repeated sampling increases confidence with fewer samples



Surveillance Sampling

- Chase and Polson, 2000
 - Based upon Cannon and Roe
 - Extrapolated for large herd sizes
 - This is where the 30 serum samples per month for PRRSV surveillance is derived
 - If PRRSV enters a negative herd, 95% confident that more than 10% will be positive

Table 1

Prevalence Estimate % Positive	Confidence Level	Population Size (Detecting One or More Positives)										
		100	200	400	600	800	1000	2000	4000	6000	8000	10000
>1%	70%	71	92	105	110	113	114	118	120	120	120	121
	80%	81	112	133	142	147	149	155	158	160	160	160
	90%	91	138	176	192	201	206	218	224	226	227	228
	95%	96	156	211	236	250	259	278	289	292	294	295
	99%	100	181	274	321	350	369	411	434	443	447	449
>2%	70%	46	53	57	58	59	59	60	61	61	61	61
	80%	56	67	74	76	77	78	80	80	81	81	81
	90%	69	88	101	105	108	109	112	114	114	115	115
	95%	78	106	125	133	137	139	144	147	148	148	149
	99%	91	137	175	191	200	205	217	223	225	226	227
>5%	70%	22	24	24	25	25	25	25	25	25	25	25
	80%	28	30	32	32	32	32	33	33	33	33	33
	90%	37	42	44	45	45	45	46	46	46	46	46
	95%	45	52	56	57	58	58	59	59	60	60	60
	99%	60	73	82	85	86	87	89	90	91	91	91
>10%	70%	12	13	13	13	13	13	13	13	13	13	13
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	95%	26	28	29	29	29	30	30	30	30	30	30
	99%	37	41	43	44	44	44	45	45	45	45	45

Chase and Polson AASV 2000



Surveillance Sampling

- Chase and Polson, 2000
 - Each month is a new “round” of testing on the herd
 - Can combine the confidence of successive rounds
 - Probability that two independent rounds fail to detect a disease is the product of the probabilities from each

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Chase and Polson AASV 2000

Surveillance Sampling

- Per Cannon (2002):
 - Combining confidence levels for rounds of random testing follows the equation:
 - $\gamma = 1 - [(1 - \gamma_1)(1 - \gamma_2)]$
 - Thus, combined confidence (γ) of 2 rounds of 30 serum samples for PRRSV surveillance would yield:
 - $\gamma = 1 - [(1-0.95)(1-0.95)]$
 - $\gamma = 0.9975$
 - Four rounds (months):
 - $\gamma = 1 - [(0.05)(0.05)(0.05)(0.05)]$
 - $\gamma = 0.99999375$
 - *One positive detection resets.*

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Chase and Polson AASV 2000

Cannon, R M. 2002. Demonstrating disease freedom – combining confidence levels. *Prev Vet Med.* 52(3-4):227-49.

Surveillance Sampling

- How Many Samples Do I Need?
 - Fixed Spatial Sampling (Rotolo et al. 2017)
 - Technically less complex
 - Collect the same location repeatedly
 - same pen(s) every time
 - Amenable to composite samples
 - Similar sensitivity as random sampling

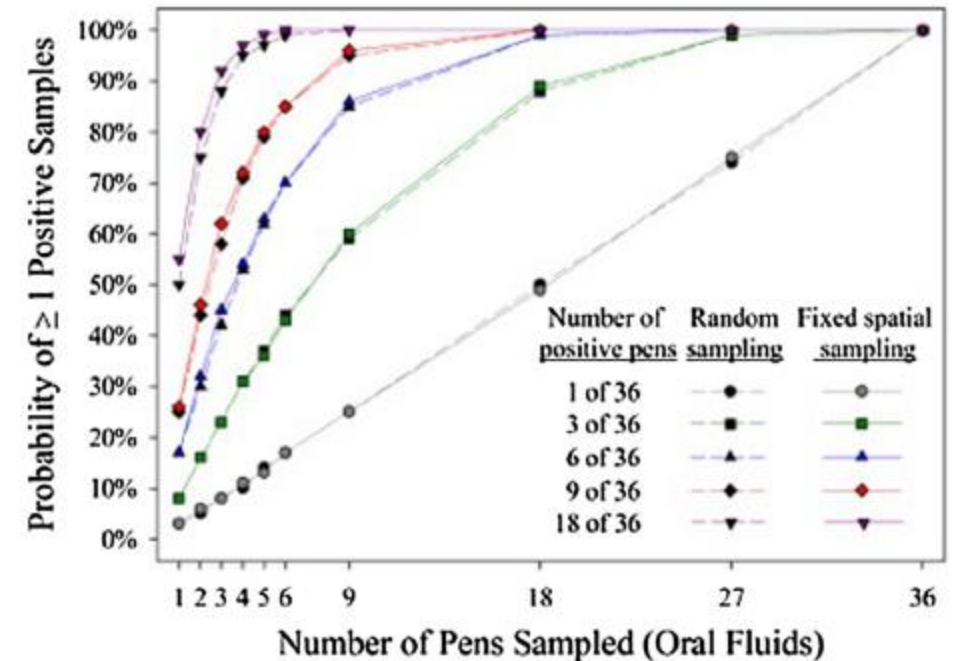


Fig. 1. Probability of detecting PRRSV in a single barn using pen-based oral fluids tested by RT-rtPCR as a function of sample allocation (simple random sampling vs. fixed spatial sampling), sample size, and prevalence.



Surveillance Sampling

- How Many Samples Do I Need?
 - Fixed Spatial Sampling (Rotolo et al. 2017)
 - In 4 weeks, 95% confidence to detect one positive with 4 or 6 oral fluids / wk
 - 4 x 4 weeks = 16 samples
 - versus 30 sera in one round randomly
 - Number of samples needed would depend upon the expected pathogen dynamics
 - Upper and lower graphs are slower vs faster spread

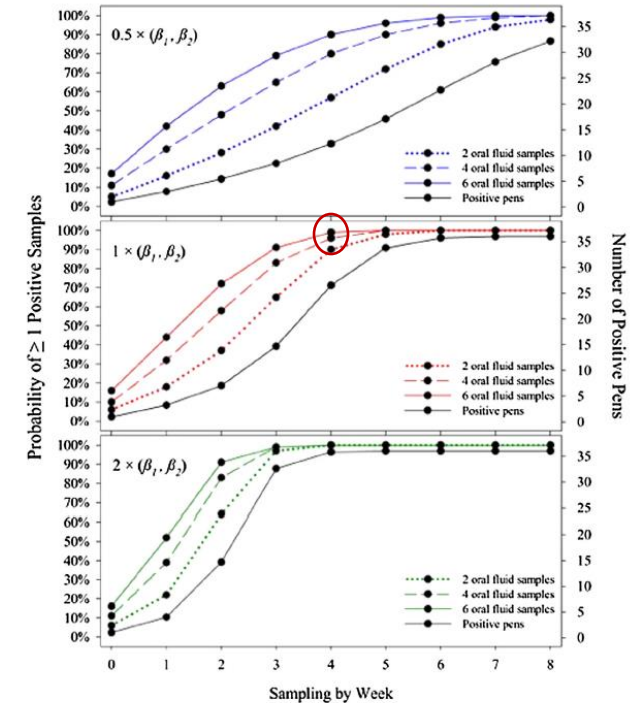


Fig. 2. Effect of spread of infection on the probability of detection by time in a single barn modeled by changing the values of β_1, β_2 in simulation studies. Fixed spatial sampling was used with sample sizes 2, 4, and 6 while allowing prevalence to change over time. For simplicity, diagnostic sensitivity and specificity were assumed to be 100%.

Surveillance Sampling

- How Many Samples Do I Need?
 - Herd surveillance does not need to be rigid and inflexible (Cannon 2002)
 - Not “one size fits all”
 - Generally, a binary approach (presence/absence)
 - Should be customized to the needs of the user (cost, convenience, speed, etc.)
 - Point in time information or ongoing assessment?
 - Must meet the needs of the customer (replacement stock versus grower/finisher)
 - Can combine different strategies:
 - Random sampling and statistical tables to establish herd or regional status initially
 - Fixed spatial sampling of fewer samples for ongoing surveillance
 - Cumulative rounds of negative testing raise confidence level over time



Surveillance Sampling

- Potential Application for Dysentery Surveillance on a Sow Farm

- Subclinical breeding herds likely have low prevalence of *B. hyodysenteriae* <2% (Duff et al. 2014)

- Traditional surveillance methods require many samples to reach 95% confidence in negative
 - ~145 samples for 2,500 hd
 - Reflects one timepoint
- Sampling specific subsets (lactating animals, just weaned pigs, etc.)

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Chase and Polson AASV 2000

Duff JW, et al. 2014. Prevalence of *Brachyspira hyodysenteriae* in sows and suckling piglets. *J Swine Health Prod.* 22(2):71-77.

Surveillance Sampling

- Potential Application for Dysentery Surveillance on a Sow Farm
 - How could fixed spatial sampling be used?
 - Select a subset of crates in farrowing
 - Sample the same crates monthly
 - Individual *Brachyspira* culture
 - ± Pooled PCR

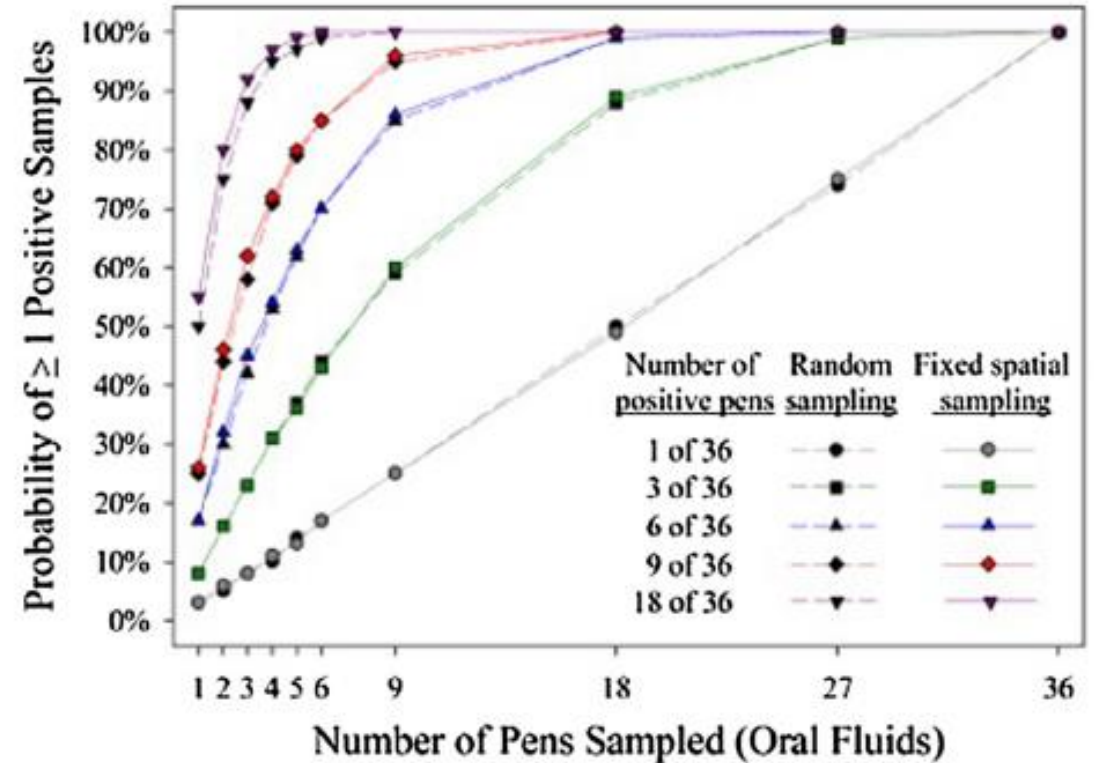
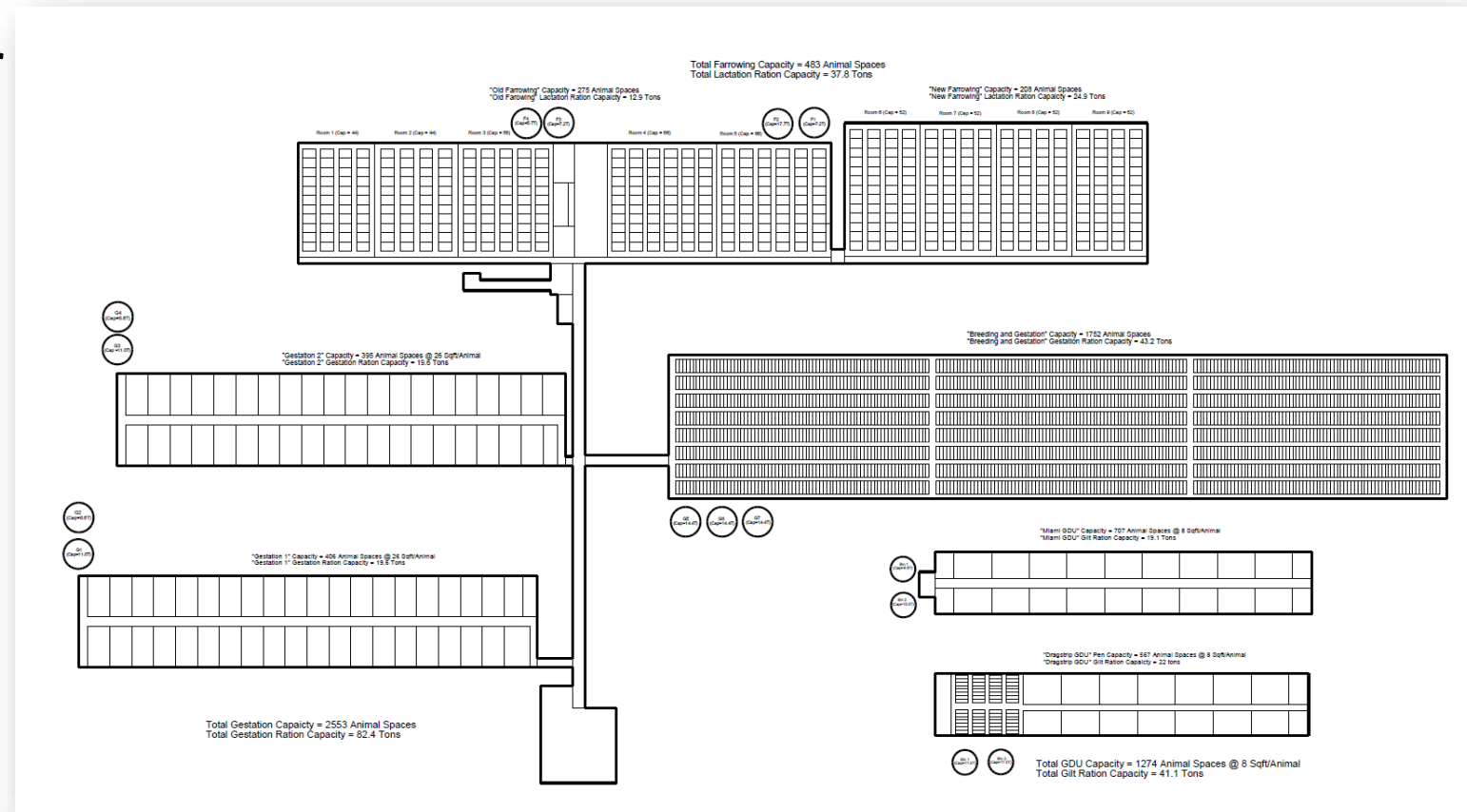


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Surveillance Sampling

- Potential Application for Dysentery Surveillance on a Sow Farm

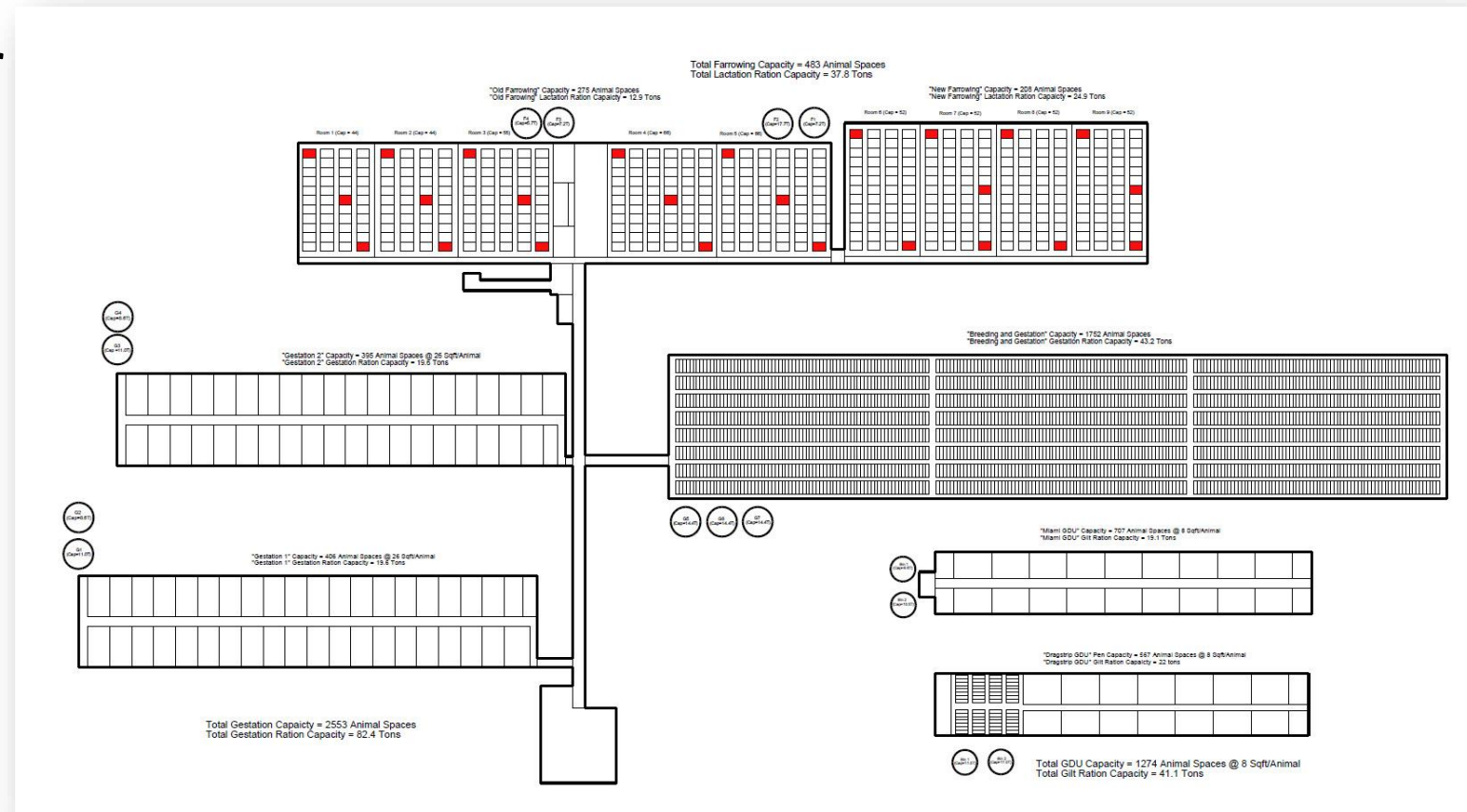
- How could fixed spatial sampling be used?
 - Select a subset of crates in farrowing (ex. 25)
 - Sample the same crates monthly
 - Individual *Brachyspira* culture
 - \pm Pooled PCR



Surveillance Sampling

- Potential Application for Dysentery Surveillance on a Sow Farm

- How could fixed spatial sampling be used?
 - Select a subset of crates in farrowing (ex. 25)
 - Sample the same crates monthly
 - Individual *Brachyspira* culture
 - \pm Pooled PCR
 - So, what is the expected confidence of 25 samples?



Surveillance Sampling

- Potential Application for Dysentery Surveillance on a Sow Farm
 - According to Cannon and Roe (1982):
 - Sampling 25 animals at 2% prev is 60.3% likely to fail to detect (39.7% DSe)
 - Recall the combined confidence eq:
 - $\gamma = 1 - [(1 - \gamma_1) (1 - \gamma_2)]$
 - Modify for n = # of repeated rounds
 - $\gamma = 1 - (1 - \gamma_1)^n$
 - $0.95 = 1 - (1 - 0.397)^n$
 - $0.95 = 1 - (0.603)^n$
 - $n = \sim 6$ months
 - After 6 months, you may assume with >95% confidence the herd is and remains negative with continued testing

Table 3: Probability of Failure to Detect Diseased Animals

The table gives the probability of failure to detect diseased animals from an 'infinite' population with the specified proportion of positives in the population.

prevalence	number of animals in sample tested									
	5	10	25	50	75	100	200	250	500	1000
1%	0.951	0.904	0.778	0.605	0.471	0.366	0.134	0.081	0.007	0.000
2%	0.904	0.817	0.603	0.364	0.220	0.133	0.018	0.006	0.000	
3%	0.859	0.737	0.467	0.218	0.102	0.048	0.002	0.000		
4%	0.815	0.665	0.360	0.130	0.047	0.017	0.000			
5%	0.774	0.599	0.277	0.077	0.021	0.006	0.000			
6%	0.734	0.539	0.213	0.045	0.010	0.002	0.000			
7%	0.696	0.484	0.163	0.027	0.004	0.001	0.000			
8%	0.659	0.434	0.124	0.015	0.002	0.000				
9%	0.624	0.389	0.095	0.009	0.001	0.000				
10%	0.590	0.349	0.072	0.005	0.000					
12%	0.528	0.279	0.041	0.002	0.000					
14%	0.470	0.221	0.023	0.001	0.000					
16%	0.418	0.175	0.013	0.000						
18%	0.371	0.137	0.007	0.000						
20%	0.328	0.107	0.004	0.000						
24%	0.254	0.064	0.001	0.000						
28%	0.193	0.037	0.000							
32%	0.145	0.021	0.000							
36%	0.107	0.012	0.000							
40%	0.078	0.006	0.000							
50%	0.031	0.001	0.000							
60%	0.010	0.000								



Cannon RM and Roe RT. 1982. Livestock disease surveys: a field manual for veterinarians. Australian Government Publishing Service

Surveillance Sampling

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 - $n = \sim 6$ months
 - *After 6 months, you may assume with >95% confidence the herd is and remains negative with continued testing*

Total tests required:

- Traditional (point in time) = 145
- Fixed spatial
 - 25/month * 6months = 150



Cannon RM and Roe RT. 1982. Livestock disease surveys: a field manual for veterinarians. Australian Government Publishing Service

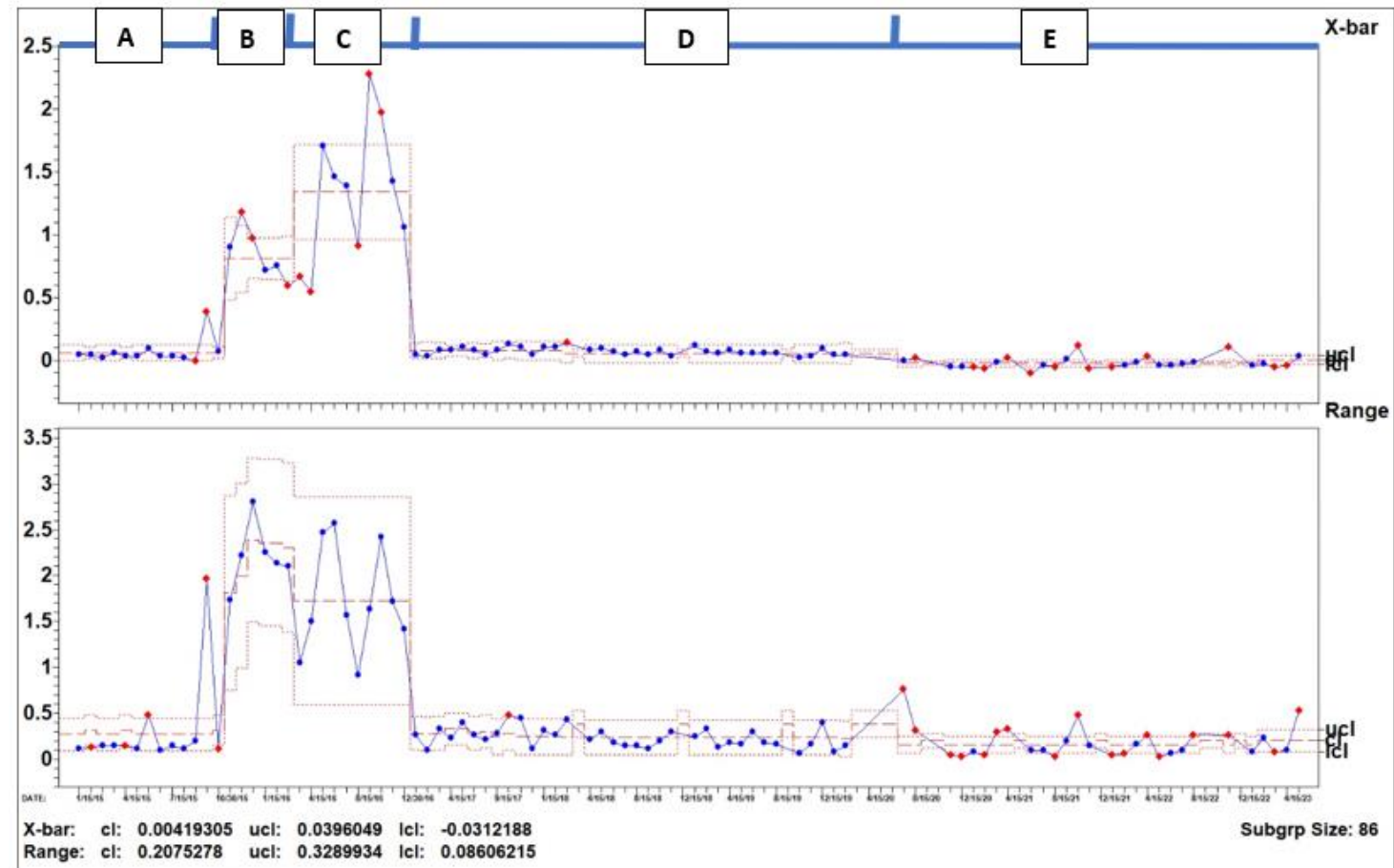
Monitoring

- If a herd is known to be positive for a given pathogen, or vaccinated, it may be desirable to temporally monitor quantitative data
 - ELISA or PCR results
- Specific Process Control (SPC) Charts
 - Well-suited for aggregated quantitative diagnostic data of individual pathogens
 - Looking for variation, loss of stability
 - Several commercial software packages:
 - Northwest Analytics Quality Analyst
 - <https://www.nwasoft.com/products/nwa-quality-analyst>
 - Microsoft Excel



Monitoring

- SPC Chart for Mhp ELISA
 - Results are reported as S/P
 - *positive/negative cutoff is 0.5*
 - The charts' three-sigma limits recalculate when a new method is introduced or if a change in output average is detected
 - A = Mhp negative
 - B = Acute Mhp infection
 - C = Herd closure + vaccination
 - D = Depop / repop
 - E = Unstable variation
 - Needs investigating

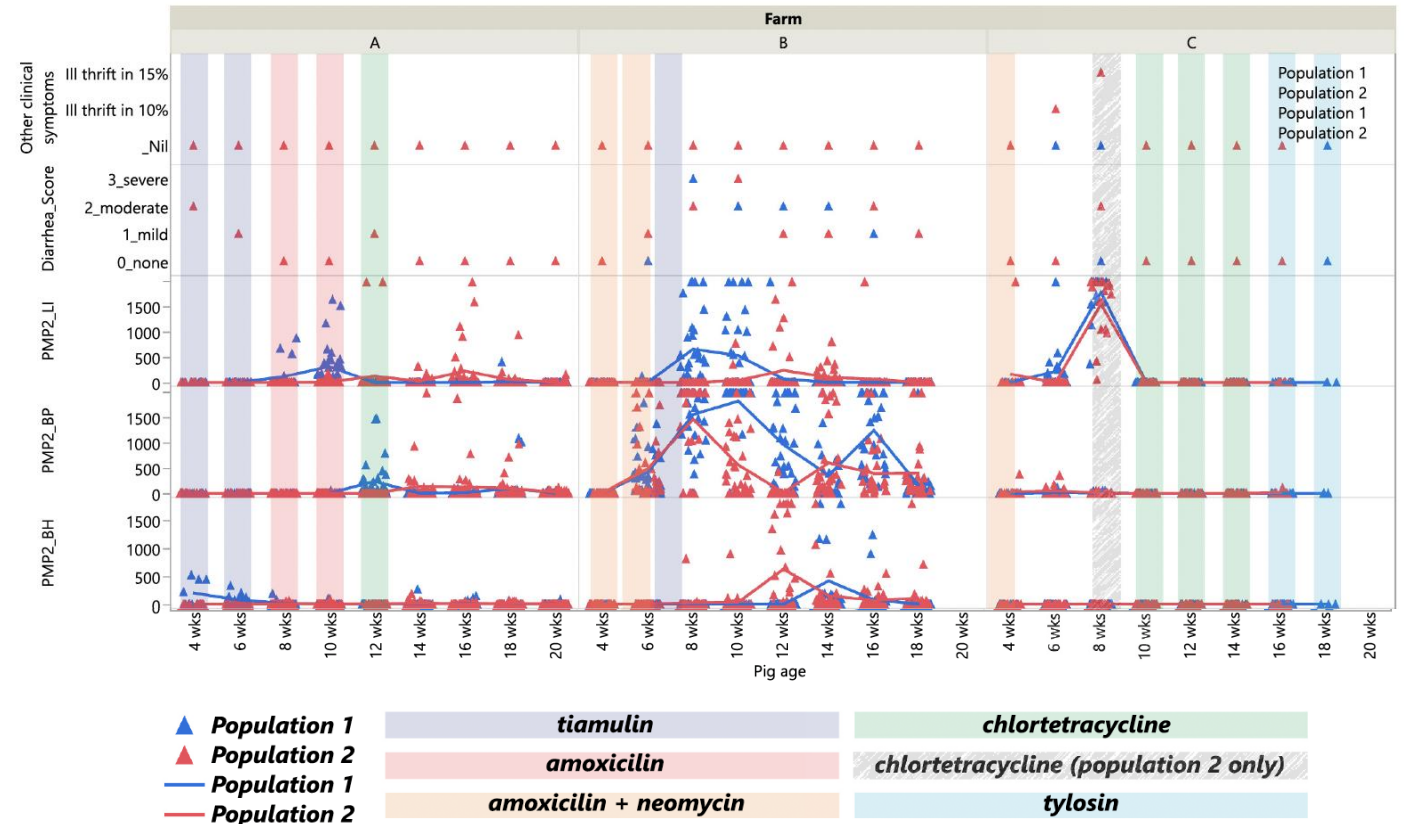


Monitoring

- PCR Panels for Endemic Pathogens

- Copy number or Ct values can be used to estimate pop pathogen burden
- Useful for composite samples over time
 - Oral fluids, feces
- Consistency of sampling is important
- Indirect assessment of mitigation effectiveness
 - Unexpected spikes warrant investigation

Pork MultiPath™ Enteric panel (PMP2) results

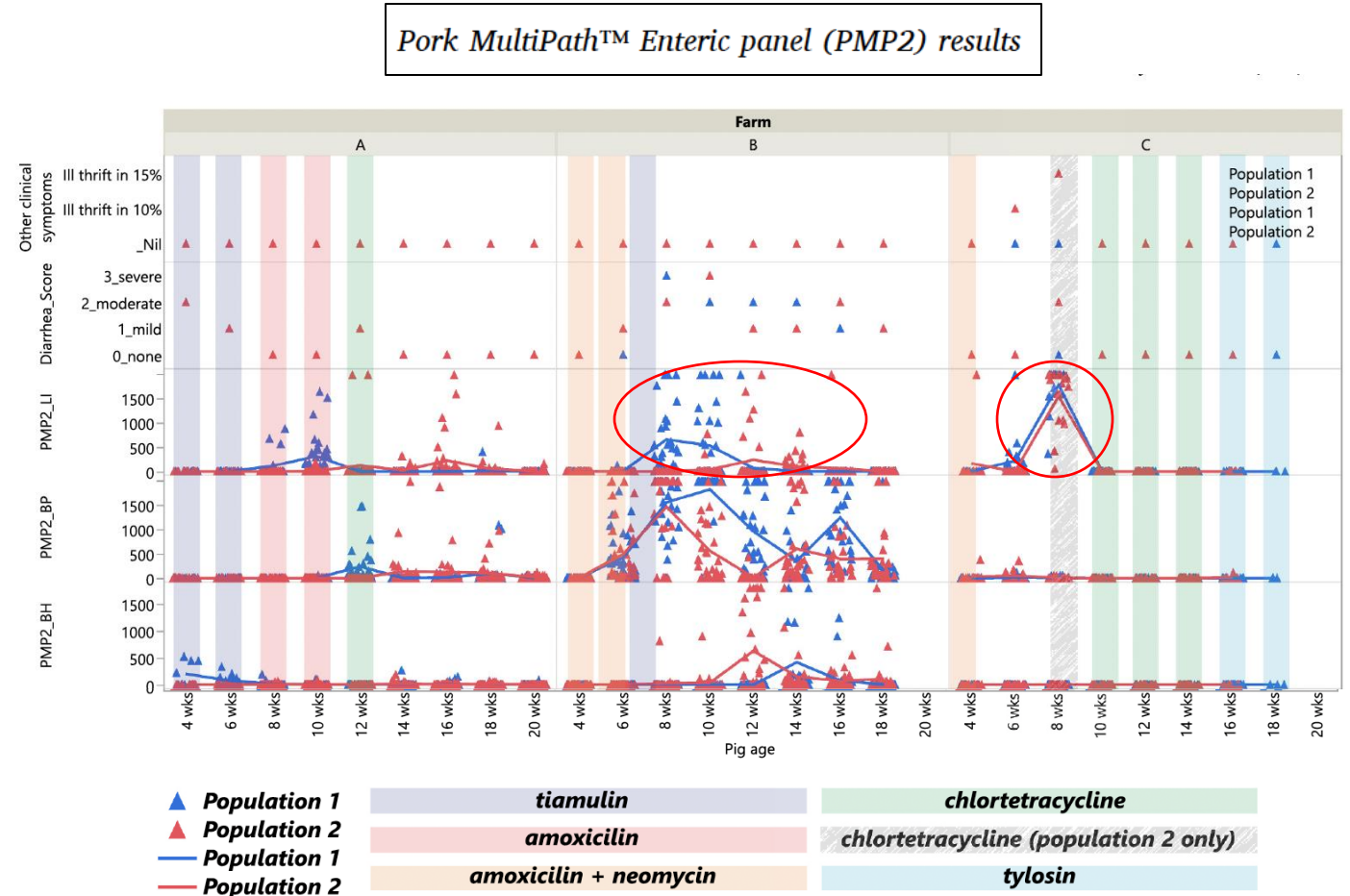


Gerszon J, et al. 2024. The use of oral fluids and sock samples for monitoring key pathogens in pig populations for surveillance purposes. *Prev Vet Med* 228:106237.

Monitoring

- PCR Panels for Endemic Pathogens

- Will generate more questions than answers
 - Requires knowledge of the herds behind the data
 - What do these *Lawsonia* detections reflect?
 - Is live vaccine used?



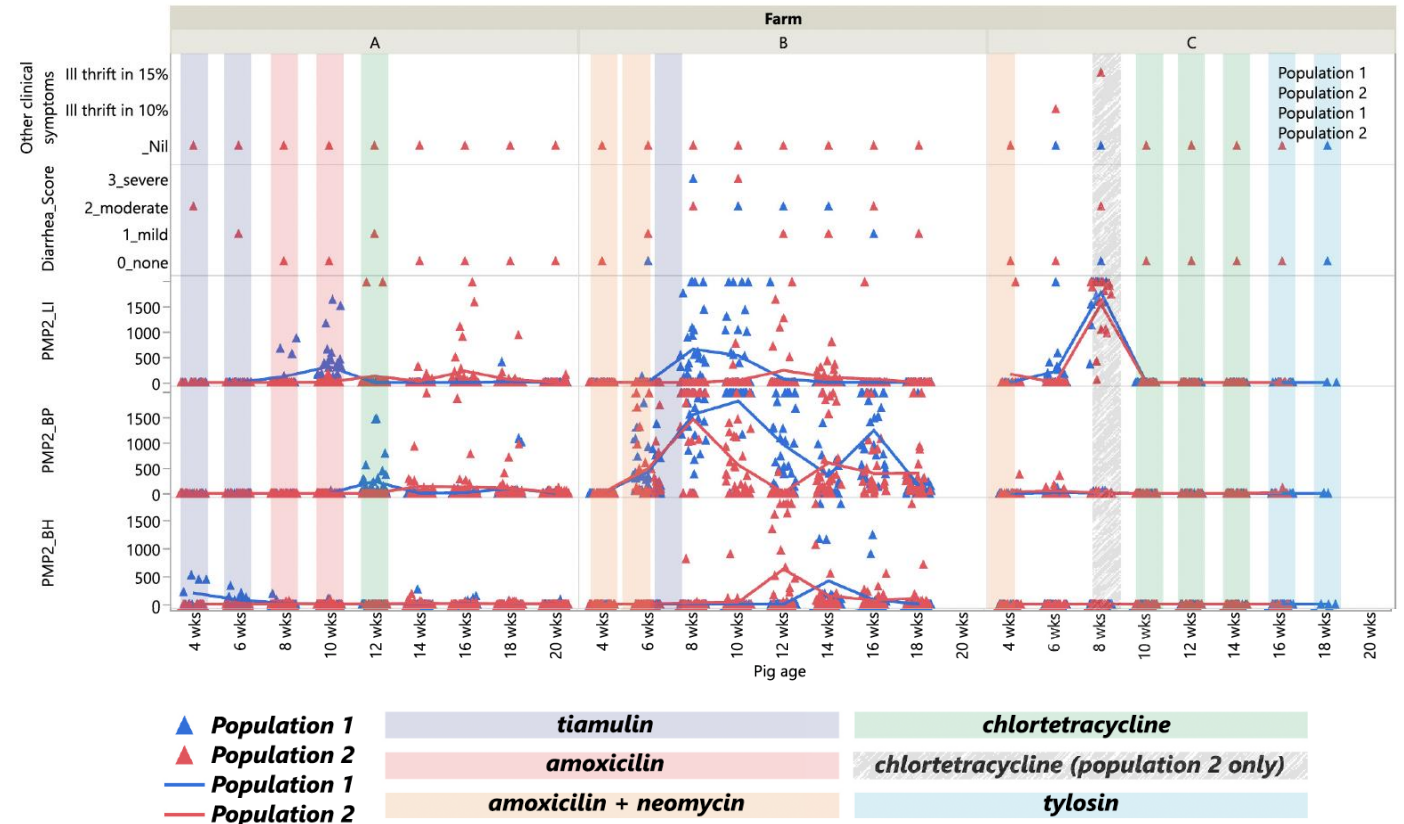
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Monitoring

- PCR Panels for Endemic Pathogens

- Will generate more questions than answers
 - Requires knowledge of the herds behind the data
 - What do these *Lawsonia* detections reflect?
 - Is live vaccine used?
 - *B. pilosicoli* appears tiamulin resistant
 - Is this spreading to *B. hyo* or are these later lateral introductions?
 - Need current MIC and genetic information of both organisms.

Pork MultiPath™ Enteric panel (PMP2) results



Gerszon J, et al. 2024. The use of oral fluids and sock samples for monitoring key pathogens in pig populations for surveillance purposes. *Prev Vet Med* 228:106237.

Large Scale Data Aggregation

Combining test data from multiple streams for zone-level monitoring





IOWA STATE
UNIVERSITY
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Diagnostic
Laboratory



Swine Disease Reporting System (SDRS)

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Project Coordinator



Dr. Guilherme
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Principal Investigators



Dr. Giovanni
Trevisan



Dr. Daniel
Linhares



Communications



Dr. Edison
Magalhães

Graduate Students



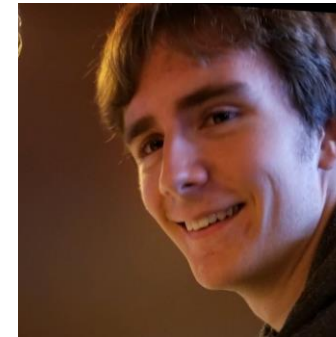
Srijita
Chandra



Dr. Elisa
De Conti



Jai
Tatinani



Alan
Moore

Software Developer



Kinath
Rupasinghe

Objective

- GOAL: to share information on the detection of endemic and emerging pathogens affecting the US swine population, thereby assisting veterinarians and producers in making informed decisions on disease prevention, detection, and management.





A collaborative project across US Vet. Diagnostic Labs

Participant Labs



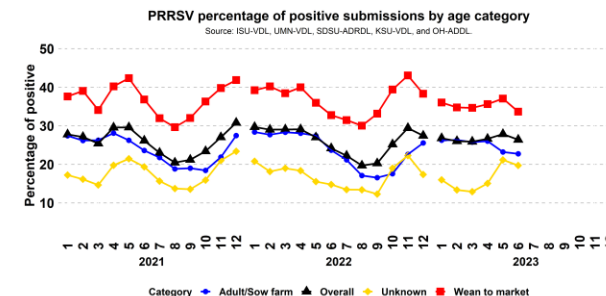
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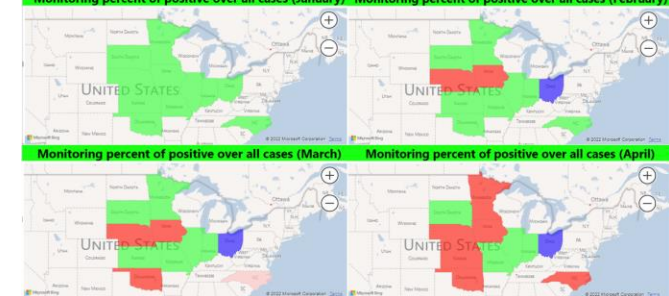
Data collating



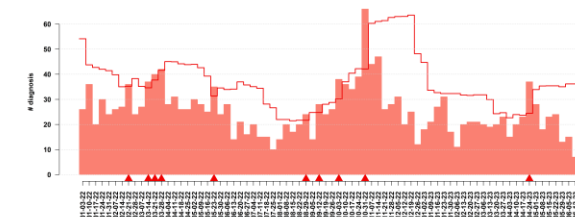
SDRS team compilation



Legend: 2-3 STD above baseline (red), 2-3 STD below baseline (green), 3+ STD above baseline (dark red), 3+ STD below baseline (dark green), Within +/- 2 STD of baseline (light green)



Influenza A diagnosis



Numbers + Field Specialists comments

Distribution



Final Report

PRRSV PCR+/- Lineage/RFLP	MHP PCR+/-
PCV2/3 PCR+/- Ct values	IAV PCR+/- subtyping
PDCoV PCR+/-	PEDV PCR+/-
TGEV PCR+/-	
Confirmed porcine tissue diagnosis (ISU VDL only)	

SDRS timeline

Participant

VDLs



Funding

PRRSV, PEDV, PEDV, TGEV PCR;
PRRSV ORF5 sequence (ISU)

Tissue-based
diagnoses (ISU)
Mar 2019

IAV PCR
Apr 2022

PCV2 PCR
May 2022

IAV
subtype
Oct 2022

PCV3 PCR
Nov 2023





Information available through monthly PDF reports

Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.

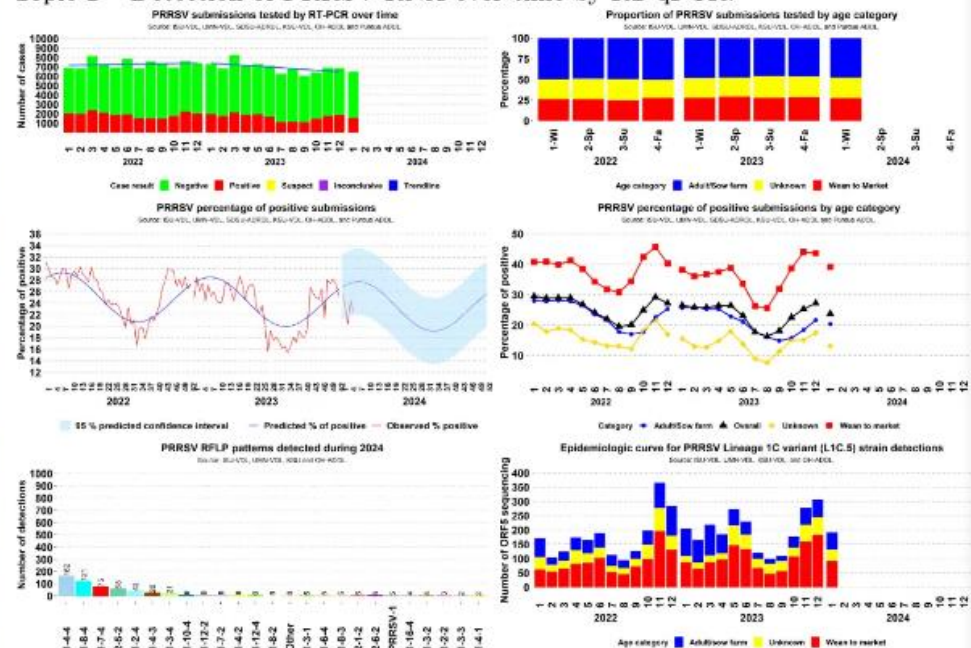


Figure 1. Top: Left: Results of PRRSV RT-PCR cases over time; Right: Proportion of accession ID cases tested for PRRSV by age group per year and season. Middle: Left: Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 3 years; Right: Percentage of PRRSV PCR-positive results, by age category, over time. Wean to market corresponds to nursery and grow-finish. Adult/Sow correspond to Adult, boar stud, breeding herd, replacement, and suckling piglets. Unknown corresponds to not informed site type or farm category. Bottom Left: The 25 most frequently detected RFLP patterns during 2024; Right: Epidemiological curve of detection for PRRSV Lineage 1C variant (L1C.5) strain.

SDRS Advisory Group highlights:

- Overall, 23.76% of 6,486 cases tested PRRSV-positive in January, a moderate decrease from 27.22% of 6,878 in December;
 - Positivity in the adult/sow category in January was 20.39% (629 of 3,085), similar to 21.67% (681 of 3,143) in December;
 - Positivity in the wean-to-market category in January was 39.1% (701 of 1,793), a moderate decrease from 43.63% (898 of 2,058) in December;
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Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

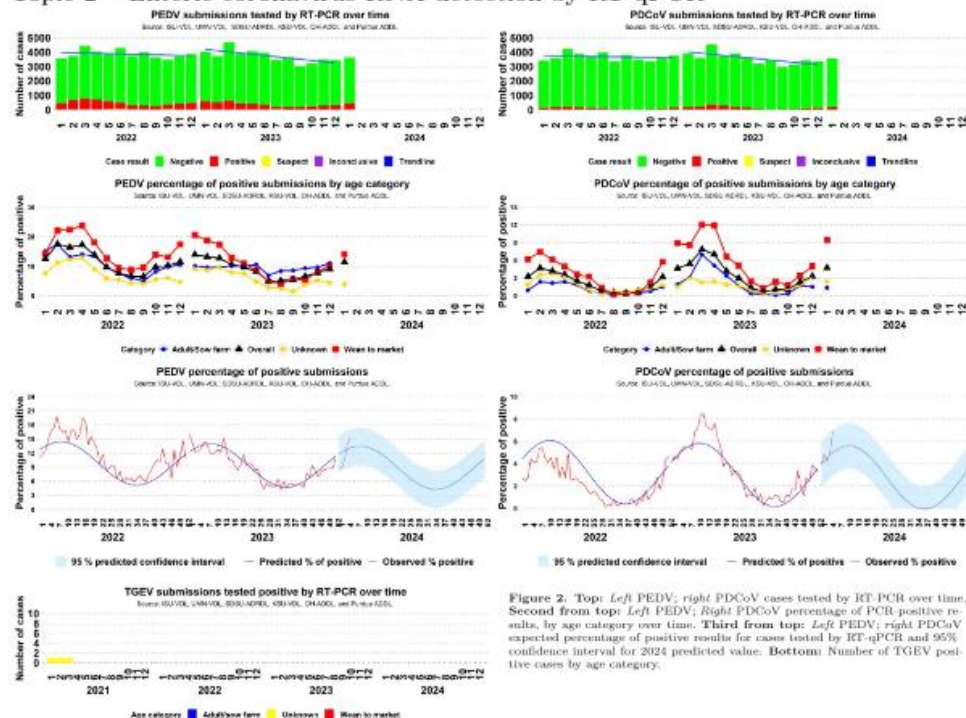


Figure 2. Top: Left PEDV; right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of PCR positive results, by age category over time. Third from top: Left PEDV; right PDCoV expected percentage of positive results for cases tested by RT-qPCR and 95% confidence interval for 2024 predicted value. Bottom: Number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

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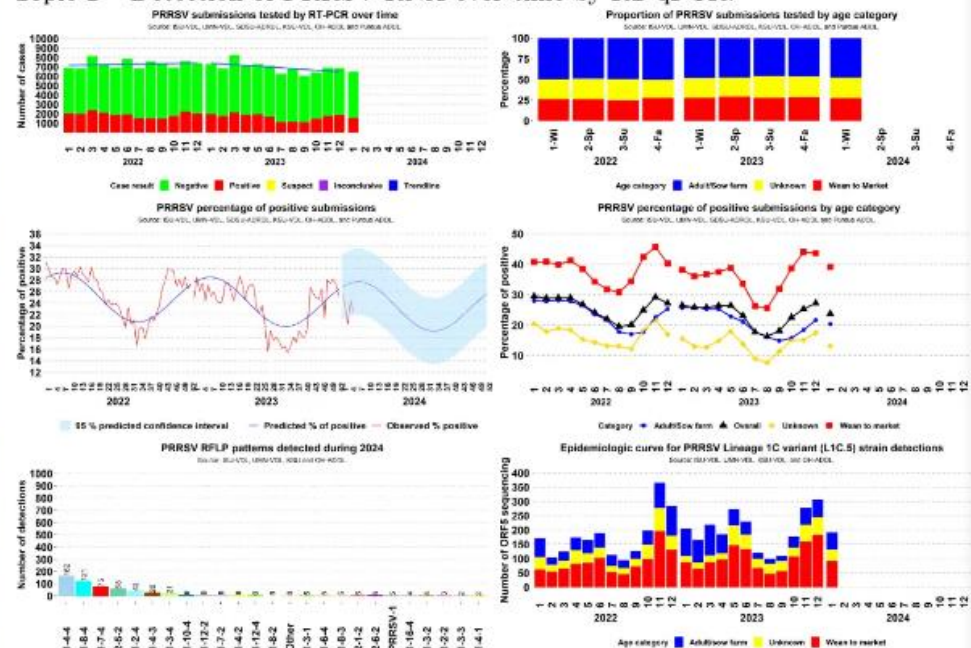


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Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

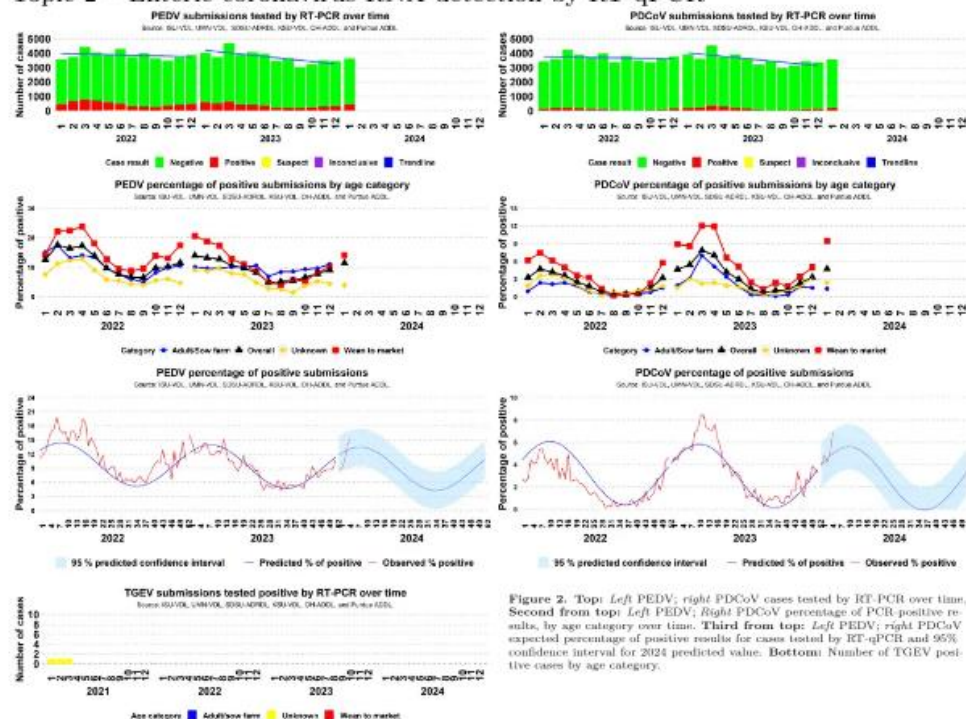


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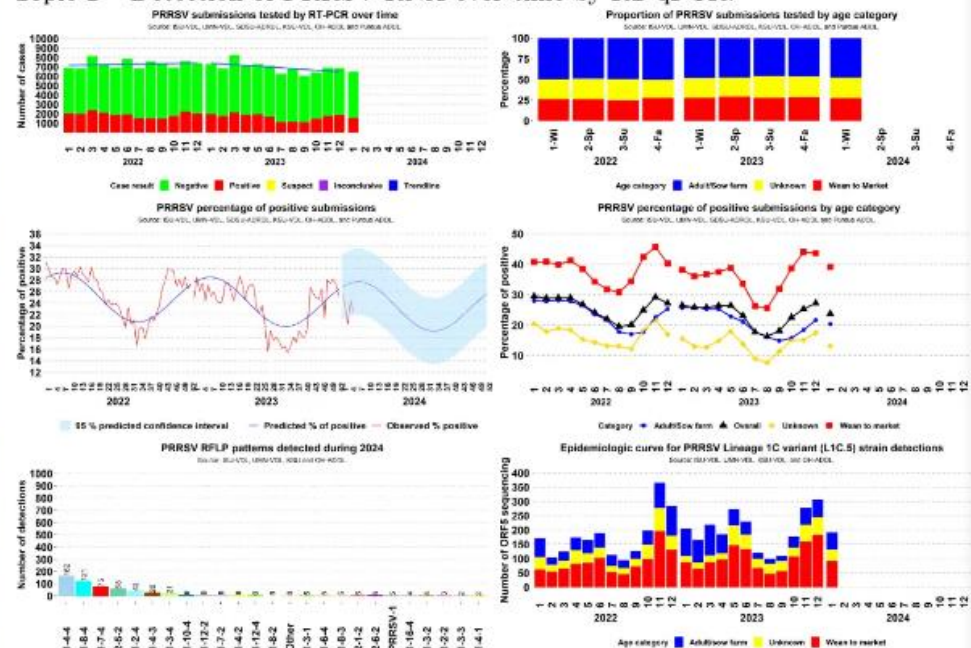


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Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

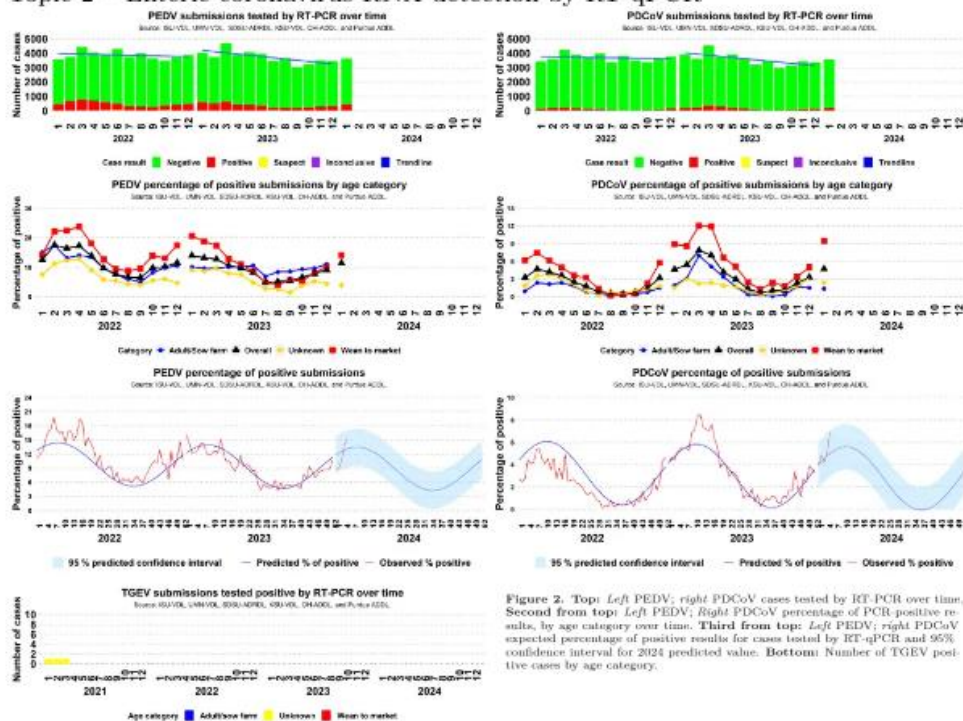


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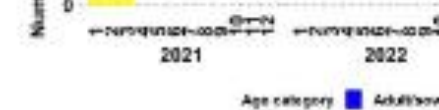
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SDRS report 72



SDRS Advisory Group highlights:

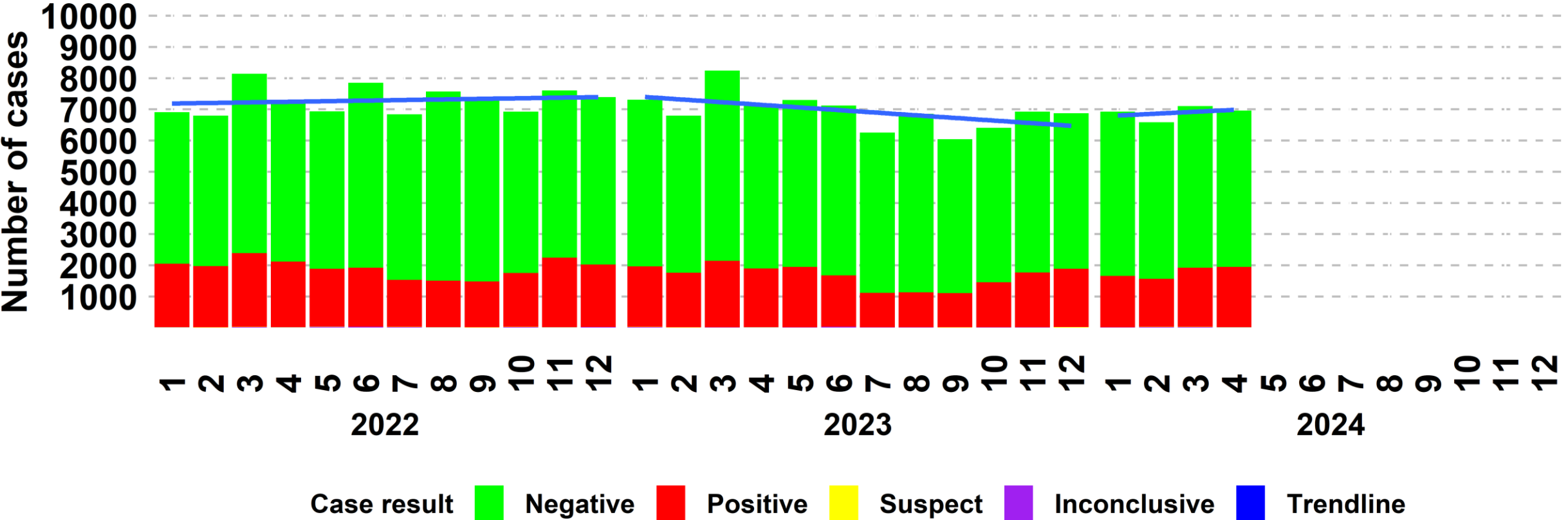
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Interpret the decrease in positivity with caution because some production systems are not sampling the animals downstream once the sow farm is positive for PRRSV

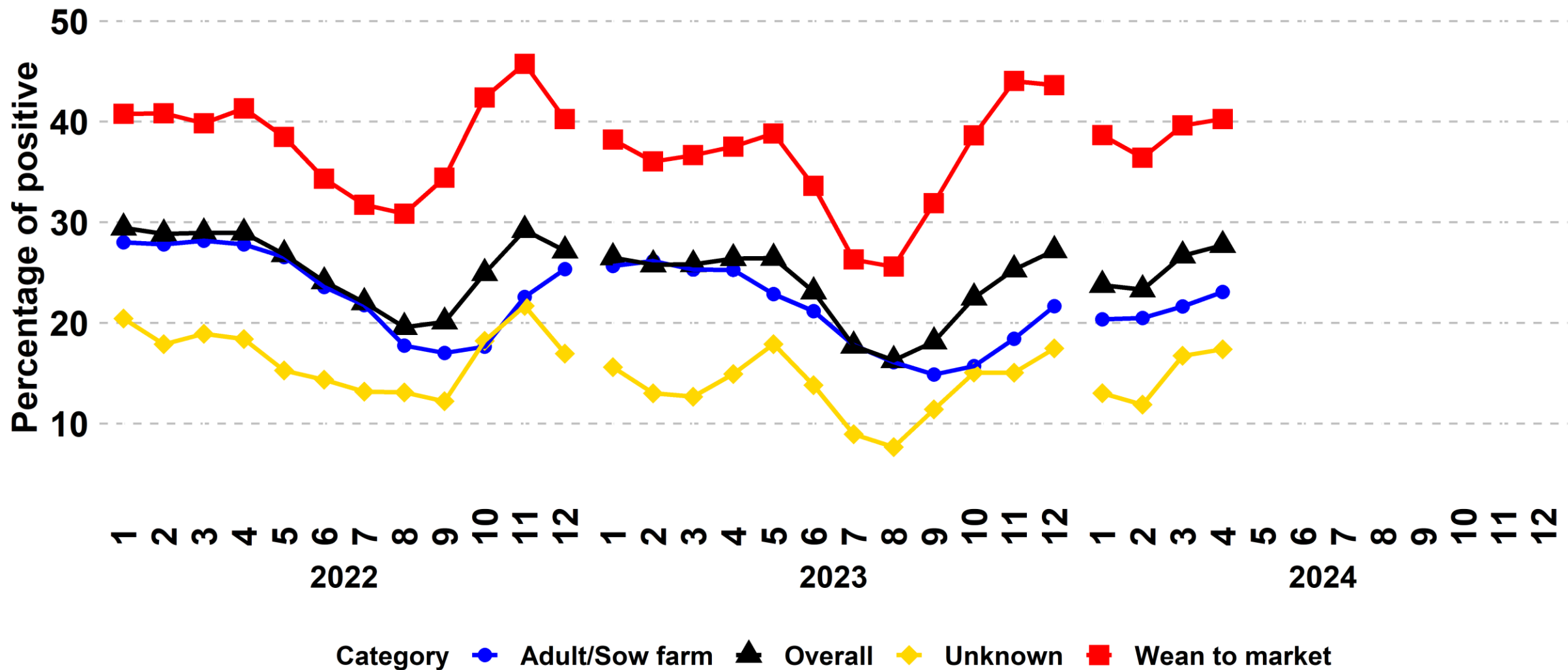
PRRSV submissions tested by RT-PCR over time

Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, KSU-VDL, OH-ADDL and Purdue ADDL.



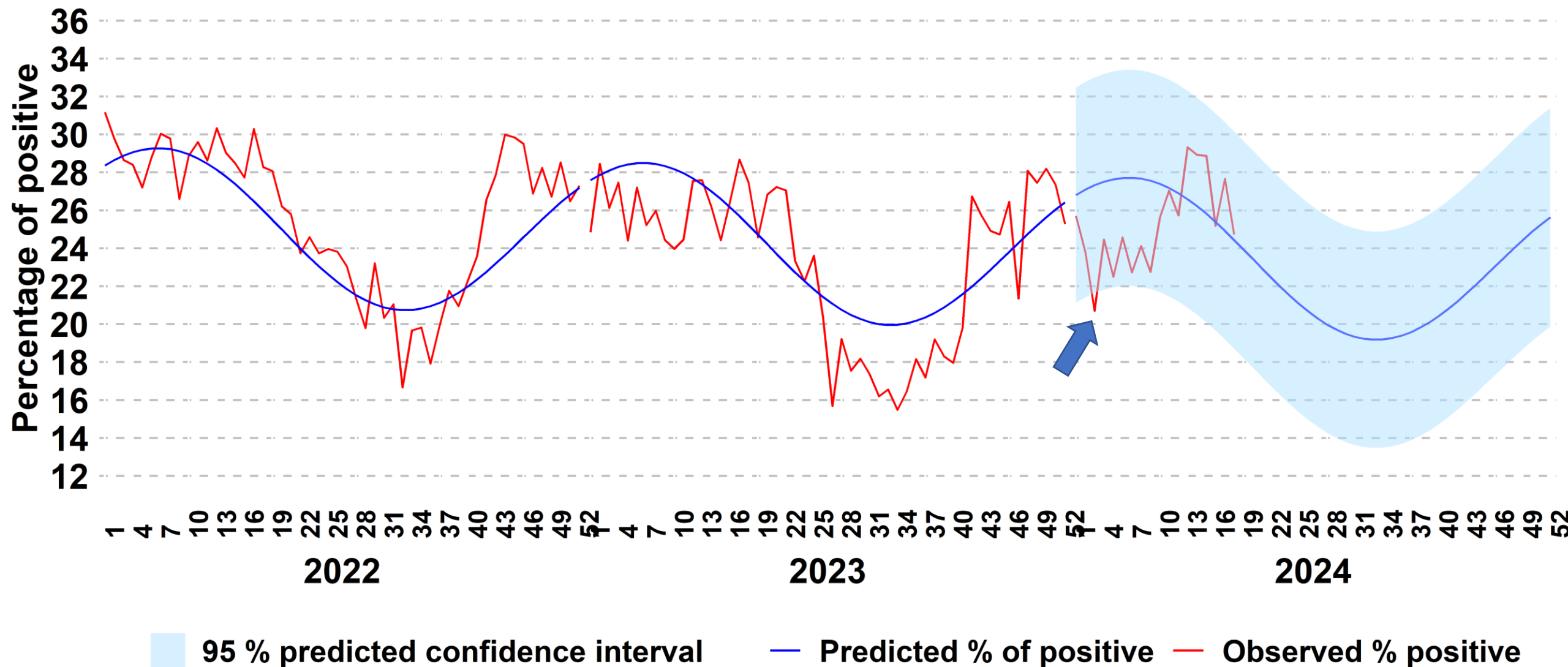
PRRSV percentage of positive submissions by age category

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IOWA STATE
UNIVERSITY
Veterinary
Diagnostic
Laboratory



Information available through online dashboards

Analyte

IAV

MHP

PCV2

PCV3

PDCoV

PEDV

PRRSV

TGEV

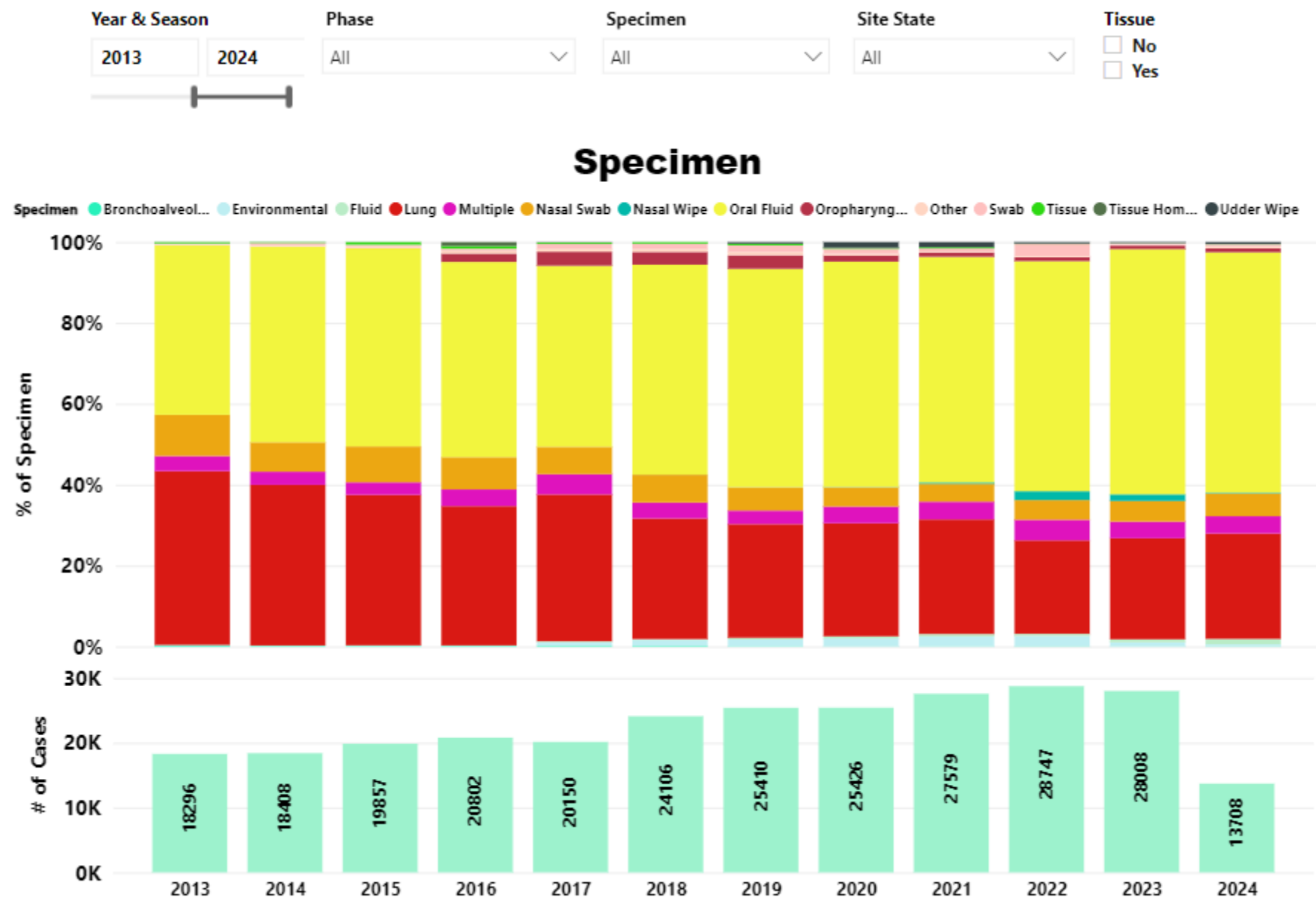
Analyte Over time

Specimen

Map

Age Category

Quality Control



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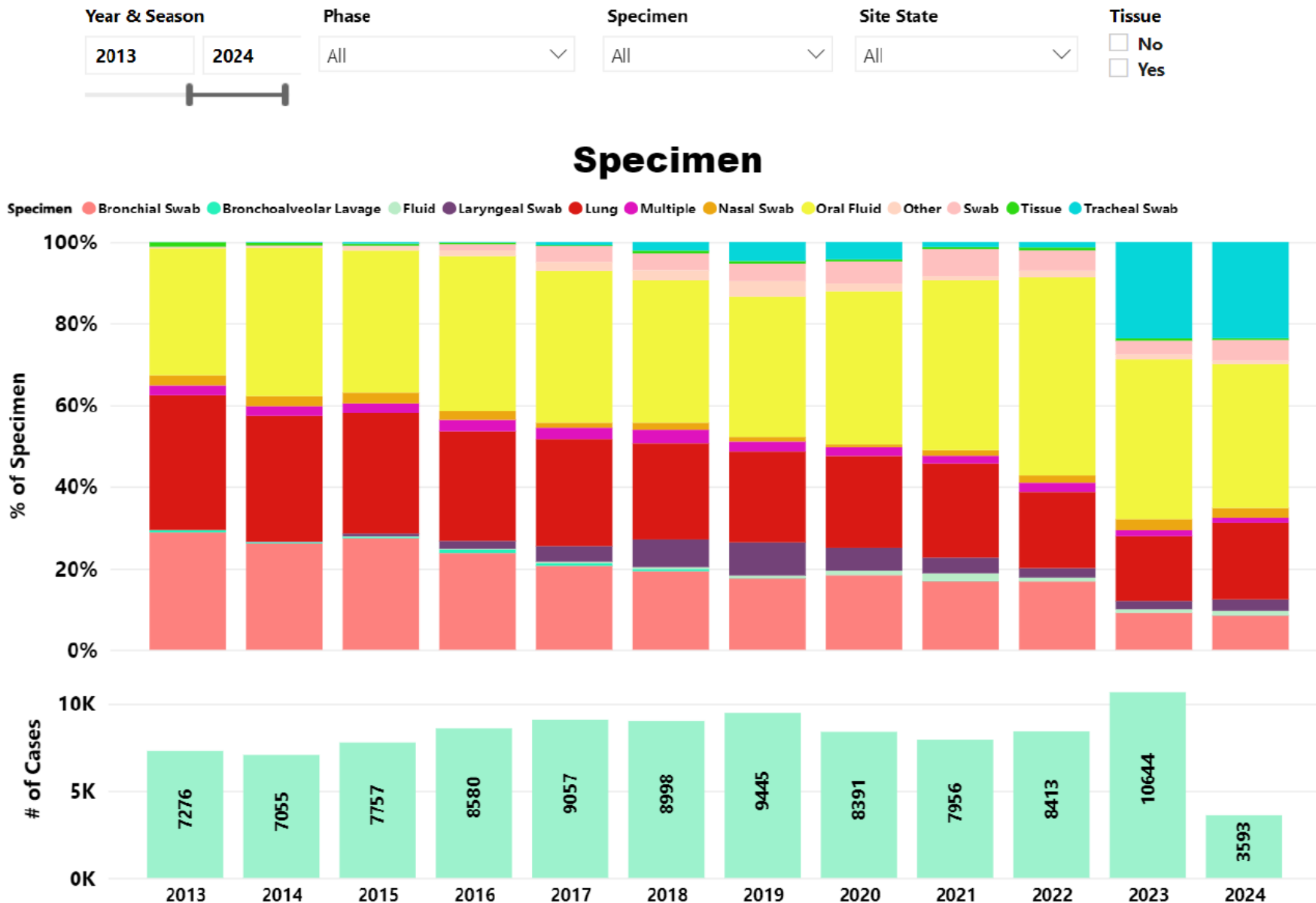
Analyte Over time

Specimen

Map

Age Category

Quality Control



Large Scale Data Aggregation

- Relatively easy to do for pathogen detection data.
- What about disease diagnosis?
 - For endemic agents, disease diagnosis requires detection + evidence
 - To be of value, there should be standardization of what is accepted as disease confirmation
 - Pathology (gross and microscopic) is the gold standard
 - The narrative nature of traditional pathology reporting makes data aggregation challenging
 - Currently, there is no uniform method for disease reporting in veterinary medicine
 - Can disease be coded in a uniform way?
 - Disease diagnostic codes can be messaged and aggregated similar to other test data



Large Scale Data Aggregation

- Disease Diagnostic Codes (Dx Codes)
 - Have been used at the ISU VDL since 2003
 - Early codes were not standardized, no clear hierarchy
 - Examples:
 - MHD = mulberry heart disease
 - ABOR PPV = parvovirus abortion
 - ENTE SERP HYOD = swine dysentery
 - In 2017, we decided a new hierarchal system was needed
 - Each disease code contains 4 components:
 - **SYSTEM** (respiratory, digestive, nervous, urogenital, etc.)
 - **INSULT** (bacterial, viral, parasitic, toxicity, etc.)
 - **LESION** (pneumonia, enteritis, arthritis, etc.)
 - **ETIOLOGY** (PRRSV, *Salmonella*, *E. coli*, etc.)



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• CBEI	NOSP	CARD	MHD	= mulberry heart disease
• UROG	VIRA	ABOR	PARV	= parvovirus abortion
• DIGE	BACT	COLI	BRACH	HYOD = swine dysentery



Large Scale Data Aggregation

- Disease Diagnostic Codes (Dx Codes)

Histopathology:

Pig 1:

Lung: Alveolar septa are variably expanded by macrophages and fewer lymphocytes and there is multifocal type II pneumocyte hyperplasia. Alveolar spaces often contain necrotic macrophages admixed with fibrin, degenerate neutrophils and cellular debris. The pleura is expanded by loose fibrous tissue and few lymphocytes and there is hypertrophy of mesothelial cells.

Heart: There is moderate multifocal infiltration of lymphocytes and plasma cells in the myocardium and endocardium.

Haired skin: The deep dermis and panniculus are expanded by coalescing abscesses. Adjacent adnexa are often surrounded by lymphocytes and plasma cells and there is orthokeratotic hyperkeratosis in the epidermis.

Lymph node, spleen, liver and kidney: There are no lesions of diagnostic significance.

Pig 2:

Lung: Lesions are similar to Pig 1.

Colon: The mesocolon is expanded by edema and few leukocytes. The mucosa is multifocally eroded and there is rare infiltration of neutrophils.

Lymph node, spleen, liver, kidney, heart and small intestine: There is significant autolysis in the intestinal tissues that impedes evaluation. Tissues are otherwise unremarkable.

Ancillary Diagnostic Tests:

Completed results appear below

Laboratory Diagnosis:

Both pigs:

- PRRSV pneumonia, subacute, moderate

Pig 1:

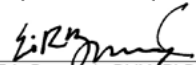
- Polyserositis, fibrinopurulent, moderate (*Streptococcus suis*)

Pig 2:

- Colitis, suppurative, multifocal, acute with mesocolonic edema

Comments:

The lung lesions are typical of PRRSV infection that was confirmed by PCR. The colitis is consistent with what is reported in *Clostridioides difficile* infection and abundant toxin was detected within colon content by ELISA. Please contact the laboratory if further testing is desired or questions arise. (6/5/24 eb/np)



Eric Burroughs, DVM PhD, DACVP
Professor

Pathology Section Leader, Diagnostic Pathologist

List of abbreviations used by the ISUVDL can be found here:

<https://vetmed.iastate.edu/vdl/diagnostic-tests/pathogen-and-testing-abbreviations>

Requester	Department	Requester ID	
Please genotype the C perf from the intestine	Bacteriology	erb	ELLIE
Please genotype the smooth mucoid E. coli from the intestine.	Bacteriology	Dr. T. Angen	ELLIE
Please send the foot in save back for culture of the skin around the joint. These are the joint for amputation.	Necropsy	erb	BURI
Please run PRRSV PCR on the pooled lung	Necropsy	Dr. T. Angen	KOLF
Please run PRRSV PCR on the pooled lung	Molecular Diagnostics	Dr. T. Angen	BURI
Please run CDR PCR on the swirle	Molecular Diagnostics	Dr. T. Angen	BURI

Codes	Research?	188 dx code(s) matched
<input type="checkbox"/> DIGE ANOM HEPA OPAT NOSP	<input type="checkbox"/>	Digestive, Anomaly, Hepatopathy, Not specified
<input type="checkbox"/> DIGE ANOM INTE STIN NOSP	<input type="checkbox"/>	Digestive, Anomaly, Intestine, Not specified
<input type="checkbox"/> DIGE BACT ABSC LIVE ABSC	<input type="checkbox"/>	Digestive, Bacterial, Abscess, Liver abscess
<input type="checkbox"/> DIGE BACT ABSC NOSP	<input type="checkbox"/>	Digestive, Bacterial, Abscess, Not specified
<input type="checkbox"/> DIGE BACT ABSC TPYO	<input type="checkbox"/>	Digestive, Bacterial, Abscess, Trueperella pyogenes
<input type="checkbox"/> DIGE BACT COLI BRAC	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Brachyspira sp.
<input type="checkbox"/> DIGE BACT COLI BRAC HAMP	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Brachyspira hampsonii
<input type="checkbox"/> DIGE BACT COLI BRAC HYOD	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Brachyspira hyodysenteriae
<input type="checkbox"/> DIGE BACT COLI BRAC MURD	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Brachyspira murdochii
<input type="checkbox"/> DIGE BACT COLI BRAC PILO	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Brachyspira pilosicoli
<input type="checkbox"/> DIGE BACT COLI BRAC SUAN	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Brachyspira suanvatitii
<input type="checkbox"/> DIGE BACT COLI CLOS DIFF	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Clostridioides difficile
<input type="checkbox"/> DIGE BACT COLI NOSP	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Not specified
<input type="checkbox"/> DIGE BACT COLI SALM	<input type="checkbox"/>	Digestive, Bacterial, Colitis, Salmonella
<input type="checkbox"/> DIGE BACT ENTE CAMP SP	<input type="checkbox"/>	Digestive, Bacterial, Enteritis, Campylobacter sp.
<input type="checkbox"/> DIGE BACT ENTE CHLA	<input type="checkbox"/>	Digestive, Bacterial, Enteritis, Chlamydia sp.
<input type="checkbox"/> DIGE BACT ENTE CLOS COLI	<input type="checkbox"/>	Digestive, Bacterial, Enteritis, Clostridium colinum

Codes	As Displayed	Research?	Creator
RESP VIRA PNEU INTE	Respiratory, Viral, Interstitial pneumonia, PRRSV	<input type="checkbox"/>	BURROUGH, ERIC R
SYST VIRA MULT PRRS	Systemic, Viral, Multiple, PRRSV	<input type="checkbox"/>	BURROUGH, ERIC R
RESP BACT PLEU STRE	Respiratory, Bacterial, Pleuritis, Streptococcus suis	<input type="checkbox"/>	BURROUGH, ERIC R
DIGE BACT COLI CLOS	Digestive, Bacterial, Colitis, Clostridioides difficile	<input type="checkbox"/>	BURROUGH, ERIC R

Large Scale Data Aggregation

- Disease Diagnostic Codes (Dx Codes)

Histopathology:

Pig 1:

Lung: Alveolar septa are variably expanded by macrophages and fewer lymphocytes and there is multifocal type II pneumocyte hyperplasia. Alveolar spaces often contain necrotic macrophages admixed with fibrin, degenerate neutrophils and cellular debris. The pleura is expanded by loose fibrous tissue and few lymphocytes and there is hypertrophy of mesothelial cells.

Heart: There is moderate multifocal infiltration of lymphocytes and plasma cells in the myocardium and endocardium.

Haired skin: The deep dermis and panniculus are expanded by coalescing abscesses. Adjacent adnexa are often surrounded by lymphocytes and plasma cells and there is orthokeratotic hyperkeratosis in the epidermis.

Lymph node, spleen, liver and kidney: There are no lesions of diagnostic significance.

Pig 2:

Lung: Lesions are similar to Pig 1.

Colon: The mesocolon is expanded by edema and few leukocytes. The mucosa is multifocally eroded and there is rare infiltration of neutrophils.

Lymph node, spleen, liver, kidney, heart and small intestine: There is significant autolysis in the intestinal tissues that impedes evaluation. Tissues are otherwise unremarkable.

Ancillary Diagnostic Tests:

Completed results appear below

Laboratory Diagnosis:

Both pigs:

- PRRSV pneumonia, subacute, moderate

Pig 1:

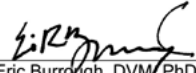
- Polyserositis, fibrinopurulent, moderate (*Streptococcus suis*)

Pig 2:

- Colitis, suppurative, multifocal, acute with mesocolonic edema

Comments:

The lung lesions are typical of PRRSV infection that was confirmed by PCR. The colitis is consistent with what is reported in *Clostridioides difficile* infection and abundant toxin was detected within colon content by ELISA. Please contact the laboratory if further testing is desired or questions arise. (6/5/24 eb/np)



Eric Burroughs, DVM PhD, DACVP

Professor

Pathology Section Leader, Diagnostic Pathologist

List of abbreviations used by the ISUVDL can be found here:

<https://vetmed.iastate.edu/vdl/diagnostic-tests/pathogen-and-testing-abbreviations>

Action request	Department	Requested by	
Please genotype the C perf from the intestine	Bacteriology	erb	ELLK
Please genotype the smooth mucoid E. coli from the intestine.	Bacteriology	Dr. Tangen	ELLK
Please send the foot in save back for culture of the skin around the joint. These culture then, joint for a new head.	Necropsy	erb	BURI
Please run PRRSV PCR on the pooled lung	Necropsy	Dr. Tangen	KOLK
Please run PRRSV PCR on the pooled lung	Molecular Diagnostics	Dr. Tangen	BURI
Please run COR PCR on the swirle	Molecular Diagnostics	Dr. Tangen	BURI

Codes	Research?	6 dx code(s) matched
<input type="checkbox"/> DIGE BACT COLI CLOS DIFF	<input type="checkbox"/>	Digestive , Bacterial , Colitis , Clostridioides difficile
<input type="checkbox"/> DIGE BACT ENTE CLOS COLI	<input type="checkbox"/>	Digestive , Bacterial , Enteritis , Clostridium colinum
<input type="checkbox"/> DIGE BACT ENTE CLOS PERF	<input type="checkbox"/>	Digestive , Bacterial , Enteritis , Clostridium perfringens
<input type="checkbox"/> DIGE BACT ENTE CLOS PERF C	<input type="checkbox"/>	Digestive , Bacterial , Enteritis , Clostridium perfringens
<input type="checkbox"/> DIGE BACT ENTE CLOS SP	<input type="checkbox"/>	Digestive , Bacterial , Enteritis , Clostridium sp.
<input type="checkbox"/> DIGE BACT HEPA CLOS NOVY	<input type="checkbox"/>	Digestive , Bacterial , Hepatitis , Clostridium novyi

Codes	As Displayed	Research?	Creator
RESP VIRA PNEU INTE	Respiratory , Viral , Interstitial pneumonia , PRRSV	<input type="checkbox"/>	BURROUGHS, ERIC R
SYST VIRA MULT PRRS	Systemic , Viral , Multiple , PRRSV	<input type="checkbox"/>	BURROUGHS, ERIC R
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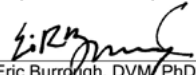
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Please run PRRSV PCR on the pooled lung	Molecular Diagnostics	Dr. Tangen	BURI
Please run CDR PCR on the swirle	Molecular Diagnostics	Dr. Tangen	BURI

Codes	Research?	1 dx code(s) matched
<input checked="" type="checkbox"/> DIGE BACT COLI CLOS DIFF	<input type="checkbox"/>	Digestive , Bacterial , Colitis , Clostridioides difficile

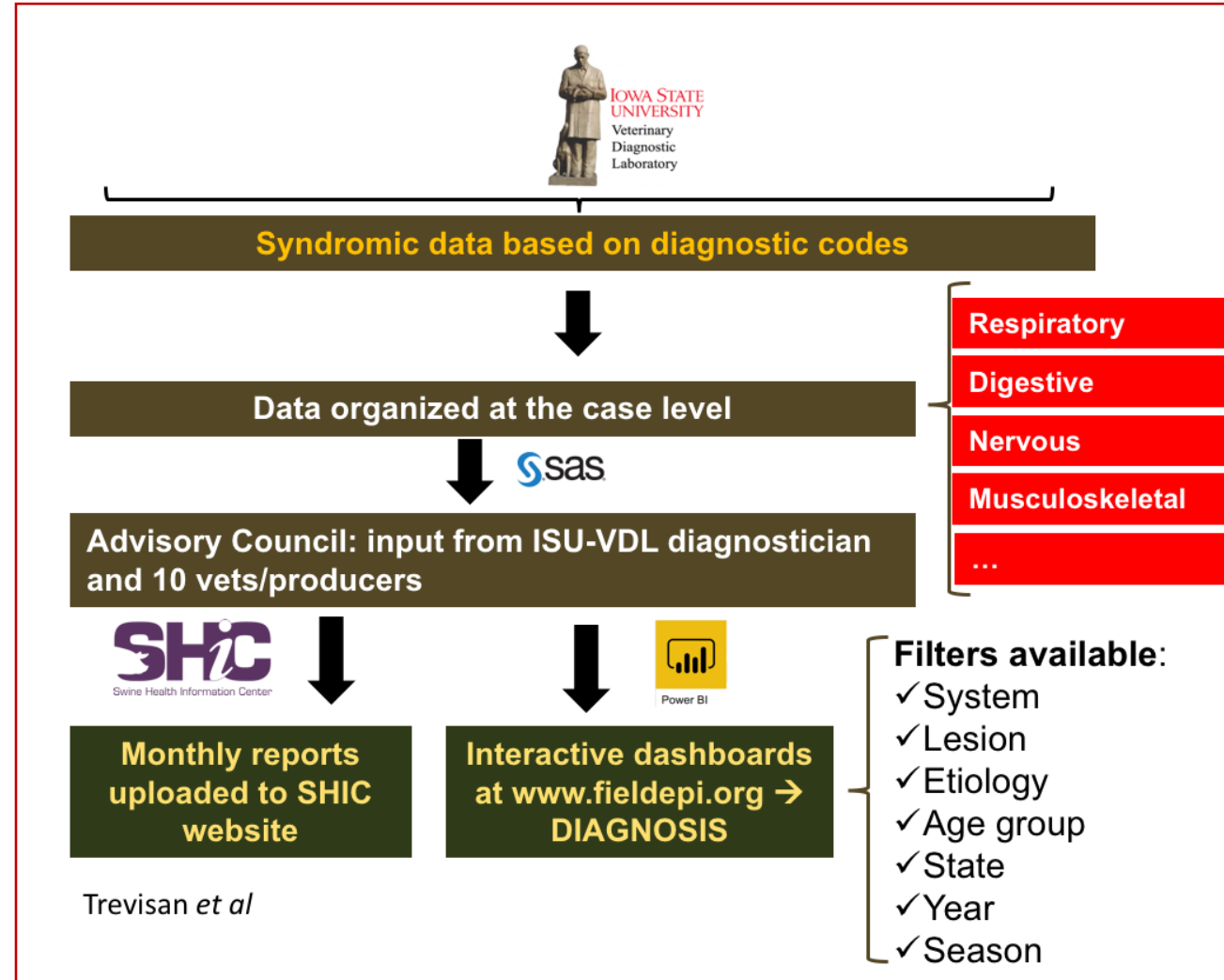
Codes	As Displayed	Research?	Creator
RESP VIRA PNEU INTE	Respiratory , Viral , Interstitial pneumonia , PRRSV	<input type="checkbox"/>	BURROUGH, ERIC R
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Large Scale Data Aggregation

- Disease Diagnostic Codes (Dx Codes)
 - Challenges
 - Requires pathologist training/retraining
 - Codes from previous system must be mapped to new system to avoid
 - This is essential to avoid loss of historical data
 - Opportunities
 - Disease data is now filterable and can be aggregated
 - A completely new stream of data is available
 - Disease data versus test result data (both useful but different)
 - Improved denominators:
 - e.g., number of IAV diagnoses in a period over:
 - Total respiratory cases received
 - Total cases with respiratory viral disease
 - Total cases with bronchitis

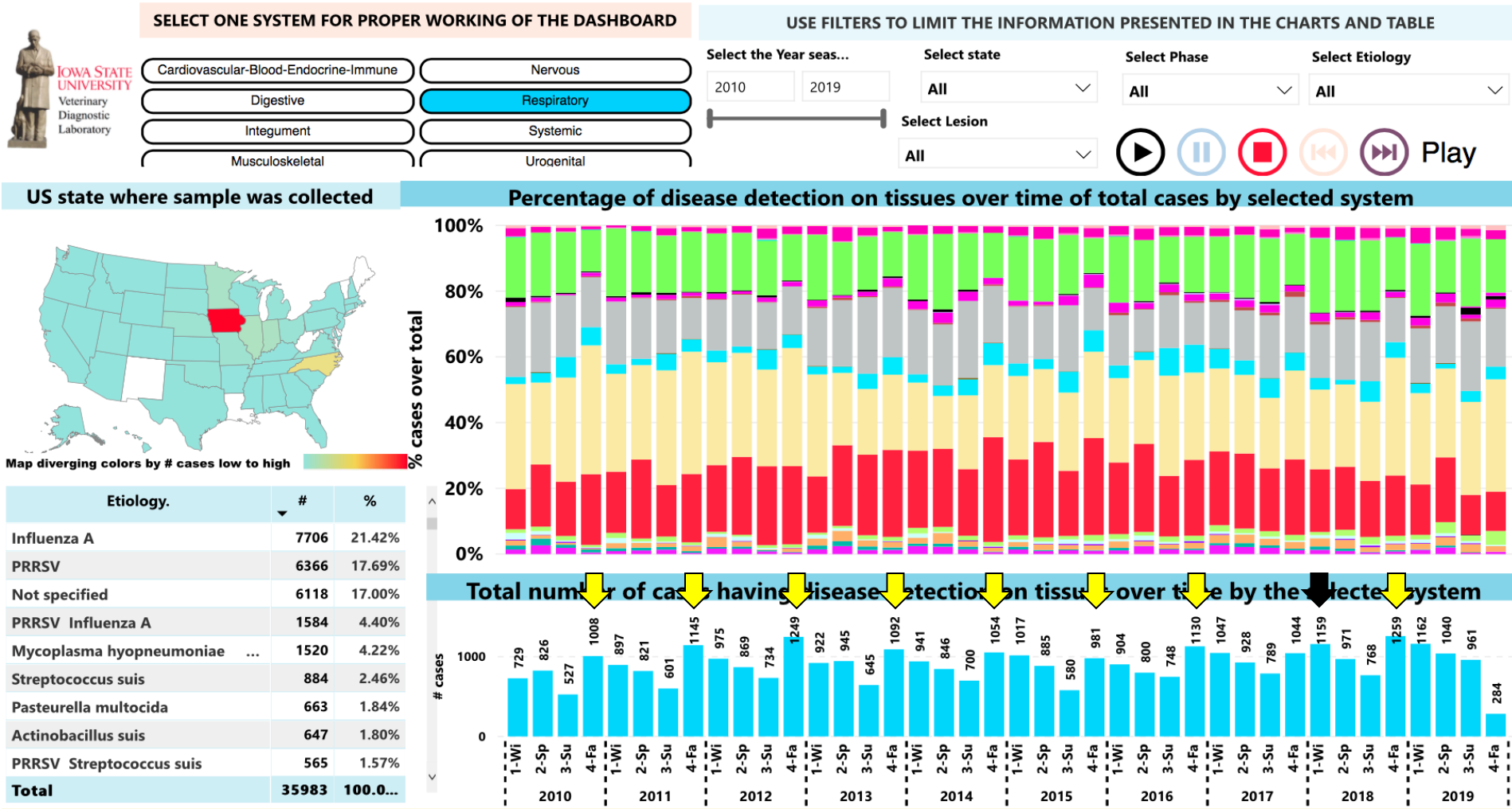


Large Scale Data Aggregation



<https://fieldepi.org/DIAGNOSIS>

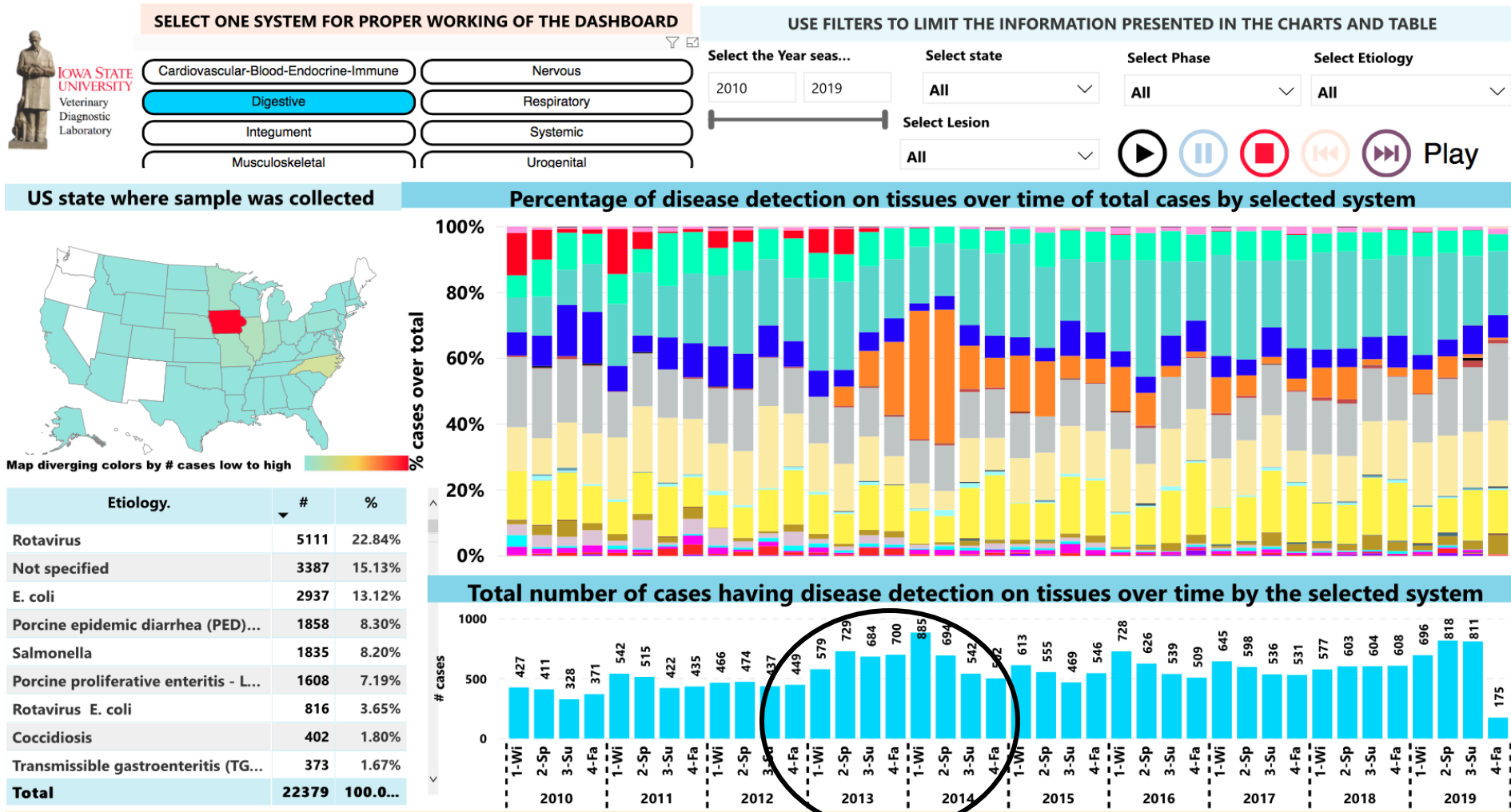
Fall / winter months have the highest number of respiratory diagnosis



Note: these communications and the information contained therein are for general informational and educational purposes only and are not to be construed as recommending or advocating a specific course of action.

<https://fieldepi.org/DIAGNOSIS>

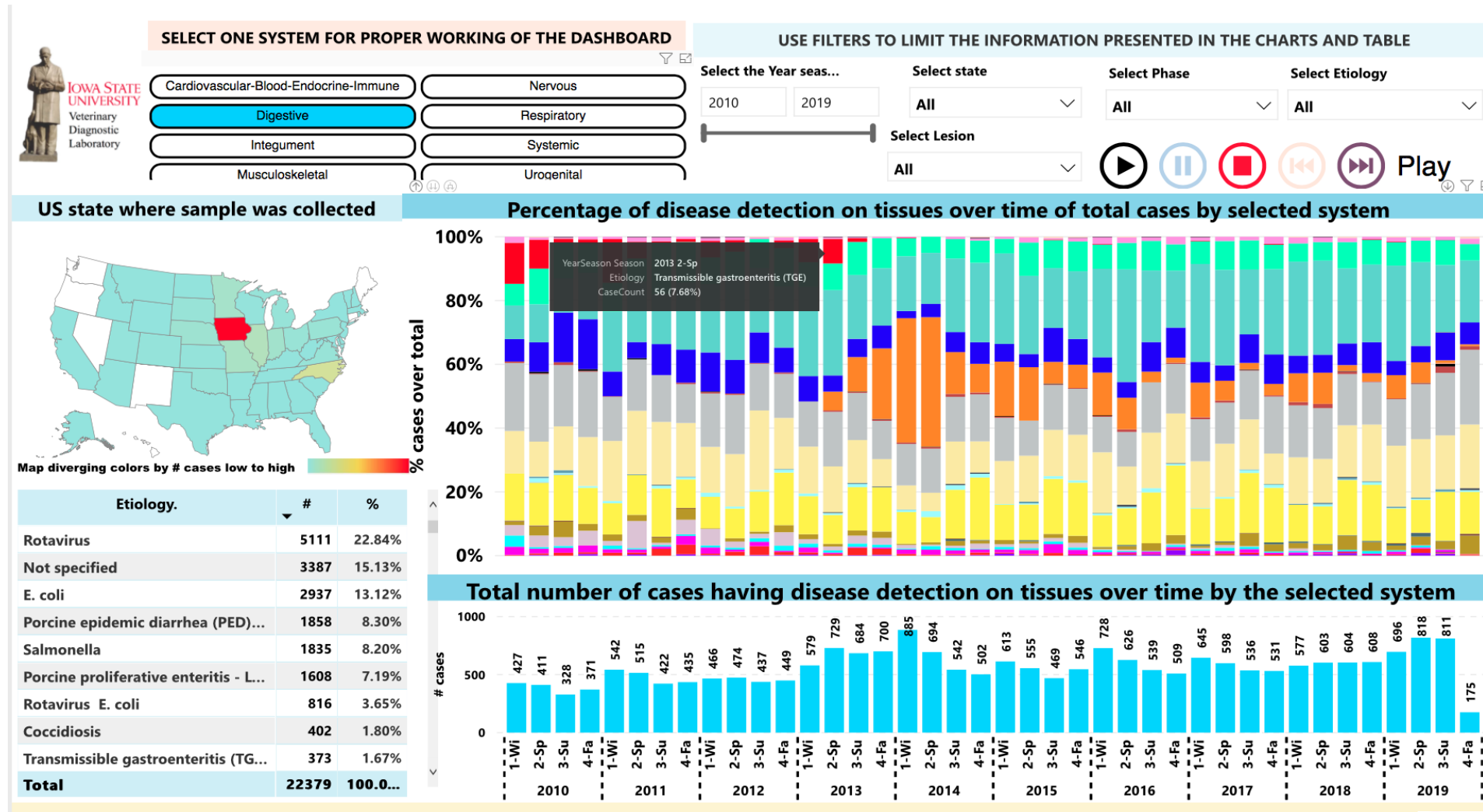
Increased number of digestive diagnosis in 2013/2014



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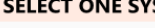
<https://fieldepi.org/DIAGNOSIS>

Low frequency of TGEV diagnosis after 2013



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<https://fieldepi.org/DIAGNOSIS>



SELECT ONE SYSTEM FOR PROPER WORKING OF THE DASHBOARD

Cardiovascular-Blood-Endocrine-Immune

Digestive

Integument

Musculoskeletal

Nervous

Respiratory

Systemic

Urogenital

USE FILTERS TO LIMIT THE INFORMATION PRESENTED IN THE CHARTS AND TABLE

Select the Year seas...

2010

2019

Select state

All

Select Phase






All

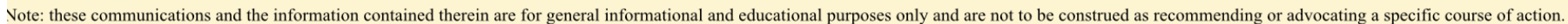
Select Etiology

All

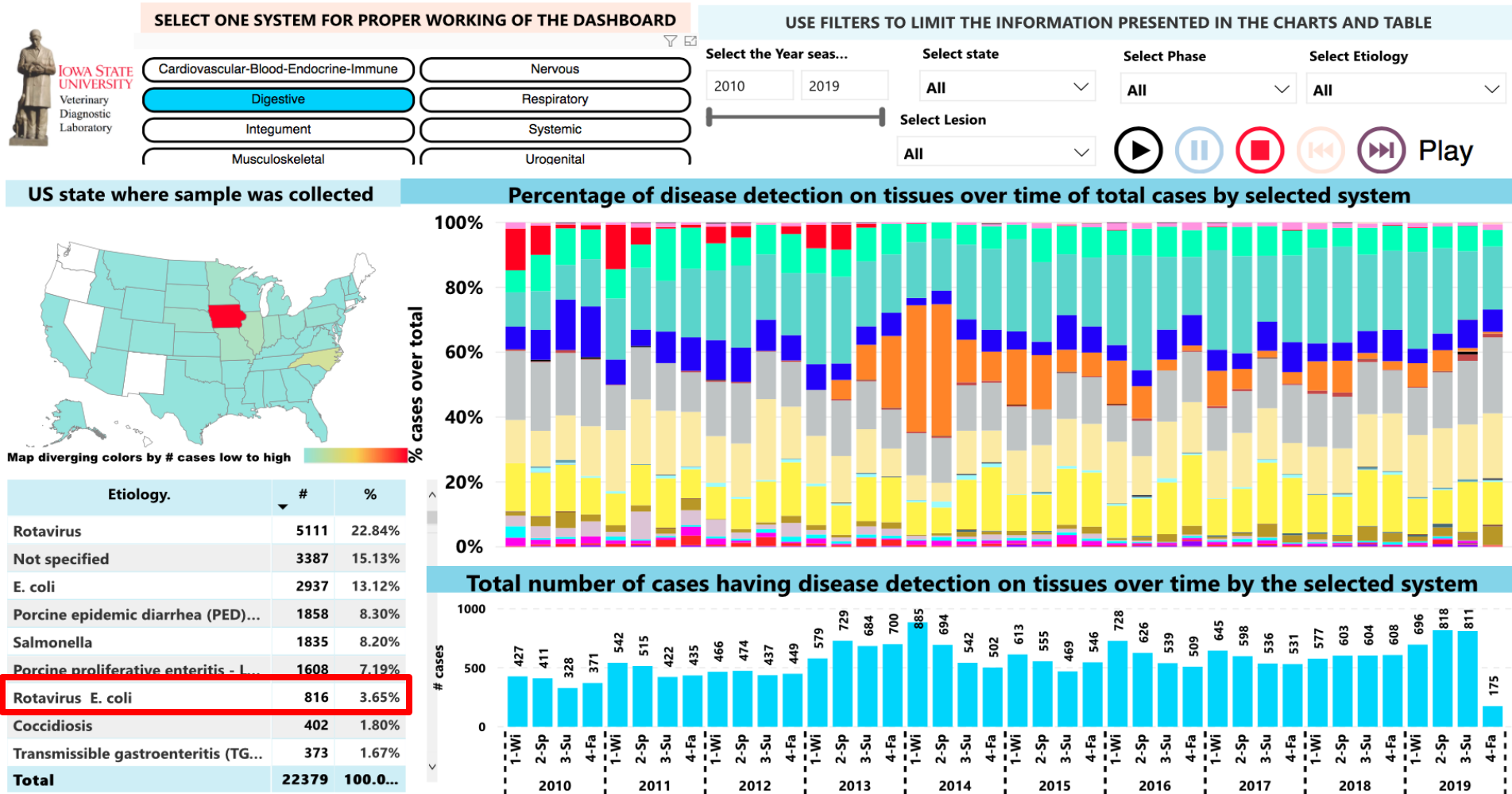
Select Lesion

All






Play



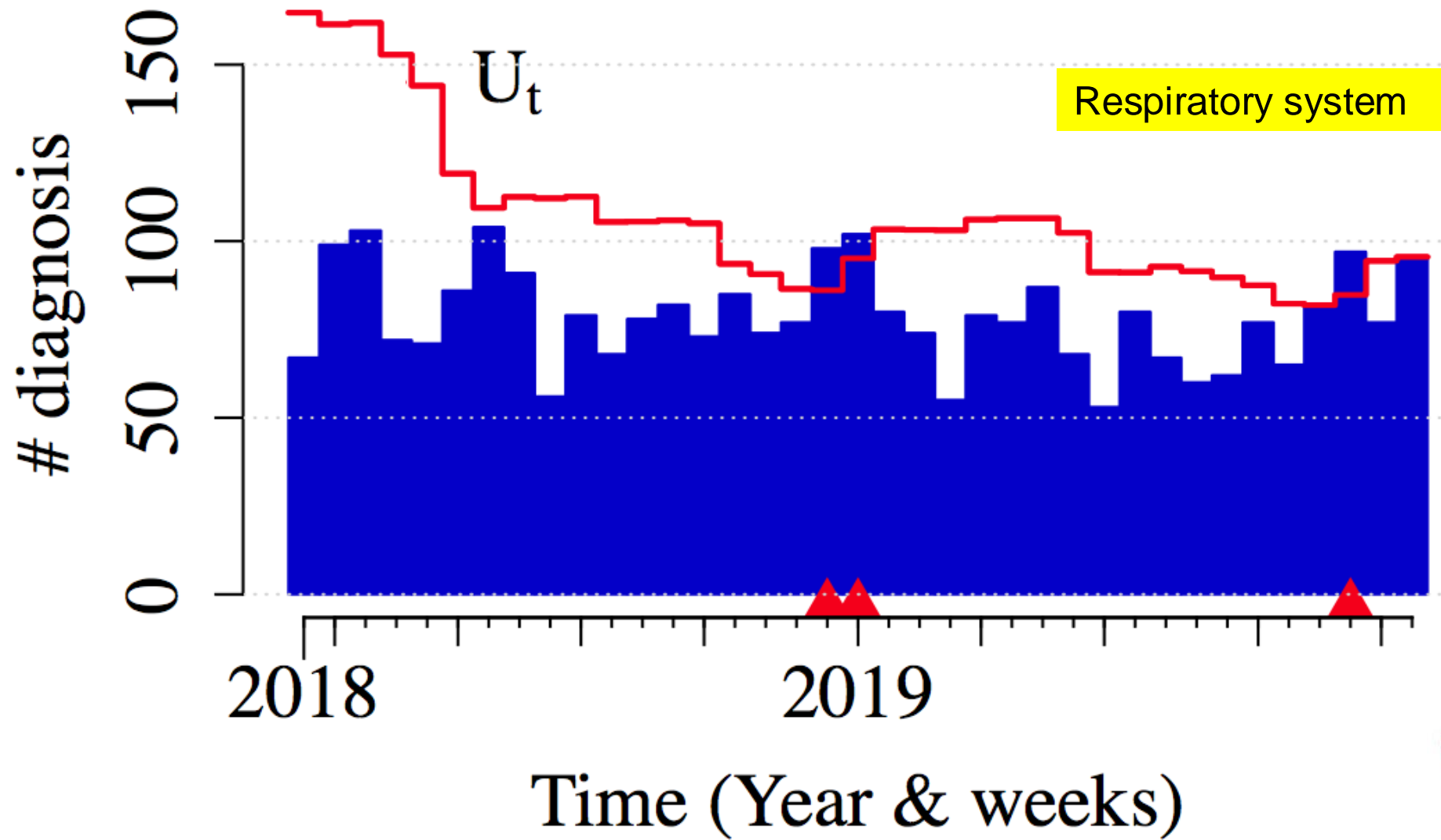
Sorted by system the tool has ability to inform multiple agents detected in a case



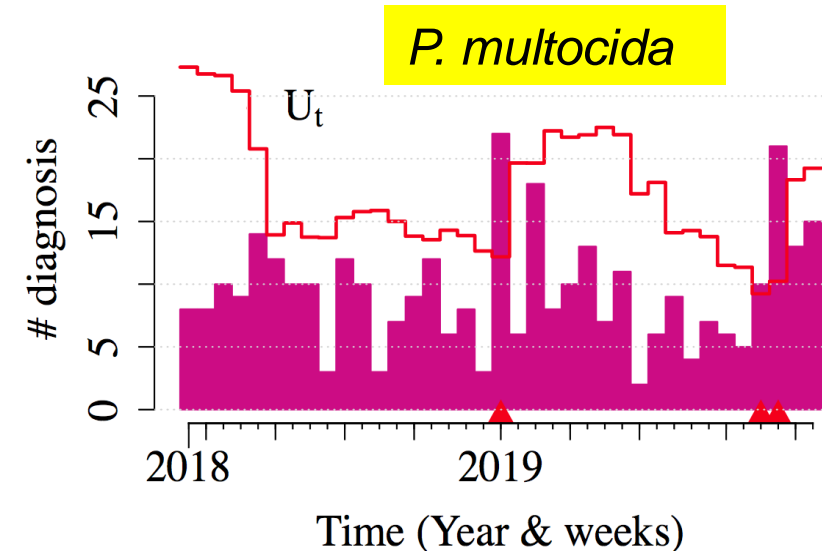
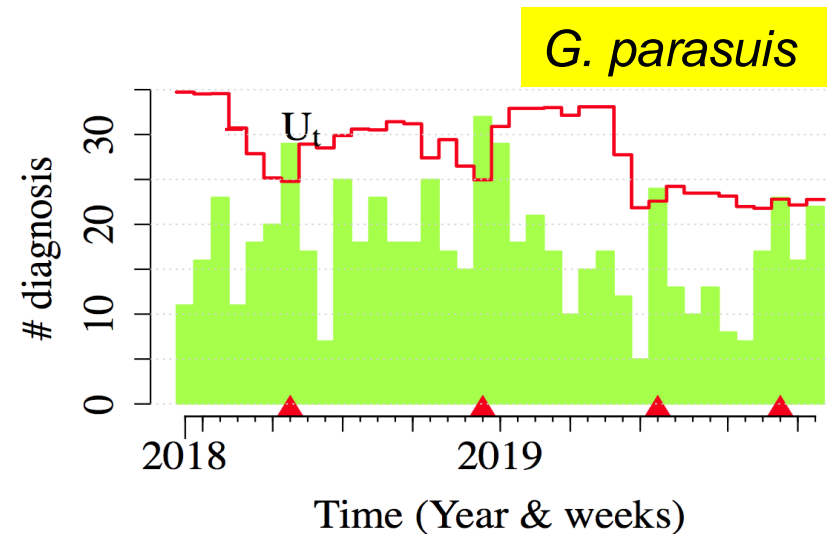
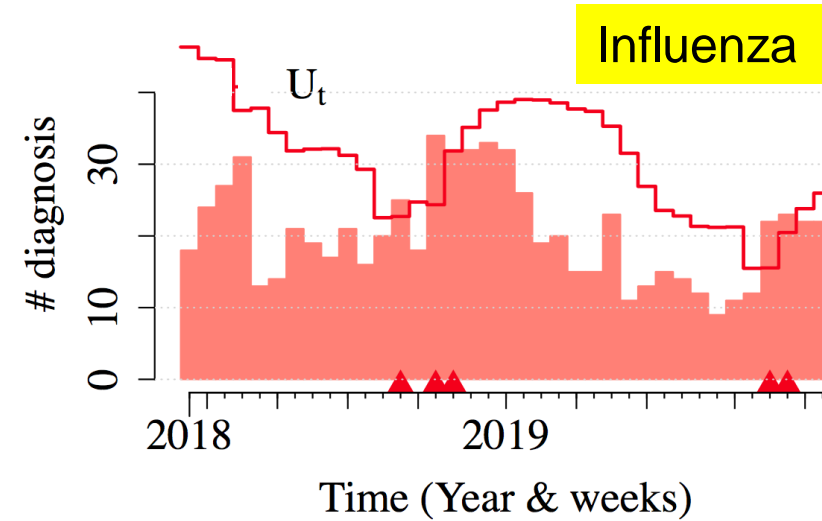
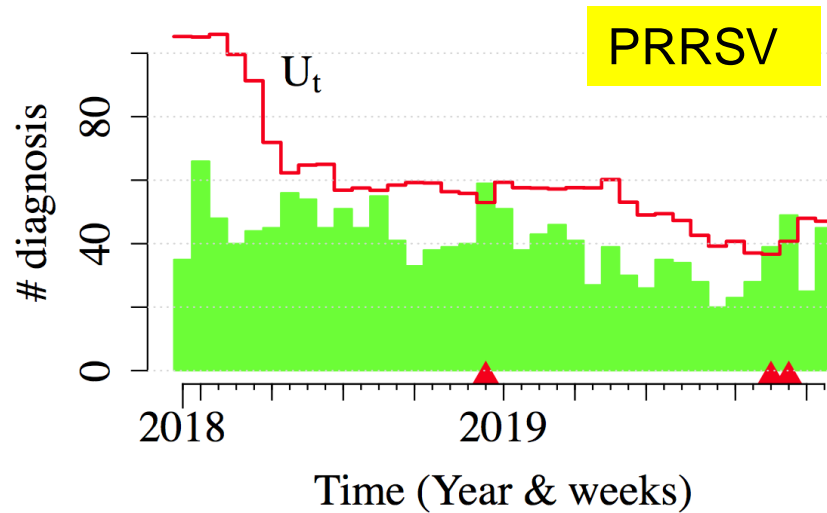
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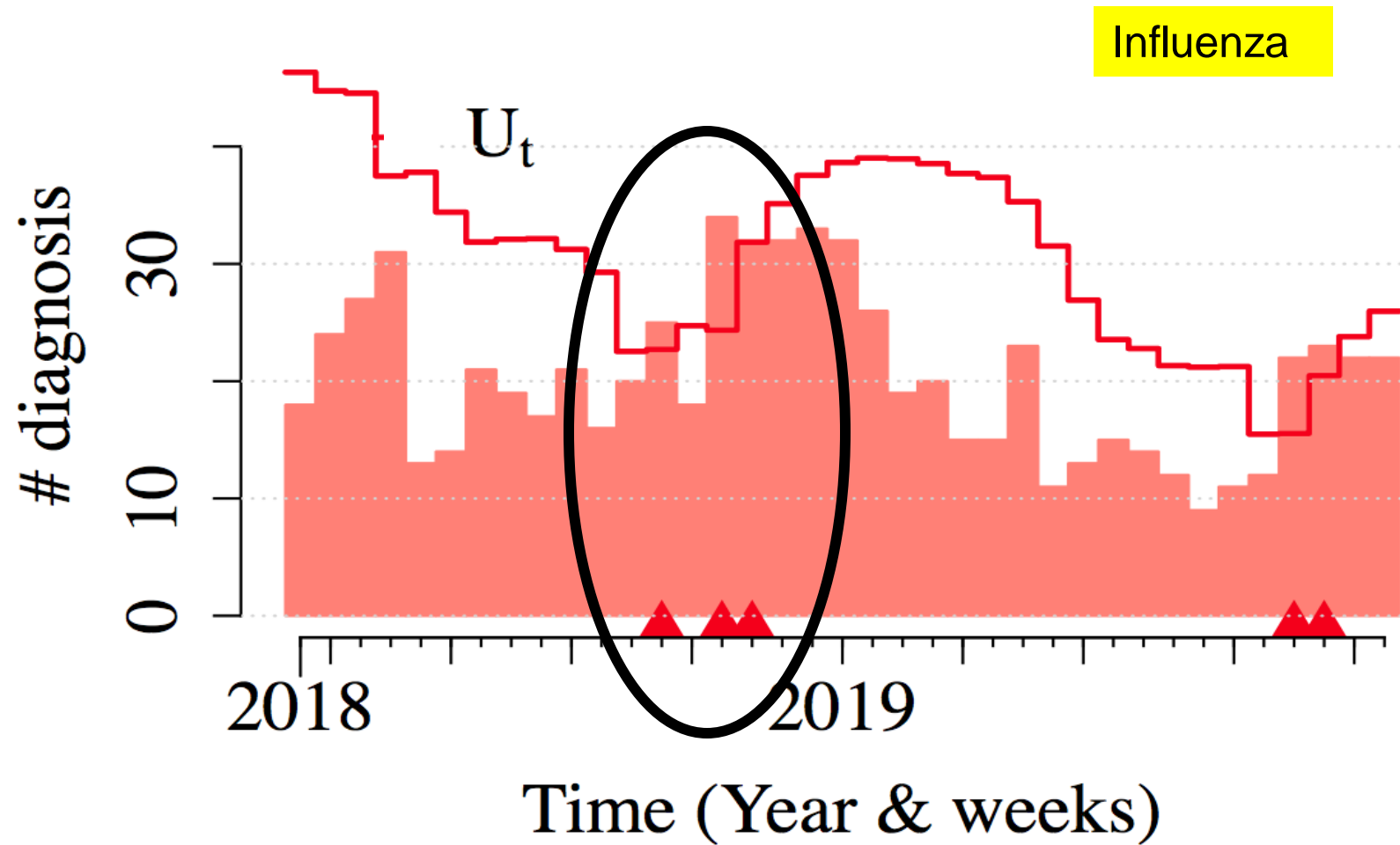
Weekly monitoring of disease diagnosis by system can create alert signals for increased diagnoses



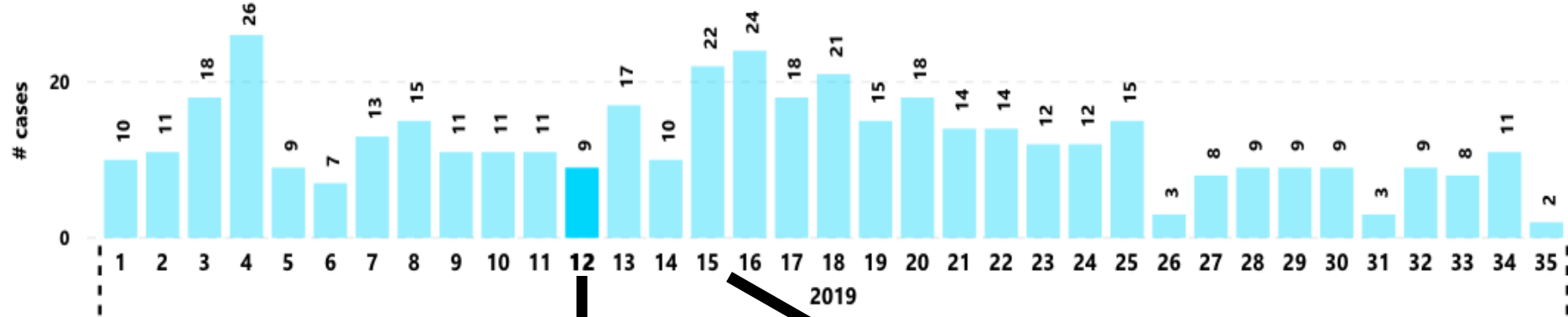
At the agent level, 2 signals in a 4 week interval are suggestive of a potential outbreak



Triggers investigation of geographical distribution of diagnosis signal in week 15

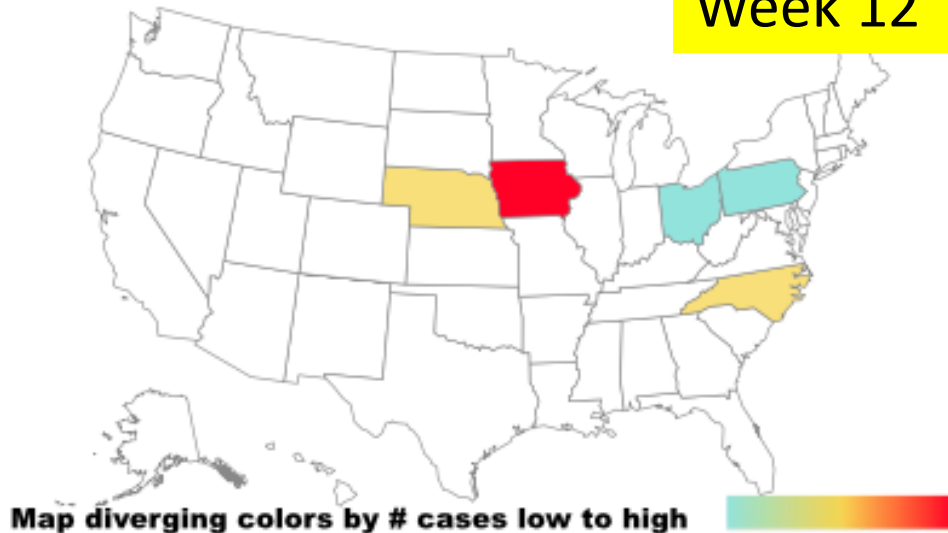


Dashboards are then used to investigate weekly cases of influenza diagnosis



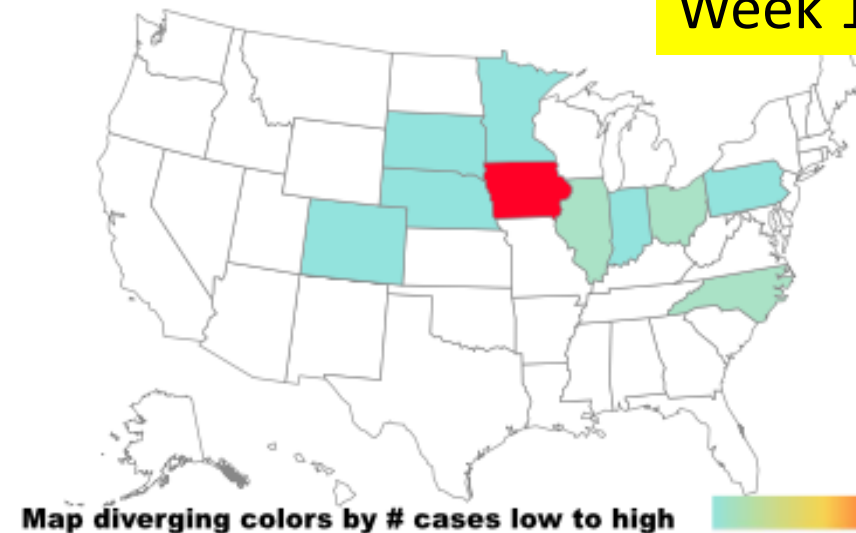
US state where sample was collected

Week 12



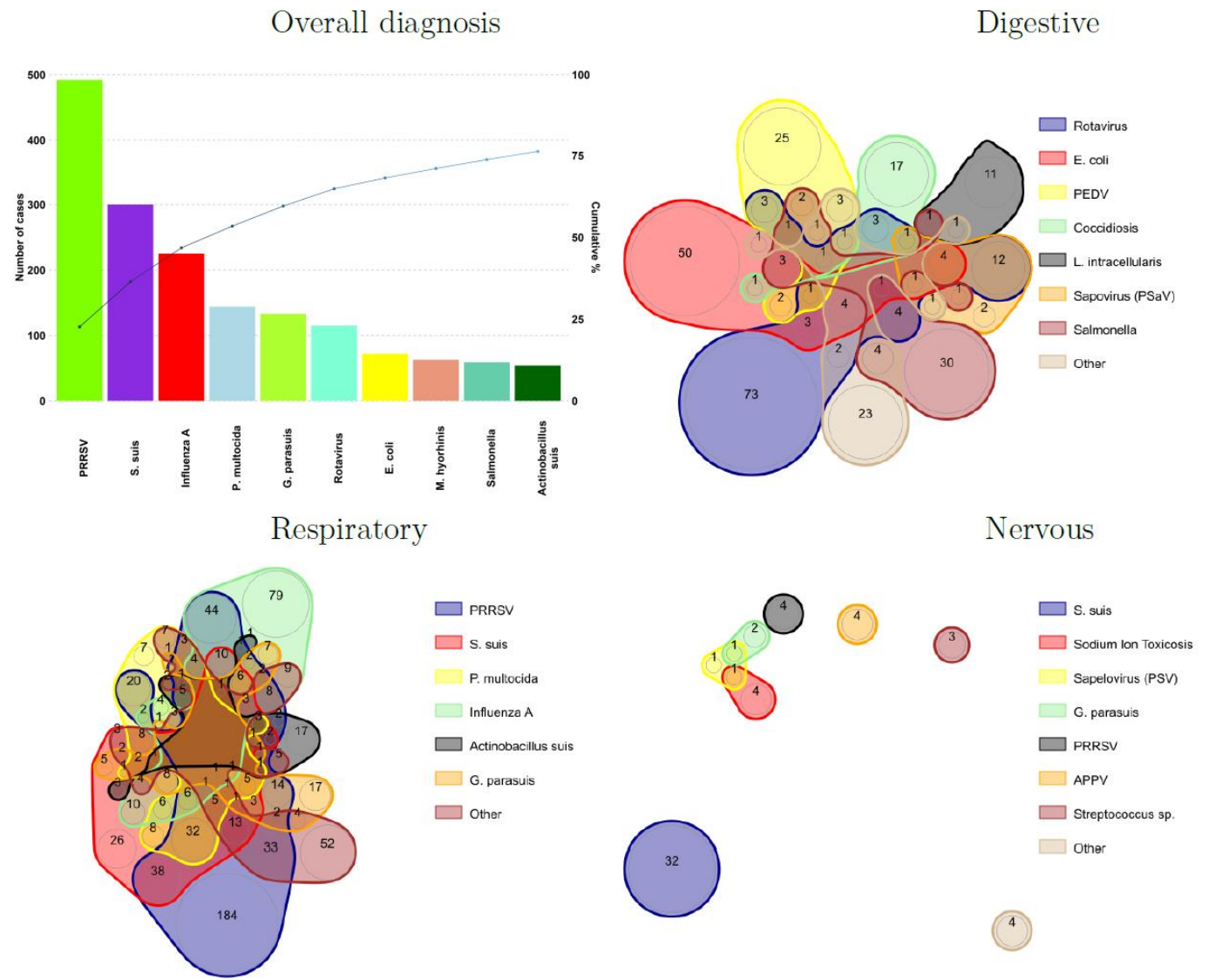
US state where sample was collected

Week 15



Dx Code Data from ISU VDL is Summarized Monthly in the SDRS Report

Topic 6 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.



Large Scale Data Aggregation – Take Home

- Use of DX code information to monitor swine disease diagnosis:
 - Can keep swine industry informed on endemic disease trends
 - Large scale monitoring of endemic disease diagnosis can help scientists, producers, and veterinarians:
 - Better understand the pattern of disease occurrence
 - Develop better disease control strategies
- Next steps:
 - Explore additional statistical tools to monitor disease diagnosis trends
 - Collaborate with other VDLs in US and globally to aggregate information?
 - Will require standardization of coding for useful messaging



Summary

- Different tools are needed for Surveillance versus Monitoring
 - Surveillance often used to prove freedom from disease
 - Is well suited for binary data (presence/absence)
 - Fixed spatial sampling and combined confidence from successive rounds of testing can reduce sample numbers per round
 - Monitoring is used to observed patterns or changes in endemic disease
 - Poorly suited for binary data (finding it is not unexpected)
 - SPC charts can be used for quantitative data
 - Disease diagnosis data is best, but harder to aggregate
- Aggregated anonymized data is useful for the swine industry
 - Requires purposeful collaboration (and funding)
 - Data access via dashboards help generate new questions



Questions?



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(515) 294-1950 | burrough@iastate.edu | @erburrough

