HEALTH 4 WEALTH

Assessment of value from reporting peri-mortem data collected at abattoirs

Final Report
Project Number (i.e. APL Project 2017/2262)

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Herd Health Pty Ltd
Dr Richard Shephard
65 Beet Road
Maffra VIC 3860

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Acknowledgements

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Executive Summary

Data was obtained from the National Sheep Health Monitoring Project (NSHMP), Enhanced Abattoir Surveillance Program (EASP) and the Export Production and Condemnation Statistics (EPACS) program for the period 2007–17. Data was examined for consistency, cleaned and re-coded for analysis to describe the distribution of endemic diseases. Only NSHMP and EASP data were suitable for detailed analysis as EPACS data was provided as 2007–17 summary counts for each state.

Endemic disease levels appear approximately constant across the period 2007–17 with both the prevalence of infected lines and the within-infected-line prevalence remaining stable. However, there were important regional and temporal differences in the prevalence of infected lines and the within-infected-line prevalence. Differences between abattoirs were observed in NSHMP suggesting inconsistency between works (and meat inspectors) in ability to identify and code endemic diseases. A precondition of any national producer reporting program must be to first ensure that meat inspection diagnoses are accurate.

Data provided did not include records of which lines/producers received feedback on the disease status of their lines. This presented a major challenge for identifying and quantifying the effect of endemic disease reporting on disease control. Because no record was provided about which lines resulted in producers being informed about disease, we were forced to assume that lines with disease resulted in notification for analytical purposes. This is certainly not the case for Western Australia and Tasmania with New South Wales and Victoria providing sporadic notifications, Queensland providing periodic notifications and South Australia providing the most consistent and complete notifications of all the states. Lines of animals were classified according to property of origin, year, class of animal and abattoir. Similar lines from the same class of animal, property and sent to the same abattoir in the preceding year were identified. Lines were classified as: previous lines positive (if they contained diseased animals); previous lines negative (if all were disease-free) or no previous lines (if no lines were identified).

A multivariable regression was then used to explore difference in previous line status on the prevalence of disease effect within the current line. No obvious effect of previous notification was observed. It must be stated that there is large potential for bias in this approach—not all producers with disease were notified and producers with disease in previous lines are likely to be different to producers without disease in previous lines. In the former, disease may be established and at an endemic prevalence. In the latter, disease may only be establishing and only at low prevalence. Lines from producers who have no preceding history may be new producers or producers from outside the region who are sending animals to a new works for the first time. These results do not exclude the possibility of benefit from reporting.

A benchmarking system was developed. This system did not rely upon an algorithm to warn a producer if disease was detected above some arbitrary and universal cut-point for disease—because this cut-point can never be known with surety. Instead, the system identified peer lines of animals. These were lines of the same class, originating from the same LGA, sent to the same abattoir and in the same year as the line being assessed. The distribution of infected lines and the within-line prevalence from these comparator lines contextualise the performance of the current line; the producer can easily see how their line compares. The prevalence of disease in identical lines of animals sent to the same works by the same producer in the preceding year was also mapped alongside the prevalence of the current line and this brings context on individual producer improvement or decline in disease control performance.

This system therefore focuses on providing the user with information on relative performance—both against their peers and against themselves from a previous period. This system is recommended because it presents information on endemic disease in a way that maintains interest and supports continual self-improvement in the understanding that eradication of an endemic disease is usually not economical. This system can be implemented now but will require working data standards and a strengthened data centralisation systems so that near-real-time reporting can occur. The LDL network is the ideal vehicle for such a system and to generate and distribute producer reports.

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1. Background to Research

The value from reporting endemic disease findings at meat inspection back to producers has not been formally evaluated. This project examined if feedback to producers from various meat inspection programs lead to discernible change in endemic disease prevalence. The project also identified challenges in disease recording and reporting and explored the potential for developing benchmarking systems to place endemic disease findings in context for individual producers.

The project requires the analyst to:

- Obtain access to data from 2007–2017 on arthritis, pleurisy/pneumonia, sarcocystis, CLA, liver fluke and sheep measles from Animal Health Australia, PIRSA, Industry and the Export Meat Program. The data should be able to be analysed to the level of state, region, abattoir and individual producer (de-identified as appropriate).
- Analyse the data using appropriate epidemiological and/or statistical methods to determine if, when supplied to producers, these data lead to a reduction in diseased animals being consigned to abattoirs.
- Conduct an analysis of every condition; incorporate seasonal trends; regional impacts at the state, regional, abattoir and producer level.
- Provide a report to the Health 4 Wealth Project Management Committee that describes the analyses undertaken and the insights and results gained. Whether structured feedback of animal health and conditions data collected in abattoirs has led to a reduction in diseased animals being consigned to abattoirs should be clearly identified.

2. Objectives of the Research Project

Endemic diseases are an important cause of trim, condemnations and losses at abattoirs. Affected carcases are devalued, incur extra processing cost and contribute to inefficiency in the meat supply chain. For many producers the dispatch of animals to the works represents the end of their involvement, however, the farmer is the person who has the most influence over the quality of lines sent for slaughter. Providing feedback to the producer on disease levels is an important component of improving meat quality and processing efficiency.

The objectives of this project are:

1. To determine if feedback to producers on the prevalence of selected diseases in animals they supply to abattoirs has resulted in a reduction in the number of affected lines and the prevalence of diseased animals sent for slaughter.
2. To identify ways to best present information on the presence and level of disease in affected lines to producers

3. Introductory Technical Information

Data extracts were provided from the National Sheep Health Monitoring Project (NSHMP) from all sheep-producing states, the Enhanced Abattoir Surveillance Program (EASP) for sheep in South Australia and the national Export Production and Condemnation Statistics (EPACS) database for cattle, sheep and goats. These are described in more detail below.

3.1 National Sheep Health Monitor Project (NSHMP) data

De-identified data from the NSHMP was received from New South Wales (46,312 lines between 2007–17), Queensland (4,386 lines between 2007–17), South Australia (76,202 [1]lines between 2007–17), Tasmania (6,500 lines between 2007–17), Victoria (31,764 lines between 2007–17) and Western Australia (14,045 lines between 2008–17). A total of 27 abattoirs provided data from sheep lines sourced from 23,894 unique property identification codes (PIC) originating from within 457 local government regions. Of these, 15,483 provided at least two lines of sheep to participating works. There were 140 individual meat inspectors listed as providing data.

3.2 Enhanced Abattoir Surveillance Program (EASP) data

De-identified EASP data was provided by the Biosecurity SA division of Primary Industries and Regions South Australia (PIRSA). Data from 70,130[2] lines of slaughtered sheep from the period January 2007 to June 2018. Data was de-identified at producer (5,749 PICs) and abattoir (2 processors) levels. There were 23 LGA regions recorded representing 10 PIC regions of South Australia. Information on 23 diseases and conditions was recorded. Data was aggregated to month and year of consignment.

3.3 Export Production and Condemnation Statistics (EPACS) data

State-level aggregate slaughter totals and disease condition counts for the combined period 2007–2017 were provided for cattle, sheep and goats.

4. Research Methodology

4.1 Introduction

The National Sheep Health Monitoring Project (NSHMP) is a surveillance system for disease in lines of sheep that operates in some abattoirs. Twenty significant animal health conditions of sheep are monitored. The objective of the program is to monitor prevalence of these conditions and to provide information to producers on their disease levels which

[1] This is EASP data plus any line of South Australian originated sheep processed in Victoria

[2] This total is only South Australian sheep processed in study abattoirs

they may use to better manage disease in their flocks. The producer-feedback systems only operate in lines of sheep sent for direct slaughter by producers; lines of sheep purchased from sale yards by abattoir buyers are not able to be traced back to the farm of origin.

The Export Production and Condemnation Statistics (EPACS) database is a notifiable disease surveillance-focused system. Studies of EPACS have shown value in reporting meat inspection findings back to producers.

The Enhanced Abattoir Surveillance Program (EASP) provides health and disease feedback to some South Australian producers who supply stock to Thomas Foods International abattoirs. This is essentially a value-add to the NSHMP in South Australia (funded primarily by the state industry fund with some support from NSHMP) to investigate the value of reporting to producers. The proportion of lines of submitted sheep with conditions recognised at meat inspection are linked to the producer Property Identification Code and information is provided to Primary Industries and Regions SA who then contact the producer by letter informing them about the percentage of the line affected with each disease and relevant fact sheets on disease control. A notification is triggered if any disease is detected at a prevalence of 5% or greater in the line. Again, only lines of sheep sent for direct slaughter by producers were able to receive reports. The EASP system also only reports back to South Australian producers—interstate producers are not contacted. South Australian producers who have processed stock in other states will be contacted if any individual disease is present in the line at a prevalence of 5% or greater.

Most abattoirs provide informal feedback to producers, but this is usually limited to a manager calling producers who provided an exceptionally poor line of sheep. Information on the source farm for sale-yard-purchased lines of sheep is generally not available and as a result feedback on these lines cannot be provided to the producer.

There is potential value from providing all sheep producers with regular and standardised feedback on the performance of every line of their sheep that are processed. Feedback to producers from an integrated meat-inspection recording system is also possible. The Livestock Data Link (LDL) is an on-line information system that links producer and processor information stored in different databases to facilitate analysis and two-way reporting. LDL has been designed primarily to provide producers with carcase compliance and animal health information. This has recently been extended to provide information to producers and processors on the conditions identified within lines of animals and, most importantly, some relative comparison of the prevalence identified in a producer's line(s). This capacity was provided through LDL from around June 2017.

This project brings a supply-chain focused approach to the problem of endemic disease impacts at meat processing. It recognises that the optimal industry solution is to move

farmers to the most cost effective control point—not necessarily disease eradication. The project will specifically examine if deployment of pilot producer-feedback systems for abattoir data have changed producer behaviour resulting in a reduction in the amount of disease subsequently sent to abattoirs. The primary determinant of success for this project will be the quality of any counter-factual data that can be extracted from the essentially observational data provided. Counter-factual data is data from producers who supply lines of animals but were not informed of the disease status of their supplied lines. Counter-factual data allows the change in disease levels as a result of feedback to be validly estimated.

Analytical techniques that can be used depend on the data; especially the amount and quality of counter-factual data available. Simple data cleaning and descriptive analysis are likely to underpin analysis. Statistical techniques such as GLM (generalised linear modelling) have been identified for use but this will be highly dependent on the quality of data. Multivariable techniques such as GLM allow inclusion of other explanatory (confounding) variables (such as season, year, class of stock etc.) into models and this can help better define impact of feedback reporting on subsequent disease rates in lines. Managing inherent biases within an observational dataset that does not specifically record which lines and which producers did and did not receive feedback on their lines is the biggest challenge for this project.

4.2 Data aggregation and cleaning

Data from the NSHMP sources were aggregated into a central database. Disease codes were standardised across jurisdictions to allow proper categorisation. Most differences related to spelling, capitalisation and abbreviation. The number of animals in the line and number inspected were recorded separately and rows (observations) that had more cases recorded for an individual condition than the number of animals inspected were deleted. Data from EASP lines were aggregated into producer, date, abattoir and class of animal totals. Producers who sent sheep to the works that were subsequently split into different processing lines, but all processed on the same day were aggregated into a single row. No data cleaning was possible (or required) for the summary EPACS data.

4.3 Analysis

Basic descriptive statistics and plots of infected line prevalence (the proportion of lines of the same class of animal that had one or more affected animal) and within-infected-line disease prevalence (the within herd/flock prevalence in lines with at least one affected animal) by region and time provided the most information.

Regression analysis was used to explore if previous information on the presence of disease resulted in a reduction in the prevalence of infected lines and/or a reduction in the within-

infected line prevalence. Multivariable regression analysis allows the effects of other confounders and predictors (e.g. year) to be isolated from each other.

A benchmarking algorithm was developed to contextualise disease findings. The benchmarking objective was to allow an individual producer to compare disease levels in their specific line of animals to similar lines presented for slaughter by the same producer in the previous year and by similar producers in the current year.

5. Results

5.1 Descriptive statistics

Basic descriptive statistics and plots of infected line prevalence (the proportion of lines of the same class of animal that had one or more affected animal) and within-infected-line disease prevalence (the within herd/flock prevalence in lines with at least one affected animal) by region and time provided the most information

5.1.1 NSHMP data

The NSHMP was examined to assess the level of 'completeness' of recording[3]. This was done by examining the number of lines of sheep reported by abattoir and by state. Results are presented in Figure 1 (abattoirs) and Figure 2 (states). This indicates great variation in the number of lines reported by works. Without information on the total number of lines processed by each abattoir the level of under-reporting by individual works cannot be estimated. However, it is likely that a large number of works reported on only a proportion of total lines processed. Given individual processors monitored on an intermittent basis this is to be expected. This may impact on accuracy of estimation of the distribution of disease at individual works and as a result the accuracy of comparators for each disease and works.

[3] Understanding that this is not a compulsory program

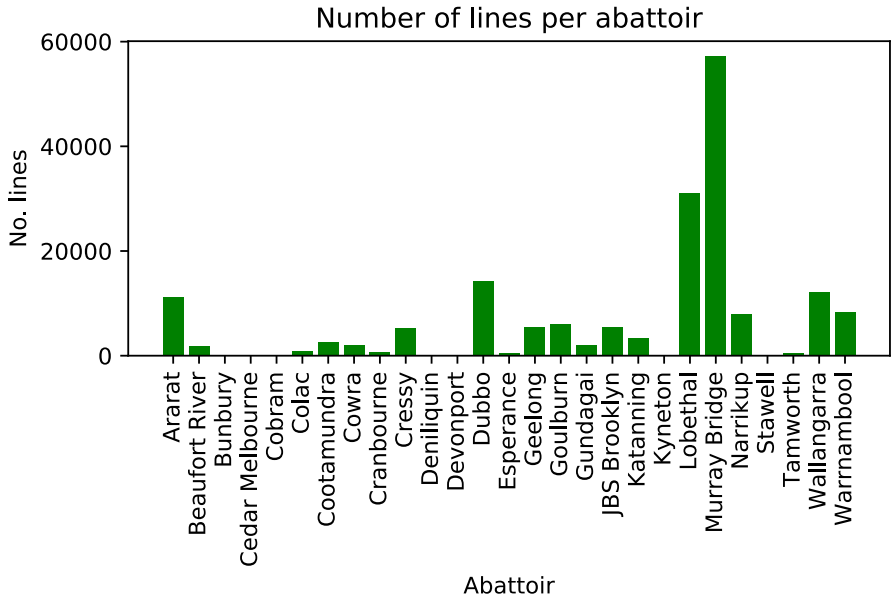


Figure 1: Number of lines processed per abattoir

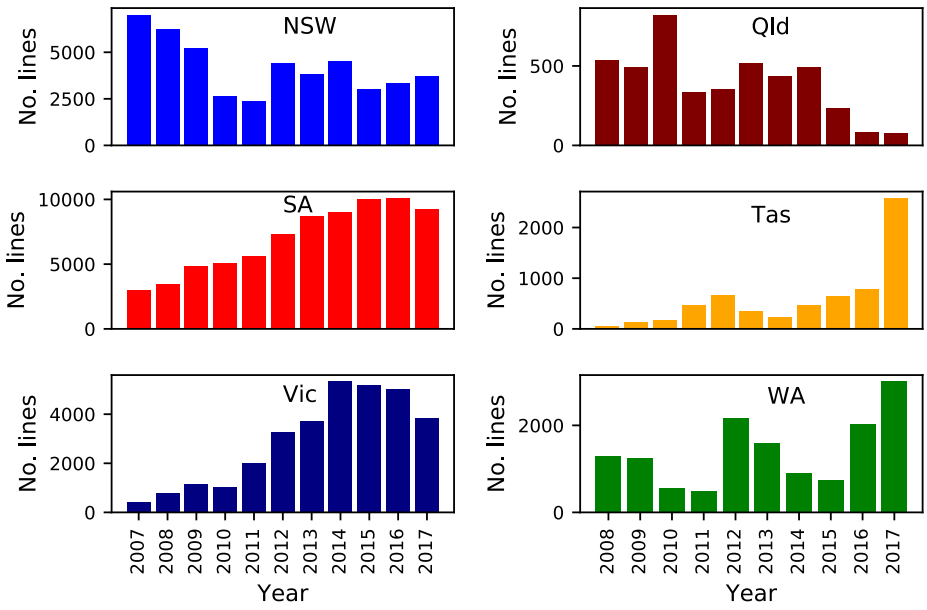


Figure 2: No lines processed per year by state

Data was provided with a regional location of the property of origin. For most states these regional groupings were local government area (LGA) classifications but some states used their own PIC-region aggregation (e.g. South Australia). In this case, the most commonly named town or identifying name used within the

region was used as the geographical identifier as a surrogate LGA. The distribution of line sizes by LGA and by state were examined to explore the variability within state and region. This was limited to regions with at least 100 lines and results are presented in Figure 3. The largest lines were presented in Queensland and the smallest in Tasmania with most states having 75% of lines being within 100 sheep of the average size for the state.

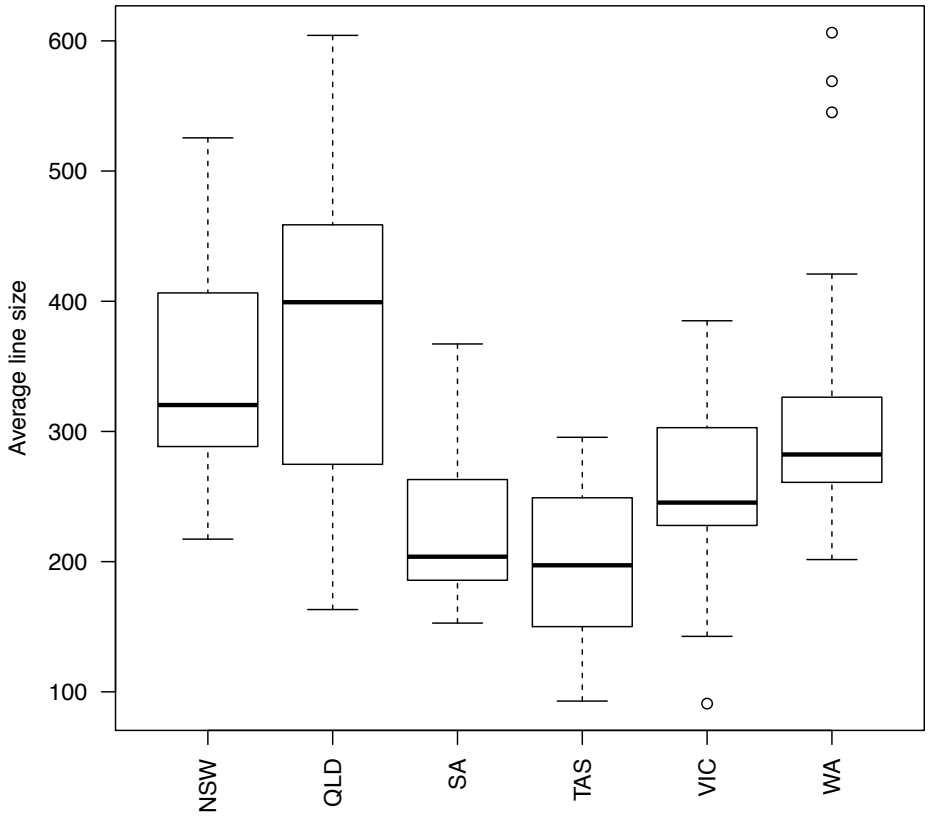


Figure 3: Average lot size by state-level LGA boxplot

The crude prevalence of affected lines (then proportion of lines with at least one affected animal) and affected animals (the proportion of animals inspected with the disease) varied by state. Crude prevalences are presented in Table 1 (animals), Table 2 (lines) and Table 3 and Figure 4 (within-infected-lines prevalence). The distribution of the prevalence of infected lines and the within-infected line (flock) prevalence by LGA and state was also examined. Aggregated LGA results are presented in Figure 5 to Figure 11 and individually listed in Table 2 (infected lines) and Table 3 (within-infected lines) below. Again, these show wide variation between LGA regions for infected line and within-infected-line (flock)

prevalence for most states and most diseases. Liver fluke is not present in Western Australia and very few South Australian flocks are exposed to fluke. These findings indicate that comparators for lines of sheep need to be regional—state-level rates are insufficient. This is to be expected for a number of diseases—such a liver fluke—due to climatic and farming environment differences that promote or suppress disease. This has implications for benchmarking and comparison. No national disease comparator exists. Individual lines will need to be compared to similar lines that originate from at least the same state.

Table 1: Percentage of animals affected (condition prevalence) by state

Condition	Arthritis	CLA	Liver Fluke	Pleurisy	Pneumonia	Sarco	Sheep Measles
NSW	0.7	4.4	6.1	1.7	0.1	0.1	4.1
QLD	0.6	5.4	2.7	0.7	0.0	0.1	1.8
SA[4]	1.4	2.7	0.0	2.2	1.2	1.0	2.7
TAS	0.3	2.5	0.9	1.6	0.0	4.8	2.1
VIC	1.4	4.6	0.5	3.9	0.6	0.7	3.6
WA	0.4	1.7	0.0	1.0	0.0	0.1	3.6

Table 2: Percentage of infected lines by condition and state

State	Arthritis	CLA	Liver Fluke	Pleurisy	Pneumonia	Sarco	Sheep Measles
NSW	22.1	41.3	28.4	29.4	1.8	2.4	54.3
QLD	12.8	50.9	11.9	12.2	0.0	2.2	29.4
SA[4]	19.5	16.8	0.3	20.6	6.4	2.7	31.5
TAS	12.5	19.9	5.0	19.7	0.2	13.3	60.4
VIC	50.1	46.6	6.9	58.6	6.1	3.0	69.5
WA	21.1	31.3	0.0	27.6	1.9	2.2	59.4

[4] This may be an underestimate as South Australia reports are only triggered if more than 5% of a line is identified with a condition

Table 3: Within-infected flock prevalence (%) by condition and state

State	Arthritis	CLA	Liver Fluke	Pleurisy	Pneumonia	Sarco	Sheep Measles
NSW	3.3	10.2	19.7	6.4	6.6	4.9	6.8
QLD	3.6	10.3	28.2	4.6	0.0	3.8	5.5
SA[4]	6.0	13.1	10.2	9.1	13.3	38.3	7.3
TAS	2.0	9.8	11.5	7.1	4.3	26.9	3.3
VIC	2.7	9.3	5.8	6.7	8.6	17.8	4.9
WA	1.5	4.4	0.7	3.1	0.3	1.6	5.4

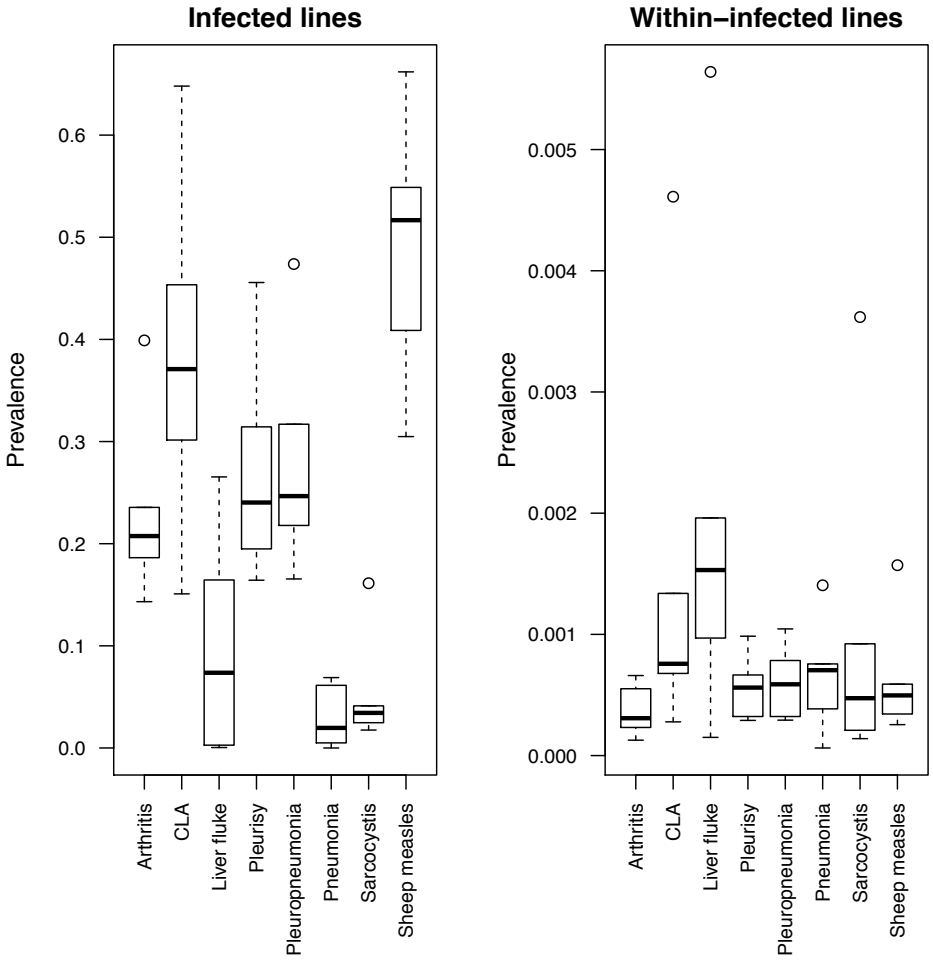


Figure 4: State-level infected line and within-infected line (flock) prevalence boxplot

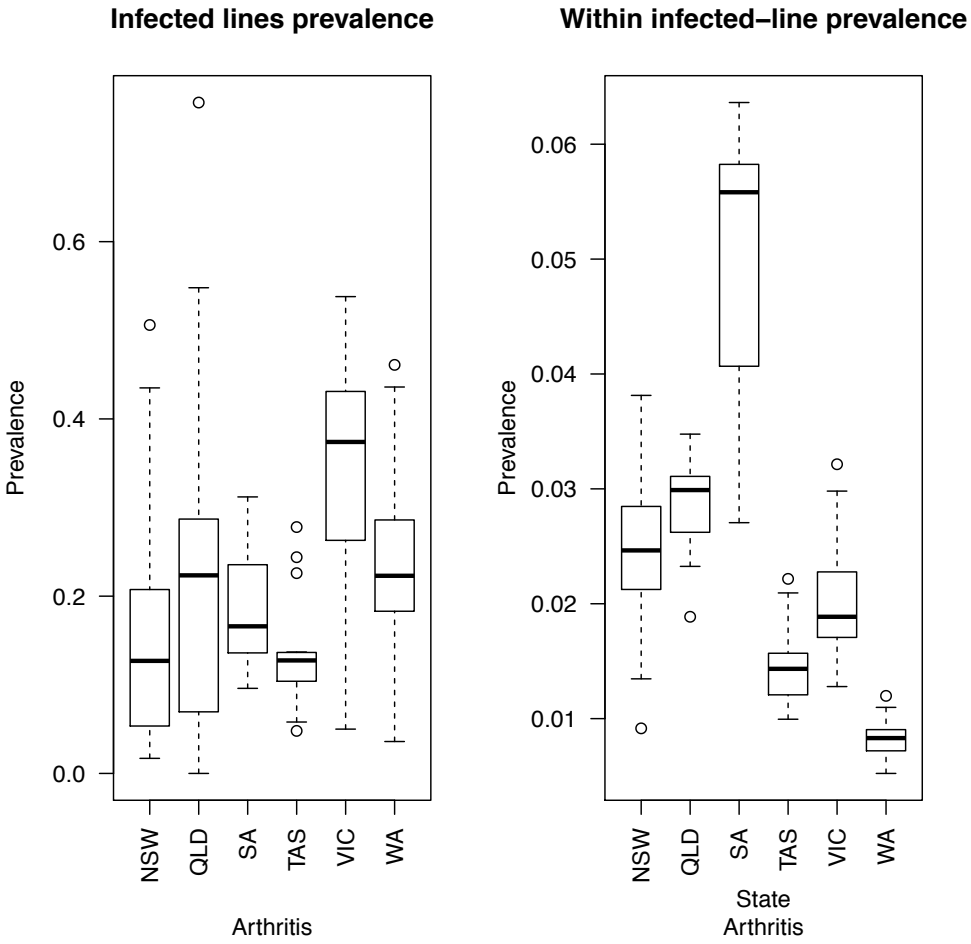


Figure 5: Arthritis infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

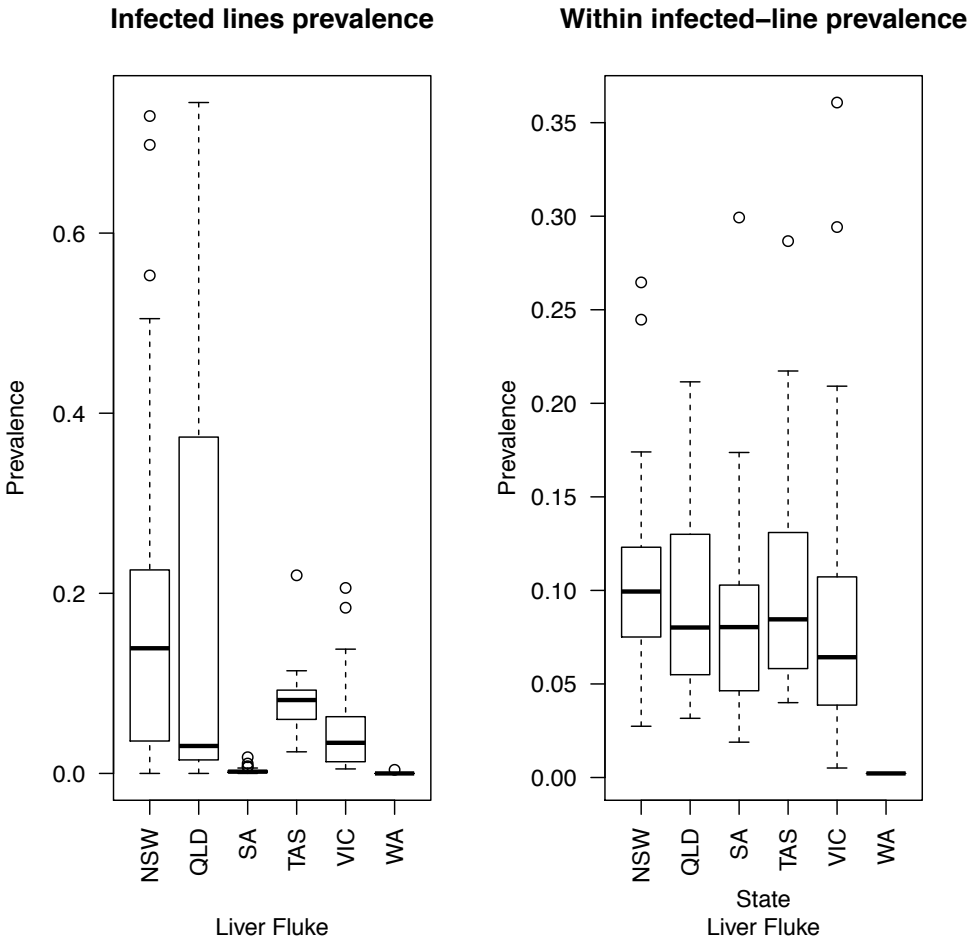


Figure 6: Liver fluke infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

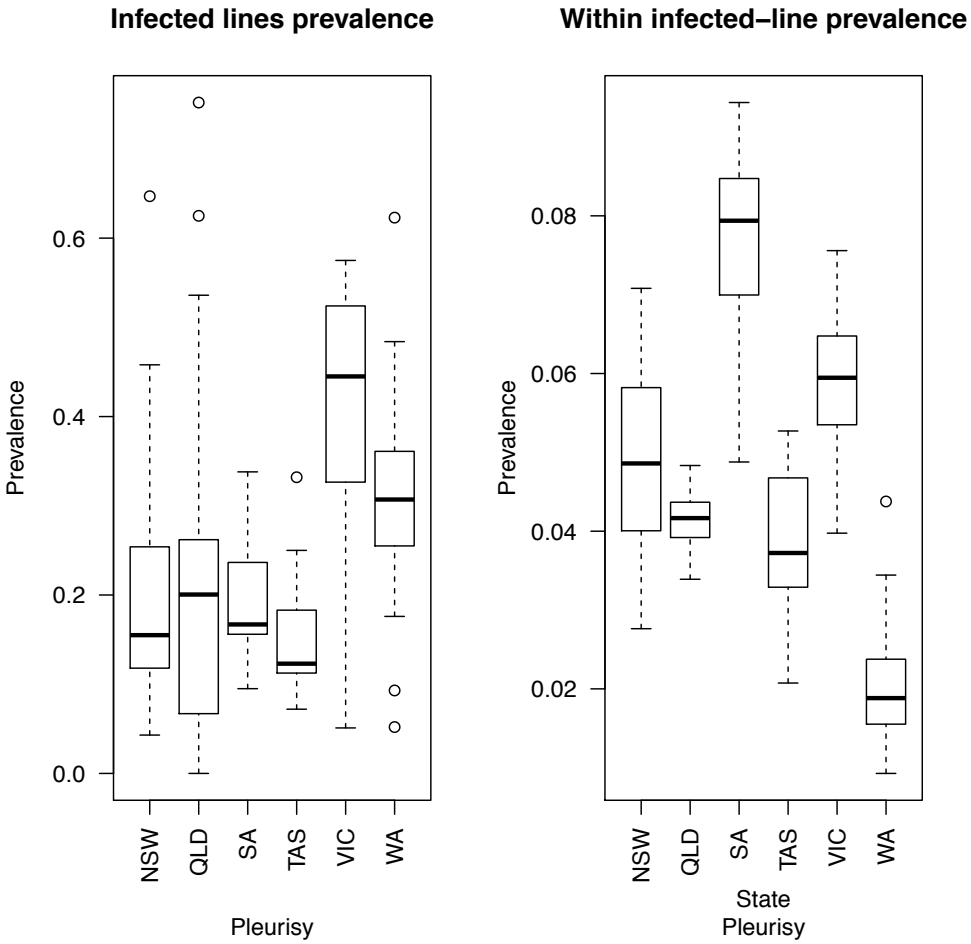


Figure 7: Pleurisy infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

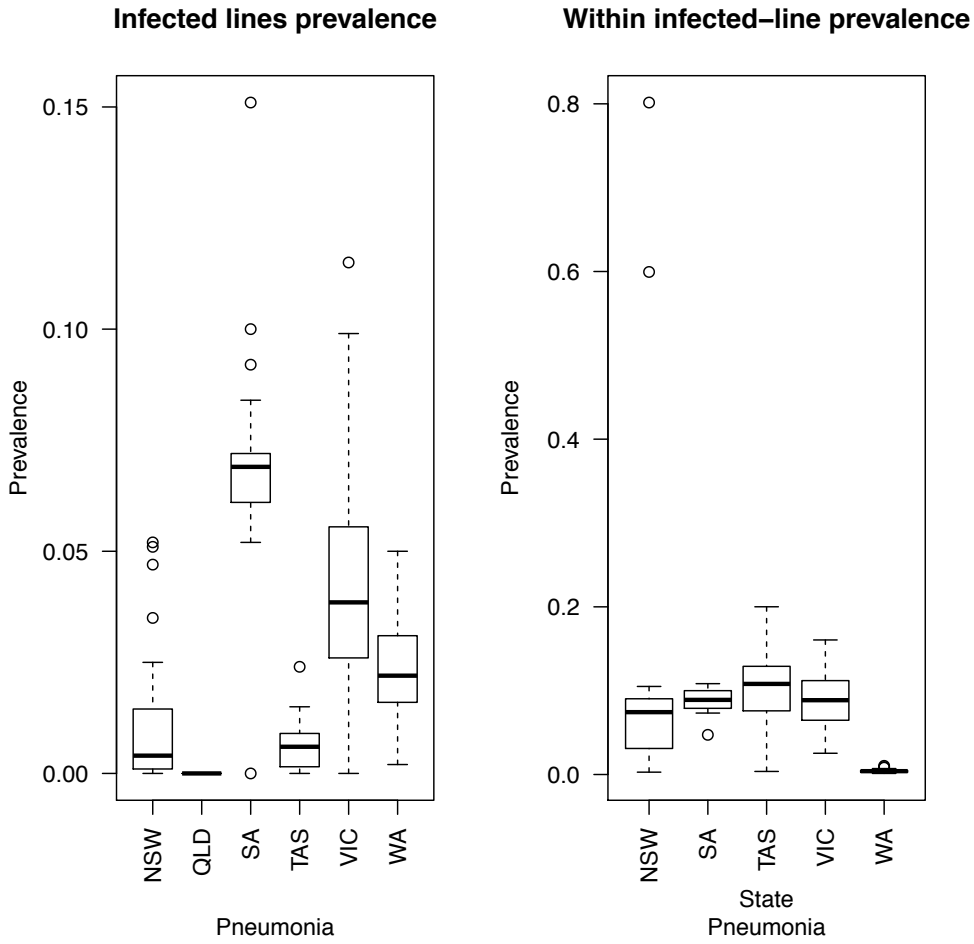


Figure 8: Pneumonia infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

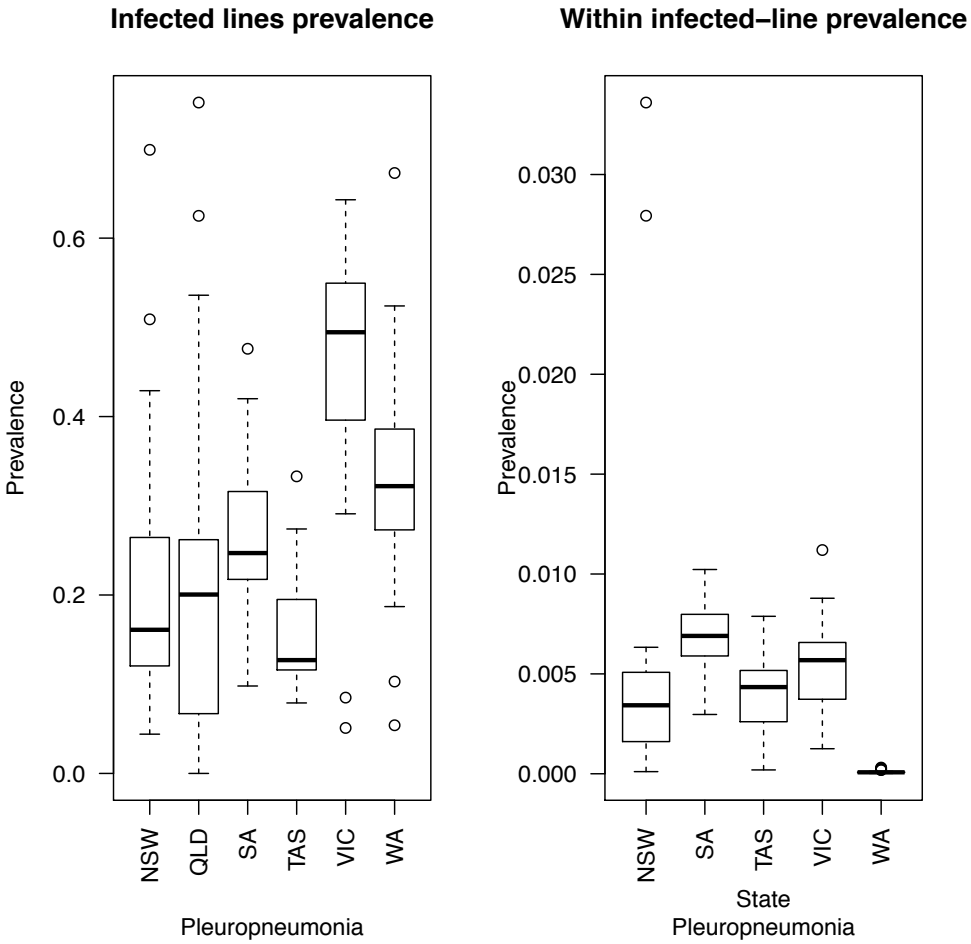


Figure 9: Combined pleurisy and pneumonia infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

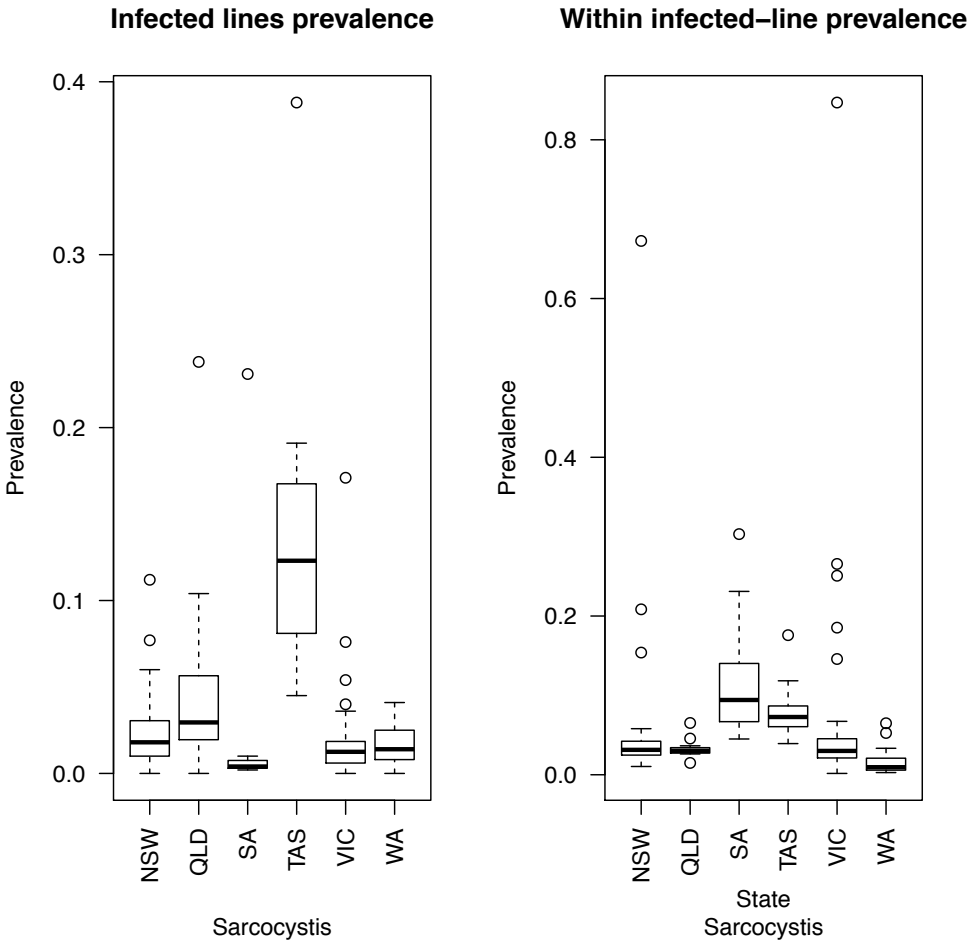


Figure 10: Sarcocystis infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

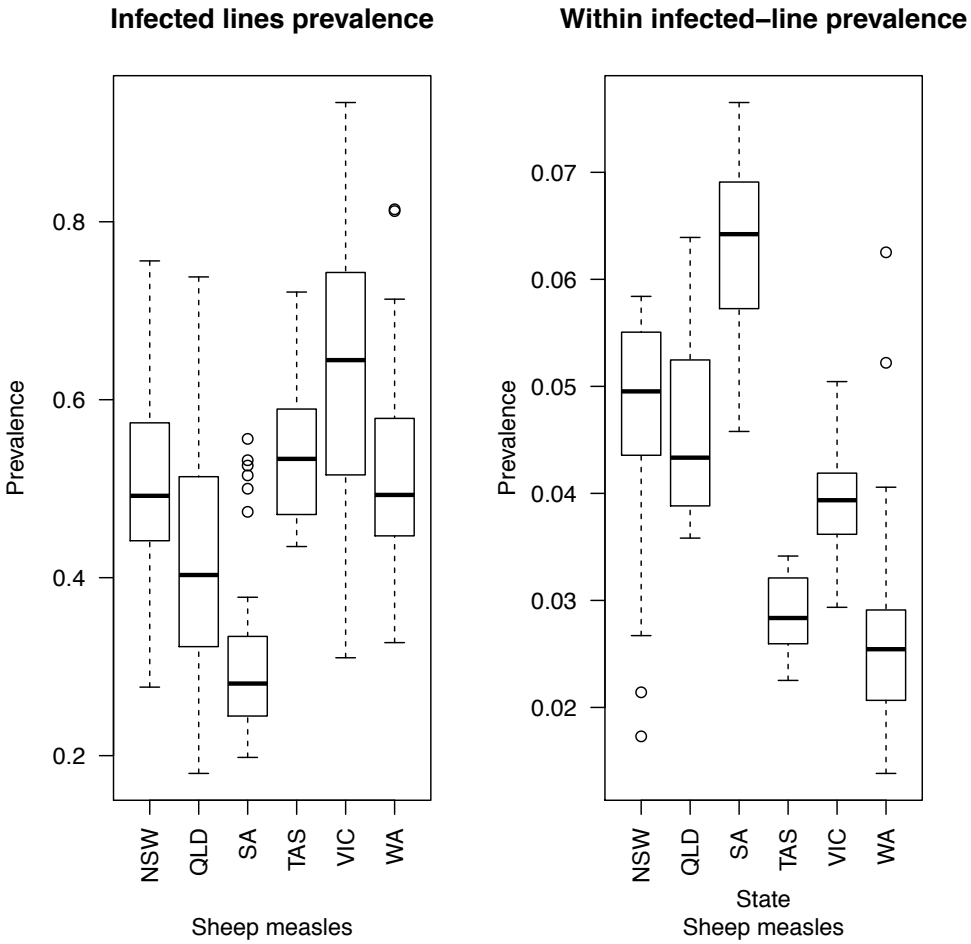


Figure 11: Sheep measles infected line prevalence and within-infected line (flock) prevalence by state LGA region boxplot

Table 4: Number of lots, average lot size, disease infected line prevalence by state LGA region

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
NSW	Armidale	3773	288.8	0.147	0.529	0.698	0.148	0.001	0.149	0.112	0.492
	Balranald	490	408.8	0.435	0.400	0.006	0.394	0.035	0.429	0.002	0.490
	Bombala	372	282.1	0.188	0.325	0.185	0.323	0.003	0.326	0.027	0.594
	Bourke	129	431.0	0.147	0.519	0.023	0.132	0.000	0.132	0.023	0.434
	Braidwood	160	217.3	0.019	0.356	0.269	0.087	0.000	0.087	0.013	0.613
	Brewarrina	186	435.0	0.048	0.387	0.027	0.043	0.005	0.048	0.016	0.457
	Broken Hill	806	444.3	0.305	0.316	0.006	0.213	0.025	0.238	0.001	0.333
	Central Tablelands	2418	294.6	0.017	0.413	0.380	0.095	0.003	0.098	0.033	0.600
	Cobar	141	342.8	0.099	0.184	0.021	0.128	0.007	0.135	0.000	0.277
	Condobolin	564	299.7	0.085	0.268	0.037	0.133	0.004	0.137	0.011	0.397
	Cooma	360	404.0	0.044	0.517	0.353	0.117	0.003	0.120	0.017	0.756
	Coonabarabran	281	320.3	0.142	0.370	0.181	0.181	0.000	0.181	0.018	0.505
	Coonamble	489	337.3	0.115	0.517	0.065	0.123	0.004	0.127	0.022	0.546
	Dubbo	3035	419.6	0.027	0.521	0.295	0.043	0.001	0.044	0.019	0.586
	Forbes	2095	288.0	0.033	0.462	0.223	0.081	0.001	0.082	0.017	0.554
	Goulburn	911	327.2	0.018	0.423	0.229	0.088	0.001	0.089	0.052	0.749
	Gundagai	1540	284.9	0.042	0.251	0.139	0.241	0.004	0.245	0.019	0.454
	Hay	279	525.5	0.384	0.351	0.022	0.355	0.047	0.402	0.011	0.530
	Hillston	309	443.9	0.259	0.388	0.036	0.246	0.003	0.249	0.003	0.450
	Hume	485	292.0	0.212	0.212	0.076	0.412	0.016	0.428	0.004	0.427
	Merriwa	204	318.2	0.186	0.431	0.279	0.191	0.000	0.191	0.034	0.618
	Milparinka	233	455.7	0.356	0.425	0.000	0.339	0.017	0.356	0.000	0.429
	Molong	498	269.9	0.102	0.285	0.141	0.253	0.014	0.267	0.016	0.394
	Moree	350	299.3	0.143	0.429	0.089	0.151	0.000	0.151	0.034	0.389
	Murray	853	295.8	0.203	0.395	0.070	0.280	0.020	0.300	0.015	0.644
	Narrabri	173	289.2	0.127	0.370	0.191	0.127	0.000	0.127	0.046	0.468
	Narrandera	652	233.2	0.075	0.373	0.140	0.110	0.011	0.121	0.008	0.531
	Northern New England	1524	238.1	0.149	0.562	0.730	0.166	0.000	0.166	0.077	0.482
	Northern Slopes	1012	268.6	0.101	0.529	0.505	0.119	0.000	0.119	0.060	0.492
	Nyngan	325	388.7	0.200	0.468	0.062	0.225	0.015	0.240	0.028	0.532
	Riverina	662	364.8	0.366	0.405	0.036	0.458	0.051	0.509	0.006	0.633
	Tamworth	1540	231.5	0.059	0.541	0.553	0.066	0.002	0.068	0.045	0.467
	Unknown NSW	9619	354.1	0.506	0.458	0.221	0.647	0.052	0.699	0.059	0.547
	Wagga Wagga	2148	365.9	0.035	0.396	0.221	0.155	0.006	0.161	0.021	0.562
	Walgett	581	390.5	0.088	0.422	0.076	0.081	0.000	0.081	0.019	0.449
	Wanaaring	107	502.9	0.299	0.477	0.009	0.290	0.009	0.299	0.009	0.374
	Wilcannia	871	463.0	0.240	0.312	0.008	0.204	0.023	0.227	0.003	0.317
	Yass	926	264.9	0.024	0.362	0.143	0.127	0.004	0.131	0.025	0.697
	Young	1681	306.1	0.063	0.260	0.133	0.255	0.007	0.262	0.018	0.463

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
QLD	Balonne	345	398.6	0.238	0.664	0.032	0.238	0.000	0.238	0.043	0.441
	Barcaldine	148	390.7	0.209	0.736	0.014	0.182	0.000	0.182	0.047	0.432
	Blackall	137	399.9	0.248	0.569	0.029	0.219	0.000	0.219	0.029	0.372
	Goondiwindi	211	288.1	0.507	0.820	0.156	0.536	0.000	0.536	0.104	0.692
	Ilfracombe	100	518.5	0.000	0.340	0.000	0.000	0.000	0.000	0.000	0.180
	Inglewood	133	457.5	0.000	0.632	0.256	0.000	0.000	0.000	0.015	0.489
	Longreach	557	459.9	0.280	0.646	0.007	0.250	0.000	0.250	0.020	0.409
	Murweh	106	409.8	0.151	0.613	0.019	0.142	0.000	0.142	0.019	0.321
	Paroo	417	433.3	0.139	0.427	0.010	0.134	0.000	0.134	0.014	0.293
	Quilpie	146	531.3	0.171	0.493	0.021	0.158	0.000	0.158	0.041	0.322
	Southern Downs	212	226.3	0.274	0.873	0.745	0.274	0.000	0.274	0.066	0.538
	Stanthorpe	102	394.9	0.000	0.686	0.471	0.000	0.000	0.000	0.029	0.363
	Unknown QLD	210	261.4	0.757	0.900	0.705	0.752	0.000	0.752	0.238	0.738
	Warwick	331	165.5	0.000	0.689	0.468	0.000	0.000	0.000	0.030	0.323
	Western Downs	104	163.2	0.548	0.971	0.279	0.625	0.000	0.625	0.077	0.635
	Winton	126	604.2	0.294	0.667	0.016	0.238	0.000	0.238	0.024	0.397
SA	Adelaide Hills	634	155.8	0.096	0.117	0.000	0.158	0.065	0.223	0.003	0.284
	Alexandrina	1776	172.9	0.113	0.083	0.002	0.138	0.070	0.208	0.005	0.230
	Barunga West	1174	213.0	0.110	0.076	0.003	0.095	0.056	0.151	0.003	0.244
	Clare/Gilbert Valleys	1186	169.6	0.159	0.128	0.000	0.225	0.072	0.297	0.006	0.291
	Cleve	3652	173.2	0.150	0.093	0.001	0.152	0.062	0.214	0.003	0.215
	Coorong	2702	193.0	0.170	0.115	0.003	0.167	0.071	0.238	0.002	0.253
	Elliston	1451	193.1	0.192	0.145	0.002	0.188	0.059	0.247	0.003	0.333
	Goyder	2230	219.1	0.157	0.133	0.001	0.183	0.078	0.261	0.004	0.281
	Grant	363	311.1	0.284	0.215	0.011	0.320	0.055	0.375	0.006	0.556
	Kangaroo Island	8062	203.8	0.166	0.123	0.002	0.149	0.065	0.214	0.231	0.250
	Karoonda East Murray	2036	195.8	0.169	0.102	0.001	0.159	0.068	0.227	0.002	0.259
	Kingston	677	307.3	0.312	0.341	0.000	0.303	0.052	0.355	0.007	0.532
	Light	2065	194.0	0.123	0.099	0.001	0.160	0.084	0.244	0.005	0.241
	Lower Eyre Peninsula	3374	172.9	0.145	0.103	0.000	0.163	0.066	0.229	0.003	0.226
	Loxton Waikerie	1660	212.4	0.231	0.136	0.002	0.243	0.078	0.321	0.003	0.284
	Mid Murray	2319	190.2	0.147	0.107	0.002	0.211	0.100	0.311	0.004	0.245
	Mount Remarkable	1440	186.9	0.121	0.096	0.000	0.156	0.072	0.228	0.003	0.223
	Murray Bridge	1034	158.7	0.147	0.097	0.001	0.155	0.061	0.216	0.008	0.262
	Naracoorte Lucindale	2678	323.7	0.287	0.273	0.008	0.288	0.070	0.358	0.009	0.526
	Northern Areas	3618	184.5	0.117	0.073	0.000	0.125	0.061	0.186	0.004	0.198
	Playford	123	266.2	0.179	0.122	0.000	0.098	0.000	0.098	0.008	0.285
	Pua	6145	253.7	0.206	0.191	0.001	0.192	0.069	0.261	0.003	0.257
	Renmark Paringa	471	274.6	0.265	0.180	0.002	0.325	0.151	0.476	0.002	0.335
	Robe	1747	323.6	0.298	0.238	0.005	0.259	0.069	0.328	0.004	0.515

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
SA	Tatiara	3229	259.9	0.240	0.215	0.003	0.264	0.064	0.328	0.005	0.378
	Unknown SA	5468	367.2	0.305	0.292	0.007	0.338	0.082	0.420	0.009	0.474
	Wakefield	3441	214.0	0.150	0.152	0.006	0.157	0.061	0.218	0.010	0.295
	Wattle Range	3098	309.7	0.282	0.203	0.006	0.230	0.071	0.301	0.008	0.500
	Wudinna	2387	194.7	0.186	0.150	0.001	0.214	0.071	0.285	0.003	0.295
	Yankalilla	757	234.9	0.125	0.083	0.018	0.156	0.092	0.248	0.008	0.244
	Yorke Peninsula	4163	152.8	0.127	0.102	0.002	0.162	0.055	0.217	0.006	0.261
TAS	Bothwell	367	256.4	0.136	0.411	0.095	0.125	0.000	0.125	0.191	0.608
	Campbell Town	475	236.4	0.107	0.389	0.084	0.112	0.002	0.114	0.128	0.512
	Deloraine	117	115.3	0.137	0.162	0.060	0.197	0.009	0.206	0.051	0.573
	Evandale	364	166.3	0.093	0.324	0.096	0.115	0.003	0.118	0.118	0.462
	Fingal	168	206.5	0.101	0.333	0.060	0.113	0.006	0.119	0.113	0.571
	Green Ponds	124	295.5	0.226	0.411	0.065	0.250	0.024	0.274	0.177	0.597
	Hamilton	273	205.8	0.128	0.300	0.114	0.121	0.004	0.125	0.147	0.582
	Longford	798	166.3	0.132	0.221	0.084	0.169	0.015	0.184	0.095	0.538
	Oatlands	567	185.9	0.123	0.332	0.037	0.120	0.009	0.129	0.138	0.529
	Richmond	124	92.9	0.048	0.218	0.024	0.073	0.008	0.081	0.089	0.435
	Ross	252	241.7	0.127	0.397	0.083	0.167	0.000	0.167	0.175	0.437
	Scottsdale	156	257.4	0.244	0.186	0.090	0.231	0.013	0.244	0.045	0.667
	Spring Bay	100	188.6	0.130	0.420	0.060	0.110	0.000	0.110	0.160	0.480
	St. Leonards	138	128.6	0.058	0.232	0.080	0.072	0.007	0.079	0.065	0.457
	Unknown TAS	1152	292.4	0.278	0.443	0.220	0.332	0.001	0.333	0.388	0.721
	Westbury	354	133.9	0.119	0.251	0.065	0.133	0.006	0.139	0.073	0.514
VIC	Ararat	1792	235.7	0.525	0.722	0.013	0.533	0.014	0.547	0.012	0.843
	Ballarat	626	350.8	0.050	0.799	0.184	0.051	0.000	0.051	0.171	0.914
	Buloke	238	234.3	0.282	0.231	0.013	0.424	0.042	0.466	0.004	0.496
	Campaspe	695	368.5	0.062	0.737	0.206	0.078	0.007	0.085	0.076	0.934
	Colac-Otway	288	161.5	0.378	0.260	0.049	0.479	0.017	0.496	0.014	0.517
	Corangamite	502	223.0	0.420	0.424	0.020	0.476	0.046	0.522	0.040	0.697
	Delatite	222	328.2	0.432	0.275	0.027	0.500	0.027	0.527	0.005	0.595
	East Gippsland	129	224.1	0.388	0.473	0.085	0.527	0.016	0.543	0.023	0.744
	Gannawarra	113	237.9	0.195	0.124	0.009	0.345	0.115	0.460	0.018	0.310
	Glenelg	1151	312.3	0.323	0.281	0.080	0.349	0.078	0.427	0.011	0.566
	Golden Plains	459	248.8	0.410	0.547	0.061	0.495	0.031	0.526	0.054	0.776
	Greater Geelong	172	91.0	0.320	0.285	0.023	0.517	0.035	0.552	0.017	0.465
	Greater Shepparton	111	220.1	0.387	0.171	0.018	0.450	0.036	0.486	0.000	0.514
	Hepburn	107	377.0	0.523	0.364	0.065	0.533	0.047	0.580	0.009	0.636
	Hindmarsh	369	240.2	0.268	0.203	0.005	0.295	0.070	0.365	0.000	0.333
	Horsham	781	293.5	0.186	0.567	0.038	0.247	0.054	0.301	0.017	0.673
	Loddon	413	257.5	0.465	0.363	0.010	0.552	0.029	0.581	0.007	0.615

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
VIC	Mildura Rural	995	272.8	0.190	0.221	0.010	0.254	0.092	0.346	0.000	0.379
	Moira	240	198.7	0.258	0.458	0.138	0.308	0.025	0.333	0.013	0.742
	Moorabool	128	254.8	0.430	0.273	0.031	0.438	0.070	0.508	0.016	0.617
	Moyne	1695	243.5	0.395	0.429	0.038	0.440	0.047	0.487	0.018	0.710
	Northern Grampians	910	206.1	0.462	0.534	0.008	0.521	0.040	0.561	0.010	0.662
	Pyrenees	662	235.0	0.498	0.699	0.005	0.542	0.020	0.562	0.015	0.826
	South Gippsland	107	247.2	0.336	0.346	0.037	0.439	0.028	0.467	0.019	0.692
	Southern Grampians	2557	348.5	0.366	0.535	0.068	0.380	0.050	0.430	0.036	0.763
	Strathbogie	354	231.5	0.424	0.280	0.028	0.573	0.037	0.610	0.003	0.653
	Surf Coast	246	142.6	0.370	0.285	0.028	0.472	0.057	0.529	0.012	0.524
	Swan Hill	213	243.3	0.188	0.338	0.056	0.249	0.042	0.291	0.005	0.451
	Unknown VIC	11422	385.0	0.487	0.448	0.067	0.559	0.084	0.643	0.028	0.656
	Wellington	186	256.6	0.538	0.489	0.059	0.575	0.016	0.591	0.005	0.774
	West Wimmera	2442	317.5	0.339	0.380	0.006	0.394	0.099	0.493	0.008	0.580
	Yarriambiack	175	283.2	0.189	0.246	0.040	0.303	0.029	0.332	0.011	0.457
WA	Albany	700	236.2	0.259	0.244	0.000	0.329	0.020	0.349	0.011	0.327
	Beverley	142	326.3	0.183	0.232	0.000	0.282	0.021	0.303	0.014	0.585
	Boyup Brook	195	245.5	0.344	0.446	0.000	0.446	0.031	0.477	0.000	0.477
	Brookton	155	280.5	0.213	0.310	0.000	0.265	0.026	0.291	0.006	0.561
	Broomehill/Tambellup	138	280.3	0.239	0.275	0.000	0.326	0.029	0.355	0.022	0.406
	Bruce Rock	181	274.2	0.436	0.298	0.000	0.448	0.022	0.470	0.017	0.414
	Chittering	194	545.1	0.067	0.253	0.000	0.093	0.010	0.103	0.026	0.814
	Coorow	114	352.5	0.351	0.325	0.000	0.412	0.044	0.456	0.026	0.430
	Corrigin	145	252.7	0.221	0.248	0.000	0.228	0.034	0.262	0.014	0.441
	Cranbrook	268	292.9	0.235	0.351	0.000	0.321	0.022	0.343	0.030	0.619
	Cuballing	165	216.8	0.158	0.230	0.000	0.255	0.018	0.273	0.006	0.400
	Dalwallinu	113	327.7	0.292	0.336	0.000	0.310	0.018	0.328	0.009	0.487
	Dandaragan	485	420.9	0.344	0.276	0.000	0.394	0.039	0.433	0.014	0.501
	Dumbleyung	191	265.3	0.257	0.304	0.000	0.361	0.042	0.403	0.016	0.529
	Esperance	599	269.7	0.222	0.245	0.000	0.252	0.012	0.264	0.008	0.447
	Gnowangerup	300	310.6	0.157	0.237	0.000	0.217	0.027	0.244	0.010	0.470
	Jerramungup	370	319.5	0.195	0.265	0.000	0.268	0.016	0.284	0.027	0.584
	Katanning	500	569.0	0.036	0.324	0.000	0.052	0.002	0.054	0.004	0.812
	Kent	123	304.0	0.179	0.276	0.000	0.309	0.041	0.350	0.008	0.350
	Kojonup	616	265.7	0.240	0.386	0.000	0.357	0.008	0.365	0.016	0.654
	Kondinin	188	254.8	0.112	0.170	0.000	0.176	0.011	0.187	0.011	0.447
	Kulin	267	282.3	0.195	0.243	0.000	0.270	0.026	0.296	0.007	0.453
	Lake Grace	355	343.3	0.217	0.256	0.000	0.285	0.031	0.316	0.023	0.476
	Merredin	137	304.8	0.358	0.285	0.000	0.350	0.036	0.386	0.029	0.518
	Moora	213	275.7	0.286	0.225	0.000	0.357	0.019	0.376	0.005	0.535
	Narembeen	217	308.3	0.313	0.341	0.000	0.424	0.046	0.470	0.023	0.535

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
WA	Narrogin Shire	257	201.6	0.280	0.335	0.000	0.471	0.008	0.479	0.016	0.463
	Pingelly	205	250.4	0.229	0.254	0.000	0.307	0.010	0.317	0.010	0.493
	Plantagenet	639	261.1	0.174	0.250	0.000	0.286	0.019	0.305	0.014	0.488
	Ravensthorpe	148	298.7	0.149	0.216	0.000	0.189	0.007	0.196	0.007	0.331
	Unknown WA	945	606.3	0.461	0.623	0.004	0.623	0.050	0.673	0.041	0.675
	Victoria Plains	113	330.9	0.212	0.221	0.000	0.248	0.018	0.266	0.018	0.690
	Wagin	196	229.3	0.184	0.357	0.000	0.286	0.015	0.301	0.036	0.526
	Wandering	114	351.6	0.254	0.272	0.000	0.316	0.026	0.342	0.035	0.535
	West Arthur	560	275.1	0.225	0.357	0.000	0.362	0.020	0.382	0.027	0.570
	Wickepin	261	249.4	0.195	0.199	0.000	0.291	0.031	0.322	0.038	0.579
	Williams	275	285.3	0.371	0.440	0.000	0.484	0.040	0.524	0.025	0.713
	Wongan/Ballidu	121	260.9	0.223	0.107	0.000	0.256	0.033	0.289	0.000	0.355
	Woodanilling	148	208.7	0.142	0.250	0.000	0.230	0.014	0.244	0.000	0.622
	Yilgarn	182	327.1	0.341	0.412	0.000	0.451	0.016	0.467	0.011	0.456
	York	113	298.0	0.159	0.195	0.000	0.212	0.027	0.239	0.000	0.451

Table 5: Number of lots, average lot size and within-infected-line disease prevalence by state LGA region

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
NSW	Armidale	3773	288.8	0.038	0.067	0.300	0.050	0.063	0.051	0.032	0.050
	Balranald	490	408.8	0.014	0.083	0.031	0.063	0.098	0.098	0.014	0.029
	Bombala	372	282.1	0.026	0.052	0.200	0.053	0.019	0.056	0.029	0.050
	Bourke	129	431.0	0.040	0.051	0.025	0.047	-	0.047	0.052	0.050
	Braidwood	160	217.3	0.040	0.050	0.149	0.061	-	0.061	0.154	0.050
	Brewarrina	186	435.0	0.025	0.097	0.100	0.039	0.100	0.044	0.030	0.050
	Broken Hill	806	444.3	0.026	0.099	0.053	0.050	0.098	0.075	0.051	0.039
	Central Tablelands	2418	294.6	0.030	0.064	0.103	0.050	0.049	0.053	0.048	0.050
	Cobar	141	342.8	0.050	0.092	0.100	0.051	0.802	0.058	-	0.050
	Condobolin	564	299.7	0.030	0.050	0.100	0.050	0.103	0.054	0.025	0.050
	Cooma	360	404.0	0.018	0.050	0.150	0.050	0.031	0.053	0.020	0.050
	Coonabarabran	281	320.3	0.030	0.050	0.100	0.050	-	0.050	0.021	0.050
	Coonamble	489	337.3	0.039	0.052	0.051	0.041	0.071	0.045	0.030	0.050
	Dubbo	3035	419.6	0.037	0.094	0.100	0.050	0.048	0.051	0.030	0.050
	Forbes	2095	288.0	0.030	0.097	0.100	0.050	0.095	0.051	0.031	0.050
	Goulburn	911	327.2	0.028	0.048	0.100	0.051	0.105	0.052	0.021	0.050
	Gundagai	1540	284.9	0.030	0.050	0.100	0.051	0.095	0.055	0.026	0.050
	Hay	279	525.5	0.017	0.051	0.055	0.050	0.060	0.097	0.030	0.030
	Hillston	309	443.9	0.013	0.075	0.098	0.060	0.599	0.063	0.020	0.030
	Hume	485	292.0	0.017	0.057	0.100	0.053	0.061	0.069	0.673	0.048
	Merriwa	204	318.2	0.030	0.051	0.100	0.050	-	0.050	0.030	0.050
	Milparinka	233	455.7	0.013	0.068	-	0.048	0.001	0.065	-	0.031
	Molong	498	269.9	0.021	0.050	0.100	0.050	0.015	0.064	0.030	0.050
	Moree	350	299.3	0.030	0.051	0.100	0.041	-	0.041	0.030	0.050
	Murray	853	295.8	0.020	0.059	0.064	0.060	0.100	0.080	0.030	0.047
	Narrabri	173	289.2	0.030	0.050	0.098	0.040	-	0.040	0.029	0.050
	Narrandera	652	233.2	0.044	0.076	0.100	0.069	0.102	0.080	0.030	0.050
	Northern New England	1524	238.1	0.035	0.058	0.251	0.049	-	0.049	0.030	0.050
	Northern Slopes	1012	268.6	0.037	0.080	0.200	0.050	-	0.050	0.030	0.050
	Nyngan	325	388.7	0.039	0.052	0.073	0.047	0.047	0.062	0.030	0.050
	Riverina	662	364.8	0.013	0.068	0.050	0.053	0.100	0.104	0.027	0.031
	Tamworth	1540	231.5	0.030	0.096	0.200	0.050	0.085	0.052	0.030	0.051
	Unknown NSW	9619	354.1	0.030	0.052	0.080	0.053	0.050	0.105	0.030	0.049
	Wagga Wagga	2148	365.9	0.041	0.080	0.100	0.050	0.090	0.056	0.033	0.050
	Walgett	581	390.5	0.032	0.055	0.123	0.034	-	0.034	0.030	0.050
	Wanaaring	107	502.9	0.007	0.051	0.050	0.049	0.027	0.058	0.049	0.011
	Wilcannia	871	463.0	0.033	0.079	0.051	0.050	0.051	0.073	0.650	0.036
	Yass	926	264.9	0.047	0.046	0.100	0.050	0.050	0.054	0.055	0.050
	Young	1681	306.1	0.043	0.050	0.100	0.051	0.100	0.058	0.050	0.050

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
QLD	Balonne	345	398.6	0.031	0.050	0.050	0.040	-	0.040	0.030	0.050
	Barcaldine	148	390.7	0.040	0.050	0.101	0.045	-	0.045	0.040	0.050
	Blackall	137	399.9	0.040	0.050	0.055	0.039	-	0.039	0.037	0.049
	Goondiwindi	211	288.1	0.031	0.049	0.079	0.047	-	0.047	0.030	0.049
	Ilfracombe	100	518.5	-	0.067	-	-	-	-	-	0.050
	Inglewood	133	457.5	-	0.100	0.100	-	-	-	0.015	0.050
	Longreach	557	459.9	0.035	0.050	0.098	0.044	-	0.044	0.030	0.050
	Murweh	106	409.8	0.029	0.050	0.050	0.040	-	0.040	0.030	0.043
	Paroo	417	433.3	0.020	0.051	0.047	0.049	-	0.049	0.039	0.050
	Quilpie	146	531.3	0.040	0.051	0.050	0.040	-	0.040	0.030	0.050
	Southern Downs	212	226.3	0.034	0.051	0.202	0.049	-	0.049	0.030	0.051
	Stanthorpe	102	394.9	-	0.100	0.100	-	-	-	0.039	0.051
	Unknown QLD	210	261.4	0.040	0.050	0.150	0.050	-	0.050	0.030	0.050
	Warwick	331	165.5	-	0.100	0.156	-	-	-	0.029	0.050
	Western Downs	104	163.2	0.031	0.050	0.050	0.044	-	0.044	0.029	0.048
	Winton	126	604.2	0.042	0.051	0.032	0.048	-	0.048	0.030	0.050
SA	Adelaide Hills	634	155.8	0.050	0.053	-	0.100	0.051	0.165	0.231	0.053
	Alexandrina	1776	172.9	0.051	0.052	0.096	0.098	0.052	0.168	0.244	0.052
	Barunga West	1174	213.0	0.052	0.100	0.100	0.097	0.053	0.153	0.089	0.052
	Clare/Gilbert Valleys	1186	169.6	0.051	0.094	-	0.099	0.098	0.171	0.055	0.052
	Cleve	3652	173.2	0.051	0.055	0.047	0.098	0.051	0.160	0.053	0.051
	Coorong	2702	193.0	0.051	0.068	0.152	0.098	0.063	0.169	0.099	0.051
	Elliston	1451	193.1	0.051	0.053	0.051	0.099	0.099	0.158	0.196	0.052
	Goyder	2230	219.1	0.050	0.100	0.048	0.099	0.098	0.177	0.050	0.051
	Grant	363	311.1	0.049	0.051	0.050	0.099	0.071	0.154	0.094	0.050
	Kangaroo Island	8062	203.8	0.051	0.098	0.110	0.099	0.098	0.164	0.302	0.052
	Karoonda East Murray	2036	195.8	0.051	0.054	0.174	0.078	0.072	0.146	0.102	0.051
	Kingston	677	307.3	0.049	0.080	-	0.073	0.054	0.125	0.100	0.051
	Light	2065	194.0	0.051	0.099	0.030	0.098	0.099	0.182	0.101	0.052
	Lower Eyre Peninsula	3374	172.9	0.051	0.097	0.299	0.096	0.052	0.162	0.101	0.052
	Loxton Waikerie	1660	212.4	0.050	0.088	0.100	0.053	0.052	0.131	0.251	0.050
	Mid Murray	2319	190.2	0.051	0.097	0.050	0.096	0.100	0.196	0.198	0.051
	Mount Remarkable	1440	186.9	0.051	0.099	-	0.098	0.053	0.170	0.052	0.053
	Murray Bridge	1034	158.7	0.050	0.052	0.100	0.098	0.098	0.159	0.156	0.051
	Naracoorte Lucindale	2678	323.7	0.044	0.053	0.049	0.051	0.053	0.121	0.050	0.050
	Northern Areas	3618	184.5	0.051	0.098	0.103	0.096	0.098	0.157	0.105	0.052
	Playford	123	266.2	0.051	0.096	-	0.078	-	0.078	0.048	0.055
	Pua	6145	253.7	0.051	0.102	0.050	0.099	0.053	0.168	0.098	0.051
	Renmark Paringa	471	274.6	0.050	0.094	0.049	0.052	0.099	0.203	0.051	0.050
	Robe	1747	323.6	0.049	0.068	0.241	0.065	0.090	0.134	0.098	0.051
	Tatiara	3229	259.9	0.049	0.070	0.100	0.060	0.054	0.124	0.051	0.050

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
SA	Unknown SA	5468	367.2	0.049	0.052	0.013	0.095	0.050	0.177	0.051	0.050
	Wakefield	3441	214.0	0.050	0.079	0.049	0.067	0.053	0.128	0.050	0.050
	Wattle Range	3098	309.7	0.050	0.051	0.020	0.051	0.052	0.122	0.050	0.051
	Wudinna	2387	194.7	0.051	0.097	0.051	0.099	0.053	0.170	0.073	0.052
	Yankalilla	757	234.9	0.050	0.099	0.173	0.099	0.100	0.191	0.190	0.053
	Yorke Peninsula	4163	152.8	0.051	0.055	0.100	0.099	0.053	0.154	0.101	0.052
TAS	Bothwell	367	256.4	0.010	0.055	0.068	0.039	-	0.039	0.130	0.027
	Campbell Town	475	236.4	0.010	0.058	0.069	0.042	0.120	0.044	0.084	0.029
	Deloraine	117	115.3	0.016	0.080	0.320	0.050	0.170	0.059	0.094	0.030
	Evandale	364	166.3	0.013	0.063	0.100	0.035	0.140	0.038	0.042	0.030
	Fingal	168	206.5	0.013	0.062	0.051	0.037	0.055	0.043	0.058	0.030
	Green Ponds	124	295.5	0.012	0.049	0.120	0.060	0.073	0.084	0.101	0.032
	Hamilton	273	205.8	0.010	0.052	0.110	0.040	0.200	0.044	0.069	0.026
	Longford	798	166.3	0.016	0.054	0.145	0.052	0.125	0.067	0.077	0.031
	Oatlands	567	185.9	0.013	0.038	0.033	0.045	0.130	0.054	0.062	0.028
	Richmond	124	92.9	0.024	0.063	0.400	0.040	0.045	0.048	0.029	0.036
	Ross	252	241.7	0.012	0.057	0.110	0.032	-	0.032	0.081	0.028
	Scottsdale	156	257.4	0.013	0.060	0.077	0.044	0.110	0.057	0.171	0.027
	Spring Bay	100	188.6	0.013	0.040	0.092	0.041	-	0.041	0.051	0.030
	St. Leonards	138	128.6	0.012	0.110	0.200	0.060	0.100	0.067	0.070	0.025
	Unknown TAS	1152	292.4	0.017	0.102	0.044	0.077	0.004	0.078	0.299	0.039
	Westbury	354	133.9	0.013	0.070	0.240	0.049	0.108	0.055	0.111	0.031
VIC	Ararat	1792	235.7	0.014	0.087	0.058	0.066	0.086	0.080	0.053	0.040
	Ballarat	626	350.8	0.013	0.099	0.030	0.065	-	0.065	0.020	0.055
	Buloke	238	234.3	0.017	0.085	0.600	0.058	0.051	0.100	0.847	0.045
	Campaspe	695	368.5	0.020	0.089	0.042	0.059	0.051	0.066	0.023	0.050
	Colac-Otway	288	161.5	0.020	0.084	0.386	0.060	0.029	0.077	0.030	0.042
	Corangamite	502	223.0	0.013	0.059	0.075	0.046	0.048	0.092	0.096	0.039
	Delatite	222	328.2	0.020	0.100	0.052	0.060	0.115	0.087	0.020	0.037
	East Gippsland	129	224.1	0.020	0.092	0.200	0.060	0.127	0.076	0.006	0.041
	Gannawarra	113	237.9	0.020	0.050	0.005	0.067	0.053	0.182	0.006	0.048
	Glenelg	1151	312.3	0.024	0.050	0.073	0.050	0.098	0.128	0.020	0.048
	Golden Plains	459	248.8	0.012	0.086	0.029	0.062	0.032	0.093	0.064	0.039
	Greater Geelong	172	91.0	0.033	0.111	0.178	0.075	0.183	0.110	0.250	0.039
	Greater Shepparton	111	220.1	0.020	0.050	0.082	0.070	0.100	0.106	-	0.040
	Hepburn	107	377.0	0.017	0.091	0.165	0.067	0.160	0.114	0.002	0.040
	Hindmarsh	369	240.2	0.030	0.090	0.209	0.063	0.126	0.133	-	0.047
	Horsham	781	293.5	0.015	0.091	0.035	0.056	0.100	0.110	0.024	0.046
	Loddon	413	257.5	0.015	0.100	0.132	0.060	0.127	0.089	0.049	0.032
	Mildura Rural	995	272.8	0.049	0.089	0.034	0.053	0.052	0.145	-	0.049

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
VIC	Moira	240	198.7	0.020	0.055	0.070	0.069	0.055	0.094	0.016	0.048
	Moorabool	128	254.8	0.015	0.104	0.059	0.060	0.110	0.130	0.040	0.045
	Moyne	1695	243.5	0.015	0.054	0.067	0.044	0.051	0.091	0.033	0.042
	Northern Grampians	910	206.1	0.015	0.088	0.057	0.066	0.052	0.106	0.033	0.036
	Pyrenees	662	235.0	0.015	0.092	0.048	0.067	0.101	0.087	0.051	0.040
	South Gippsland	107	247.2	0.010	0.097	0.113	0.055	0.070	0.083	0.146	0.029
	Southern Grampians	2557	348.5	0.014	0.072	0.037	0.056	0.056	0.106	0.020	0.045
	Strathbogie	354	231.5	0.020	0.079	0.092	0.064	0.110	0.101	0.251	0.037
	Surf Coast	246	142.6	0.024	0.083	0.120	0.064	0.130	0.121	0.223	0.035
	Swan Hill	213	243.3	0.019	0.070	0.078	0.064	0.049	0.106	0.002	0.039
	Unknown VIC	11422	385.0	0.025	0.086	0.024	0.071	0.051	0.155	0.029	0.049
	Wellington	186	256.6	0.020	0.083	0.034	0.067	0.100	0.083	0.027	0.040
	West Wimmera	2442	317.5	0.020	0.069	0.019	0.051	0.053	0.150	0.051	0.049
	Yarriambiack	175	283.2	0.015	0.080	0.050	0.060	0.057	0.089	0.028	0.047
WA	Albany	700	236.2	0.007	0.009	-	0.012	0.006	0.032	0.011	0.016
	Beverley	142	326.3	0.011	0.015	-	0.026	0.004	0.047	0.003	0.040
	Boyup Brook	195	245.5	0.010	0.049	-	0.035	0.003	0.066	-	0.021
	Brookton	155	280.5	0.005	0.020	-	0.021	0.005	0.047	0.021	0.040
	Broomehill/Tambellup	138	280.3	0.009	0.030	-	0.024	0.004	0.053	0.004	0.022
	Bruce Rock	181	274.2	0.009	0.013	-	0.017	0.005	0.039	0.002	0.020
	Chittering	194	545.1	0.005	0.045	-	0.013	0.004	0.023	0.013	0.056
	Coorow	114	352.5	0.008	0.007	-	0.020	0.003	0.064	0.018	0.014
	Corrigin	145	252.7	0.008	0.031	-	0.016	0.006	0.050	0.008	0.039
	Cranbrook	268	292.9	0.009	0.029	-	0.019	0.003	0.041	0.015	0.030
	Cuballing	165	216.8	0.007	0.019	-	0.020	0.012	0.038	0.007	0.034
	Dalwallinu	113	327.7	0.010	0.011	-	0.020	0.003	0.038	0.003	0.023
	Dandaragan	485	420.9	0.006	0.008	-	0.012	0.002	0.051	0.008	0.020
	Dumbleyung	191	265.3	0.006	0.020	-	0.021	0.003	0.063	0.031	0.022
	Esperance	599	269.7	0.010	0.042	-	0.022	0.003	0.034	0.002	0.032
	Gnowangerup	300	310.6	0.010	0.020	-	0.022	0.005	0.049	0.009	0.031
	Jerramungup	370	319.5	0.008	0.017	-	0.017	0.005	0.033	0.003	0.040
	Katanning	500	569.0	0.011	0.080	-	0.050	0.007	0.052	0.053	0.052
	Kent	123	304.0	0.008	0.035	-	0.027	0.004	0.068	0.004	0.022
	Kojonup	616	265.7	0.010	0.049	-	0.033	0.003	0.041	0.027	0.029
	Kondinin	188	254.8	0.008	0.017	-	0.024	0.002	0.035	0.007	0.034
	Kulin	267	282.3	0.008	0.018	-	0.026	0.005	0.052	0.005	0.027
	Lake Grace	355	343.3	0.010	0.031	-	0.024	0.002	0.055	0.023	0.030
	Merredin	137	304.8	0.008	0.022	-	0.019	0.004	0.055	0.012	0.020
	Moora	213	275.7	0.007	0.008	-	0.018	0.002	0.037	0.033	0.048
	Narembeen	217	308.3	0.010	0.012	-	0.021	0.005	0.067	0.003	0.021
	Narrogin Shire	257	201.6	0.012	0.046	-	0.035	0.009	0.043	0.044	0.020

State	LGA	No. lots	Avg. lot size	Arthritis	CLA	Liver fluke	Pleurisy	Pneum.	Pleur/ Pnu.	Sarco	Sheep measles
WA	Pingelly	205	250.4	0.010	0.020	-	0.022	0.004	0.032	0.033	0.030
	Plantagenet	639	261.1	0.008	0.016	-	0.020	0.003	0.039	0.006	0.032
	Ravensthorpe	148	298.7	0.009	0.035	-	0.014	0.001	0.021	0.021	0.048
	Unknown WA	945	606.3	0.008	0.022	0.001	0.030	0.002	0.080	0.007	0.019
	Victoria Plains	113	330.9	0.004	0.007	-	0.009	0.002	0.027	0.003	0.049
	Wagin	196	229.3	0.010	0.048	-	0.029	0.011	0.044	0.019	0.027
	Wandering	114	351.6	0.007	0.015	-	0.023	0.005	0.049	0.174	0.021
	West Arthur	560	275.1	0.010	0.038	-	0.028	0.005	0.048	0.020	0.025
	Wickepin	261	249.4	0.008	0.014	-	0.020	0.004	0.051	0.009	0.037
	Williams	275	285.3	0.009	0.020	-	0.021	0.006	0.061	0.007	0.027
	Wongan/Ballidu	121	260.9	0.005	0.004	-	0.016	0.004	0.049	-	0.030
	Woodanilling	148	208.7	0.010	0.051	-	0.033	0.002	0.047	-	0.046
	Yilgarn	182	327.1	0.006	0.015	-	0.015	0.007	0.031	0.004	0.021
	York	113	298.0	0.008	0.042	-	0.015	0.005	0.042	-	0.030

The trends in infected line and within-infected-lines prevalences for each disease and by state are presented in Figure 12 to Figure 18. In general, most diseases are stable within and between lines, but liver fluke line prevalence and within-line prevalence appear to trend lower whereas combined pleurisy and pneumonia[5] line prevalence and within-line prevalence appear to be trending up. Arthritis line prevalence is essentially constant but there is evidence that the prevalence of disease within infected lines is trending higher. Sheep measles appears to have a constant within-infected-line prevalence, but the prevalence of infected lines may be trending downwards.

[5] Pleurisy and pneumonia were reported together until 2014 when they were split into separate diseases. It is possible that some affected animals since 2014 were classified singly as either pleurisy or pneumonia with some classified as having both conditions.

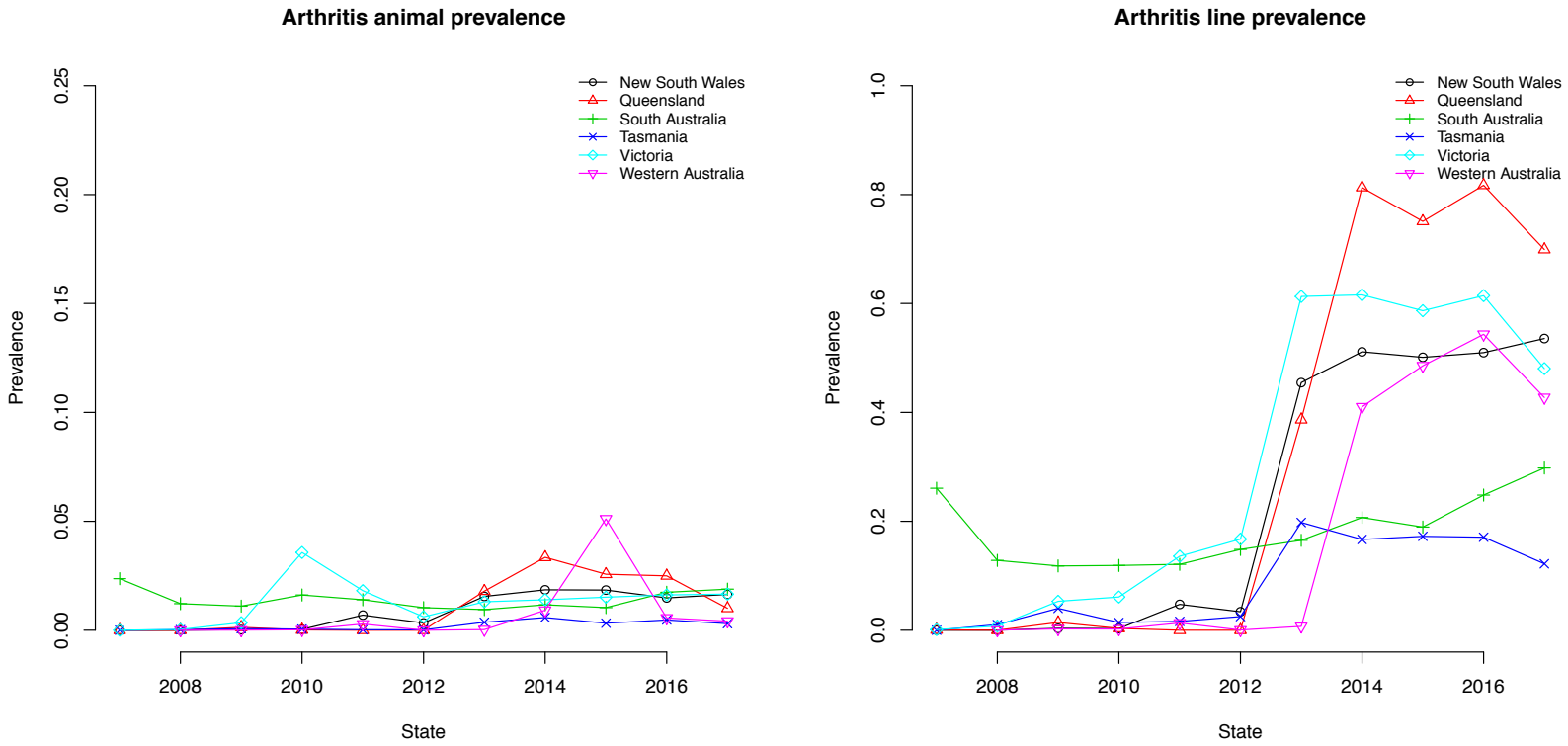


Figure 12: Arthritis animal and line prevalence by state and year

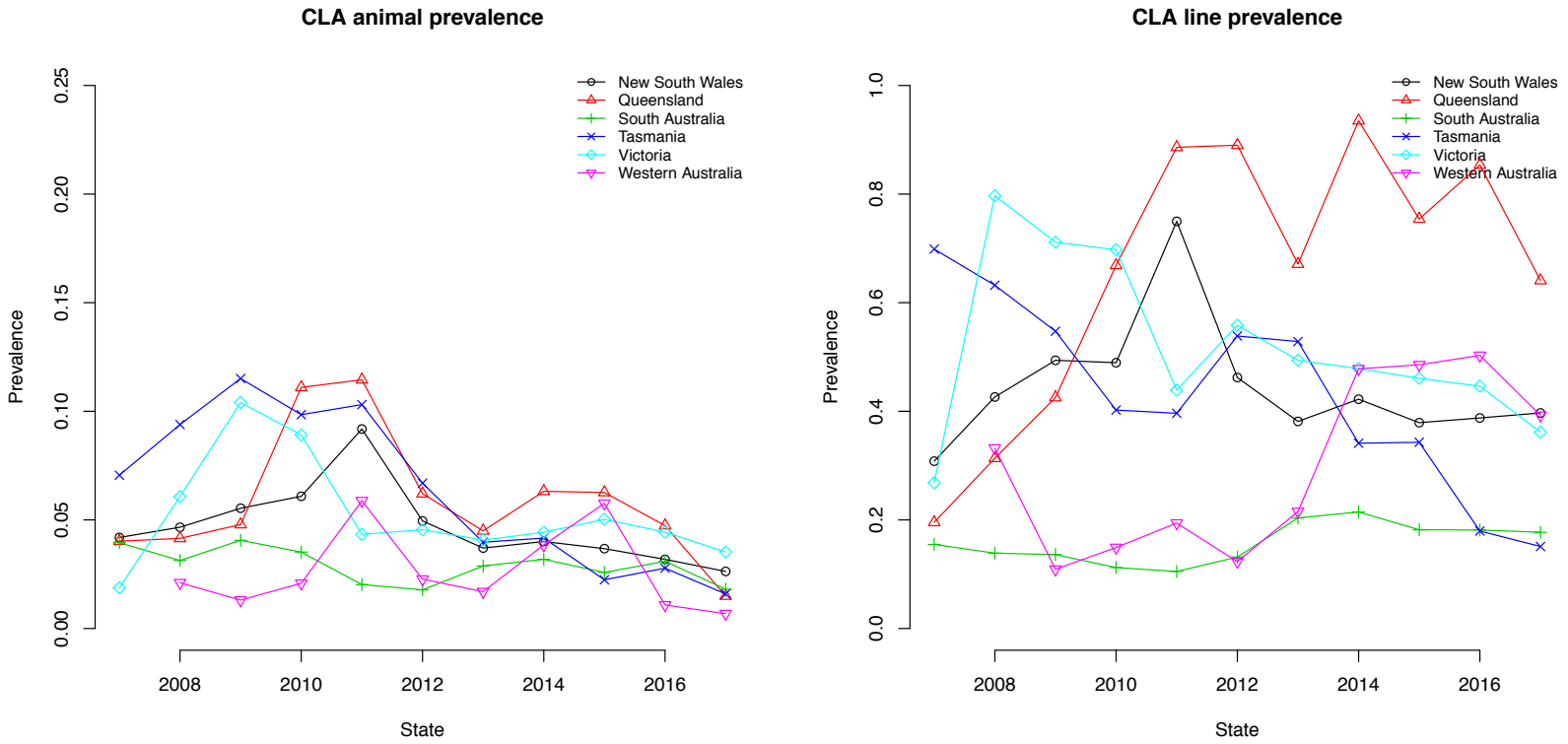


Figure 13: CLA animal and line prevalence by state and year

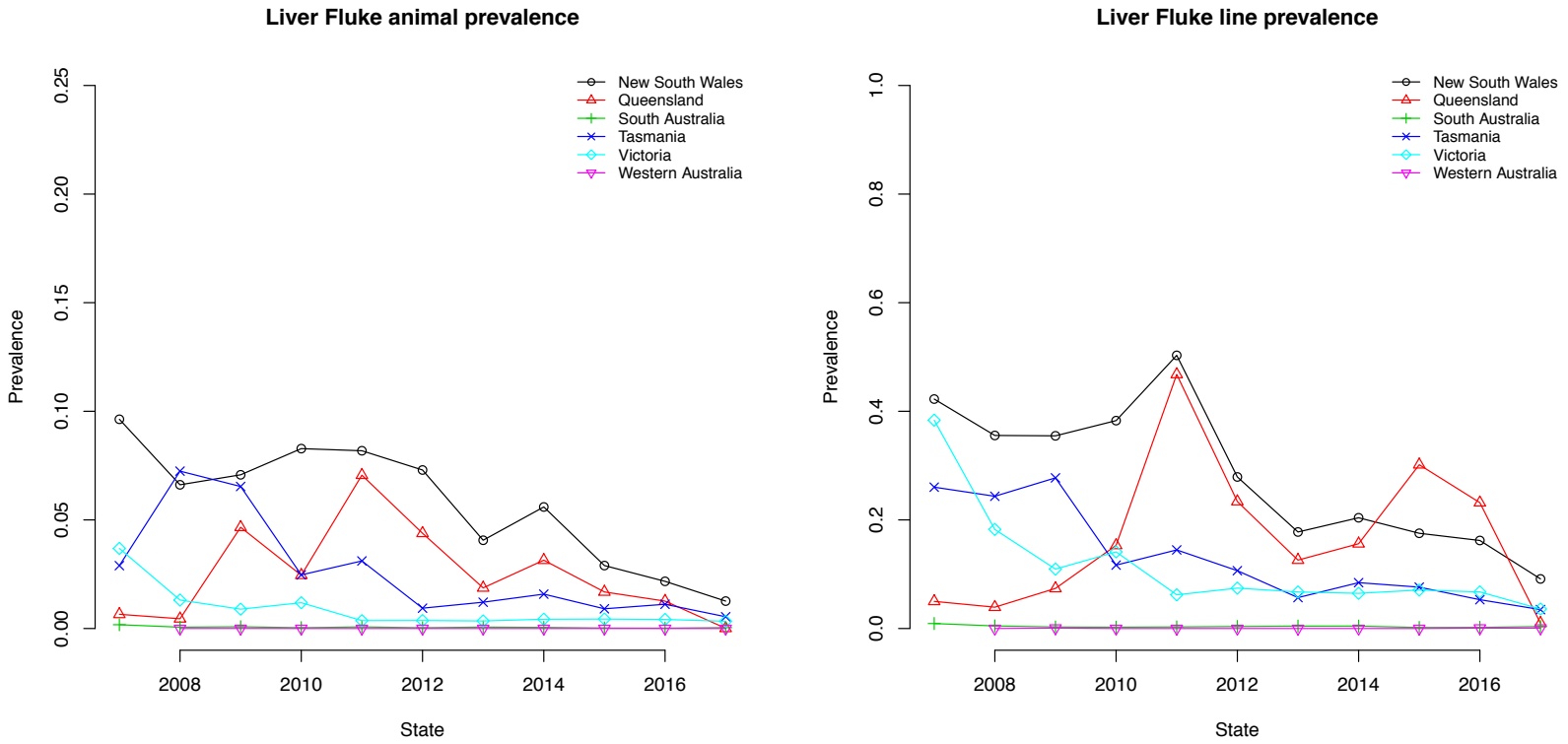


Figure 14: Liver fluke animal and line prevalence by state and year

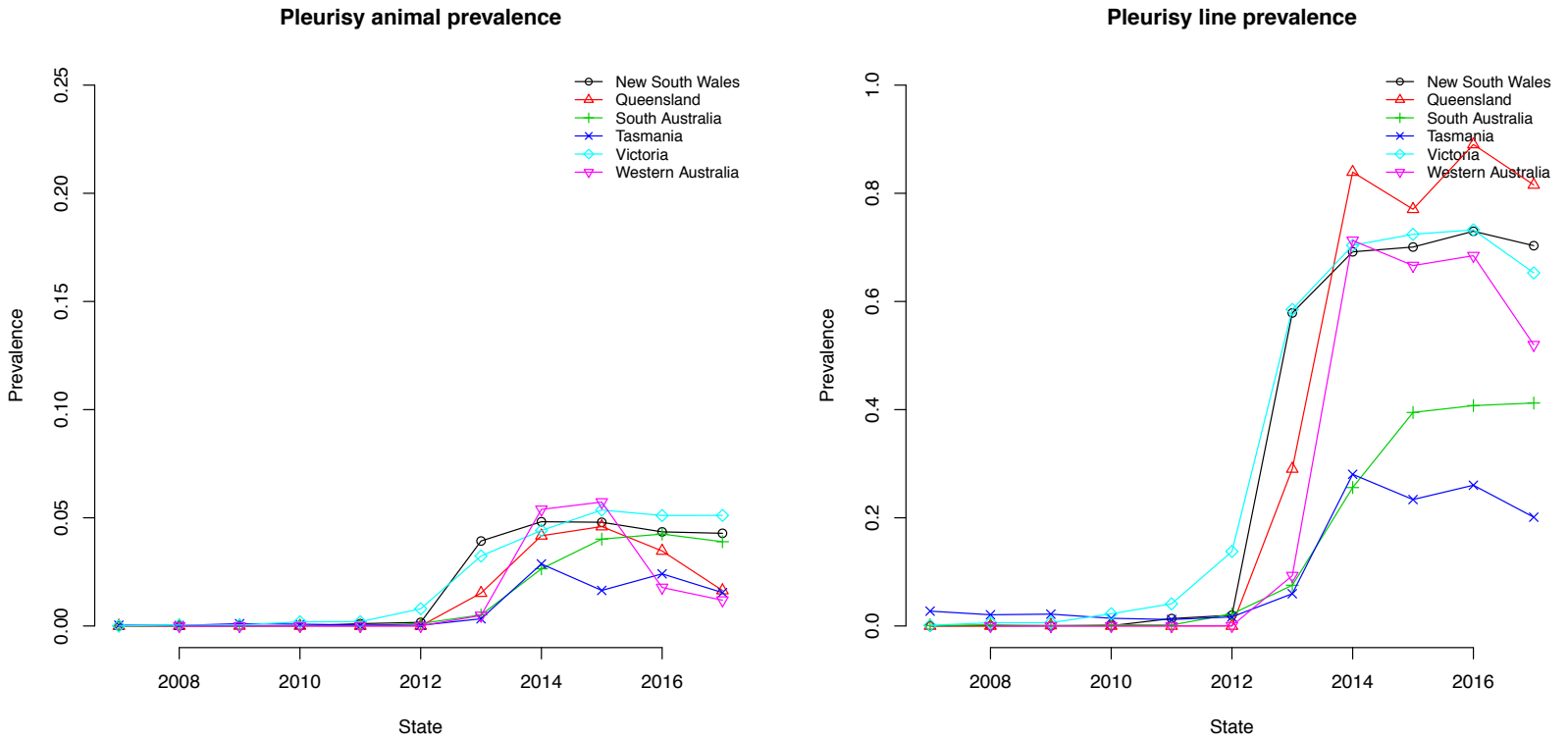


Figure 15: Pleurisy animal and line prevalence by state and year

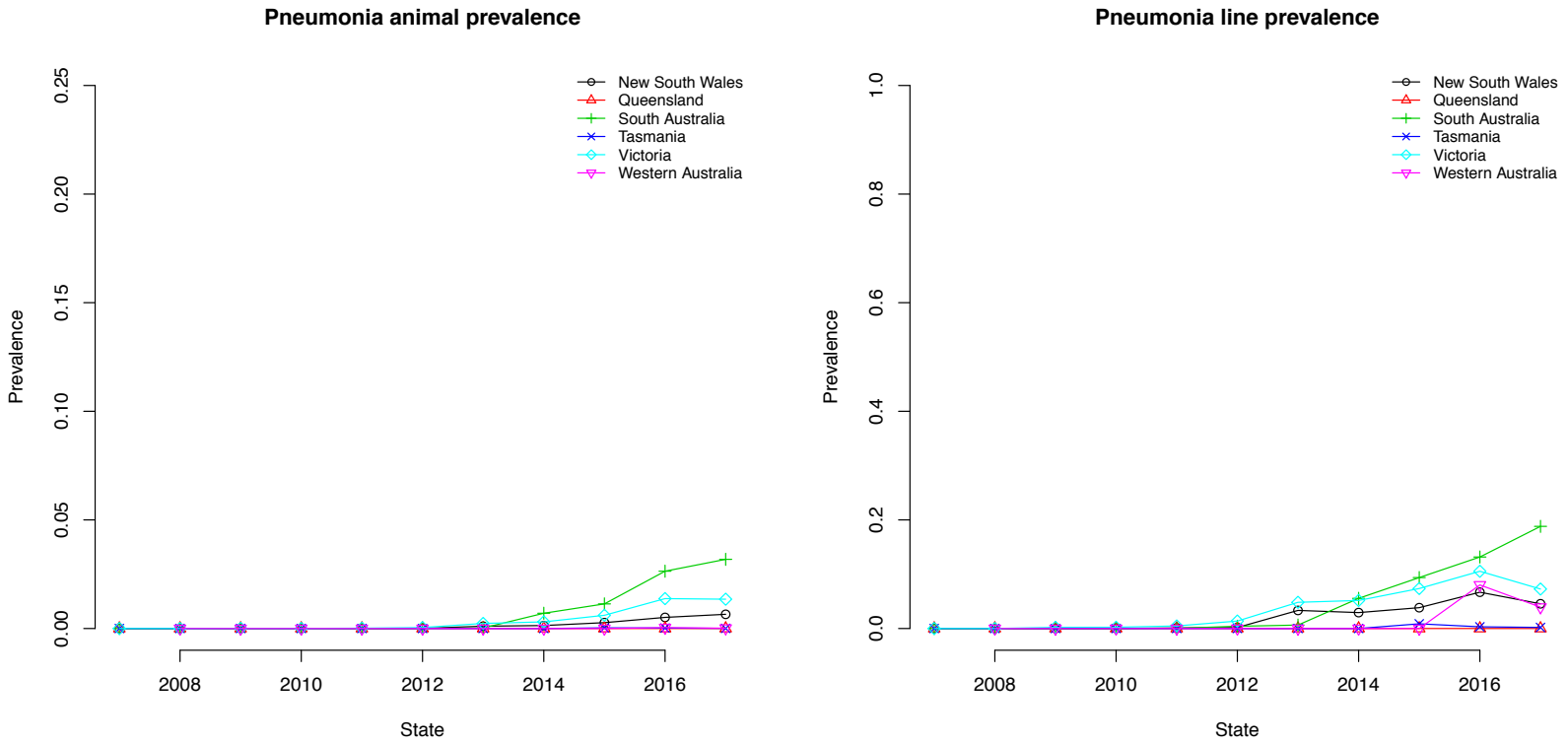
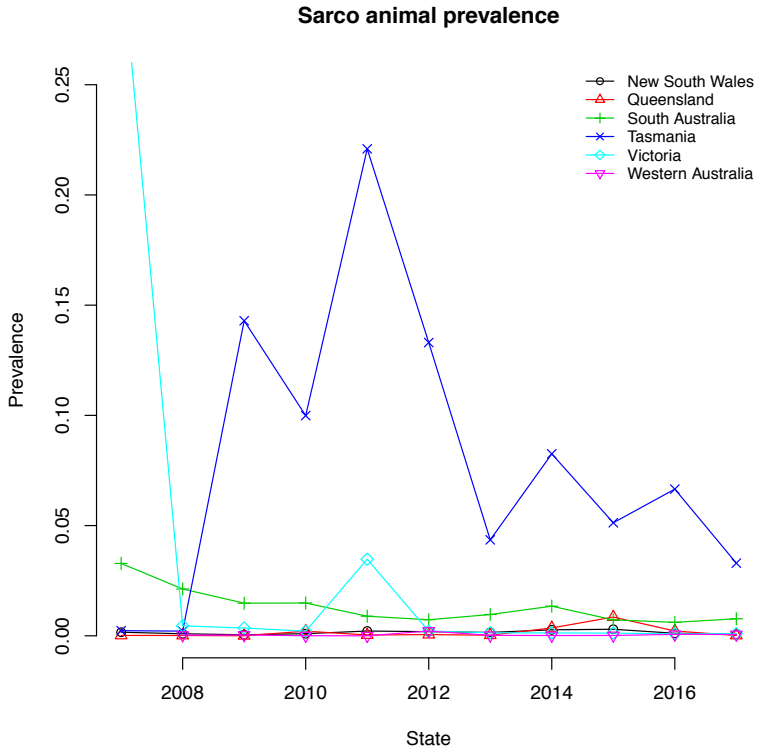


Figure 16: Pneumonia animal and line prevalence by state and year



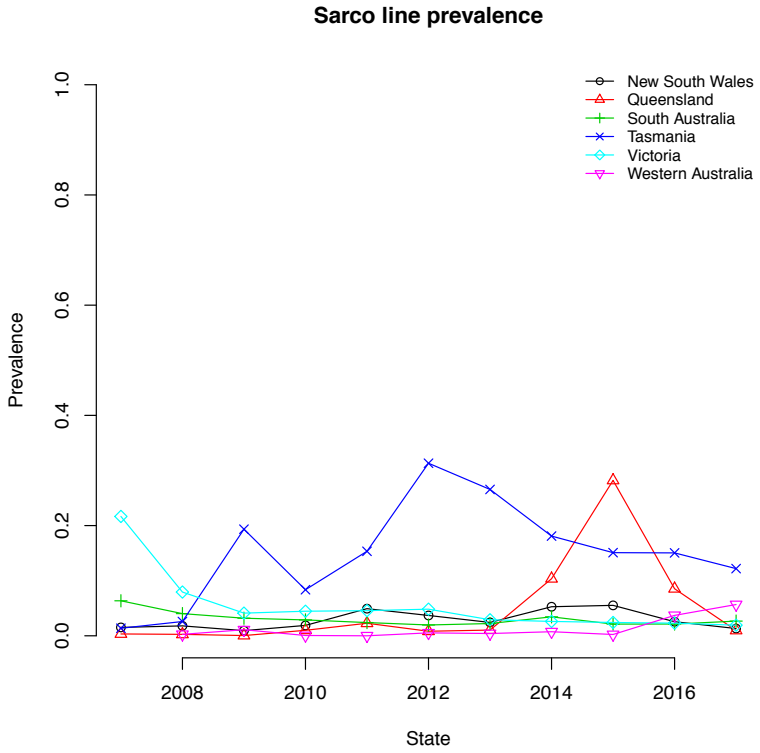


Figure 17: Sarcocystis animal and line prevalence by state and year

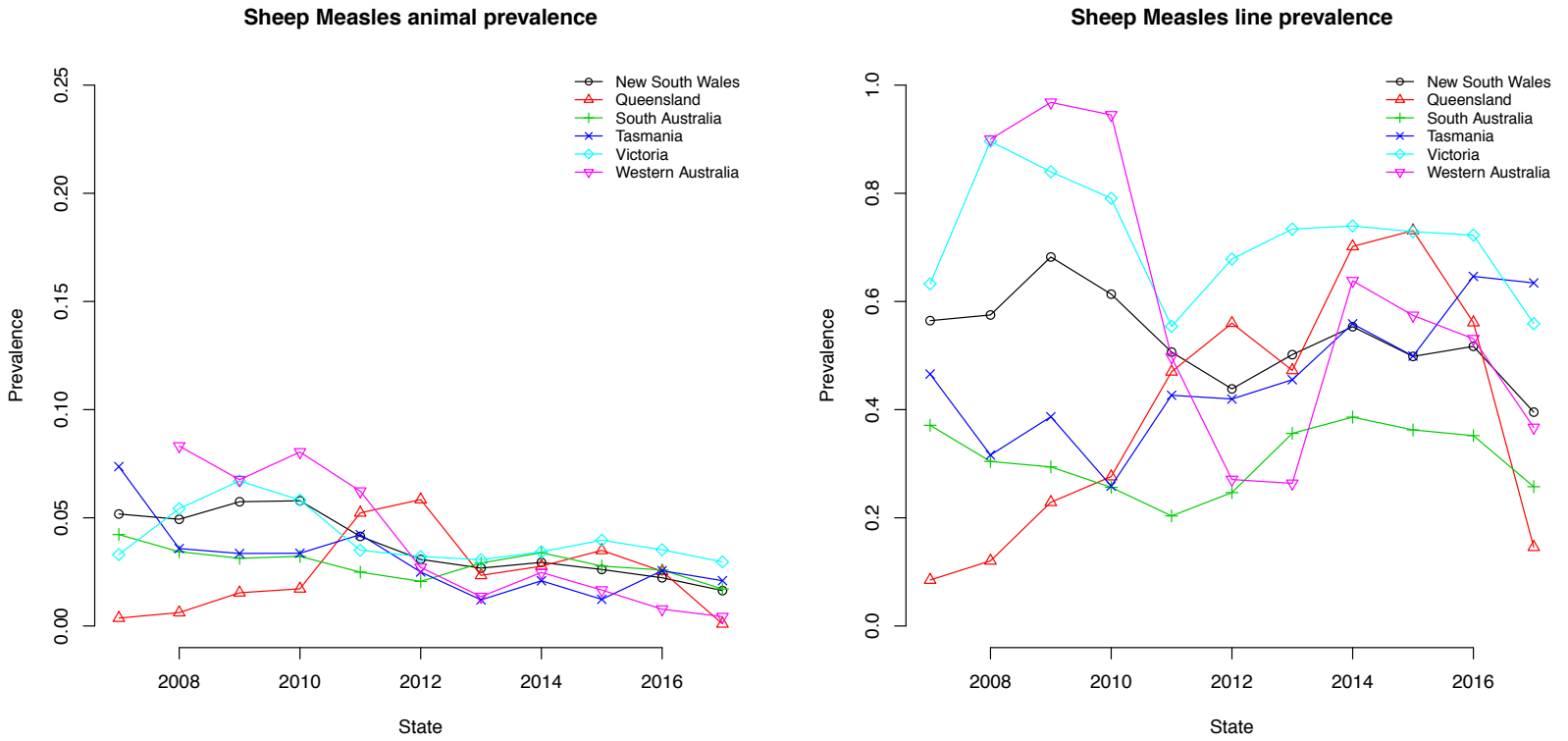


Figure 18: Sheep measles animal and line prevalence by state and year

5.1.2 EASP data

Because the EASP program focused on all lines of sheep submitted to two abattoirs, the data was not examined for completeness. A similar approach to NSHMP descriptive analysis was undertaken with focus on examination of the trends within infected line prevalence and within-infected-line (flock) prevalence for each condition. EASP data is essentially a census and this meant the preceding year disease history for each (de-identified) producer line was (mostly) able to be determined. Each line of sheep was examined to determine if the same producer had submitted a similar line of sheep (same class and age) to the same abattoir[6] in the preceding year. The preceding year history for the line of sheep were classified as:

1. Previously infected: When lines were submitted in the preceding year and at least one affected sheep was submitted for slaughter in the preceding year's lines
2. Previously uninfected: When lines were submitted in the preceding year and no affected sheep were submitted for slaughter in the preceding year's lines
3. Unknown status: No relevant lines were submitted in the preceding year.

Prevalence of infected lines and within-infected lines were plotted over time for each condition for all lines. This was supplemented by plotting prevalence for lines that were from properties with previously infected line prevalence in the preceding year and for lines from properties with only uninfected lines from the preceding year. Year and month-of-year prevalence plots were also produced to explore yearly and seasonal trends in prevalence. These plots are presented in Figure 19 to Figure 32.

In general, most diseases have consistent prevalence of infected lines and within-line prevalence. Infected line prevalence trend exceptions include knotty gut and nephritis (tending up) and sheep measles (trending down) and for within-infected line prevalence include cirrhosis, CLA, grass seeds and sheep measles (trending down).

[6] To avoid any abattoir effect that may or may not be present

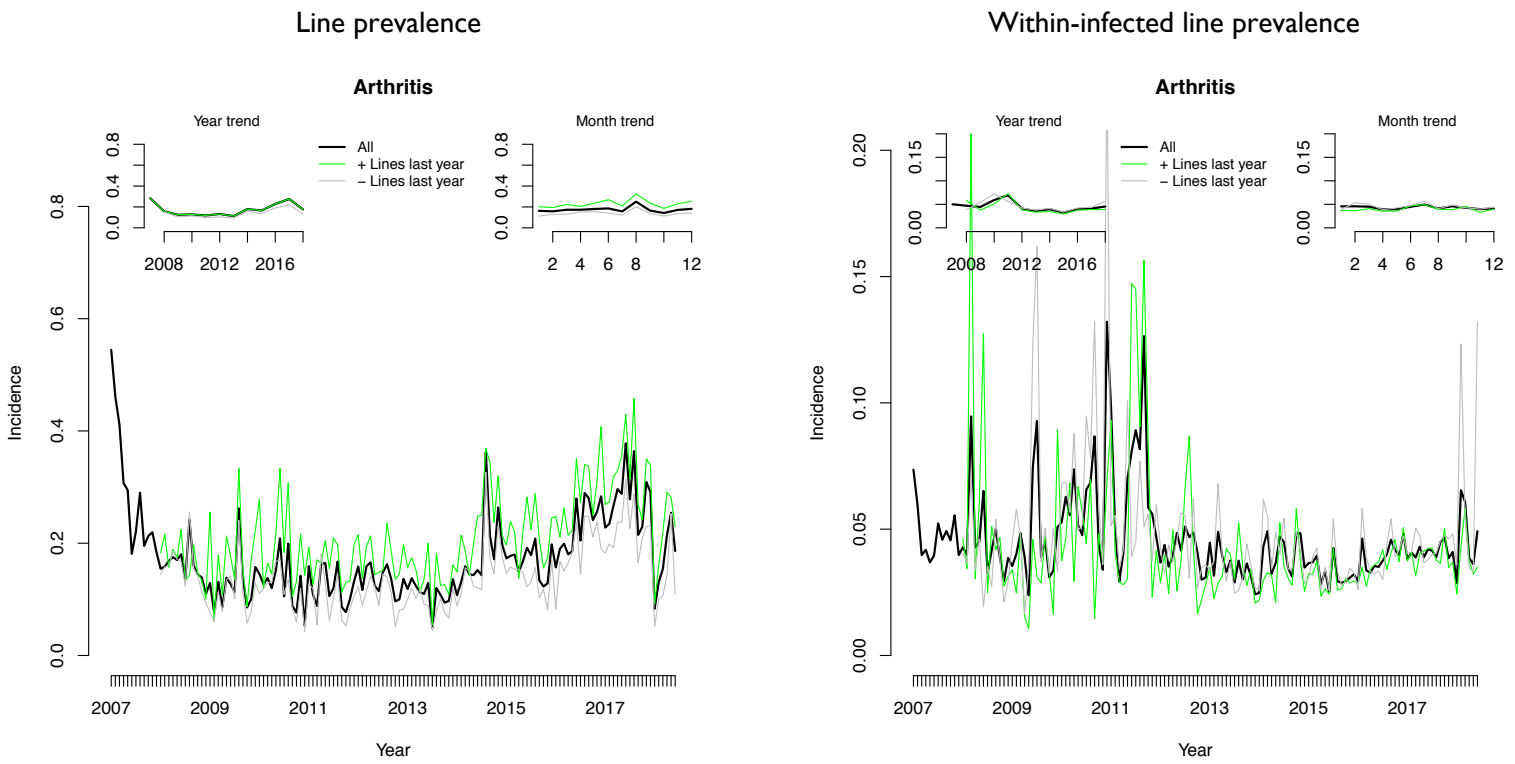


Figure 19: EASP line and within-infected-line arthritis prevalence plot by time

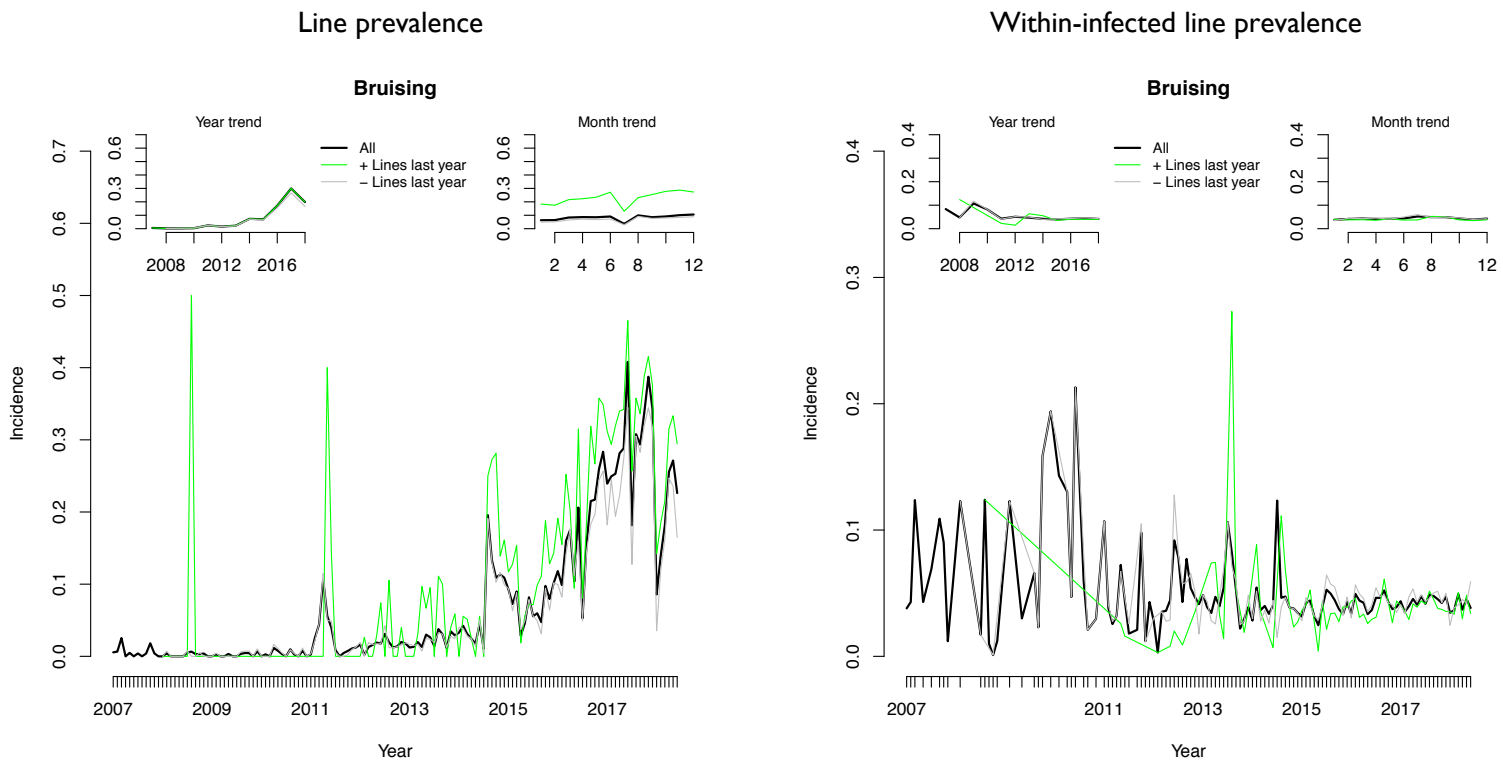


Figure 20: EASP line and within-infected-line bruising prevalence plot by time

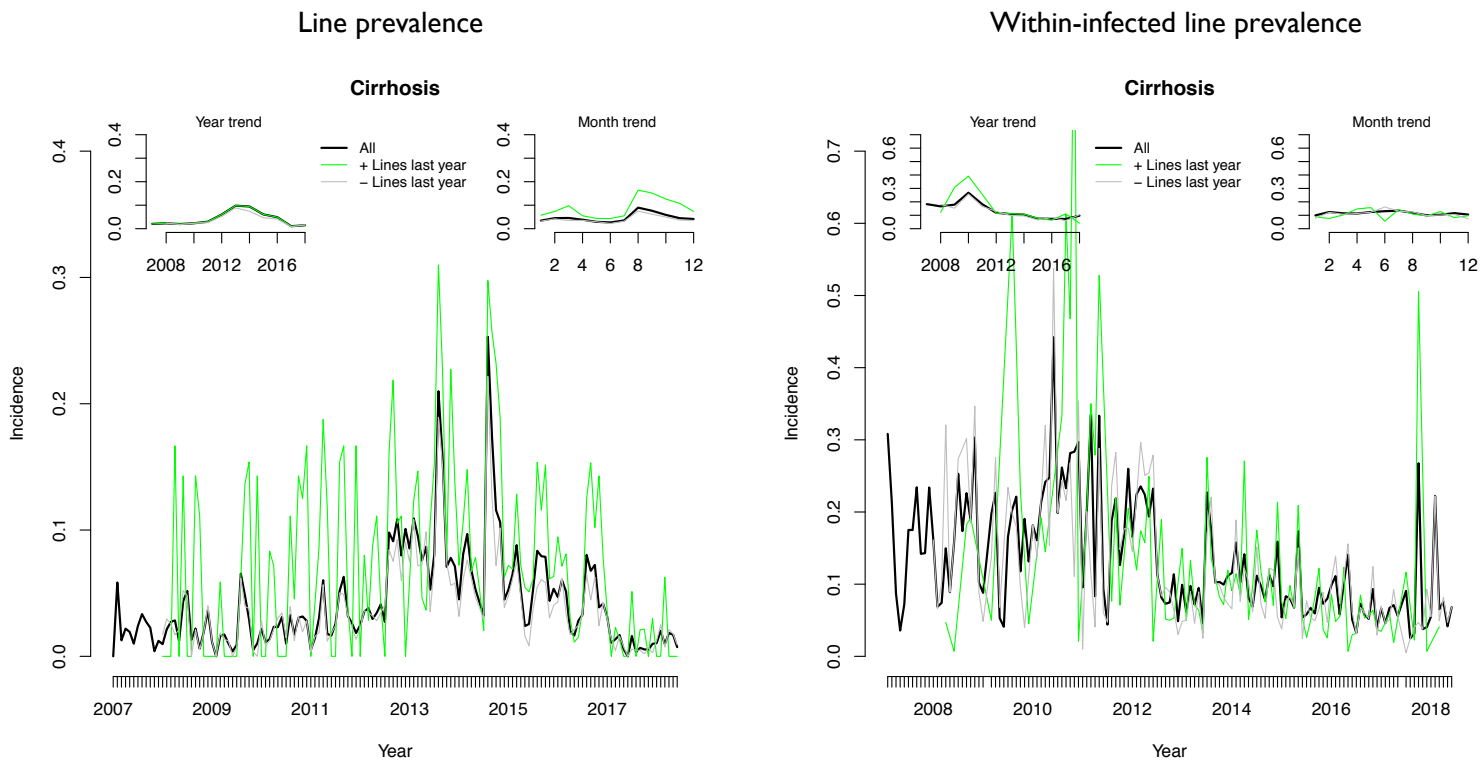


Figure 21: EASP line and within-infected-line cirrhosis prevalence plot by time

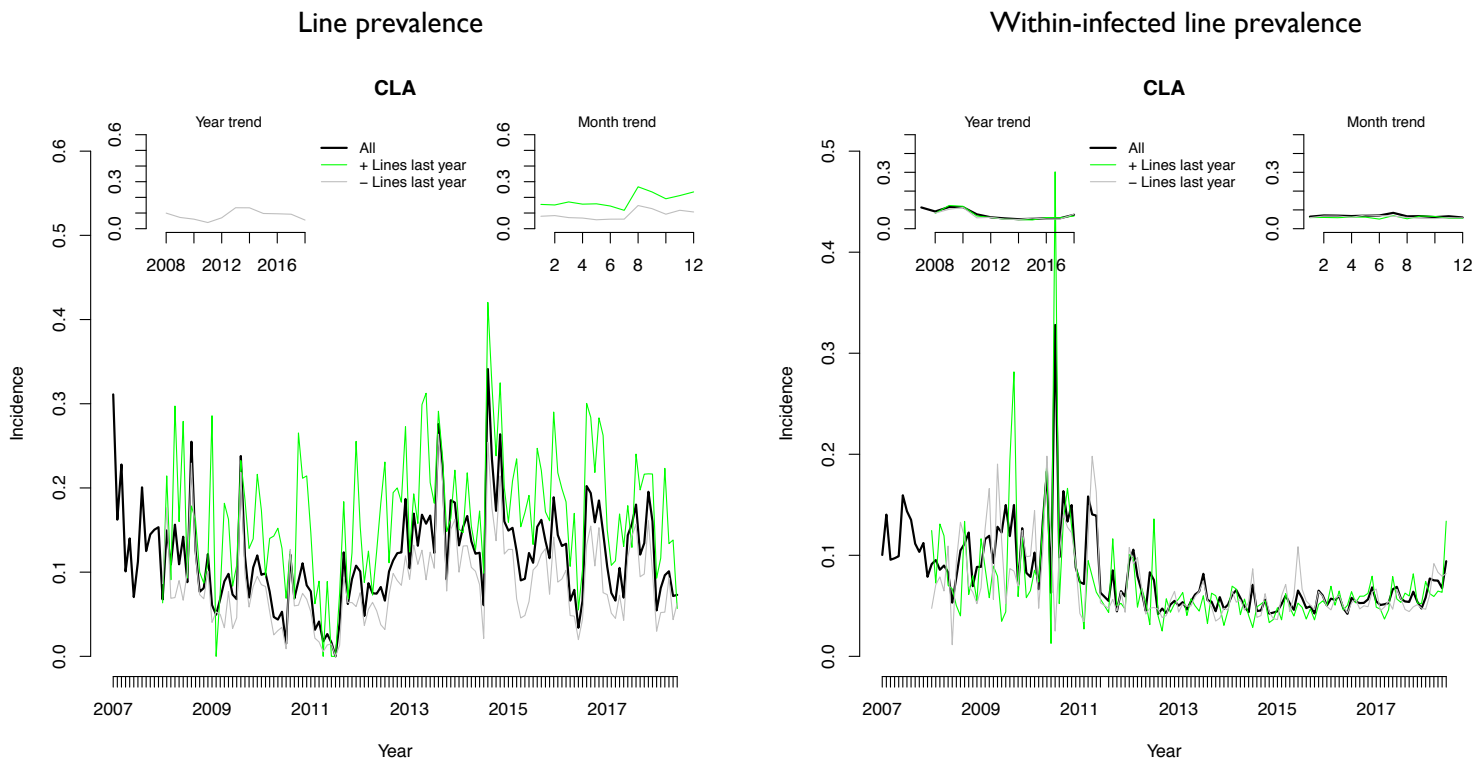


Figure 22: EASP line and within-infected-line CLA prevalence plot by time

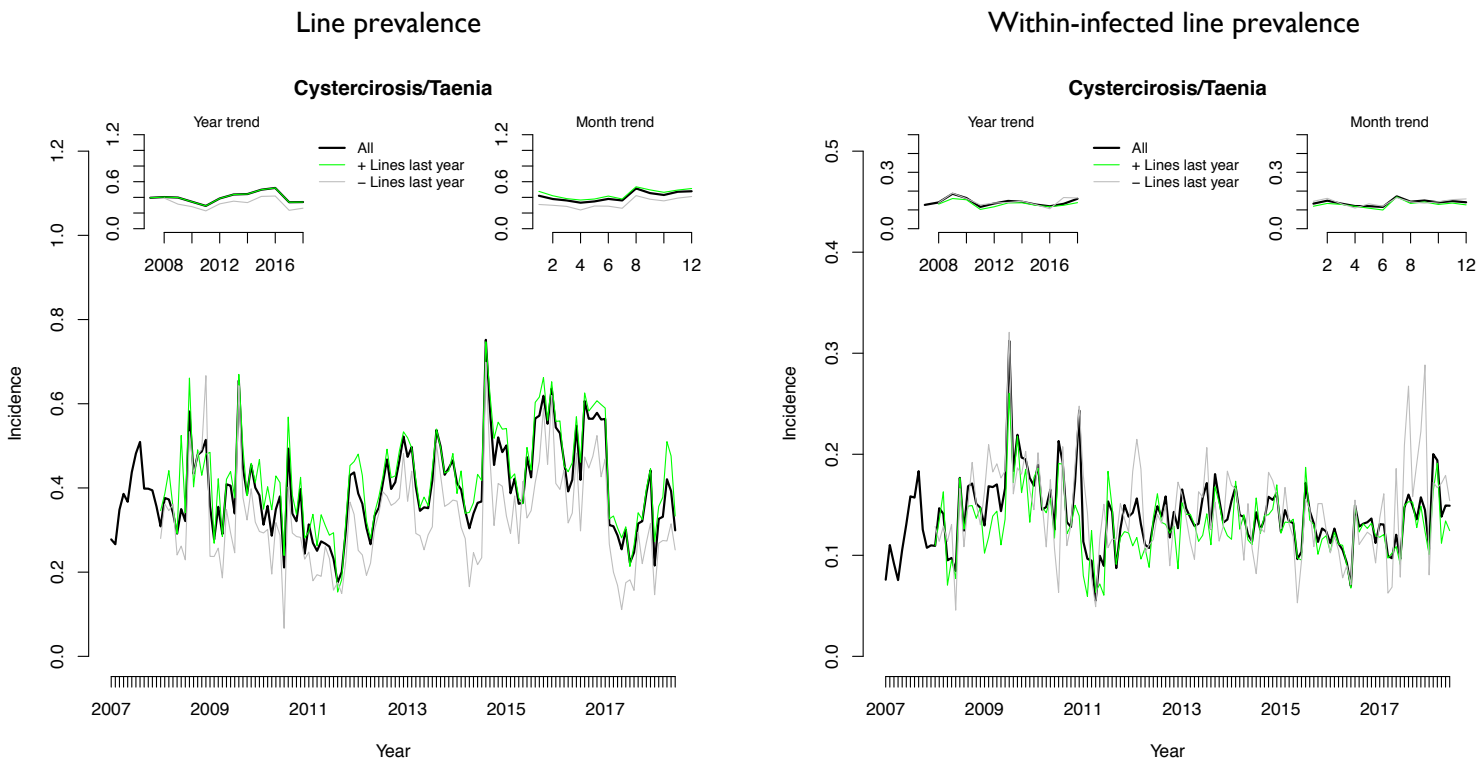


Figure 23: EASP line and within-infected-line cysticercosis/taenia prevalence plot by time

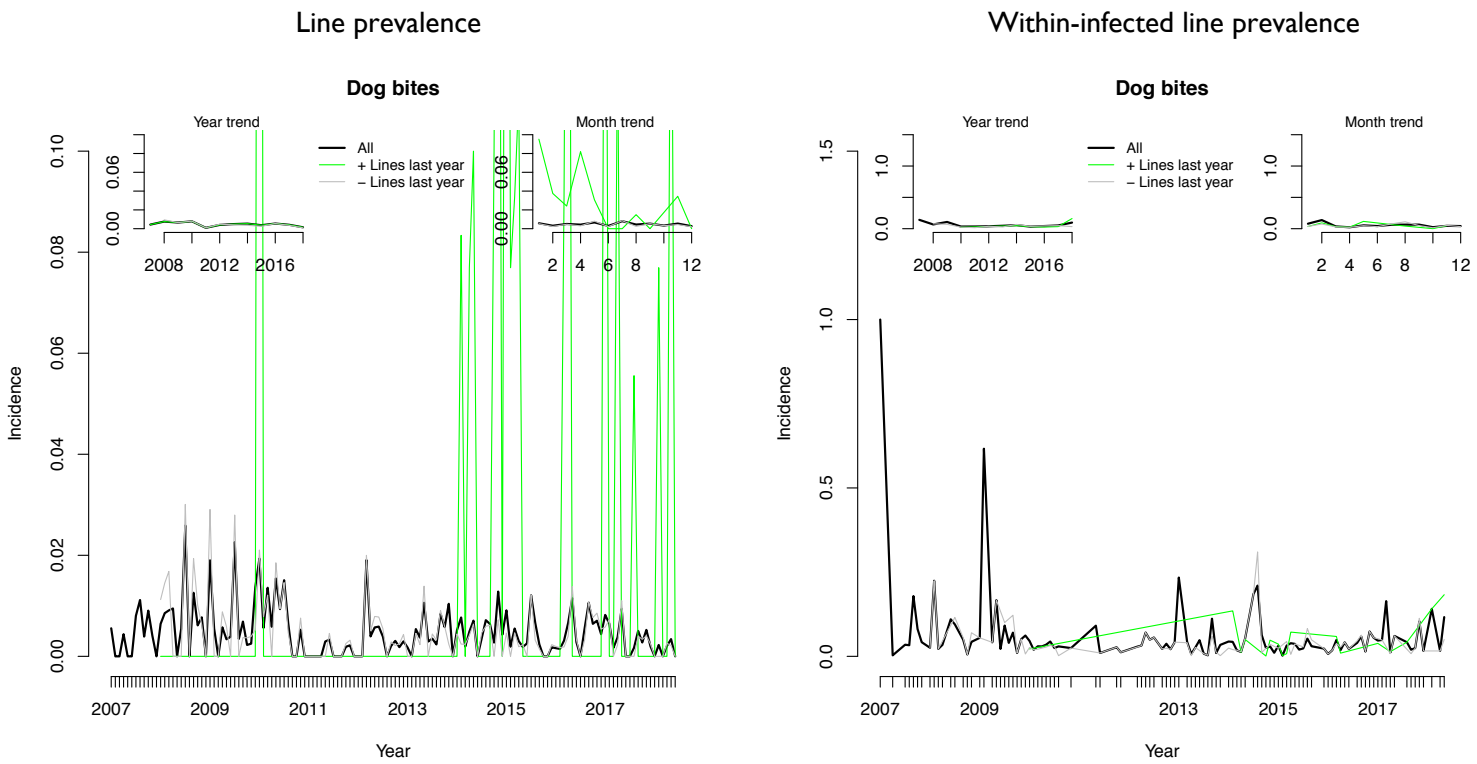


Figure 24: EASP line and within-infected-line dog bite prevalence plot by time

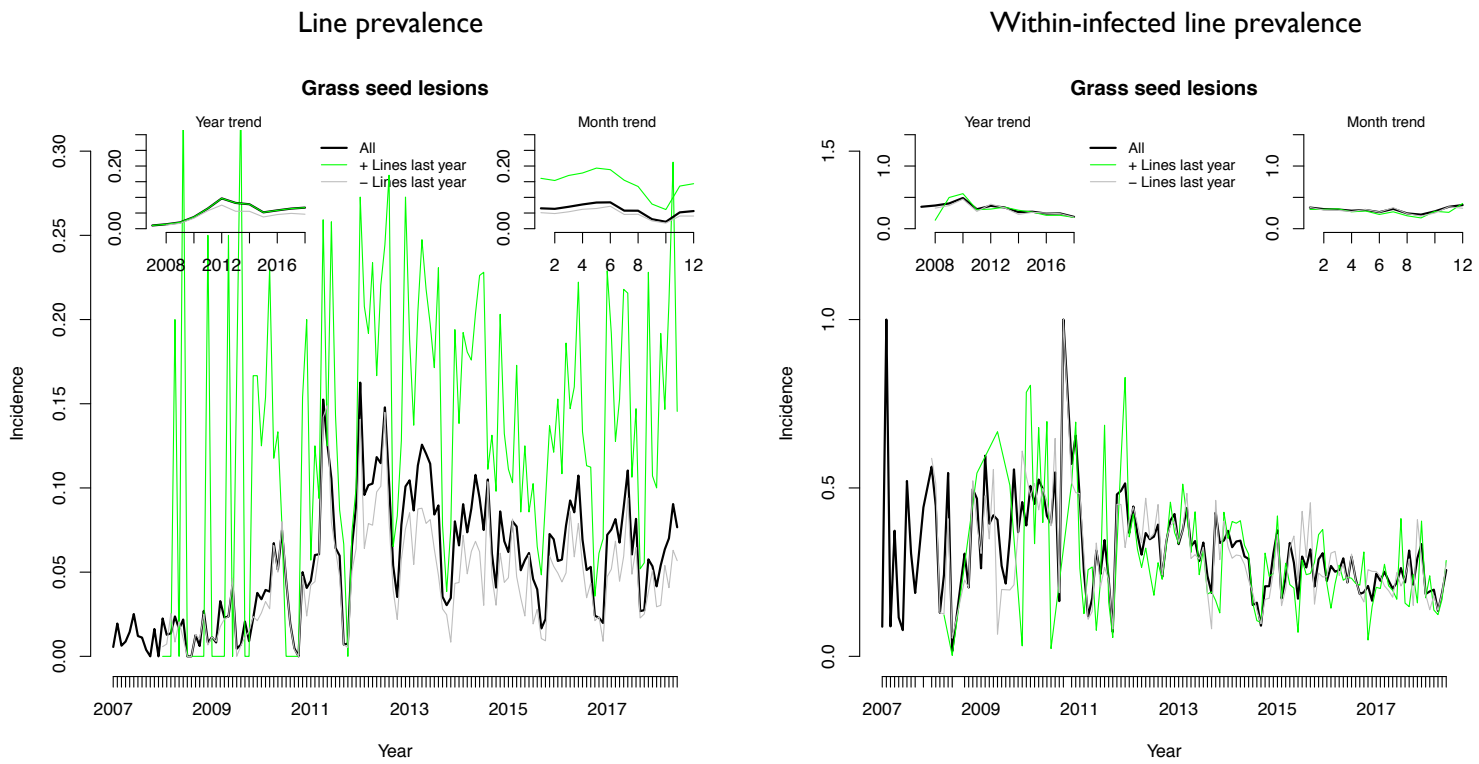


Figure 25: EASP line and within-infected-line grass seed lesion prevalence plot by time

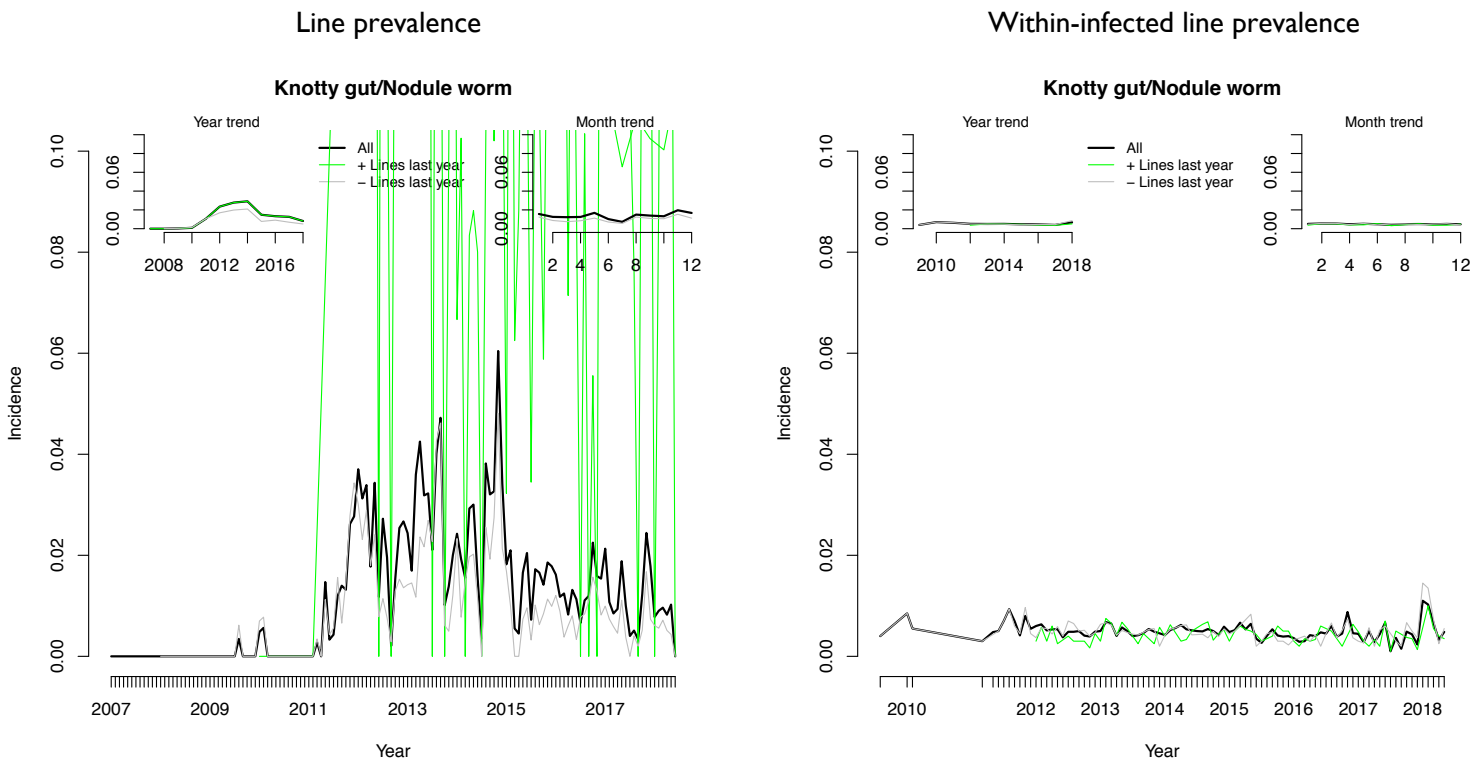


Figure 26: EASP line and within-infected-line knotty gut/nodule worm prevalence plot by time

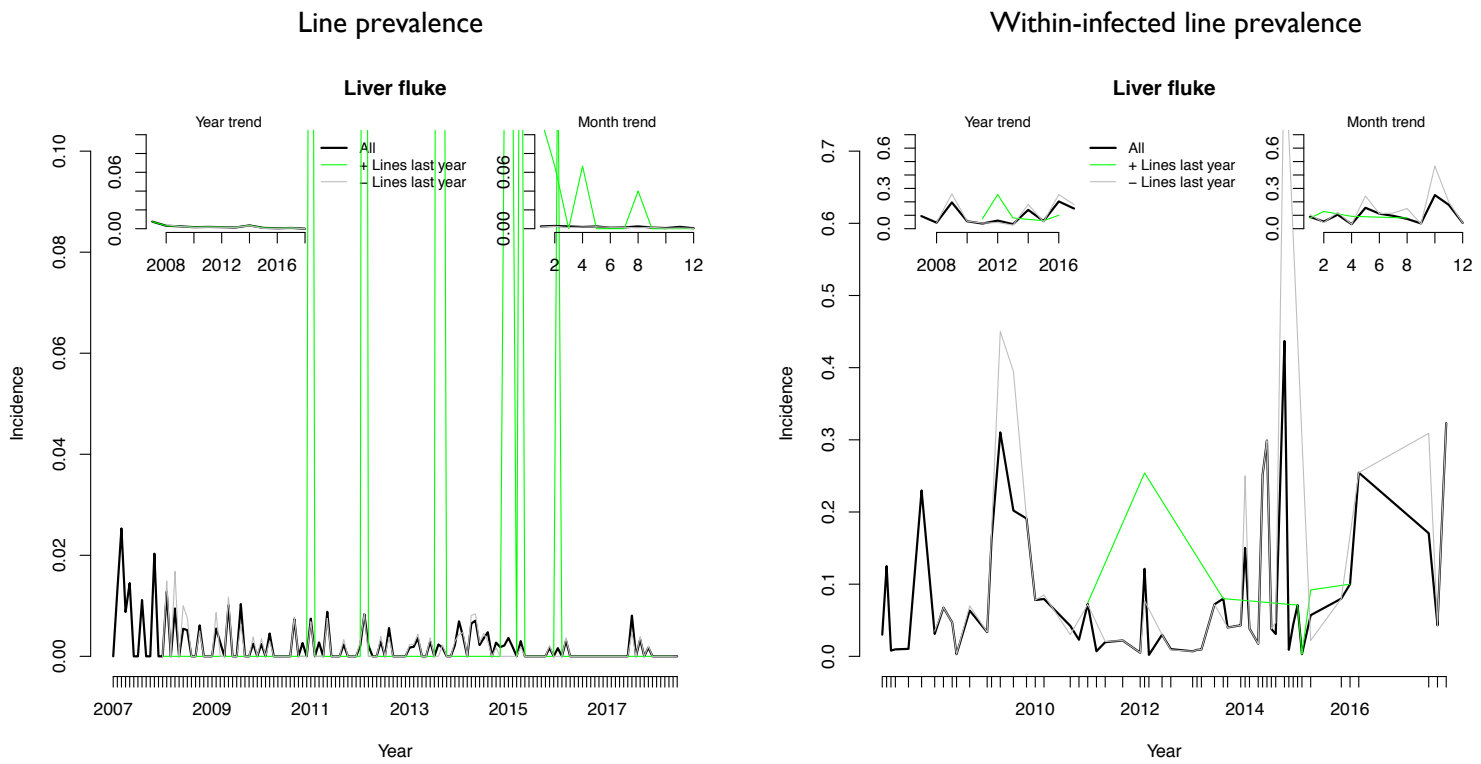


Figure 27: EASP line and within-infected-line liver fluke prevalence plot by time

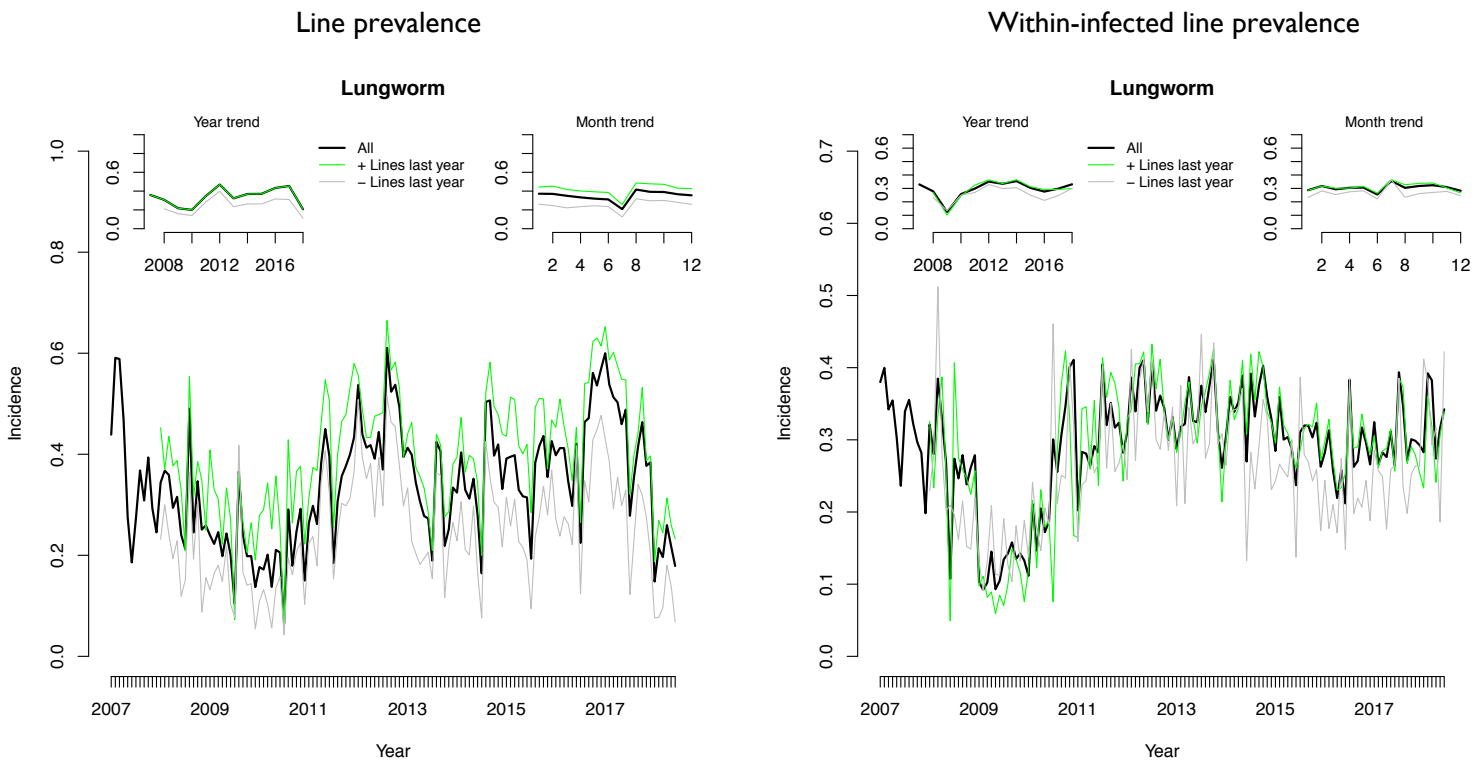


Figure 28: EASP line and within-infected-line lungworm prevalence plot by time

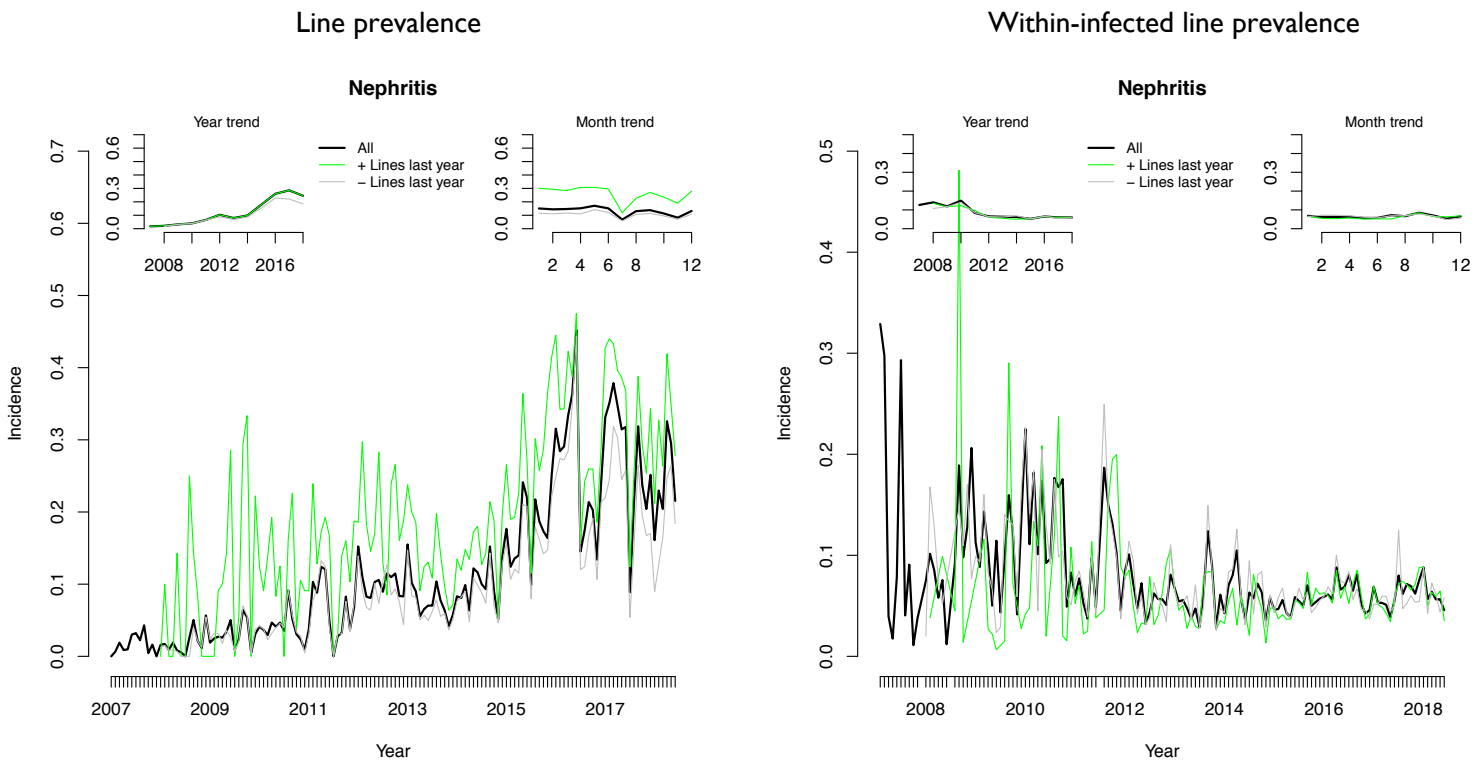


Figure 29: EASP line and within-infected-line nephritis prevalence plot by time

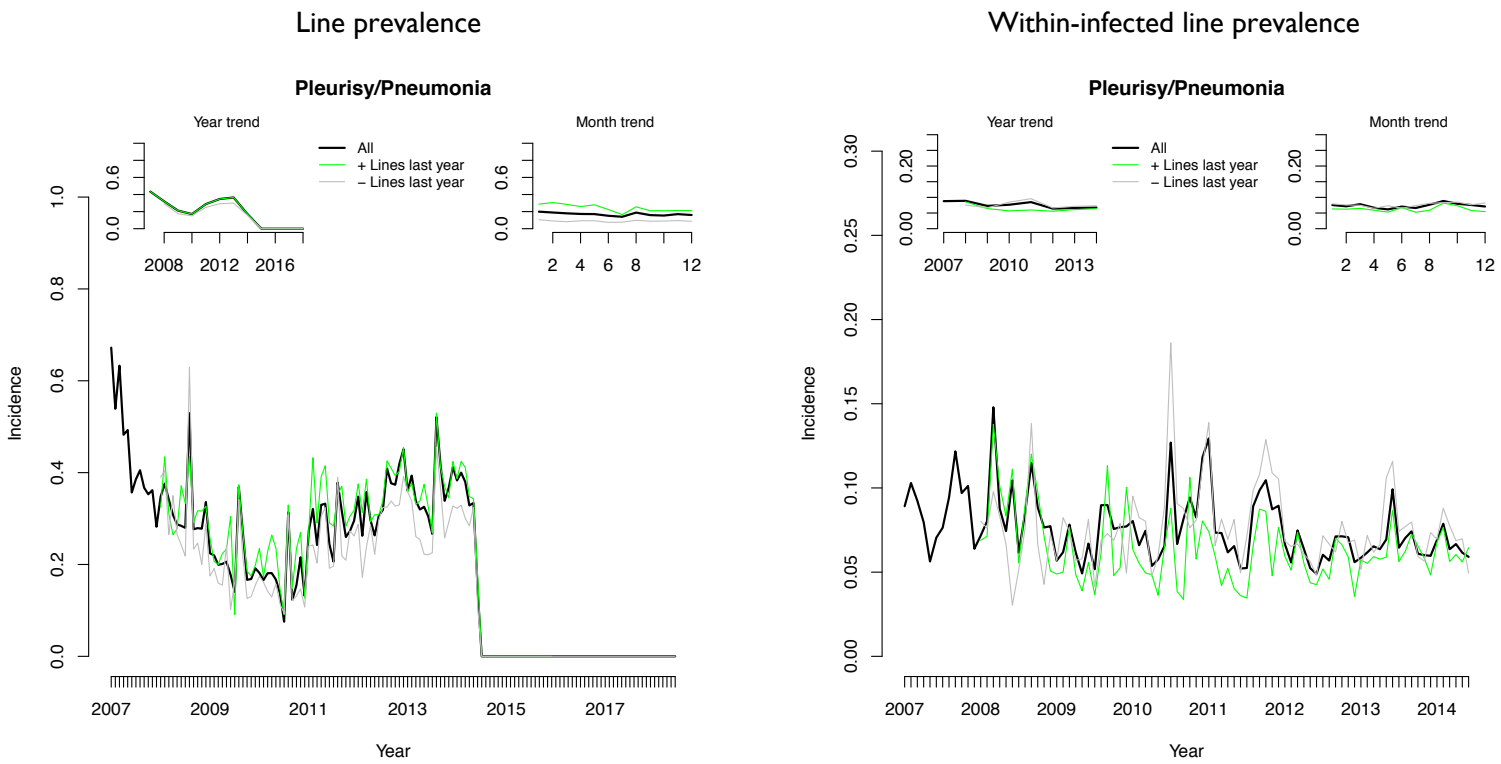


Figure 30: EASP line and within-infected-line pleurisy/pneumonia prevalence plot by time

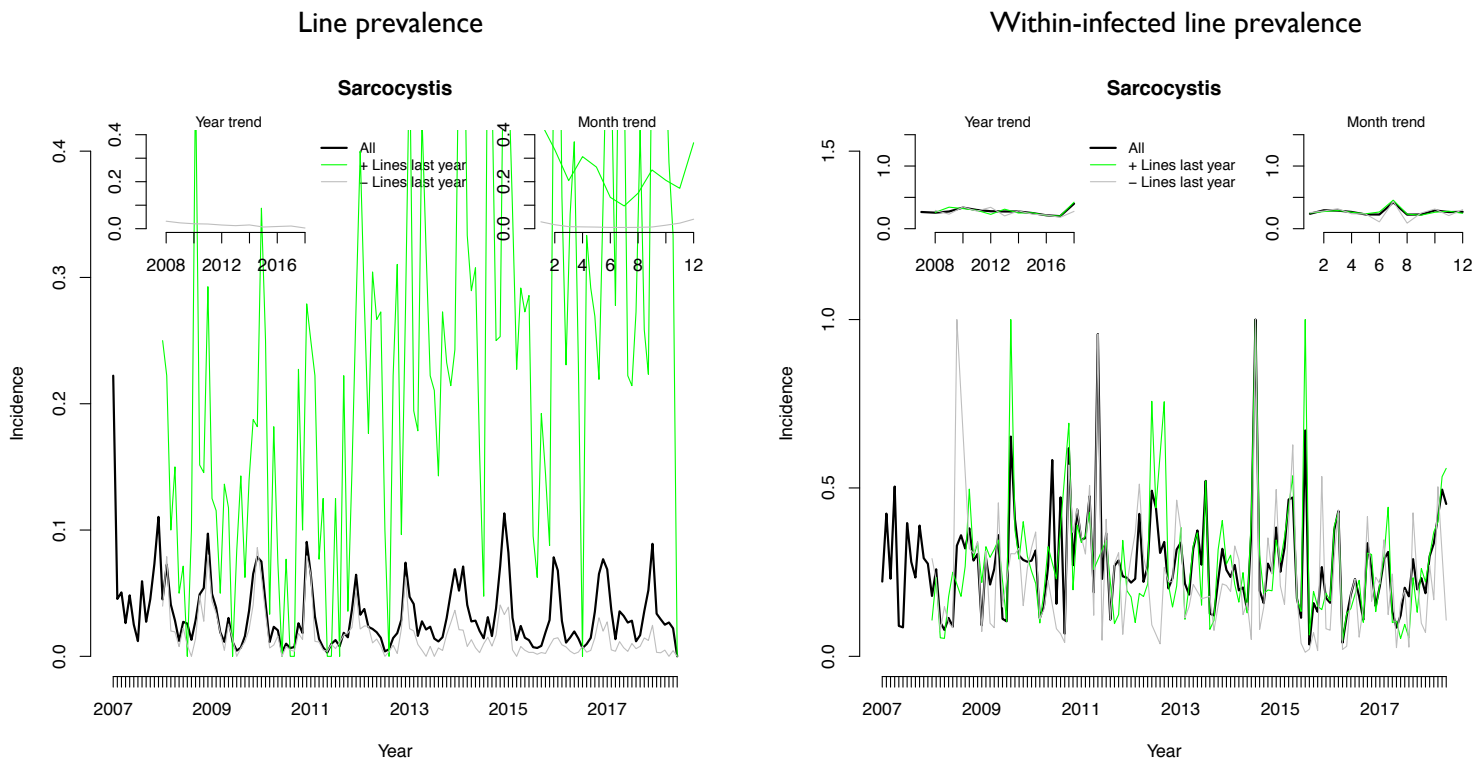


Figure 31: EASP line and within-infected-line sarcocystis prevalence plot by time

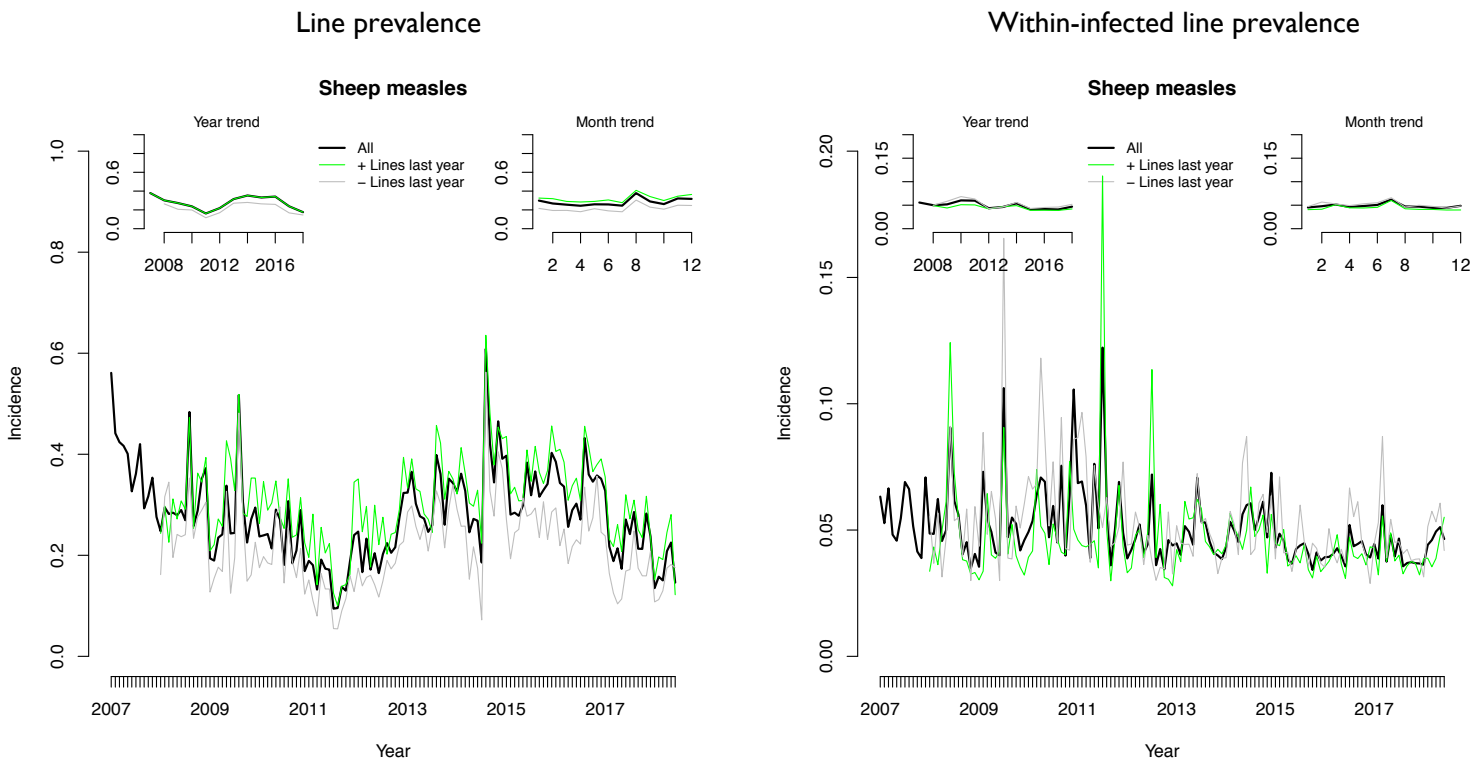


Figure 32: EASP line and within-infected-line sheep measles prevalence plot by time

5.1.3 EPACS

Only summary statistics were able to be calculated for EPACS data. These are presented as histograms in Figure 33. Unfortunately, little can be gleamed from the EPACS data as it has been aggregated across lines, multiple years and multiple regions.

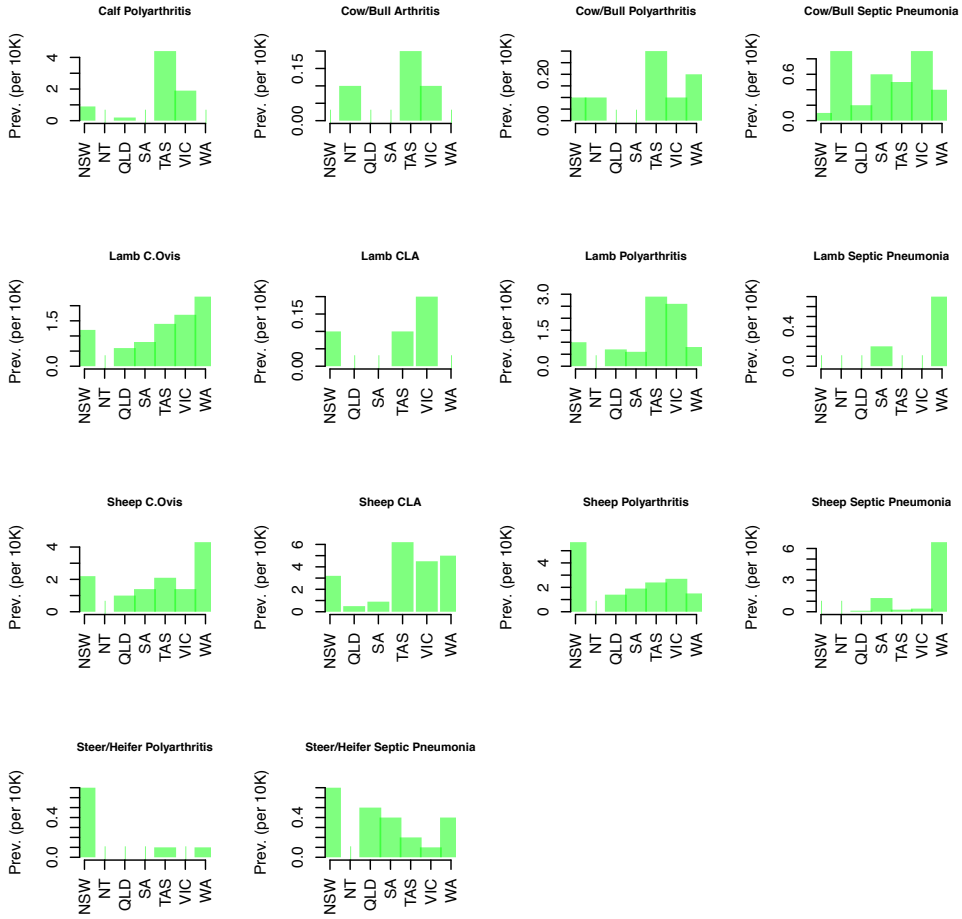


Figure 33: EPACS summary histogram of species, class and condition prevalence by state for the period (2007–17)

5.2 Regression analysis

Statistical analysis was only possible for NSHMP data and EASP data. Summary data that aggregated all lines, properties of origin, dates and abattoirs only was provided in the EPACS summary dataset. This prevented any meaningful analysis.

The predictor variable of interest was to see if previous year disease status (presuming this information was provided to the producer) resulted in a reduction in the infected line prevalence and/or the within-infected line prevalence. Comparing the prevalence in lines of sheep that had similar lines inspected (and presumably) reported in the previous year may provide insight into the effectiveness of the program. However, there are potential biases that may exist:

1. Producers who regularly submit lines of sheep to an abattoir may differ from producers that submit a line of sheep to a works for the first time;
2. Producers with infected lines in the preceding year may have more established disease than a producer with uninfected lines in the preceding year; and importantly,
3. Feedback on the disease status of preceding lines may not have provided to the producer. Feedback is necessary in order for producers to take action.

Regression analysis was undertaken for NSHMP data and EASP data. There were three levels of the previous line disease status: no lines submitted, preceding lines included positive animals (infected), and no diseased animals were detected in preceding lines (uninfected). The relative risk of the predicted within-line prevalence comparing previously infected to previously uninfected, previously infected to no previous lines and previously uninfected to no previous lines were calculated.

5.2.1 NSHMP Data

A series of multivariable regressions were used to estimate the impact of NSHMP feedback on the within-flock prevalence of infected lines for each disease. Only infected lines were included in analysis. Predictor variables included in the model included year, state and the status of similar lines of sheep submitted to the same abattoir in the preceding year. Results are provided in Table 6 and should be viewed in light of the potential biases discussed above.

South Australia has been the most active state in providing feedback on the disease status of lines of sheep examined[7]. Feedback to producers requires the producer to have a South Australian address and PIC. Examination of the relative risks for South Australia appears to demonstrate that the presence of infected lines in the preceding year—with subsequent feedback to the producer—resulted in a reduction in the prevalence of infection in the current line when compared to producers with previously uninfected lines. All disease relative risks for this comparison in South Australia were below 1.0 indicating that the prevalence of disease in the infected line is less than expected. This suggests that the information on disease status and prevalence from the previous year was used by the producer and resultant action taken to better control the disease.

It is difficult to interpret the relative risk comparing positive previous lines to no preceding lines or negative previous lines to no preceding lines for the reasons discussed above. Producers with no

[7] Mostly via EASP through specific abattoirs, but NHSMP reporting back to producers from non-EASP abattoirs may be more active than for other states

previous lines submitted to this abattoir may have submitted lines to other abattoirs in previous years, received feedback and taken (or not taken) corrective actions to better control disease. The relative risks for these comparisons fluctuate around 1.0.

Table 6: The relative risk of within-infected-line prevalence for lines of sheep from properties with positive (infected), negative (uninfected) and unknown (unsubmitted) lines of sheep in the preceding year.

		Relative risk		
State	Disease	Pos. vs no lines	Pos. vs Neg. lines	Neg. vs No lines
New South Wales	Arthritis	1.11	0.81	1.38
	CLA	1.33	1.47	0.91
	Liver fluke	0.57	0.69	0.83
	Pleurisy	1.16	1.03	1.13
	Pleuropneumonia	1.14	1.03	1.11
	Pneumonia	0.57	0.58	0.99
	Sarcocystis	1.42	58.89	0.02
	Sheep measles	1.18	1.12	1.06
Queensland	Arthritis	1.29	0.94	1.37
	CLA	0.81	0.94	0.86
	Liver fluke	0.79	0.52	1.52
	Pleurisy	1.14	1.11	1.03
	Pleuropneumonia	1.12	1.05	1.07
	Sarcocystis	0.63	90.42	0.01
	Sheep measles	1.22	1.01	1.21
South Australia	Arthritis	1.23	0.89	1.39
	CLA	0.98	0.98	1.00
	Liver fluke	0.88	0.41	2.17
	Pleurisy	1.15	0.95	1.22
	Pleuropneumonia	1.22	0.95	1.28
	Pneumonia	1.01	0.90	1.12
	Sarcocystis	0.79	0.62	1.28
	Sheep measles	1.11	0.90	1.24
Tasmania	Arthritis	0.96	1.10	0.87
	CLA	1.26	1.79	0.70
	Liver fluke	0.40	0.62	0.64
	Pleurisy	1.32	2.29	0.58
	Pleuropneumonia	1.25	2.18	0.57
	Pneumonia	0.72	0.74	0.97
	Sarcocystis	1.52	2.56	0.59
	Sheep measles	1.01	1.06	0.95

State	Disease	Relative risk Pos. vs no lines	Pos. vs Neg. lines	Neg. vs No lines
Victoria	Arthritis	1.22	0.97	1.25
	CLA	1.23	1.42	0.86
	Liver fluke	0.71	1.62	0.44
	Pleurisy	1.12	1.11	1.01
	Pleuropneumonia	1.09	0.99	1.1
	Pneumonia	0.63	0.66	0.95
	Sarcocystis	11.91	116.9	0.1
	Sheep measles	1.28	1.34	0.95
Western Australia	Arthritis	0.74	0.59	1.24
	CLA	0.95	0.5	1.89
	Liver fluke	0.26	0.25	1.05
	Pleurisy	0.88	0.68	1.3
	Pleuropneumonia	0.81	0.61	1.33
	Pneumonia	0.55	0.49	1.13
	Sarcocystis	2.4	1.35	1.78
	Sheep measles	0.49	0.43	1.15

5.2.2 EASP data

The difficulty of finding an appropriate comparator is also present in the more complete EASP data. The same regression-based approach as used above was applied to examine impact of provision of feedback on previous diseased lines of sheep on current infected line prevalence and within-infected line prevalence in infected mobs. Results are presented in Table 7 (line prevalence) and Table 8 (within-infected-line prevalence) below. Relative risks for diseases with few positive lines (such as cancer and fever/septicaemia) should be viewed with caution.

Table 7: EASP RR for infected line prevalence

Disease	RR Pos. vs none	RR Pos vs neg	RR neg. vs none
Arthritis	1.31	1.54	0.85
Bruising	1.38	1.30	1.07
Cancer	3456.12	3456.12	1.00
Cirrhosis	2.98	4.32	0.69
CLA	1.35	2.29	0.59
Cysticercosis / Taenia	1.03	1.40	0.74
Dog Bites	2.75	2.57	1.07
Fever/Septicaemia	32.10	32.10	1.00
Grass seed lesions	2.37	3.01	0.79
Hydatids	30.25	30.25	1.00
Jaundice	3.67	4.37	0.84
Knotty gut / Nodule worm	5.32	7.13	0.75
Liver fluke	3.66	4.38	0.84
Lungworm	1.31	2.14	0.61
Nephritis	0.00	0.00	1.00
Pleuropneumonia	1.79	1.64	1.09
Pleurisy	1.61	1.61	1.00

Disease	RR Pos. vs none	RR Pos vs neg	RR neg. vs none
Pneumonia	1.25	1.41	0.89
Rib fractures	1.74	1.74	1.00
Sarcocystis	4.61	4.76	0.97
Sheep measles	9.73	11.03	0.88
Vax. lesions	1.09	1.61	0.67

Table 8: EASP RR for within-flock prevalence

Disease	RR Pos. vs none	RR Pos vs neg	RR neg. vs none
Arthritis	1.31	1.54	0.85
Bruising	1.38	1.30	1.07
Cancer	3456.12	3456.12	1.00
Cirrhosis	2.98	4.32	0.69
CLA	1.35	2.29	0.59
Cysticercosis / Taenia	1.03	1.40	0.74
Dog bites	2.75	2.57	1.07
Fever/Septicaemia	32.10	32.10	1.00
Grass seed lesions	2.37	3.01	0.79
Hydatids	30.25	30.25	1.00
Jaundice	3.67	4.37	0.84
Knotty gut / Nodule worm	5.32	7.13	0.75
Liver fluke	3.66	4.38	0.84
Lungworm	1.31	2.14	0.61
Nephritis	0.00	0.00	1.00
Pleuropneumonia	1.79	1.64	1.09
Pleurisy	1.61	1.61	1.00
Pneumonia	1.25	1.41	0.89
Rib fractures	1.74	1.74	1.00
Sarcocystis	4.61	4.76	0.97
Sheep measles	9.73	11.03	0.88
Vax. lesions	1.09	1.61	0.67

It is interesting to note that there was a consistent trend for relative risks to be greater than 1.0 in lines of sheep that were from properties with a preceding history of disease when compared to the previously-free and unknown previous status categories. This appears to contrast the trend for this category in the South Australian NSHMP data where the relative risks were consistently below 1.0. The South Australian NSHMP data will include lines of South Australian sheep that were processed in Victoria whereas these lines are excluded from analysis in the EASP data set.

Examination of the infected line and within-infected line trends for EASP data (Figure 19 to Figure 32) reveal little change in long-term trends for most diseases. Exceptions may be claimed for CLA, cirrhosis and pleuro-pneumonia (stable infected line prevalence but reduced within-infected-line prevalence) and grass-seed lesions (reduced infected line prevalence and reduced within-infected-line prevalence). However, bruising and arthritis have a trend for increasing line prevalence whilst within-infected-line prevalence appears stable and nephritis has an increasing infected line prevalence combined with a falling within-infected-line prevalence.

5.3 Benchmarking

Endemic disease reporting has intrinsic difficulties. By their nature they are common—even ubiquitous for some diseases—making notifying producers of their presence uninteresting at best and uninformative at worst. It is difficult for a producer to understand if they have an excess of many of these ubiquitous diseases without some form of valid comparison. This is the benchmarking challenge.

Finding an appropriate comparator in order to assess the impact of producer feedback of findings at meat inspection is difficult. The automated benchmarking challenge is to develop a system that relies upon a machine (an algorithm) telling a human (a producer or processor) about potential problems in their animals with confidence. There are two types of errors such a system can make: failure to inform a producer that has a problem that the system has detected the problem (a false negative); and informing a producer that the system has detected a problem when they don't (a false positive). It is unrealistic to expect a system to make no errors, so an important aspect of operation and management is how to present findings to the user.

A false negative report (i.e. failing to notify of a problem) is less damaging for a newly developed system. This is because no alternative notification system exists (so the producer remains ignorant of their problem) whereas a false positive report (erroneously informing a producer that they have a problem) is potentially more damaging. Once a system matures, damage from false negative reports will increase as individuals learn to trust and rely upon the feedback provided. In the early stages, false positive alerts are much more damaging. These can cause affected producers/processors to lose faith in the system.

A cautionary approach is needed in algorithm development (i.e. identifying 'problem' lines and separating them from 'clean' lines) and in the report wording of the findings. Both aspects are important. A recommended approach is to present results without the use of (arbitrary) cutpoints to delineate 'problem' from 'clean' lines, but instead to focus on contextualising the results. This can be done by presenting comparators against line results accompanied by words that do not declare a problem but instead encourage the producer to consider their result and perhaps investigate further if they compare poorly to themselves in a previous year or to their peers. A set of hypothetical examples are provided to demonstrate this potential problem.

<u>Reporting example 1</u>
A part-time producer chooses to sell some ewes. His business model includes opportunistic buying and selling of livestock. He also has no real control programs for endemic diseases. He has 70% prevalence of CLA in his line of cull adult ewes. The automated system informs him as follows:

> Option 1: Tells him he has 70% of the ewes with CLA and that he has a serious problem and is losing money. He is encouraged to follow links to (basic) information on CLA control and to contact her vet to help him manage the problem
>
> Option 2: List the 70% prevalence of CLA in this line of ewes and map this against similar lines of sheep sent in that year and to the average prevalence in all submitted lines of sheep by this same producer last year. No statements about disease severity are made but links to CLA control are provided.

Both options can work in this case—note that this is a true positive detection. Under Option 1, over a number of years the producer may respond to being continually told he has a problem with CLA by becoming motivated to take action or he may decide CLA is something everyone has and there is not much you can do about it. Under Option 2, the contextualised performance of this line and last years' lines against peers shows this producer to be particularly bad. This may motivate him to take action.

Reporting example 2

A highly-competent producer decides to cull some old ewes as a result of drought. She goes through her ewe flock and pulls the bottom 10% out and sends them to the works. Of this line, 70% of the cull ewes have CLA lesions, however, the prevalence in the remainder of her flock is 5% as a result of her effective vaccination and control program implemented over the past five years. The automated reporting system could inform her as follows:

> Option 1: Inform her that 70% of the cull ewes had CLA and that this indicates that she has a serious problem[8] with CLA in her flock and is losing money. She is encouraged to follow links to information on CLA control and to contact her vet.
>
> Option 2: List the 70% prevalence of CLA in this line of cull ewes and map this against similar lines of sheep sent in that year and to the average prevalence in all submitted lines of sheep by this producer last year. No statements about disease severity are made but links to CLA control are provided.

In this case, the CLA notification is an overstatement of the problem (bordering on a false positive notification as the disease is under control in the rest of the flock). As such Option 1 presents a risk of insulting the producer. She may now place no value on information provided by the system and ignore future reports. Option 2 makes no judgement on her control ability. By presenting last years' (within-flock) comparator alongside the population averages this could help the producer to see how effective her CLA control program is performing.

The initial challenge is to build a system that makes no judgement calls on individuals but presents enough information to the user that they make their own assessment of their performance. The ongoing challenge then becomes on refining the system to reduce the false negative rate.

The following applies to the NSHMP data only. This dataset was chosen because it contained data from many states. The principles are universally applicable and can easily be adapted for other datasets (e.g. EASP). Exploratory analysis has demonstrated clear state, regional, abattoir (inspector?), stock class, year (and seasonal) variation in disease rates as identified by inspection. This has major implications for benchmarking as all benchmark comparators will need to be calculated at each of these level to provide a responsible comparison.

5.3.1 Algorithm pseudocode

A benchmark comparator system algorithm was derived. The pseudocode describing the algorithm is as follows:

1. The producer PIC code is identified.
2. The list of diseases present within the consignment are identified.
    a. Identified diseases are listed.
    b. If 100[9] or more animals of the single and same class are present within the lot, the within-lot prevalence for each disease is calculated.
3. Lots from the same producer and for the same class of animal for the preceding year (12-month period) are identified.

[8] This requires an arbitrary prevalence cut-point for each disease to identify lines with 'excess' disease.

[9] A pragmatic lot size must be selected that provides suitable accuracy in the prevalence but does not exclude too many lines of animals. This number is likely to be different for sheep and cattle.

    a. If data exists and there 100 or more animals in total. The aggregate within-flock prevalence for each disease is calculated.
    b. If there is not data from the preceding year or there are fewer than 100 animals in total, then no previous-year comparator statistic is calculated.
4. For lines of at least 100 processed the shape parameters that define the beta distribution that describes the within-infected-lot prevalence for each disease in the same class of animal, submitted to the same abattoir and originating from properties within the same LGA region and in the same year is obtained from reference to a look-up table.
5. If the lot contains 100 or more animals of the same class a plot is generated that:
    a. Maps the baseline population for the disease. Using the beta distribution that defines the baseline infected line population (see above) using either a colour gradients to map the centre and extremities of the distribution or marking 25%, 50% and 75% prevalence points for the population of infected lines.
    b. The average prevalence of infected lines of the same animal class originating from the same LGA and presented to the same abattoir in the year of submission of the current line is marked onto the plot using an arrow.
    c. The prevalence of the current line is plotted as a point overlain onto the population distribution in a unique colour/point combination that is described in the legend.
    d. If a valid prevalence was calculated for the same class of animal for the preceding year was identified, this is plotted as a point over the population distribution as a unique colour/point combination that is described in the legend.
    e. The proportion of infected lines for the year is printed on the plot with associated text.
6. If the plot does not contain 100 or more animals of the same class, the disease/conditions identified in the lot are presented as a text listed (no plot)

5.3.2 Example benchmark plots

Examples of benchmark plots generated using the algorithm described above on NSHMP data are presented in Figure 34 to Figure 38. It should be noted that these plots are wholly machine generated; no individual tweaking or commentary was included. This is how a working industry-level benchmarking system has to be.

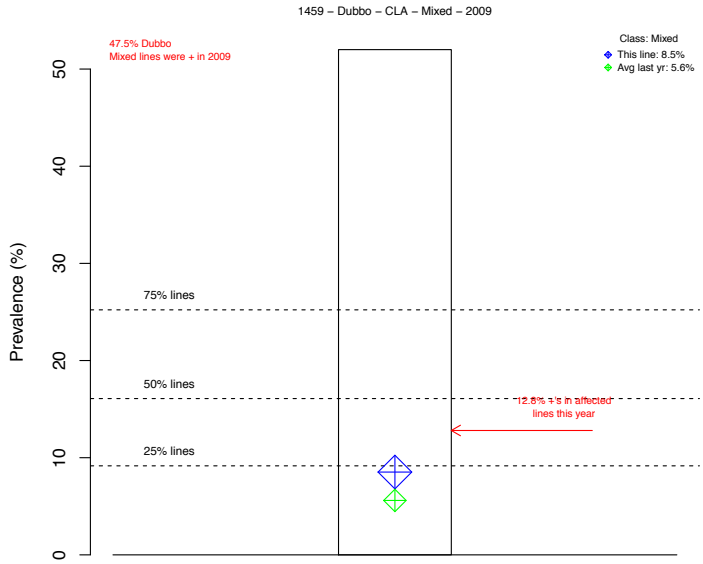


Figure 34: Example benchmark plot

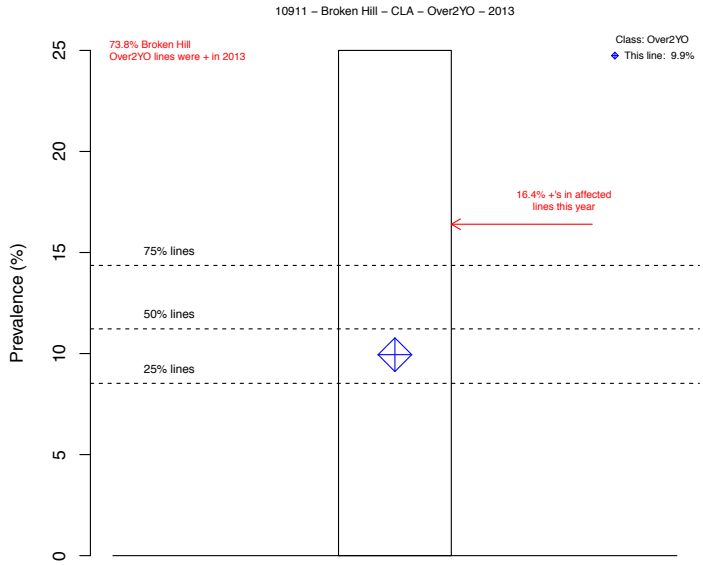


Figure 35: Example benchmark plot

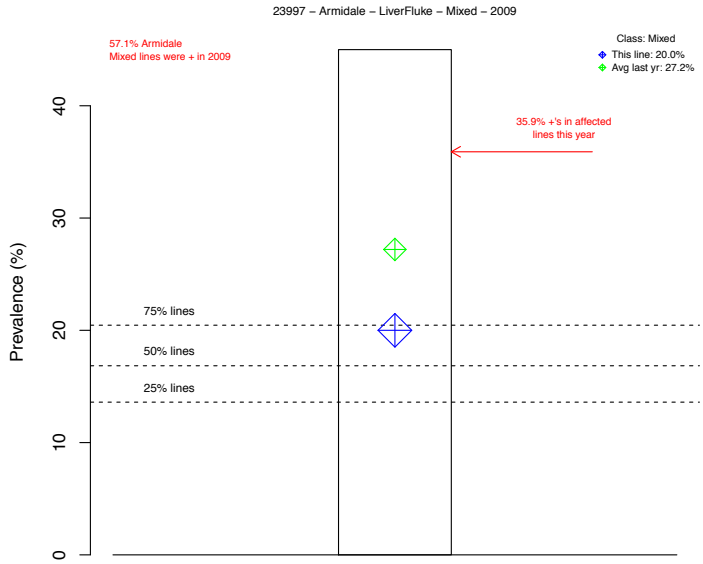


Figure 36: Example benchmark plot

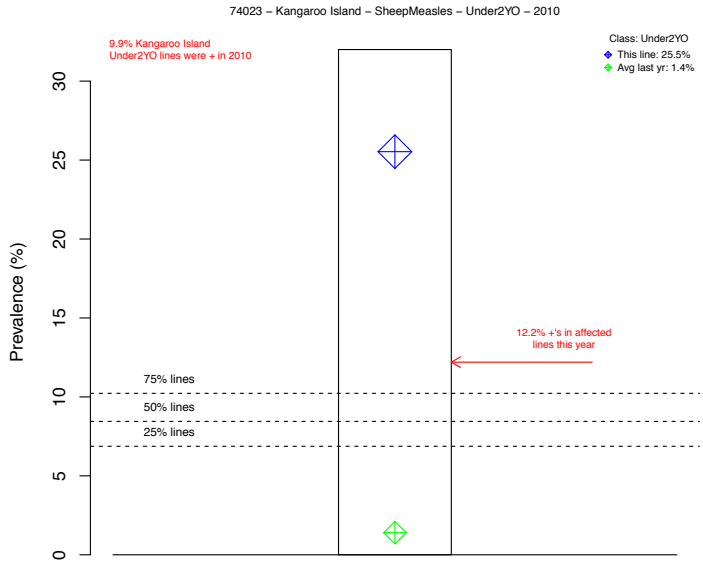


Figure 37: Example benchmark plot

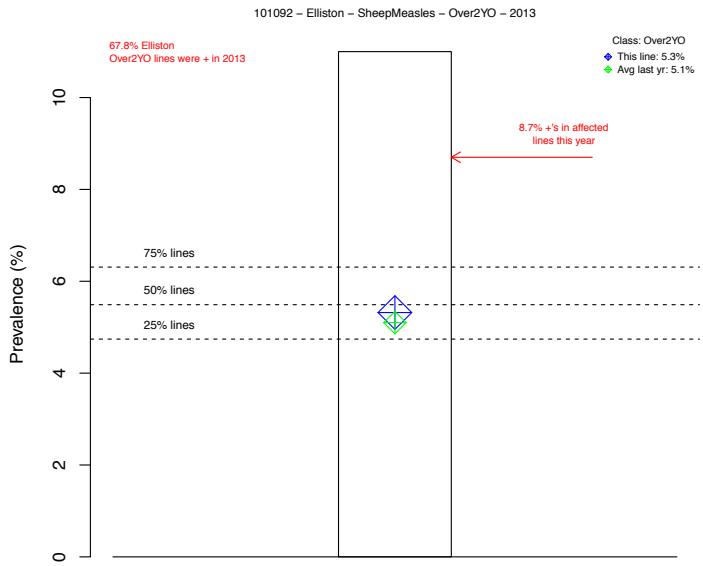


Figure 38: Example benchmark plot

6. Discussion

Analysis of abattoir data has revealed limited evidence of a reduction in disease over time. This is both for the level of infected lines, and the proportion of affected animals within infected lines. Whilst long-term stability in both these measures can be expected for endemic diseases this does not mean that effective reporting back to producers of these conditions is without merit. It is pertinent to note that there is limited evidence of an increase in these diseases over time as well—it may be possible that notifications have helped producers to better contain disease and thereby limit spread within their flocks.

Producers need to know how to best control endemic diseases such that the extra benefit the get from improved control outweighs the expense of any extra control. This requires them to both understand how to control each disease and to measure the disease in their herd or flock. Understanding if there is an excess of disease is essentially a continuous benchmarking exercise.

There is limited evidence in NSHMP and EASP data that feedback resulted in a subsequent reduction in disease in future lines. However, it must be noted that this absence of strong evidence does not lead to the conclusion that feedback has been ineffective. This is because information on who was and who wasn't provided feedback on their lines of animals was not recorded. The data was analysed in the knowledge that only some producers received consistent feedback when disease was identified in submitted lines. The proportion of producers receiving feedback was not known. The comparator population became those lines from producers who did not submit lines in the previous year or who submitted only disease-free lines in the previous year.

The comparison between (potentially) reported lines and previously unreported lines is therefore problematic and the power of this analysis depends on the proportion of 'reported' lines that actually received a report. If low, then there is low power in the analytical approach used. The absence of reporting information meant there was no alternative but to compare this way.

The potential for bias in the three comparison groups may also have been significant. Producers with previous lines that were not infected may not have disease and any disease present in the current line may be at low prevalence as disease is yet to firmly establish. Comparing this group to producers with lines that are consistently infected may also introduce a bias against the informed group. Similarly, producers who did not send a similar line to the abattoir in the previous year may be intrinsically different to producers who consistently send similar lines to the same works. These may represent new herds or flocks or producers from other regions that have decided to send their stock to this new abattoir for the first time. Herds and flocks from different geographical areas may have different average levels of disease. These biases are unpredictable and the direction of their biases unknown. What this lack of a clearly defined and effective comparator tells us is the need for integration between databases.

More effective linkage between the NSHMP or EASP data and the LDL such that reporting can also be recorded will greatly enhance and enable future analysis. This integration is happening for NSHMP through LDL. Systems will need to be developed to record users who access the system and seek information on disease in submitted lines as well as accessing information on the management of the disease.

The major challenge in reporting endemic disease levels back to producers is that for most of them it is not economical (or even possible) to eradicate these diseases from their herds and flocks. The implications are that the most economical strategy that a producer can have is to control each disease down to a level where any further expense on control cannot be returned and that simply reporting to producers that they have an endemic condition in their lines of animals has little relevance[10].

Another consideration is that for most producers the abattoir is the logical offload point for cull-for-age animals. These animals have a (long) lifetime history of exposure to endemic diseases and the prevalence of disease in older animals tends to be higher than for younger animals. Even knowing that lines of older animals carry a significant disease burden, the most rational option for most producers is still to send them for slaughter and accept the trim and downgrades as a cost of doing business.

Solely reporting the endemic disease levels in lines of sheep to producers is unlikely to motivate them towards better control—the producer expects some disease. It is important to note that 'less' disease may not be 'more' for the producer as control beyond a certain point is inevitably uneconomical for most endemic diseases. This means the level of endemic disease in the line of animals must be contextualised in order to motivate those with an excess of disease. Contextualised reporting also provides assurances to producers who have good control over endemic diseases—but have not eradicated them—by showing superior performance. Benchmarking can provide this contextualised information by ranking a producer against their peers and against themselves from a previous time period. A producer may well expect to see disease X but may be motivated to improve control if it is clear that they have significantly more disease than their peers or that disease levels in their herd/flock

[10] Besides explaining why carcase(s) was/were trimmed

have increased over previous years. Without this contextual information, continuous reporting of only the disease levels in the line provided by the producer will rapidly lose relevance and impact for the producers.

Endemic diseases are just that—they are common, produce impact on the farm and at the abattoir, and require a pragmatic approach to control. Farmers need to identify the optimal level of control for disease in their flock. To do this requires them to understand the cost of various controls and the level of reduction of disease that they can expect from implementing these controls efficiently. This is an economic question. It is often difficult to clearly identify the 'sweet spot' for control—should I have also undertaken control B alongside control A? Are all my existing controls working as efficiently as possible? How much can I expect disease to increase if I stop using control A? These questions can be very difficult to answer. They are even harder to answer without measuring disease impact—the abattoir is an important site for measuring disease impact.

A system that can standardise the measurement of endemic disease impact on trim and condemnations of lines of animals at abattoirs is an essential part of the information system for producers. Another important component is inclusion of capability for comparison against peers—do I have more or less condemnations than other producers in this class of animal and from the same region as me and with the same production system I employ? Is my suite of controls working? Have my recent changes to my controls made a difference?

Disease levels in individual lines need to be linked to historical disease levels for that producer and to the range of disease levels seen in lines of sheep sent by the producer's peers to maintain impact. This would help a producer to better contextualise their report. The LDL provides this essential linkage. Finally, tailoring of control information would also maintain report variety and relevance to producers. This is beyond the scope of this project but a system that can identify and rate the quality of the control activities by the producer may allow areas of weakness to be identified and focused information on these areas provided. We lead an MLA-funded project that is aiming to deliver this very feature—described in more detail below. This project is part of suite of developments to improve information flow in the supply chain.

The project underpins an information feedback loop to producers that they can use to improve quality of sheep they supply to the market and to improve on-farm performance. The other components of the information system that producers need include a system for assessing impact of endemic diseases on their herd/flock performance. Herd Health leads an MLA-funded project to develop an endemic disease information system for sheep farmers. The project is developing a web-based app to help individual producers to benchmark financial impact of endemic disease in their flock and compare the quality of their individual disease control programs. This project is currently pilot testing an endemic disease app that has potential to link to industry data through a single *myMLA* log-in. Data that can contribute to the economic assessment of endemic disease in flocks include NLIS and LDL data streams.

We have recognised that data is the most limiting component of these systems. The less manual data entry that is required by a producer to use a system the more likely they are to participate. The automated capture of abattoir disease and condemnation data would significantly improve appeal to busy producers. This project requests and processes the specific disease control activities and costs used by the producer. This supports benchmarking of control spend and lets producers assess the

effectiveness of their controls (through the performance of lines of sheep sent for slaughter). The ultimate goal is to direct farmers to the most economical control point for their flock. It must be emphasised again that for most endemic diseases and for most flocks that eradication of the disease is not the most economical choice. Whilst industry reviews have estimated and reported the cost of individual endemic diseases to processors, reducing the level of some endemic diseases in individual flocks may not be cost effective for many producers.

We need this data to exist if we are to compare change in producers who received feedback on the condemnations in their lines of sheep by the abattoir to similar producers who did not. Careful focus will be required to determine if there are characteristics of farms that received abattoir feedback that differ from farms that did not receive feedback (i.e. is there evidence of a reporting bias?) Adjusting for any difference in reporting bias will be important (if possible) to ensure that appropriate inference is drawn from any change in behaviour as a result of feedback and to allow meaningful extrapolation of results to the whole of industry. Examining raw data for seasonal, year, production system and region trends in level of condemnation in lines of sheep for each endemic disease will be undertaken. This, combined with above, will be used to adjust change in endemic disease level for: season, year, production system and region[11]. Once these adjustments are included, one of the remaining causes for a reduction in disease may be the information feedback provided from abattoirs, may be more clearly seen.

7. Implications & Recommendations

A wide range of organisations and systems collect data on endemic diseases and conditions identified at meat inspection. In general, these are part of active surveillance systems for monitoring the amount and distribution of disease within the population. Currently, there are some isolated producer feedback reporting systems (e.g. EASP) but there is no national program for providing feedback on diseases identified at meat inspection to producers and processors. Such a system exists in the LDL which facilitates links between producer and processor PICs, NVDs and even individual animals (via NLIS for cattle) providing easier and more complete access to animal health and performance data.
However, examination of disease prevalence trends suggests simply reporting the presence of or count of cases of endemic disease has not resulted in a reduction in disease. It must be noted that the likely presence of intrinsic biases in the observational data may have confounded any analysis looking for a systematic reduction in cases as a result of feedback. However, other (concurrent) work in this space suggests that simply reporting counts of cases of endemic disease back to producers is most likely not motivating—these diseases are to be expected. Any report that does not motivate the recipient is unlikely to be sustainable.

The most pressing (and perpetual) questions a producer has on endemic disease in their herd or flock are: do I have an excess of disease? And how effective have my controls been? These questions cannot be directly answered through providing isolated counts of cases within lines of animals sent for slaughter. They need to be placed into context. Contextualising the information is the challenge of reporting endemic diseases.

Contextualising the numbers is in practical terms the benchmarking of performance. Benchmarking is the comparison of individual performance to the performance of a comparable group of results. Here

[11] Similar to seasonal adjustments used for monitoring unemployment rate or influenza incidence

lies the challenge—what is the comparable group? The results of this (and other) analysis strongly show that national benchmark rates (line prevalence and within-infected-line prevalence) of disease do not exist. This means taking the combined national data plus the considered expert opinion to derive desirable and maximum prevalence of each disease cannot be applied. An example will best show why this should not occur. Liver fluke has distinct spatial distributions. The fluke requires the presence of the host snails and they in turn depend on water. The snail and the fluke are sensitive to temperature with cold temperatures significantly slowing snail and fluke intermediary stage activity, growth and development. Therefore the 'benchmark' fluke prevalence depends upon where the property is located and the time of year. A national average 'benchmark' has no meaning for any producer—including those in fluke-affected regions and those in fluke-free regions.

Benchmarks must be developed on a regional basis. The best regional dividers are property of origin LGA and abattoir. Traditional benchmarking uses a combination of the population performance with domain expert knowledge to identifying cutpoints or critical levels where action is recommended. We believe that the nature of abattoir meat inspection observational data does not support the derivation of cutpoints for use with benchmarks. Continuing the fluke example above, season has much to do with the fluke infection burden such that wet and warm springs can result in significant challenge whereas cold, dry winters followed by dry springs and hot summers may reduce challenge.

The other challenge for benchmark cutpoints is they assume all diagnostics perform equally well and are applied uniformly. Evidence from this and other meat inspector analyses suggests that this is not the case. Until it can be confirmed that all meat inspectors perform to the same diagnostic[12] and classification standard then it is recommended that benchmarks are developed at an abattoir level. Both the lack of universality in disease cutpoints and the potential for different diagnostic sensitivities at abattoir level mean a one-size-fits-all cut-point cannot apply.

We have developed a benchmarking system with these limitations in mind. The system uses no fixed cutpoints or warning levels, operates at the individual abattoir level and compares performance to a suitable population. The comparators are: lines of the same class of animal sent by the same producer to the same works in the preceding year; and lines of identical stock class supplied by other producers from the same region to the same abattoir and in the same year. The performance of the line in question is mapped against these comparators with no rule-based statements about excess of cases. This system allows the producer to see how they compare to their peers and most importantly to themselves in the previous year. It avoids having an algorithm (i.e. a machine) telling a producer (i.e. a human) they have done a bad job. This is acceptable if the machine gets it right but is extremely damaging when the machine gets it wrong! Presenting relative performance without statements (or with carefully worded statements) prevents this from occurring. Importantly, such a system provides answers to the perennial producer questions on endemic disease—do I have too much? And are my controls effective? This should maintain interest and support for the reports and avoid distrust in a developing system.

The system will require ongoing development and refinement of effective data standards for recording and coding diseases with suitable accuracy[13], effective data centralisation systems that allows near-real

[12] Noting that technically meat inspectors do not make a 'diagnosis', they make a disposition. The term diagnosis is used here in the context of performance of a diagnostic test.

[13] Or effective application programming interfaces (APIs) for aggregating diverse processor data

time data processing and reporting and ongoing maintenance. Long-term maintenance of this benchmarking system requires little ongoing work. Once algorithms to identify peers for comparison are developed, these can easily be run to capture the population of comparator lines and their distribution mapped.