final report

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Analysis of ESAM data

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Executive summary

The *E. coli* and *Salmonella* database (ESAM) is an ongoing system for monitoring carcase hygiene in the Australian meat industry. ESAM provides objective evidence of processing performance in the form of counts of *E. coli* and total viable count (TVC) per unit of carcase surface area and the presence or absence of *Salmonella*. ESAM data has the potential to be used by establishments to monitor and manage levels of bacteria on carcases and to demonstrate the integrity of their processing. ESAM can also be used on an industry-wide basis in the context of meeting the requirements of international trade by using it to document microbiological attributes of Australian red meat carcases. The data within ESAM is also a rich resource for investigating the causes of variation in carcase microbiology measurements. To demonstrate these benefits this project examined six years of ESAM data consisting of half a million microbiological observations.

Approach

The Australian Quarantine Inspection Service provided ESAM data for the period 1 January 2000 to 31 December 2005. Initially data were screened for correctable errors, collated into a single file, and formatted for analysis by statistical software. Graphical analyses were used to explore data, generate a descriptive overview for the entire study period, and evaluate the variability of measurements over the study period as a time series. Analyses were performed for each microbiological outcome (presence or absence of generic *E. coli*, total viable count (TVC) per unit area and presence or absence of *Salmonella*) and type of carcase. A more sophisticated time series approach was used to decompose variations in log TVC cfu.cm^{-2} into long-term trend, monthly effects and weekly effects for several establishments. The performance of attribute sampling plans were studied by developing computer algorithms for analysis and applying these to the six years of ESAM data at an individual establishment and industry-wide level.

Findings

The key findings from this project were:

A system can be established that provides a timely and informative analyses of ESAM data on demand. This is provided that some simple improvements are made to the way ESAM data are collected. The benefit would be rapid and informed responses to queries from customers and trading partners. Analyses could be performed for particular establishments or across the industry.

Improvements are needed in the collection of data on TVC. TVC data needs to be consistently collected and interpreted (particularly missing data) by more establishments and using standardised laboratory protocols. The result would be data of more uniform quality – a necessary precursor for industry wide analysis. It would also assist individual plants to verify their process control. The *E. coli* and *Salmonella* data, although of good quality, are not on their own as suitable for describing performance as log transformed TVC data.

Proportion of tests yielding positive for *E. coli* and *Salmonella* in this work are similar but generally lower than those reported in the industry baseline study (2004). In general, within ESAM there has been a decline in the rate of detections across all species from 2000-2005.

This project has identified substantial variation in microbiological measurements made on meat carcases. A large amount of variability occurs within establishments (between carcases produced on the same day, week, month and season) and between establishments. Seasonal effects have been observed for some carcase types and for some establishments. This is the first time the extent of variation has been comprehensively documented at a national level.

The analysis of attribute sampling plans showed how individual establishments and the industry performed under different monitoring schemes from 2000-2005. The algorithms that were developed are available as a tool for industry and AQIS to refine this approach to monitoring.

Contents

1 Background on the project

1.1 Introduction

Data on the occurrence of generic *E. coli* and *Salmonella* on meat carcases have been collected in Australia since 1998 as part of the ESAM program. ESAM is coordinated by the Australian Quarantine Inspection Service (AQIS) and provides data to meet the requirements of trading partners (particularly the United States of America). Establishments that return an excessively high frequency of positive *E. coli* or *Salmonella* tests in ESAM may be required to review and correct aspects of their processing.

The key features of the ESAM program that relate to this project are:

- All slaughter establishments registered with AQIS participate in the program.
- Sampling of carcases is ongoing and performed in a systematic fashion. For example, one in every 300 beef carcases and one in every 1,000 sheep carcases produced are sampled.
- Carcases are sampled by a standard technique based on surface swabbing applied to a pre-determined site of the carcase.
- Swabs are analysed for the presence or absence of *Salmonella*. The density of generic *E. coli* in swabs and hence carcase area is obtained from enumeration procedures.
- Establishments can voluntarily enumerate total viable count (TVC) and submit this data along with the compulsory data on *Salmonella* and generic *E. coli*.
- The Australian Quarantine Inspection Service provides detailed instruction on carcase sampling, swabbing, specimen handling and laboratory analysis.
- ESAM data is collected and maintained by AQIS and to date has not been subject to in-depth analysis.

Descriptions of all aspects of the conduct of ESAM are publicly available in AQIS meat notices. The relevant documents are AQIS meat notices: 2005/13, 2000/09, 2003/06 and 2005/06 and are readily available from the Australian Department of Agriculture, Fisheries and Forestry web site.

1.2 Rationale for the analysis of ESAM data

The Australian meat industry expends considerable effort complying with the requirements of the ESAM program. One immediate benefit is continued access to particular international markets. However, ESAM has resulted in an accumulation of data that is potentially valuable as a descriptor of hygienic standards of meat processing in Australia. The large amount of data now stored can be studied using modern statistical tools for describing and explaining variation in hygiene levels across the industry and within individual establishments over time. The data therefore could be of assistance to plants wishing to improve the safety and shelf life of their products. ESAM data also has the potential to improve the objective basis of decisions on meat hygiene and processing made at the industry level.

An emphasis on evidence-based management of food safety issues strongly suggests that in the future stakeholders and customers will demand a greater volume and quality of objective evidence defining the hygienic performance of the Australian meat industry. It thus seems prudent to develop analysis systems for ESAM data and ensure that future analyses can be conducted in a timely and efficient manner.

1.3 Approach

Section 1. This background chapter.

Section 2. Obtain the ESAM data from AQIS for the years 2000-2005 inclusive. Convert the data into a format suitable for importing into statistical analysis packages. Perform an exploratory analysis to identify any errors or inconsistencies in the data. Prepare and store a corrected data set so that it can be interrogated on an ad-hoc basis in the future according to industry requirements. Make recommendations on handling ESAM data in the future.

Section 3. Describes an overview of the hygienic performance of the meat industry according to type of animal being slaughtered and microbiological outcome. Some analyses are performed by geographic region. Here the data are pooled across time to provide summaries for the entire study period plus breakdown by each year.

Section 4. Perform a basic time series analysis of microbiological outcomes in ESAM for all major class of livestock. This uses data aggregated from all plants and shows how 'national average' levels of indicator bacteria vary through time.

Section 5. Perform an in-depth analysis of specific establishments. Firstly to explore what could form the basis of a routine periodic analysis. Secondly to illustrate the type and extent of information and interpretation that is possible using modern statistical methods and software applied to the ESAM data on a plant-to-plant basis.

Section 6. Perform an evaluation and comparison of attribute sampling schemes used to monitor the hygiene of red-meat carcases. This entails the development of computer algorithms to mimic the function of attribute sampling schemes and application to the data within ESAM.

2 Collation of data

2.1 Introduction

The ESAM data set is collated and managed by AQIS. AQIS staff located at each establishment enter their data on a regular basis into a single large data base. In this work we only consider the data from 2000 to 2005 inclusive. Data prior to 2000 is excluded because it was during this period that the meat industry was adapting to the new requirements and the data may not be as reliable as that post 2000 and which is the subject of this study.

The size and complexity of the ESAM database demands that the information is carefully migrated from the data storage environment to the analysis environment. The purpose of this section is to describe the manner in which ESAM data were collected and handled to prepare them for authoritative analysis. This process, or a similar process, will need to be repeated whenever there is an attempt to analyse ESAM data in the future. The results in this section do not discuss the data themselves (that is left for other parts of this report) but address the strengths and deficiencies of the data, approach used and experience gained. The recommendations issued at the end of this section are intended to streamline future collection and use of the ESAM data for periodic analysis.

2.2 Methods

Acquisition of data
Electronic files were obtained from AQIS on several occasions. Each file contained the ESAM data base for one of the years 2000, 2001, 2002, 2003, 2004 and 2005. The files were provided in two main formats to assess which of these best suited the future extraction of data from ESAM. The file formats were:

Microsoft Excel spreadsheet format: Microsoft Excel is ubiquitous and flexible software for managing data. However, it does have serious limitations particularly when data files are large and complex and Excel is only capable of basic statistical analysis. The ESAM data is so extensive that it cannot fit onto a single Excel file and so was received as a series of Excel files (one for each year). Within each file data for each ‘species’ were on a separate worksheet.

Comma delimited format: Data were provided in comma delimited format (text files) or comma separated value format (an excel export format). The data in these formats exist as ASCII codes, one line to each record, with variables within each record separated by a comma.

In both cases the data base consists of records containing various fields or variables (Table 2.1).

Collation of electronic data
In this study we used the statistical analysis package Stata SE version 9.2 (StataCorp, College Station, Texas, USA) for much of the analysis with the remaining performed using the S-Plus package (Version 6, Insightful Corporation, USA). Both of these analysis programs have the capacity to explore very large data sets and are fully programmable (i.e. they use script files to record a sequence of instructions that perform an analysis). Programmable analyses are required for tasks of this size because each analysis procedure can be easily repeated as often as desired, the analysis techniques can be audited and the analyses can be easily modified.

Electronic files (Excel and delimited formats) received from AQIS were processed into the native data file format for Stata using the software conversion package Stat/Transfer (Circle Systems Inc, Seattle, WA, USA). All pre-processing of the data (joining of data files for each year into one single data file) and preliminary checking of data for errors and inconsistencies were then performed in Stata 9 using a program file (called a “do file” in Stata terminology). Although the

proportion of records with errors and inconsistencies was very small, derivation of the final data file was a time consuming process because of the variety of different errors, each requiring authoring of specific code to be rectified. The overall management of the data prior to analysis is shown in Figure 2.1.

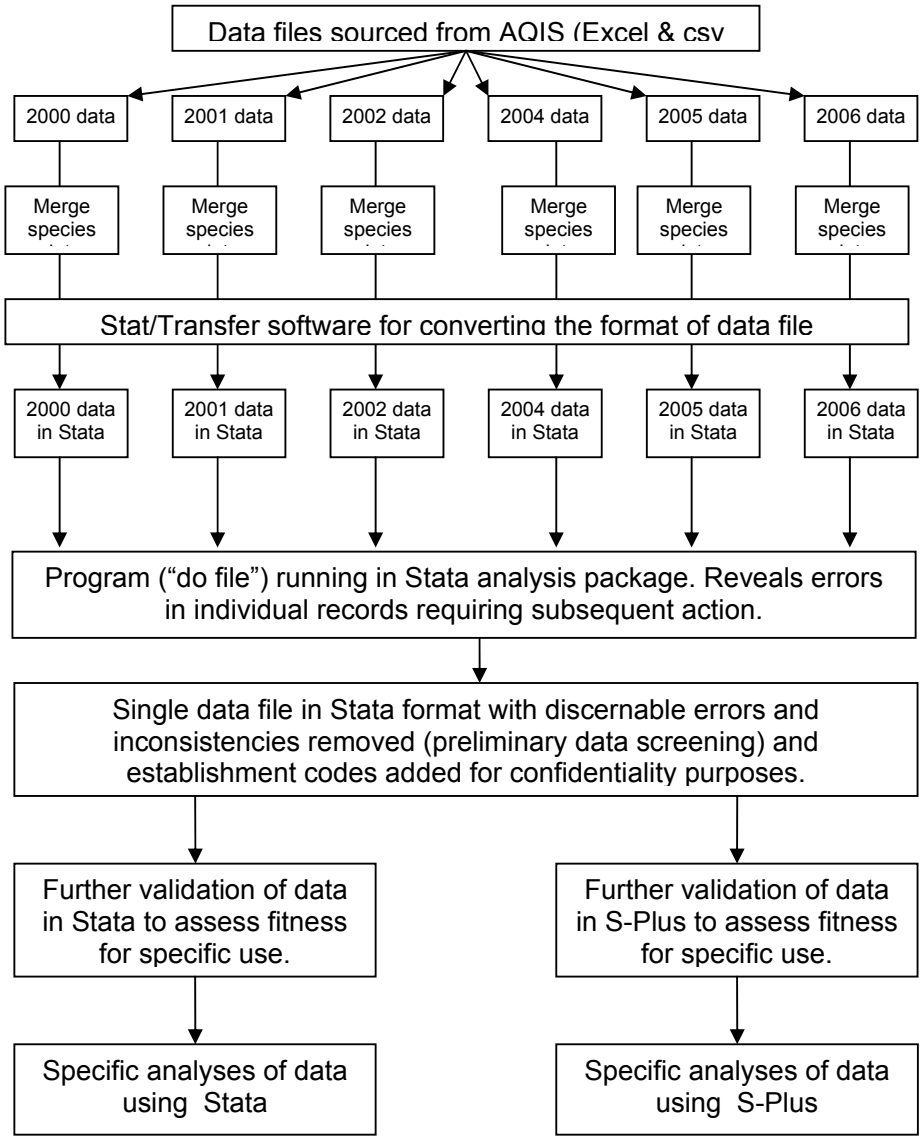

Figure 2.1. Overview of the acquisition of data from the AQIS managed ESAM database and its preparation in readiness for analysis using statistical software.

As part of the preliminary processing of data the following checks, corrections and additions were made:

Generate and assign a unique “establishment code” corresponding to each “establishment number” enabling description of establishments to occur in the analysis but with the establishment remaining anonymous.

Joining of data files from each species and each year into one large file.

Remove from the data those records and variables that serve no purpose having arisen as an artefact of the file transfer process. Typically these are empty records (rows) or empty variables (columns).

Validate each data entry to ensure they are within the legal range of values (numerical data e.g. tvcreading) or within the legal set of values (string data e.g. species).

Remove semi-colons from *Salmonella* serotype data so semi-colons can be inserted as variable delimiters when the data are exported from Stata for use in S-Plus.

Log transformation of enumeration data. Where required, enumeration densities were transformed as follows: log count = log10(count+1), this being necessary for effective graphical analysis and interpretation of findings.

Exploratory analysis
Studies based on examination of large data sets first require an initial exploration to assess the integrity of the data. This process identifies characteristics of the data that impact on the ability to perform particular analyses and defines appropriate limits on the interpretation of analyses. A large number of such procedures were undertaken over the course of the project with the most important described below.

2.3 Results

Data acquisition
Some difficulties were experienced in assimilating the data from multiple years into a single electronic file for analysis. These mostly related to the process of exporting from the main ESAM data base and dividing the files into multiple Excel files for transfer to the investigators. This process introduced some side-effects, for example: insertion of additional empty rows and columns in the data set and inconsistent case formatting of variable names between versions of the data. It was also noticed that the *Salmonella* serotype data contained punctation marks (commas, semi-colons etc) that interfere with the use of “delimited file formats”. Once recognised, these issues can be dealt with but before they are diagnosed as the cause of data corruption they caused considerable delay in completion of the analysis.

Data and variable definitions
The working data set arrived at after the compilation and importation process comprised 499,858 microbiology measurements in 325,586 lines (records) of information. Table 2.1 gives a detailed description of the data fields (variables) used in the analysis of ESAM data. Table 2.2 gives additional information on the definitions of values appearing in the Salmonella Result variable of the data.

Table 2.1. Data fields and their definitions, data validation and error trapping steps in the preliminary analysis of ESAM data prior to each periodic and full analyses.

Data field	Data type	Definition	Data validation procedure(s)	Treatment of missing values
estabnum	Integer	AQIS assigned, unique and confidential numeric code identifying each processing establishment	Check against an AQIS supplied list of valid values for establishment numbers.	Missing values are errors.
testid	Integer	Unique within establishment and sequentially allocated reference number for each carcase test	Nil, not relevant to analysis.	Not appraised.
species	String (length = 12)	Categorical variable describing the livestock species and class of carcase tested	Check each entry against a list of valid values for species.	Missing values are errors.
date	Floating point (in date format)	Date and time of the acquisition of carcase specimens for microbiological analysis	Check date within legal range for the analyses being performed.	Missing values are errors.
tvcreading	Floating point	Total viable count of bacteria per square centimetre of swabbed area of carcase	For non-zero counts check that the enumeration result is a 'legal value' for that species.	Missing values are allowed because TVC testing is not compulsory.
ecolireading	Floating point	Number of generic *E. coli* per square centimetre of swabbed area of carcase	For non-zero counts check that the enumeration result is a 'legal value' for that species.	Missing values are possible errors. They do occur when there has been *Salmonella* testing but no *E. coli* testing suggesting additional voluntary *Salmonella* testing.
salmonellatested	String (length = 1)	Not used in this analysis	Nil, information in the *Salmonella* result field used instead.	Not appraised.
salmonellaresult	String (length = 1)	Culture result for presence or absence of *Salmonella* in carcase swabs. See Table 2.2 for definitions.	Check each entry against a list of valid field values.	Missing values are errors.
serotype	String	Serotype of any *Salmonella* detected	Tabulation of all serotypes identified with manual checking for validity.	Missing values are allowed.
boningmethod	String (length = 1)	Type of boning method employed (affects the timing of swab collection)	Check each entry against a list of valid field values.	Missing values are allowed.
ecoliresultreg	String (length = 1)	Categorical interpretation of *E. coli* enumeration results as passed, marginal or not acceptable.	Check each entry against a list of valid field values.	Missing values are allowed.

Table 2.2. Definition of values for the Salmonella result variable in the ESAM data base.

Value	Definition
F	Failed test (*Salmonella* was detected)
N	No sample was taken
P	Passed test (*Salmonella* was not detected)
W	Waiting for the test result to become available
Z	Not applicable

Salmonella serotypes

When *Salmonella* serotype data were tabulated considerable inconsistencies became evident in the spelling and formatting used. Effectively, this makes it difficult and time consuming to undertake further analysis on serotypes. An example tabulation of *Salmonella* serotypes isolated from lamb carcases (Table 2.3) shows some of the types of errors present in this part of the data base. Note that in Table 2.3 the important zoonotic serotype S. Typhimurium is spelt or formatted (case, spaces and period) five different ways. Also the data field is being used for comments.

Table 2.3. Example of raw data on *Salmonella* serotypes obtained from lamb carcases showing interpretation and analysis difficulties created by errors in the data. This example shows repeatedly inconsistent spelling, capitalisation and formatting of S. Typhimurium.

Serotype	Count
Not Tested	1
Not serotyped - some mix up at lab	1
S. Typhimurium	1
S. adelaide	1
S. anatum	1
S. bovismorbificans	5
S. infantis	1
S. javiana	1
S. muenchen	1
S. newport	1
S. rubislaw	1
S. singapore	2
S. tennessee	1
S. tyhimuruium	1
S. typhimurium	19
S. typhmurium	1
S. wejikade	1
S.typhimurium	1
Salmonella isolated was a laboratory co	1
Sample recorded as to hot by lab, not t	1
Total	43

2.4 Discussion

Future management of ESAM data

ESAM is a growing body of useful data. Improving the quality and accessibility of data will improve the yield and usefulness of information. At present, performing an analysis requires substantial manual manipulation of files and data (e.g. splitting information into multiple files and then re-joining) – a task that demands the availability of expertise. Technological advances make it possible to greatly improve aspects of the management of ESAM data to reduce the burden on AQIS staff and to deliver analyses in a more timely manner. The standard of information entering the system may in future be improved by providing establishments and on-site AQIS officers with rapid feed back on the data that has been submitted. A range of suggestions are outlined below for improving the data quality.

AQIS establishment numbers

Establishment number codes should ideally be unique. There are game processing works and abattoirs with the same EstabNum. Ideally these are given different values if they are a different licence. They can be the same company but with different EstabNums. As well, EstabNum codes are best kept entirely numeric. Alphanumeric values should be avoided. For example, there is an establishment 505A and when the list is sorted this establishment is not adjacent to 505. In general, variables (data in the one column) should contain only one data type.

A documented process is required for entering new establishments into the list and for classifying others as being disbanded. Retain in the file all those establishments that are disbanded and create another field for date of disbandment. This will assist with future analysis or any auditing by another party.

Salmonella serotypes

Tabulated data on *Salmonella* serotypes revealed inaccuracies in this aspect of ESAM. If the information on *Salmonella* serotypes is to be relied on then greater care will be needed with the entry of data. Minor errors in the spelling or formatting of serotype data when it is being entered introduce substantial difficulty and delay when a detailed analysis is later attempted. Possible solutions include the use of a drop down data entry fields (referencing a dictionary of *Salmonella* serotypes), plus training for individuals responsible for entering this data.

Acquisition of data from plants

Perhaps the most important area for review is the entry of data into the system. The safest and most efficient way of creating a robust data set is to validate the data at the time of entry. In the medium and long term an automated system of validation will be needed if there is to be frequent examination of the data as part of a periodic summary analysis. By validating data upon input into the data base subsequent analysis and interpretation is streamlined.

A major issue in data entry is the interpretation of 'missing data' by individuals who enter data. This is a particular problem for TVC where (see later chapters) there is confusion on how to represent zero counts and counts that have not been performed. It is essential to address this deficiency.

Export of electronic data

The information should take a direct path from data base to analysis. Splitting the data up into multiple files should be avoided as this risks the introduction of errors when the files are re-joined. For example, in some Excel files there were whole columns or whole rows with blank data arising from the spreadsheet export and file joining process.

Microsoft Access database files should be suitable as an export format but this could not be evaluated because data were only supplied in Excel and comma delimited formats. Of the two latter formats, Excel spreadsheet files are preferable. Comma delimited files, although a more standard format, were problematic because there are commas already present in the data (in some entries of the *Salmonella* serotype field) and these additional delimiters results in corruption of the data when imported for analysis.

It is critical that the same variable or field names and same case are used each time the data are exported. Inconsistent naming of fields, or variations in the case of field names, requires the analysis program to be re-edited to accept the data.

Recommendation: A review of the process used to store, extract and export information from the ESAM data base for analysis is strongly recommended. A consistent export protocol should be devised and documented to avoid the issues mentioned above. Thus the complex procedures illustrated in Figure 1. would be greatly simplified reducing the cost and time of the analysis and reducing the risk of errors. Suggested elements of such a review are:

A single data file is used to export data.

Robust data file format is used which is compatible with analysis software import process (eg. MS Access).

Consistent field headings across all data exports.

Data is validated at point of entry into ESAM (as much as possible). This may require upgrading of the software currently being used to capture data.

Salmonella serotype data is corrected at entry or periodically corrected by reference to a serotype dictionary file.

Documentation produced on file structure and field definitions and data quality control procedures to be followed at by AQIS officers on plant and centrally in the handling of the data base. Such documentation should be regarded as essential as that for laboratory and sampling protocols.

Training of on-plant officers inputting data, particularly with respect to discrimination between missing values (test not done) and zero counts (this refers to TVC data).

Provide on-plant officers with regular feed back in the form of results for the establishments under their responsibility.

3 Descriptive overview of ESAM data

3.1 Introduction

Basic descriptive techniques are applied in this part of the report to give an overview of the data entered into ESAM for the six years of 2000-2005 inclusive.

3.2 Overview of TVC data

This section provides an overview of the TVC component of ESAM data from 2000 to 2005 inclusive.

Samples, Plants and Species
A total of 160120 valid (not missing or out of range) TVC records are in the data base. The observations cover sixteen animal classes although almost 95% of the observations are from the five most common classes. Further analysis here is constrained to red meat species, with the number of observations by species shown in Figure 3.1 and the distribution of observations by species in Figure 3.2.

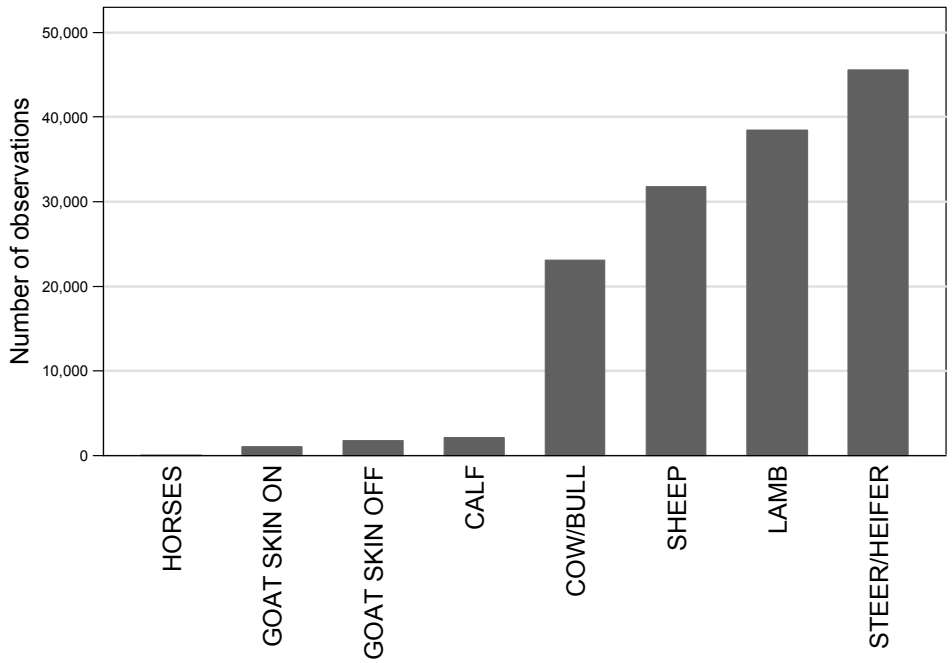

Figure 3.1. Number of TVC submissions to ESAM (including zero counts) for various red meat species for the period 1 Jan 2000 to 31 Dec 2005.

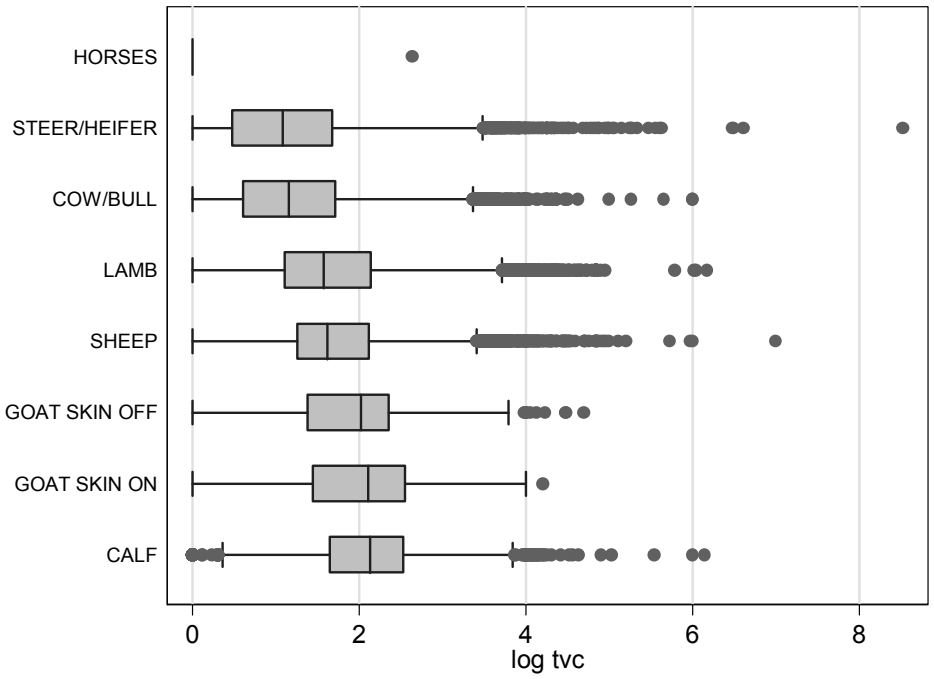

Figure 3.2. Crude log TVC data by species. Some of the data are possibly inaccurate as there is evidence to suggest reporting deficiencies in TVC measurements.

Integrity of TVC data

In the analysis a series of issues arose with the integrity of TVC data. These are discussed below.

Confusion between zero counts and missing data

For most if not all classes of livestock it is unlikely that a TVC concentration of 0 cfu.cm^{-2} is possible. Therefore most 0 cfu.cm^{-2} results represent incorrect specimen collection, laboratory error in enumeration, error in the recording of data or misinterpretation of how missing data should be represented. When establishments were evaluated on an individual basis it was common to find establishments where a value of 0 cfu.cm^{-2} was repeatedly entered, often in long sequences. An example of incorrect entry of missing data is Figure 3.3 while Figure 3.4 is an example of correct entry of missing data for comparison. Similar plots from other establishments does suggest there is confusion about how to enter missing values (i.e. those occasions when the TVC test was not done). Values of 0 cfu.cm^{-2} should not be submitted to ESAM when no test for TVC has been performed.

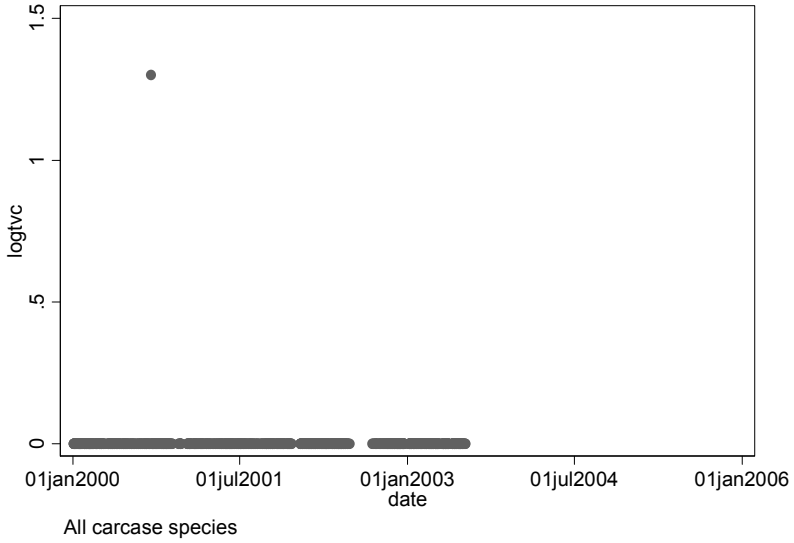

Figure 3.3. Example from an anonymous establishment of monotonous zero counts of TVC data instead of entry of missing values. TVC data has been almost exclusively and continuously entered as zero cfu.cm^{-2} from Jan 2000 to April 2003 and thereafter as missing value.

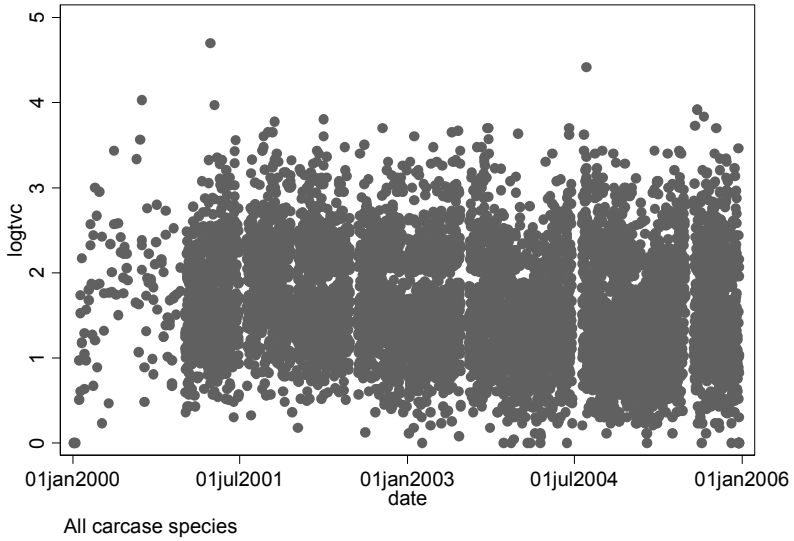

Figure 3.4. Example from an anonymous establishment of apparently correct entry of missing data in periods for which there was no TVC testing performed. Here missing data occurs very early in the study period where only sparse data on TVC are collected and during periods when the establishment is apparently non operational. Periods of missing data are not represented by zero counts (this is the correct method for representing missing data).

Intermittent TVC data

Collection of data on TVC is not compulsory in ESAM and there are no prescribed protocols for laboratory component of TVC testing for ESAM samples. From the exploratory analysis it is evident that there is variable adoption of TVC testing across the processing sector and substantial variation in test protocol. Only a minority of establishments had continuously collected TVC data over the duration of the study period. Figure 3.5 shows the case for STEER/HEIFER data, by displaying the pattern of collection of TVC data over time for various

establishments. Figure 3.6 gives an example of missing data at the level of an individual establishment. Figure 3.7 shows the overall trend in number of tests submitted to TVC over the study period (bearing in mind some of these are missing counts coded as 0 cfu.cm^{-2}.

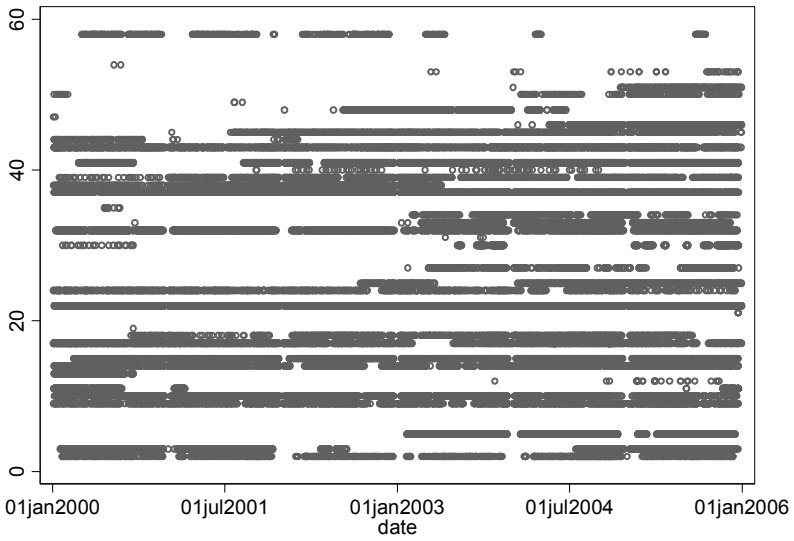

Figure 3.5. Graphic representing each plant as a row of points with dots corresponding to the dates where TVC data were recorded for each plant. Gaps on lines of dots represent periods when establishments did not collect TVC data.

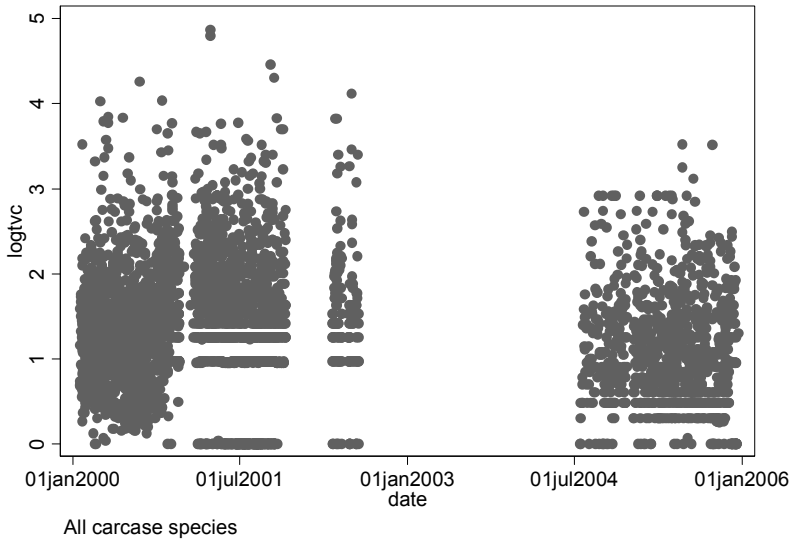

Figure 3.6. Example of an anonymous establishment with a large block of missing data from about September 2002 until July 2004.

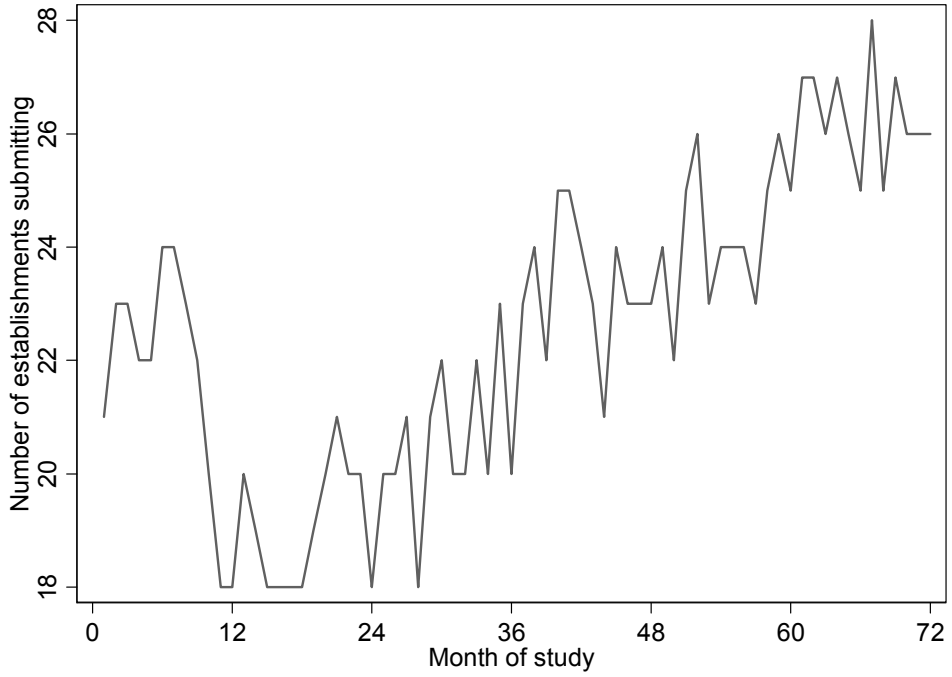

Figure 3.7. Number of establishments submitting any TVC data from STEER/HEIFER carcases for each month of the study (Jan 2000 to Dec 2005).

Units of measurement and measurement error of TVC data

Time series plots of log TVC were produced for individual plants. As well as exhibiting intermittent data and inappropriate treatment of missing values as described above, unusual horizontal banding patterns and range restrictions were observed for some plants. Both these features are illustrated for an anonymous example establishment in Figure 3.8.

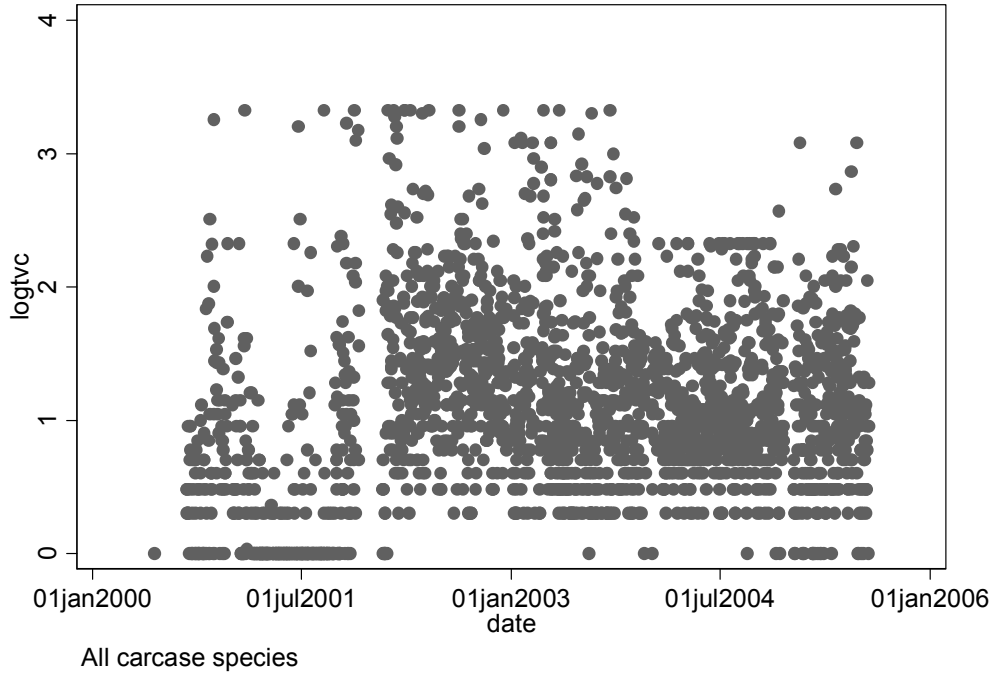

Figure 3.8. Data from an anonymous establishment showing banding indicative of inappropriate enumeration of TVC, possibly explained by the plating of limited dilutions on solid media. In addition to banding there are upper range restrictions evident (e.g. July 2004).

The banding of data is due to the way in which swabs are diluted and inoculated for TVC count on solid media. The banding itself is not an incorrect result provided it is restricted to the low range of concentrations and provided the banding lines occur at values of log TVC cfu.cm^{-2} that are consistent with an appropriate protocol for dilution and plating. If the gaps between bands are large then the method of dilution and plating provides poor accuracy at that concentration range (typically less than 1 log). If banding occurs at integer values then it is unlikely that the data are actually in units of log TVC cfu.cm^{-2}. It appears that at some establishments the colony count from a single dilution has been recorded without it being converted to log cfu.cm^{-2} i.e. the number of colonies per plate is recorded. Evidence in support of this is the large variation in banding patterns between establishments and the occurrence of data points at values of cfu.cm^{-2} that are not expected from acceptable dilution and plating protocols. Further evidence is given as an example in Table 3.1 which lists each result for the 'tvcreading' field for a particular establishment and shows that integer counts are common.

Inappropriate banding patterns (large gaps between bands and bands at inappropriate values) are commonly observed when TVC data are viewed on an individual establishment basis. It suggests there is substantial error in the TVC data from many plants, particularly at low concentrations of TVC. Moreover, without a detailed plant by plant investigation of the techniques used to enumerate TVC, it is necessary to assume that the amount of error is variable, that it cannot be estimated and that it cannot be compensated for in the analysis.

Table 3.1 Extract of data from an anonymous establishment performing TVC testing (tvcreading <= 19). It appears that at least some of the data for 'tvcreading' equates to a number of colonies growing on single agar plate (i.e. cfu per plate for a particular dilution) because of the clustering of observations around integer values. It is unclear how to explain the remaining data (possibly they are averages of multiple dilutions, or some but not all are in units of cfu.cm^{-2}, or they are errors of some kind) . It thus appears unlikely that all of the data for this establishment are in the correct units of cfu.cm^{-2}.

tvcreading	Freq.	Percent
0	4	0.17
.4	1	0.04
.5	1	0.04
.83	1	0.04
1	10	0.42
1.5	1	0.04
1.6	2	0.08
1.7	2	0.08
1.75	1	0.04
2	24	1.02
2.5	10	0.42
3	54	2.29
3.3	4	0.17
3.5	7	0.30
4	34	1.44
4.1	1	0.04
4.5	6	0.25
5	50	2.12
5.5	3	0.13
5.75	1	0.04
5.8	4	0.17
6	49	2.08
6.5	5	0.21
6.6	2	0.08
7	26	1.10
7.5	13	0.55
8	44	1.86
8.3	4	0.17
8.5	8	0.34
8.75	1	0.04
9	32	1.36
9.1	2	0.08
9.5	6	0.25
10	47	1.99
10.5	4	0.17
10.8	10	0.42
11	41	1.74

11.5	7	0.30
11.6	3	0.13
12	25	1.06
12.5	12	0.51
13	38	1.61
13.3	14	0.59
13.5	4	0.17
14	33	1.40
14.1	12	0.51
14.5	2	0.08
15	37	1.57
15.8	5	0.21
16	25	1.06
16.5	7	0.30
16.6	4	0.17
16.8	1	0.04
17	24	1.02
17.5	14	0.59
18	29	1.23
18.3	5	0.21
18.5	7	0.30
19	19	0.80

Caveats for aggregated TVC data

From the above investigations of TVC data it is evident that there are problems in the way TVC data have been collected and recorded in many establishments:

Missing data not distinguished from zero counts.

Absent or intermittent data.

Measurement error related to plating of limited dilutions on solid media.

Uncertain units of measurement. It is not clear whether some establishments record colonies per plate or cfu.cm^{-2} of carcase surface or even a mixture of these.

The number and type of the above errors varies from establishment to establishment and thus from species to species. Given that any one establishment may be affected by one or more of these problems it is inappropriate to perform any further detailed analysis on aggregated TVC data other than to demonstrate the great potential that improved collection of TVC data holds for describing the levels of hygiene in individual establishments and across the industry.

Descriptive summaries of TVC data (caveats apply)

Although the aggregated TVC data do appear to be deficient, the data does have some uses. Firstly, it demonstrates the type of plots that could be produced in the future for distribution to industry and stakeholders provided that the quality of TVC data can be improved. Secondly, it shows the utility of data that is recorded on a continuous scale and with very few zero counts (we do not expect any zero counts when testing is performed correctly) which is generally more informative than the type of data produced by monitoring *E. coli* cfu.cm^{-2}.

All TVC data aggregated for a species

The data can be aggregated (establishment identifications ignored) and plotted without reference to any particular time period. Output for this type of analysis of log TVC for SHEEP is shown as an example in Figure 3.9.

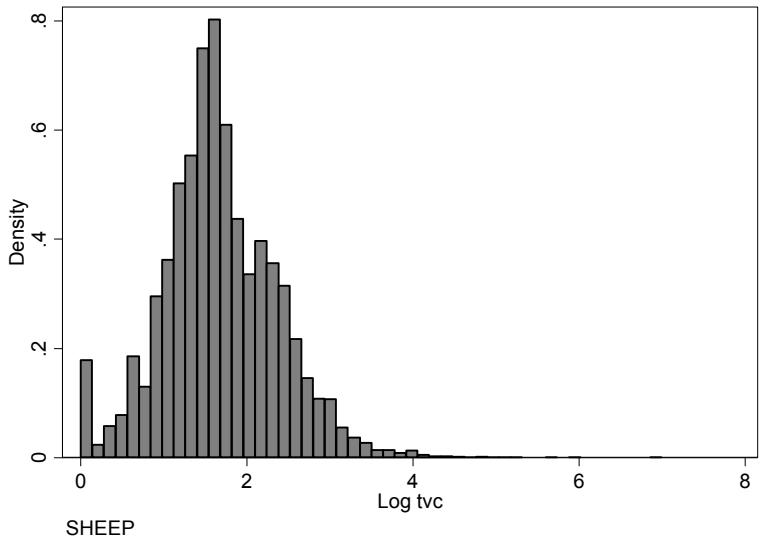

Figure 3.9. Pooled log TVC cfu.cm^{-2} for SHEEP carcases for the entire study period (data subject to above caveats).

Comparison of establishments using log TVC

Log TVC cfu.cm^{-2} can be grouped by establishment and presented in the form of a box plot. This has been performed for the SHEEP data for the entire study period (above caveats apply) in Figure 3.10.

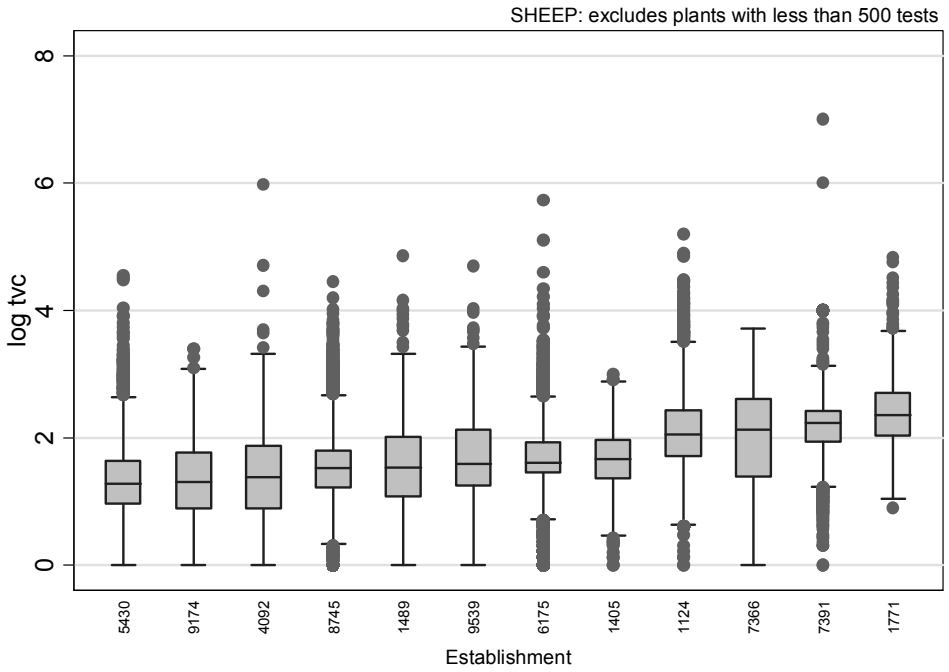

Figure 3.10. Example comparison of establishments by log TVC cfu.cm^{-2} using box plots. Establishments with less than 500 observations are excluded. The data covers the entire study period (years 2000-2005 inclusive) and may not be accurate due to data deficiencies as noted in the text.

3.3 Overview of generic *E. coli* data

The data for generic *E. coli* is distinctly different from that for TVC in the following ways:
Collection of data on *E. coli* is compulsory.
Data is always collected at the specified interval for each species. Thus establishments are represented in the data base and in any pooling of the data according to their level of production.
Specimens for *E. coli* isolation and enumeration are processed at accredited laboratories by approved methods.
Zero counts are commonly encountered particularly in swabs from cattle carcases, this effectively providing less sensitivity for detecting changes in the hygienic performance of processing.
As a result of the above attributes for *E. coli* data the presentation and interpretation of the analysis of generic *E. coli* data is very different to that for TVC.

Samples, establishments and species

A total of 273,692 observations on *E. coli* are present in the data base. The distribution of observations amongst different classes of carcases reflects that observed for TVC and is shown for red meat species in Figure 3.11. Also shown are crude percentages of positive test for *E. coli* by carcase species (Figure 3.12), by year and carcase species (Figure 3.13) and by geographic region and carcase species (Figure 3.14). Figures 3.15a to 3.15e show establishment specific percentage of carcases tests positive for *E. coli* for each species.

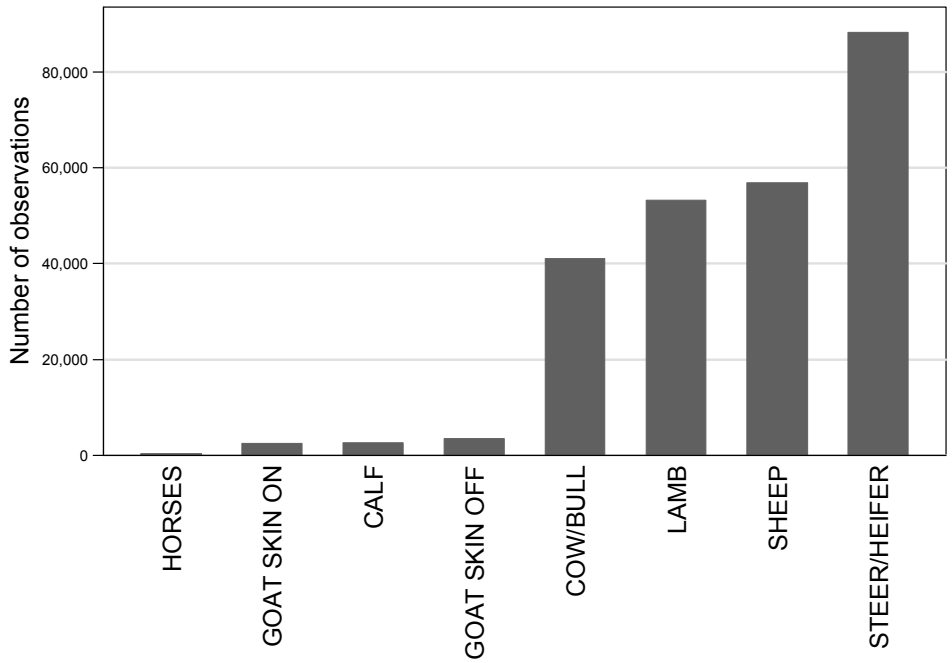

Figure 3.11. Number of *E. coli* submissions to ESAM (including zero counts) for various red meat species for the period 1 Jan 2000 to 31 Dec 2005.

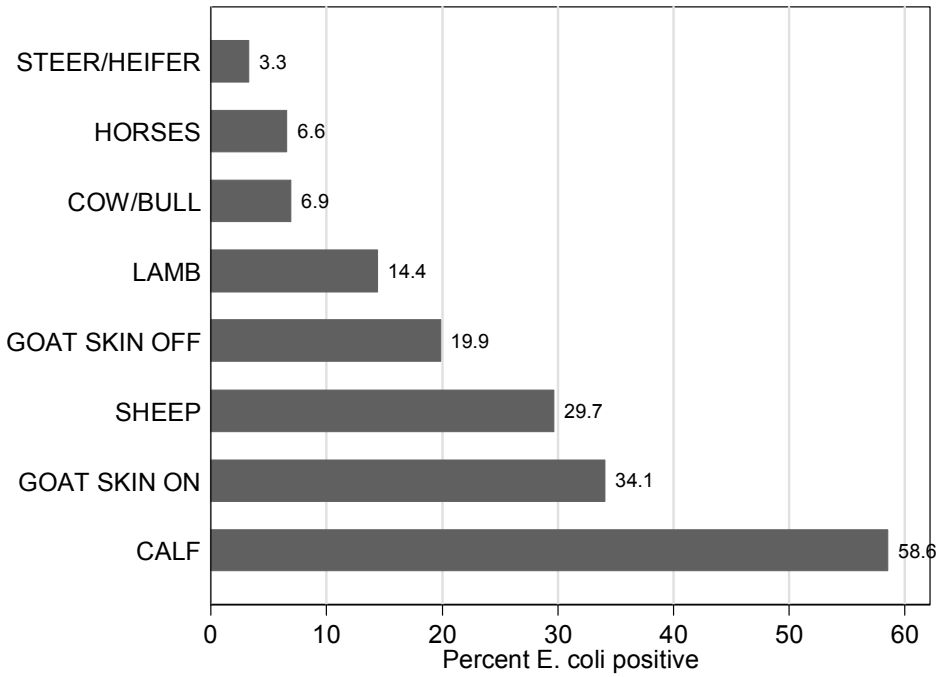

Figure 3.12. Overall prevalence of carcase tests positive for *E. coli* for the period 2000-2005 by species of carcase.

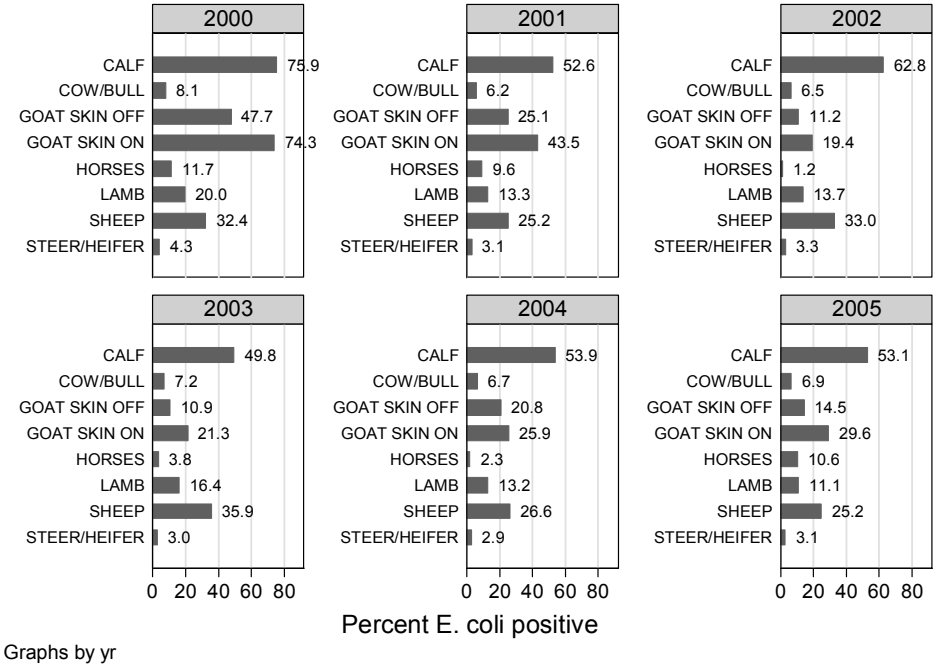

Figure 3.13. Prevalence of carcase tests positive for *E. coli* by species of carcase by year.

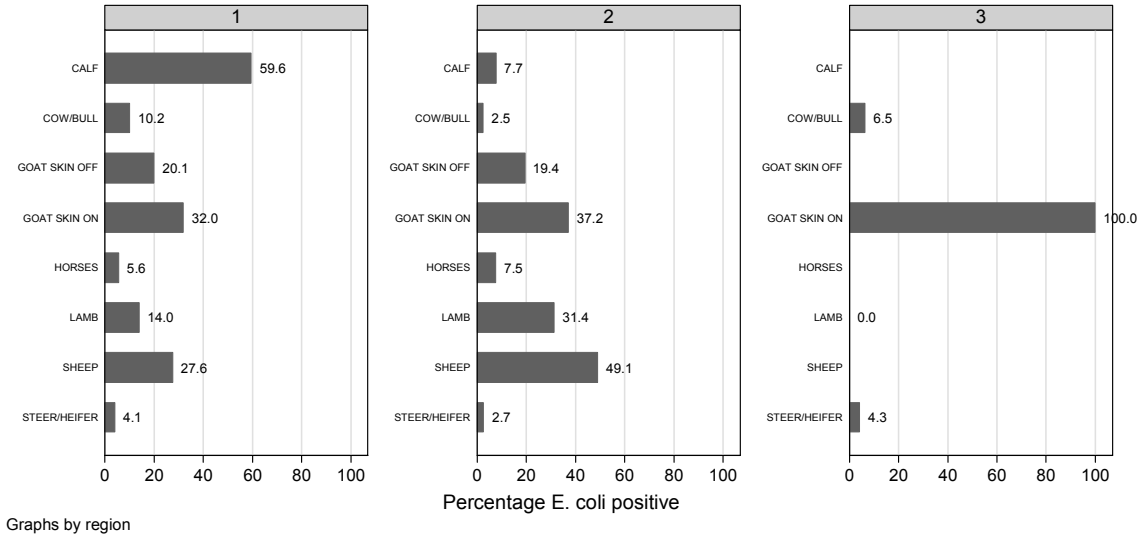

Figure 3.14. Percentage of carcase tests positive for *E. coli* from 2000 to 2005 by carcase species and by region. Region 1 is south of latitude 30° S, Region 2 is between latitudes 30° S and the tropic of Capricorn, Region 3 is north of the tropic of Capricorn).

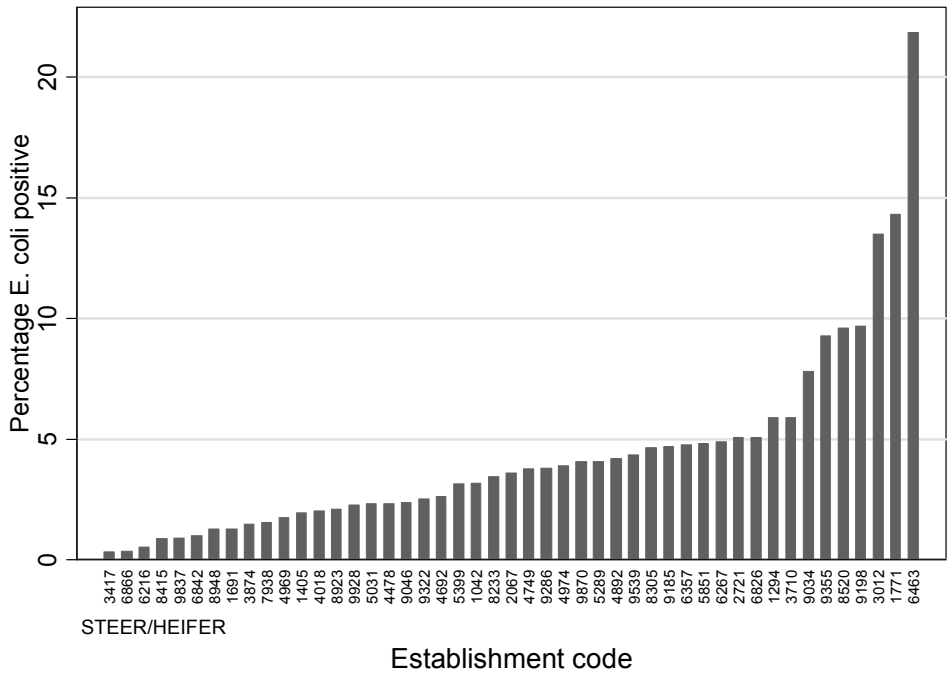

Figure 3.15a. Establishment specific values for percent of STEER/HEIFER carcases giving positive test results for *E. coli*, over the entire study period (years 2000 to 2005, establishments submitting less than 50 test results excluded).

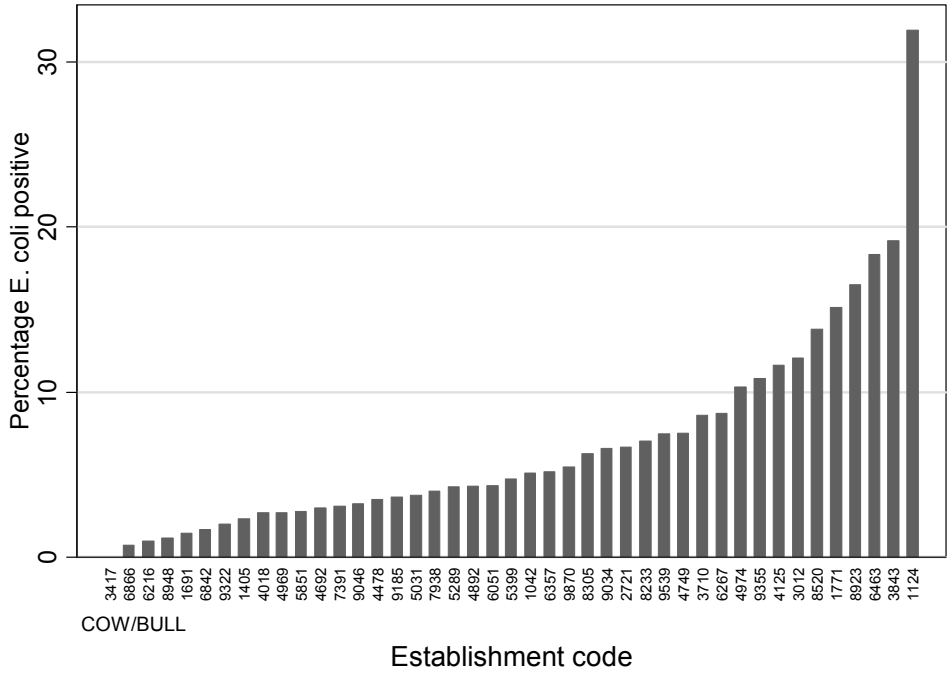

Figure 3.15b. Establishment specific values for percent of COW/BULL carcases giving positive test results for *E. coli*, over the entire study period (years 2000 to 2005, establishments submitting less than 50 test results excluded).

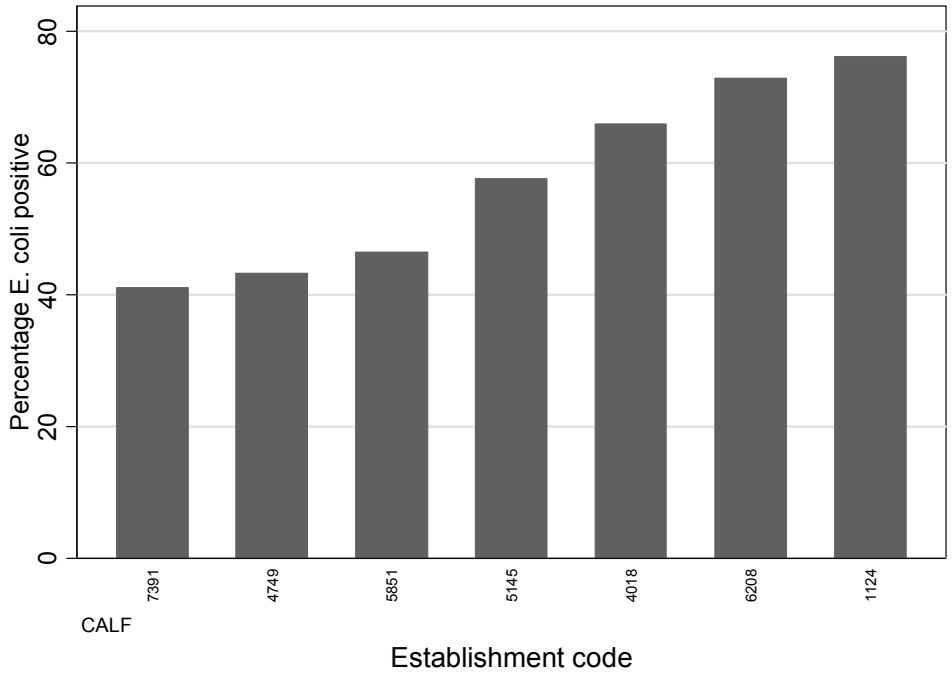

Figure 3.15c. Establishment specific values for percent of CALF carcases giving positive test results for *E. coli*, over the entire study period (years 2000 to 2005, establishments submitting less than 50 test results excluded).

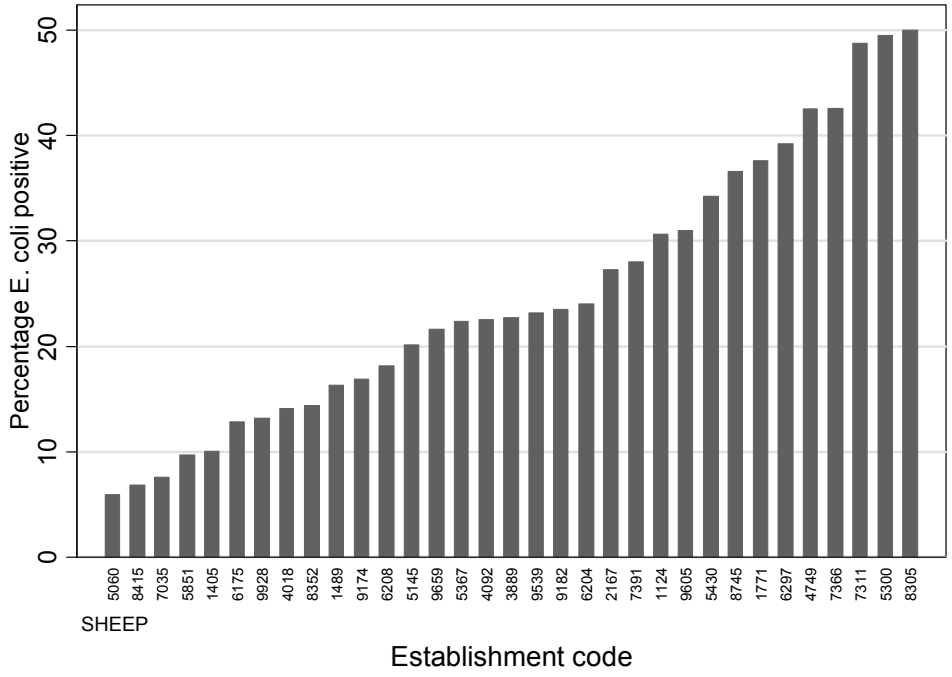

Figure 3.15d. Establishment specific values for percent of SHEEP carcases giving positive test results for *E. coli*, years 2000-2005 (establishments submitting less than 50 test results excluded).

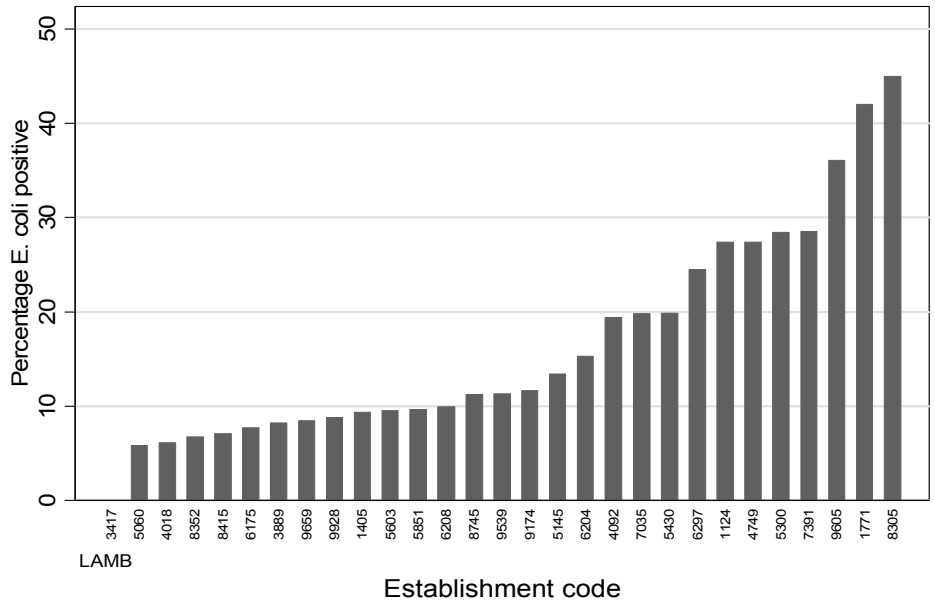

Figure 3.15e. Establishment specific values for percent of LAMB carcases giving positive test results for *E. coli*, years 2000-2005 (establishments submitting less than 50 test results excluded).

3.4 Overview of Salmonella data

The data on detection of Salmonella has the following important attributes:
Collection of data on Salmonella is compulsory (as for E. coli).

- The data only describes presence versus absence of Salmonella in the swab samples (dichotomous data).
- Data is collected at the specified interval for each species. Thus establishments are represented in the data base according to their level of production.
- Specimens for Salmonella detection are processed at accredited laboratories by approved methods.
- Detection is quite rare particularly in swabs from cattle carcases. As in the case of E. coli, the low rate of occurrence of Salmonella in swabs makes it difficult to identify methods for improving the process.
- Analysis of data on Salmonella has some similarities to E. coli, particularly with respect to STEER/HEIFER and COW/BULL carcases. This is because E. coli detection is rare and Salmonella detection is very rare.

Samples, establishments and species

A total of 65,959 conclusive tests were performed for Salmonella (all species). The distribution of number of observations amongst different classes of carcases for the entire study period is shown for red meat species in Figure 3.16. Also shown are crude percentages of positive test for Salmonella by carcase species for the entire study period (Figure 3.17), by year and carcase species (Figure 3.18) and by geographic region and carcase species (Figure 3.19). Figures 3.20a to 3.20e show establishment specific percentage of carcases tests positive for Salmonella for each species.

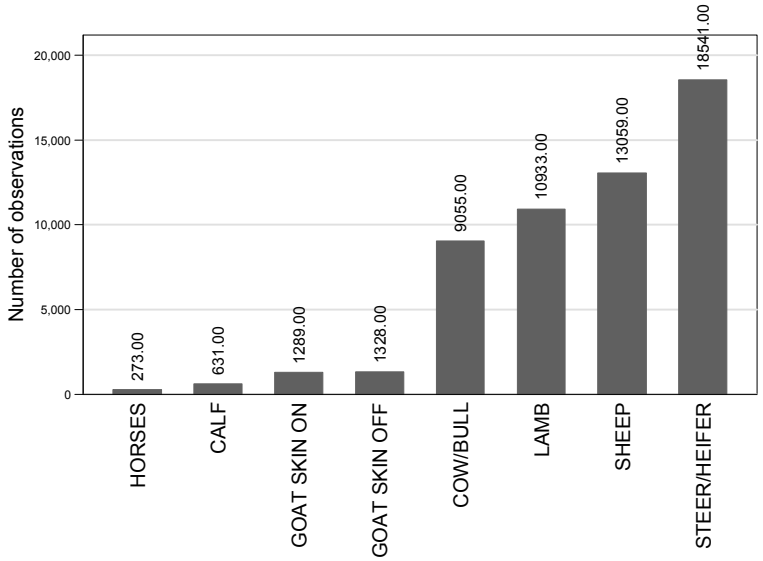

Figure 3.16. Number of *E. coli* submissions to ESAM (including zero counts) for various red meat species for the period 1 Jan 2000 to 31 Dec 2005.

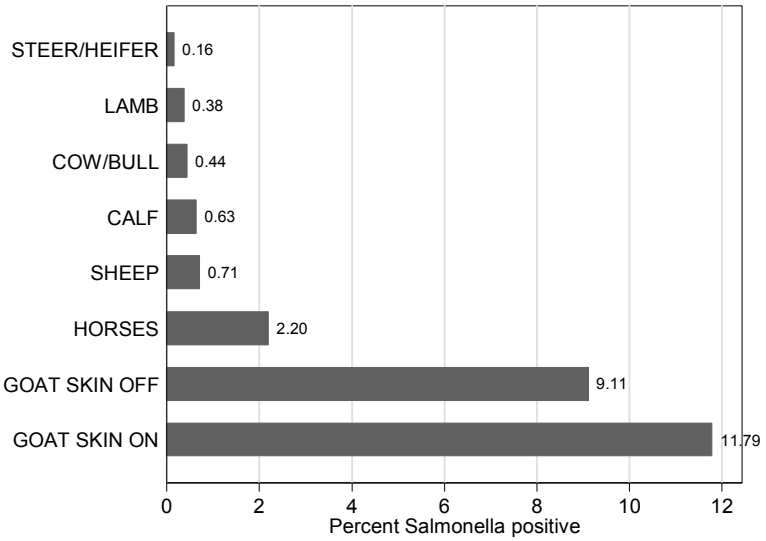

Figure 3.17. Overall prevalence of carcase tests positive for *Salmonella* for the period 2000-2005 by species of carcase.

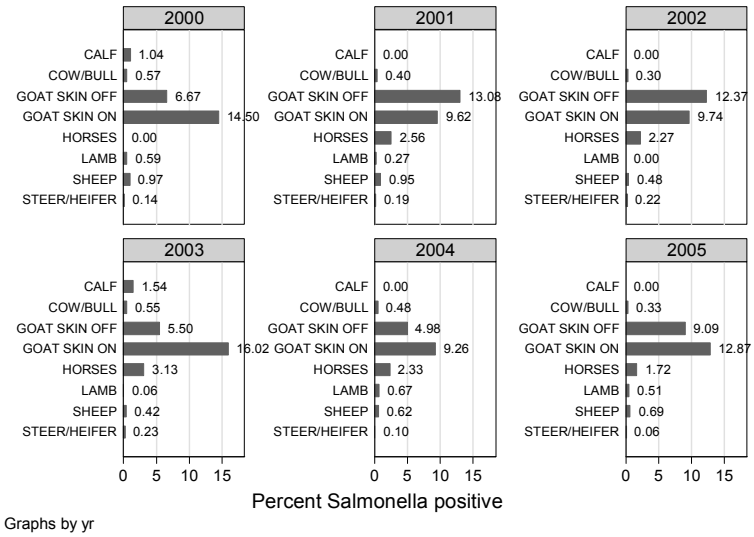

Figure 3.18. Prevalence of carcase tests positive for *Salmonella* by species of carcase by year.

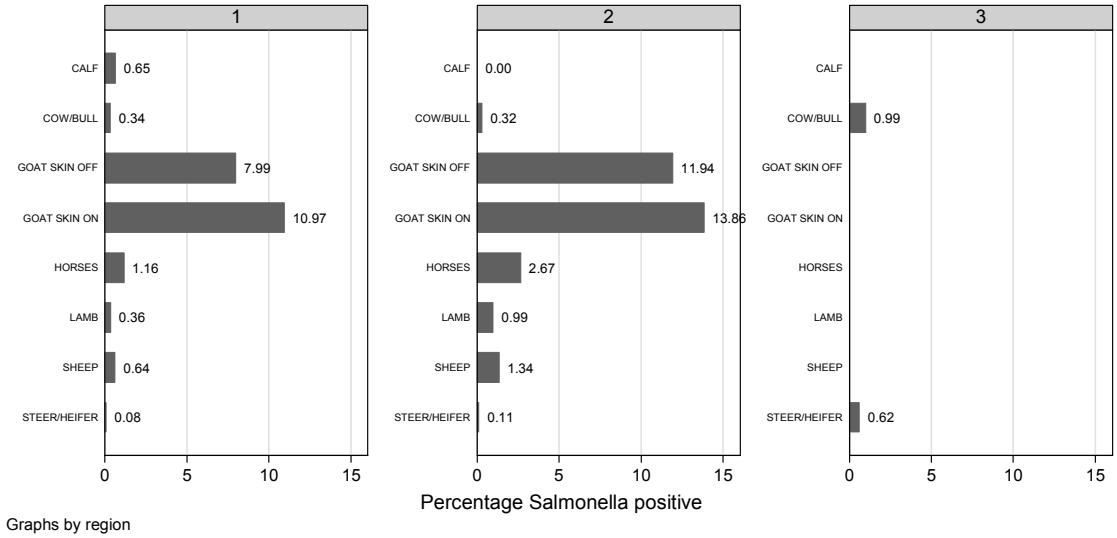

Figure 3.19. Percentage of carcase tests positive for *Salmonella* from 2000 to 2005 by carcase species and by region. Region 1 is south of latitude 30° S, Region 2 is between latitudes 30° S and the tropic of Capricorn, Region 3 is north of the tropic of Capricorn).

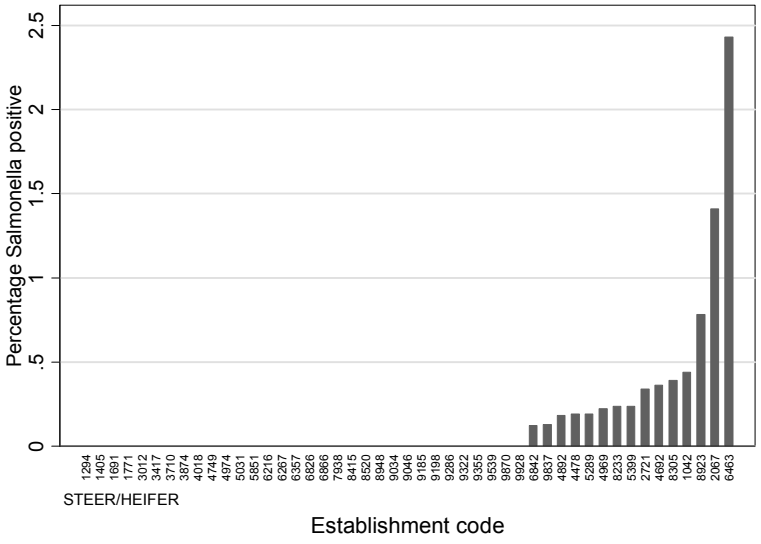

Figure 3.20a. Establishment specific values for percent of STEER/HEIFER carcases giving positive test results for *Salmonella*, years 2000-2005 (establishments submitting less than 10 test results excluded).

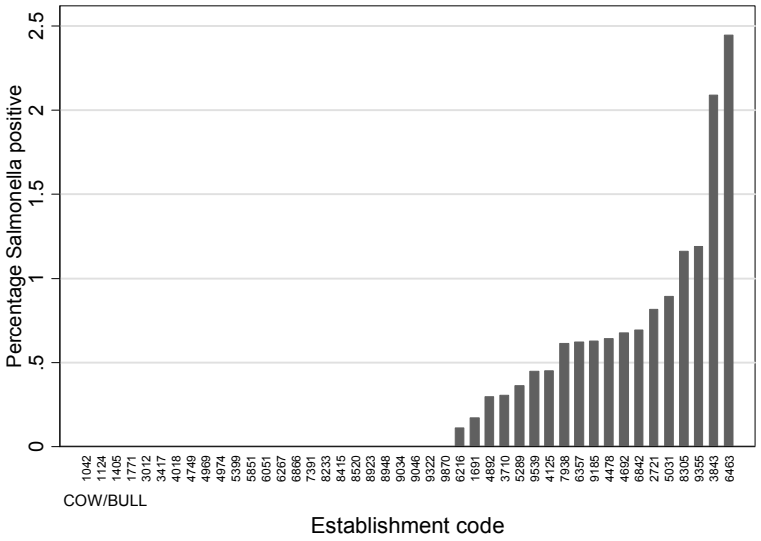

Figure 3.20b. Establishment specific values for percent of COW/BULL carcases giving positive test results for *Salmonella*, years 2000-2005 (establishments submitting less than 10 test results excluded).

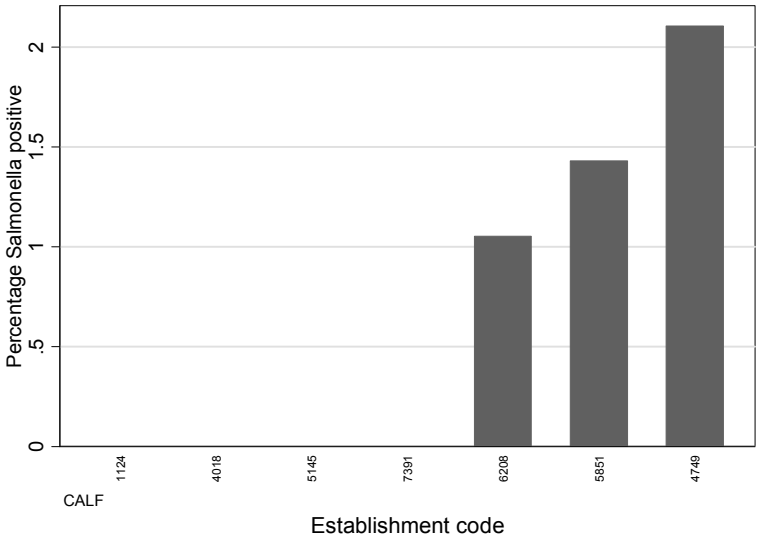

Figure 3.20c. Establishment specific values for percent of CALF carcases giving positive test results for *Salmonella*, years 2000-2005 (establishments submitting less than 10 test results excluded).

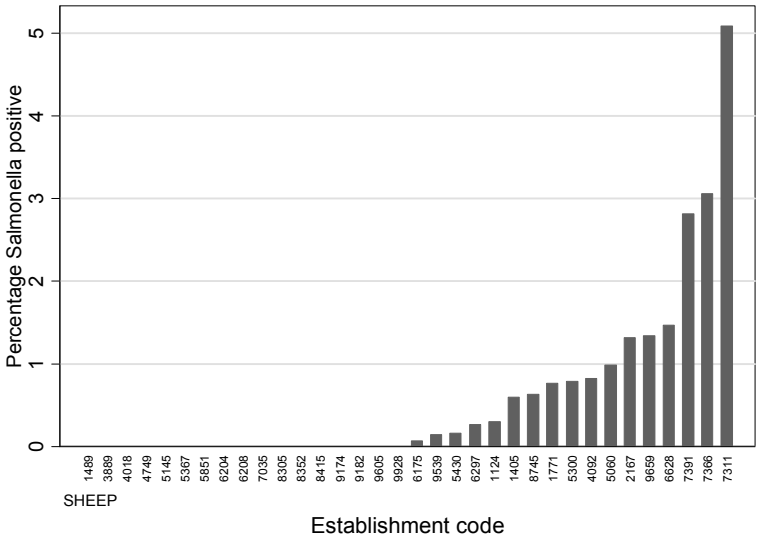

Figure 3.20d. Establishment specific values for percent of SHEEP carcases giving positive test results for *Salmonella*, years 2000-2005 (establishments submitting less than 10 test results excluded).

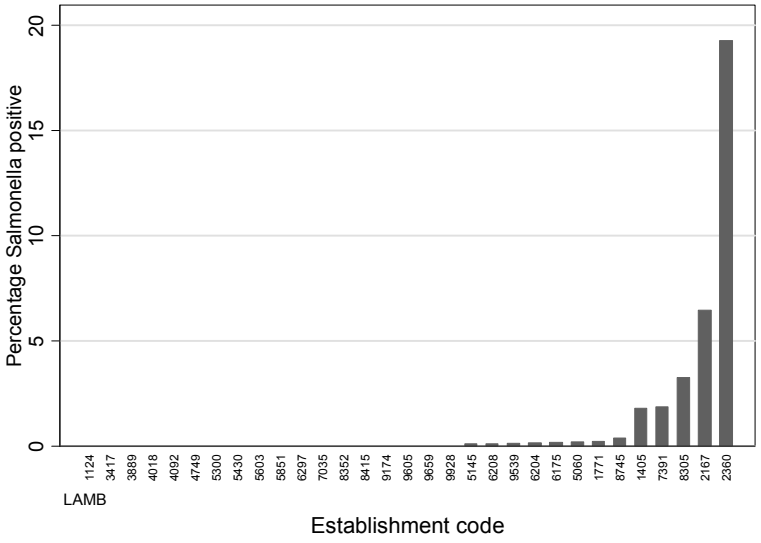

Figure 3.20e. Establishment specific values for percent of LAMB carcases giving positive test results for *Salmonella*, years 2000-2005 (establishments submitting less than 10 test results excluded).

4 Time series analysis of aggregated data

4.1 Introduction

Time series analyses are useful for describing data, explaining variations in the data over time, predicting future patterns in the data and as a tool in managing quality issues in a production process (3). In this section the ESAM data are aggregated across establishments and where appropriate subjected to time series analysis. For log TVC the outcome is the median value on each calendar day of the study period. For *E. coli* cfu.cm^{-2} the outcome of interest is the percentage of tests positive for *E. coli* on each calendar day. *Salmonella* is treated in the same manner as *E. coli*. Analysis is performed separately for each species of carcase being produced. The objectives are to provide basic descriptive overview of changes over time, assess the occurrence of seasonal variation, and note any features of the data relevant to the control of microbial contamination on carcases.

The aggregated ESAM data on detection of *E. coli* is very suitable for time series analysis and for forming a national picture on trends over time. This is because it is compulsory for establishments to collect samples at a set interval (number of carcases) then submit these to testing according to defined protocols in accredited laboratories. Thus the data is provided with very few deficiencies due to missing values, establishments are represented in the data according to the amount of production they contribute to the national output of carcases, and quality of measurements are higher than in the case of voluntary testing in non-accredited laboratories (as happens for enumeration of TVC). Nevertheless, some care is always needed in interpretation of the data from swab or excision testing of carcases for microbiological contaminants as the findings only relate to a particular region of the particular carcases tested.

4.2 Method

In these analyses the data on detection (generic *E. coli* and *Salmonella*) and enumeration (log TVC cfu.cm^{-2}) are separated out for each species of carcase and subjected to the following analysis. For *Salmonella* and generic *E. coli*, for each calendar day of the study period the percentage of tests positive for *E. coli* is calculated for all the data pooled across all establishments testing that particular kind of carcase on that day. Here the outcome for each day is then the percent of carcase swabs positive for *E. coli* or *Salmonella*. In the case of log TVC cfu.cm^{-2} it is the median value of all of the data from the pooled observations that is the outcome of interest. It is expected that these quantities could each vary substantially with time and so the data are subsequently processed in several ways using a time series plot:

a) The raw time series data is plotted against time. For median log TVC cfu.cm^{-2} and generic E. coli the data from each year of the study period is graphed as a separate time series and then each of these six plots (for each year) are assembled one under the other in chronological order. In the case of salmonella only a single plot is produced this covering all six years of data.
b) Before plotting as above, the raw time series data is subjected to a 31 day (monthly) moving window average (effectively a rolling average of 31 days) to smooth out excessive variation in the data that interferes with recognition of seasonal and long term trends.
c) Where necessary 91 day (quarterly) moving window average is derived and plotted to more clearly demonstrate seasonal effects.

Extensive analysis of the aggregated TVC data is not performed here because of the data quality issues identified earlier in this report. Only an example analysis is performed for SHEEP carcases, this to highlight the substantial potential for enhancing ESAM by promoting the need for higher quality TVC data.

4.3 Results

The findings for time-series analysis are an extension on the more basic descriptive analysis provided earlier in this report. In the results reported here much more information on the pattern of temporal change in outcome (log TVC cfu.cm^{-2}, *E. coli* detection and *Salmonella* detection) is revealed. Plots specific for each class of carcase are shown in separate figures. Where the plots consist of yearly panels stacked vertically this is to make it convenient to assess whether or not there are seasonal patterns repeated throughout the study period. An important feature to notice in each plot is the extent of variation in the outcome in the short and long term.

Descriptive time series of aggregated log TVC data (caveats apply)

In this section we provide a simple time-series descriptions for log TVC cfu.cm^{-2} data from SHEEP carcases. Again we emphasise that interpretation is greatly constrained due to the earlier detailed caveats for TVC data. While it is possible to produce similar plots for other species these are not presented because of the earlier detailed caveats and because mere presentation of these plots could invite inappropriate interpretation and false conclusions. The time series analysis on sheep is provided as an example of the opportunity for future analysis should the collection of TVC data improve.

In time series analysis, we need to use a single figure to summarise the outcome for each time step in the study period. In these plots the time step is equivalent to one day (calendar date) and the outcome is the median of the log TVC cfu.cm^{-2} for all entries in the data base for that day (i.e. the national median of log TVC cfu.cm^{-2} on each day). Another issue encountered in time-series is the need to smooth the data to remove excessive and nuisance variation that interferes with the interpretation of medium and long term trends. In descriptive analyses, we use a “moving-average-window” whereby the smoothed value for any day is the average of the value for that day and h days either side. Thus, a 31 day moving average has a value of h=15 and has a window width of approximately one month. Increasing and decreasing h results in an increase and decrease in the amount of smoothing respectively. Although the value of h is arbitrary, we generally use the monthly window (h = 15) and a quarterly (ninety-one day) window (h = 45). In Figure 4.1. we show the log TVC cfu.cm^{-2} data for SHEEP as a time series with different amounts of smoothing.

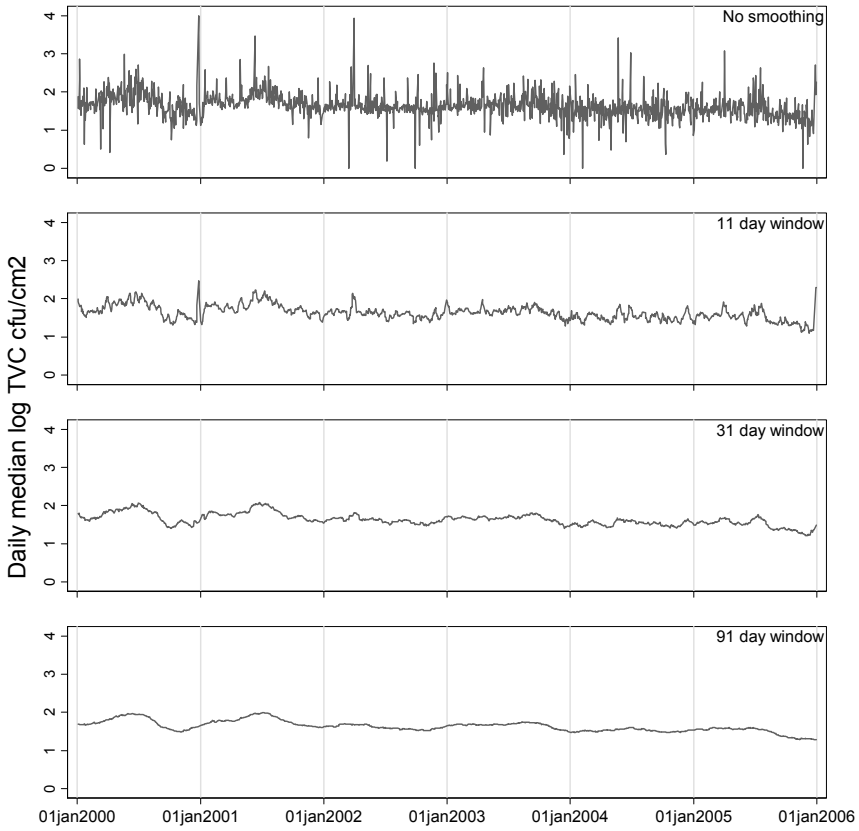

Figure 4.1. Time series of the daily median of log TVC cfu.cm^{-2} (presumed) for SHEEP with different amounts of smoothing, showing how increasing the smoothing reduces the noise but also removes the features of the data that may provide useful interpretation.

In the above plots, 31 day smoothing seems useful because it does not destroy all the variation that is present but does not exhibit so much variation as to make interpretation difficult. A problem with the above plots is that the x-axis (time) scale is compressed and this interferes with the ability to detect patterns of variation. More useful plots for assessing season and year variation are provided in Figure 4.2 where each year is given as a separate plot and plots are stacked vertically so that seasonal patterns can be examined. This effectively gives more exaggeration in the y-axis direction to help with interpretation.

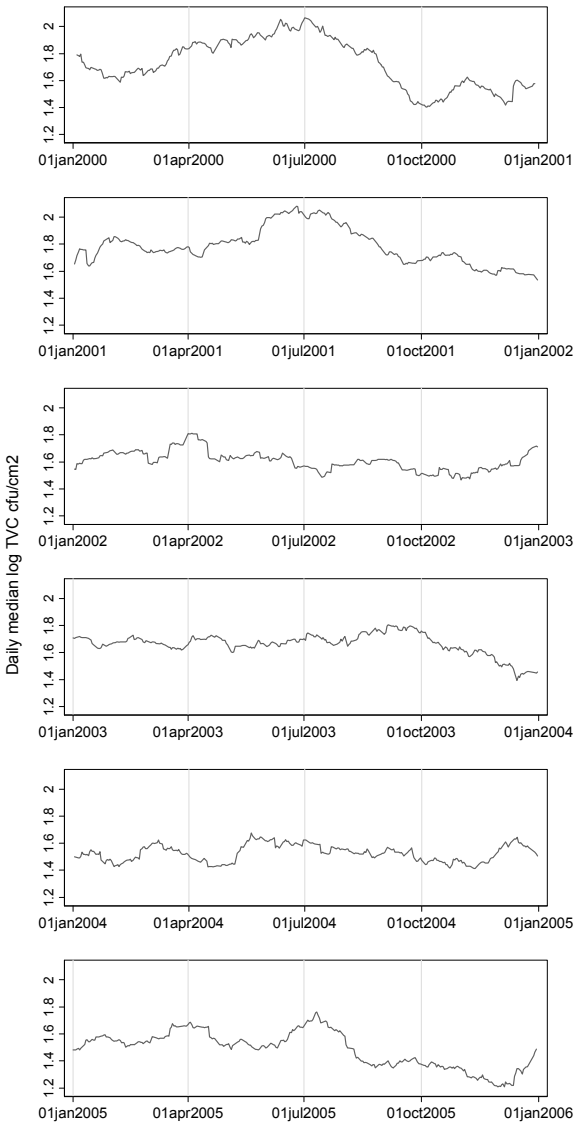

Figure 4.2. Six panel plot of time series data for SHEEP, one panel for each year of the study data, showing median log TVC cfu.cm^{-2} smoothed using a 31 day moving average window. By spreading the data over six panels it is possible to show greater detail in the variability on the y-axis compared to the previous figure.

One use for the above data is to define performance standards from historical data. Performance standards could be widely disseminated to the industry on a periodic basis along with information to each establishment on its own performance over the same time period.

Descriptive time series analysis of E. coli detection by species

The data on *E. coli* can be analysed as a proportion of tests yielding positive results. For *E. coli* the data on density per unit area of carcase is less useful because *E. coli* counts are frequently zero (although this varies with species of carcase). The techniques used in the following time series are similar to those used for log TVC cfu.cm^{-2} except that the outcome is the percentage of tests for *E. coli* being positive, this percentage derived from an aggregate of the data from all establishments on each day of the study period. Below is presented a sequence of time series plot for each carcase with and without smoothing of the data on percentage of *E. coli* detections.

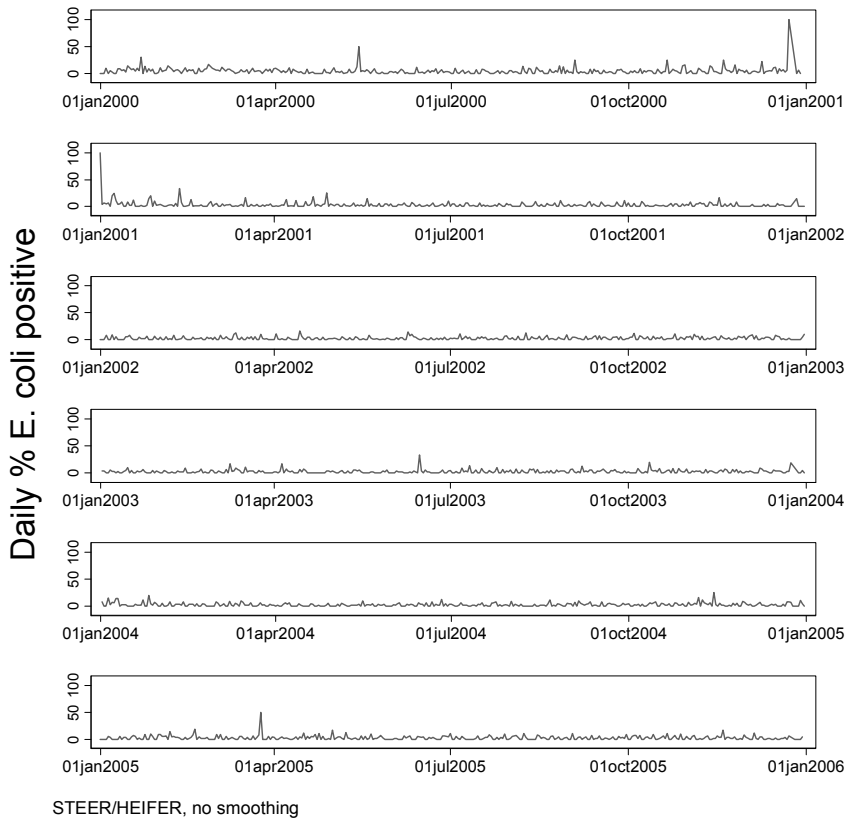

Figure 4.3a. Time series of the percentage of STEER/HEIFER carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) depicted without any application of smoothing algorithms.

Interpretive notes: Of interest are two dates (23 December 2000 and 01 January 2001) where there was a 100% detection rate. On both of these dates only one test was recorded for STEER/HEIFER carcases and both of these tests were positive. This feature of the data demonstrates one of the utilities of applying smoothing algorithms as shown in the next figure. The variation in the data is difficult to see because the two 100% spikes force the plots to be drawn with a y-axis scale unsuitable for showing detail. Nevertheless, detections are very low as reflected in the earlier analysis and there is no suggestion of a seasonal trend in the data.

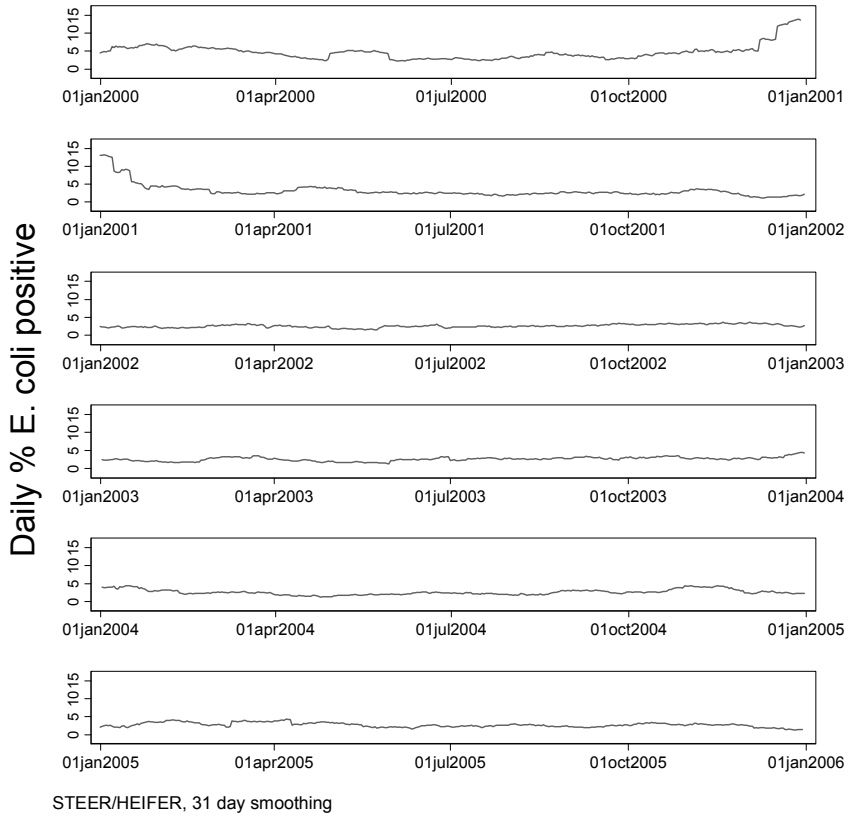

Figure 4.3b. Time series of the percentage of STEER/HEIFER carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 31 day moving average.

Interpretive notes: Here the larger spikes of the previous figure have been smoothed to a reduced size. The underlying proportion of test positive results is gently undulating but has no apparent seasonal pattern.

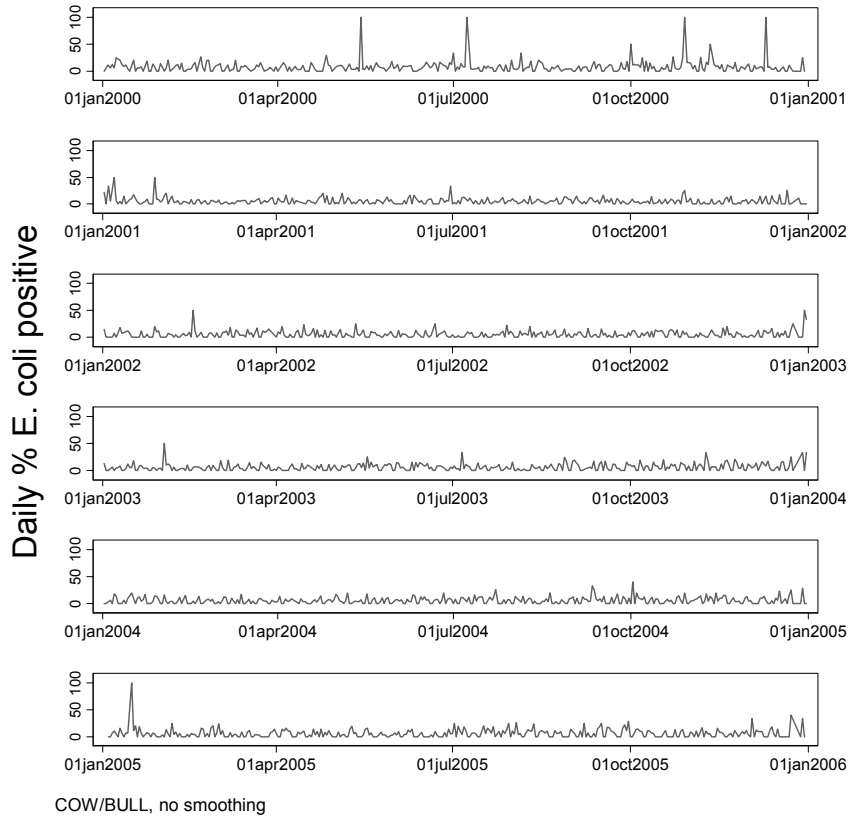

Figure 4.3c. Time series of the percentage of COW/BULL carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) depicted without any application of smoothing algorithms.

Interpretive notes: Similar to STEER/HEIFER but with a higher average percentage positive.

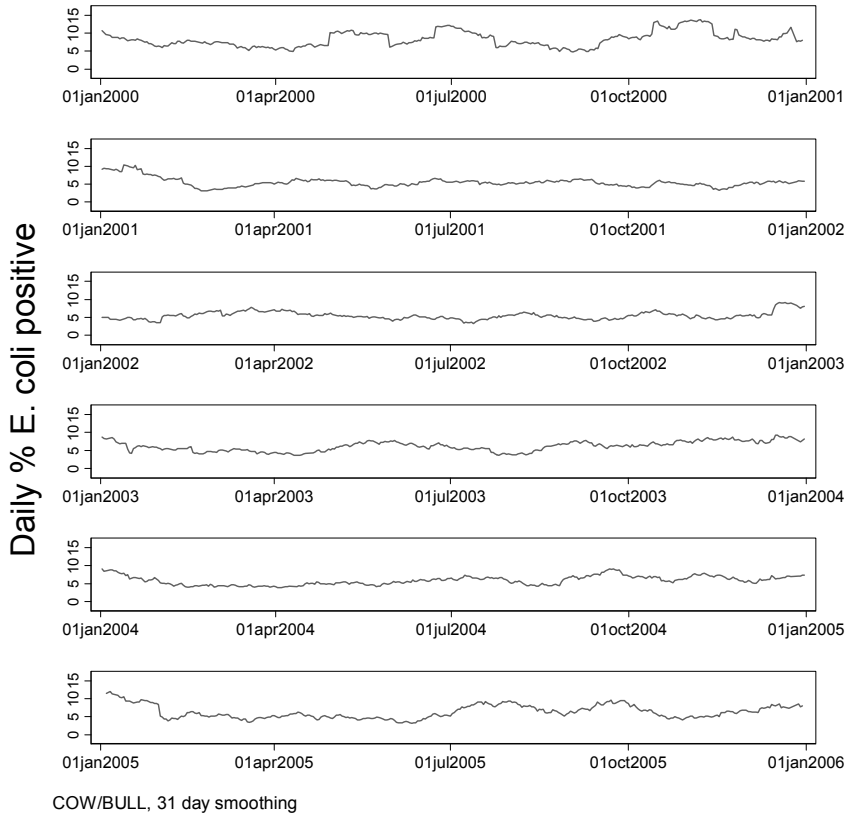

Figure 4.3d. Time series of the percentage of COW/BULL carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 31 day moving average .

Interpretative notes. After smoothing there is greater undulation than in STEER/HEIFER reflecting greater underlying variability. It is unclear if there is a seasonal effect or not.

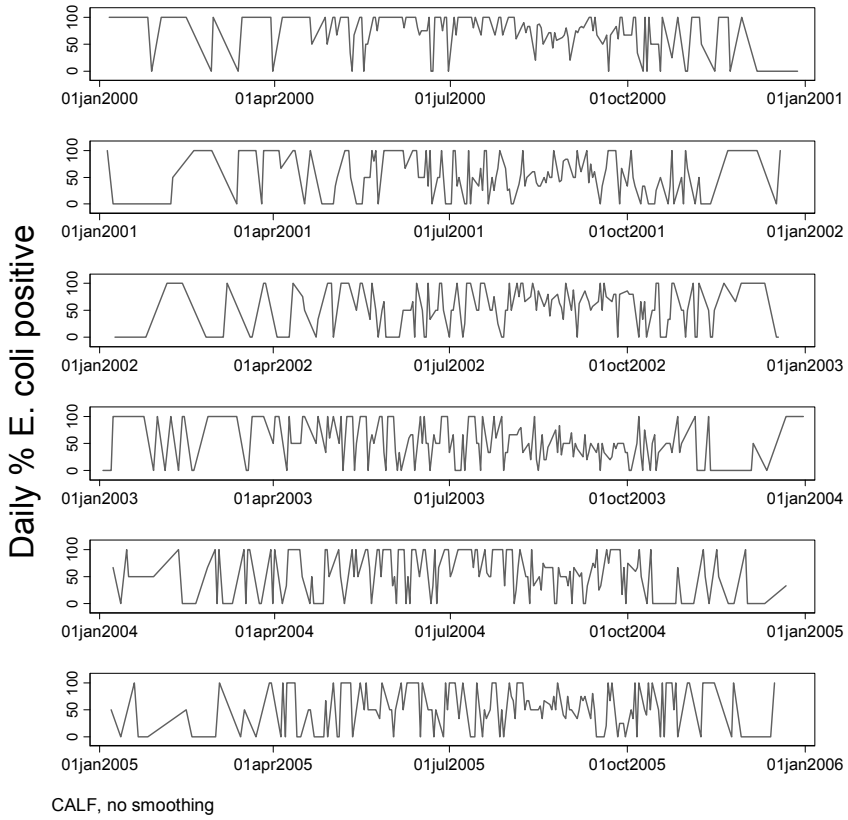

Figure 4.3e. Time series of the percentage of CALF carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) depicted without any application of smoothing algorithms.

Interpretive notes: excessively large variation in this data are due to variation in the number of calves being processed resulting in smaller numbers of test observations on some calendar dates this combined with an underlying mean prevalence of close to 50% results in substantial deviations from the mean.

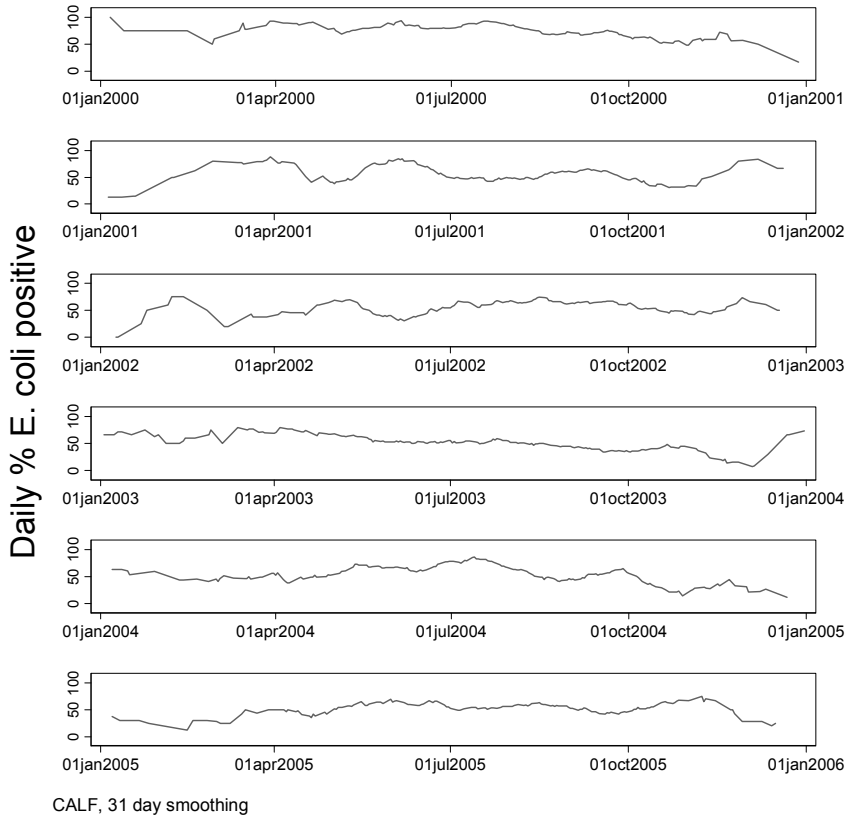

Figure 4.3f. Time series of the percentage of CALF carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 31 day moving average

Interpretive notes: excessively large variation of the previous figure has been removed by smoothing revealing undulation without an obvious seasonal effect.

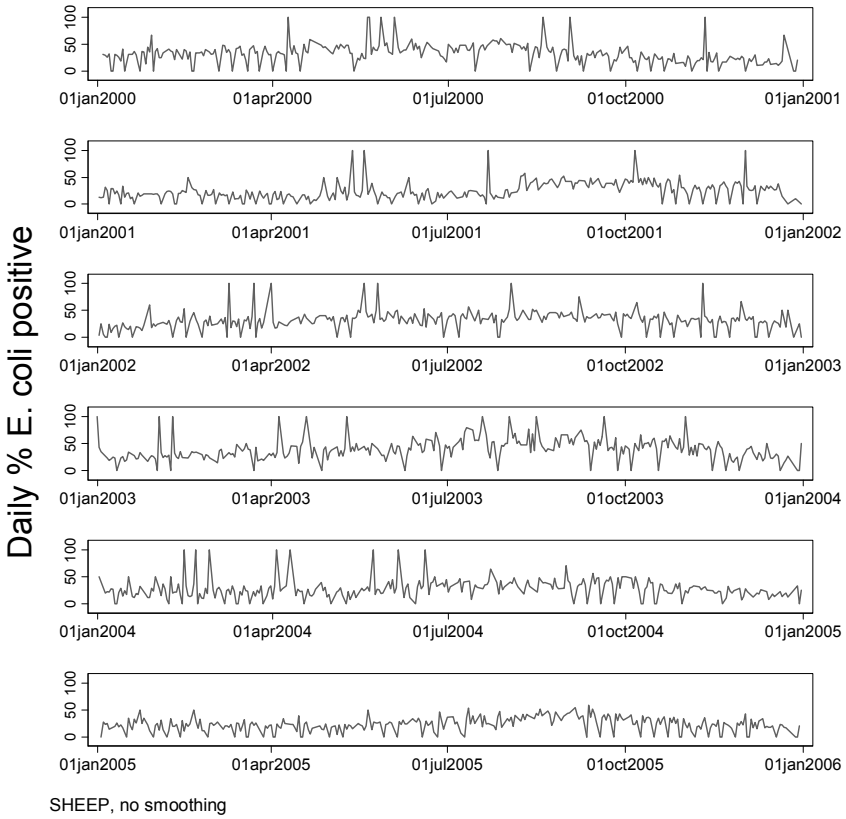

Figure 4.3g. Time series of the percentage of SHEEP carcases test positive for E. coli, from 2000 to 2005 inclusive (one year per panel) depicted without any application of smoothing algorithms.

Interpretive notes: There is a suggestion of higher frequency of positive tests in the mid-year period but excessive noise in the time-series curve makes confirmation of such a trend difficult without further analysis.

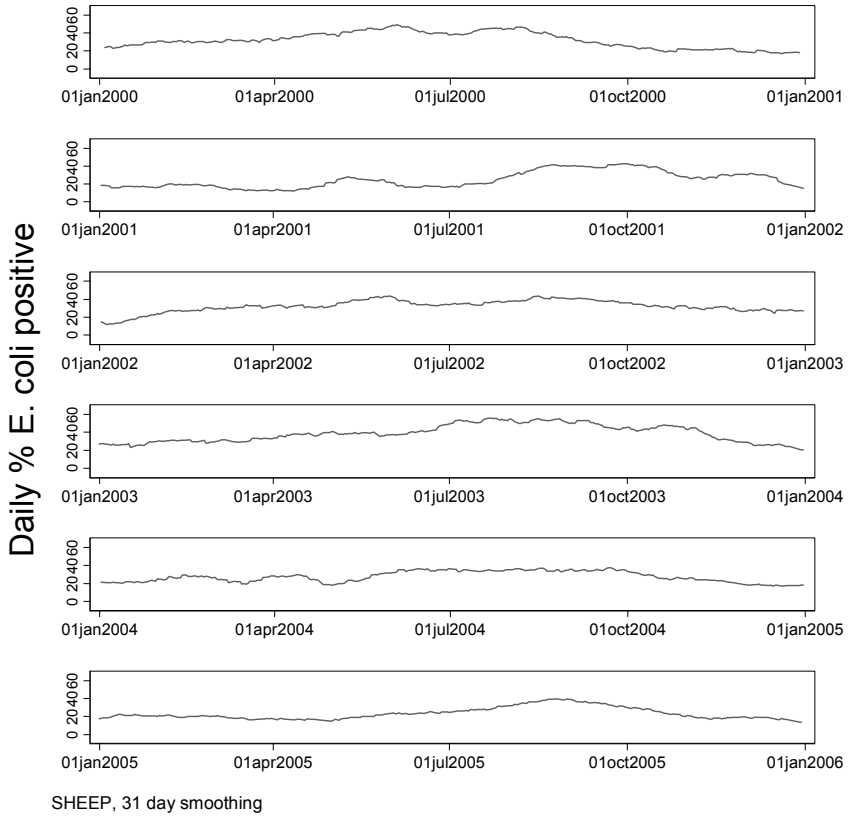

Figure 4.3h. Time series of the percentage of SHEEP carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 31 day moving average

Interpretive notes: After smoothing of the data in the previous figure, it appears very likely that during the mid-year the frequency of positive *E. coli* tests is higher than at other times of the year for SHEEP carcases. Further confirmation of the seasonal effect is sought with the next figure.

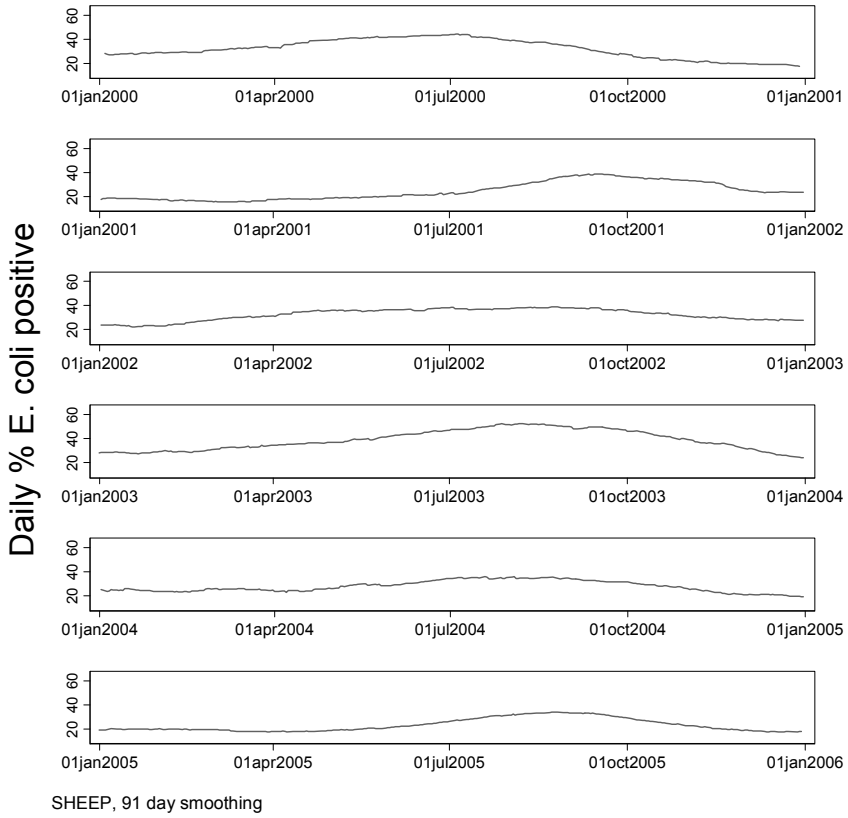

Figure 4.3i. Time series of the percentage of SHEEP carcases test positive for E. coli, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 91 day moving average.

Interpretive notes: More distinctive evidence of a regularly recurring mid-year peak in frequency of positive E. coli test results from SHEEP carcases is displayed in this figure.

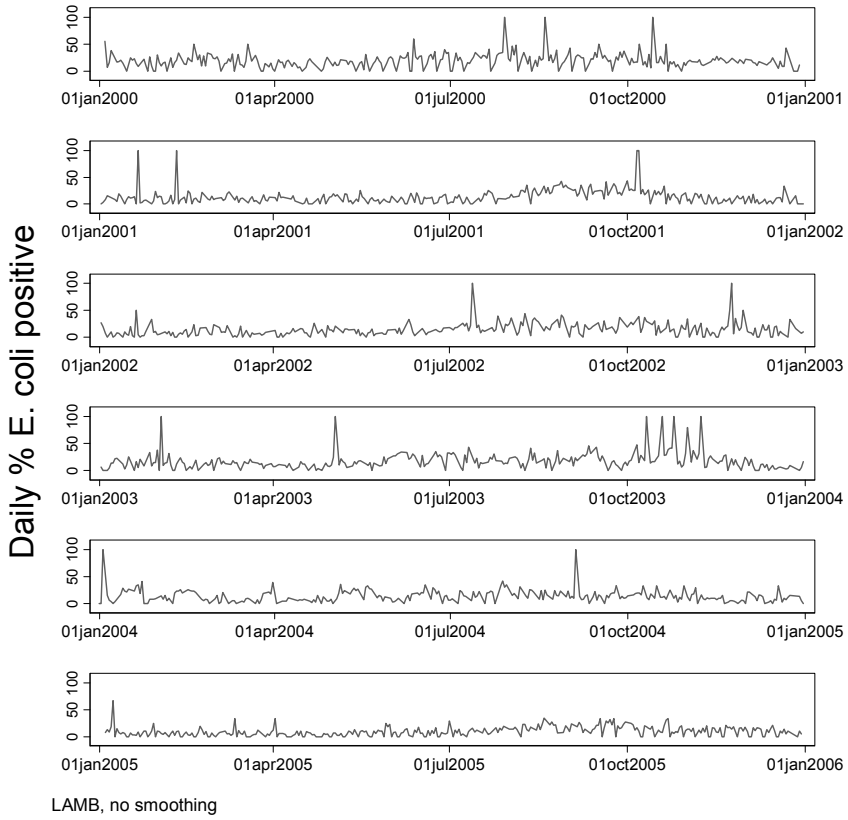

Figure 4.3j. Time series of the percentage of LAMB carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) depicted without any application of smoothing algorithms.

Interpretive notes: In LAMB carcases as in SHEEP carcases there is again a suggestion of a mid-year peak in frequency of positive *E. coli* test results. The effect is further investigated in following figures.

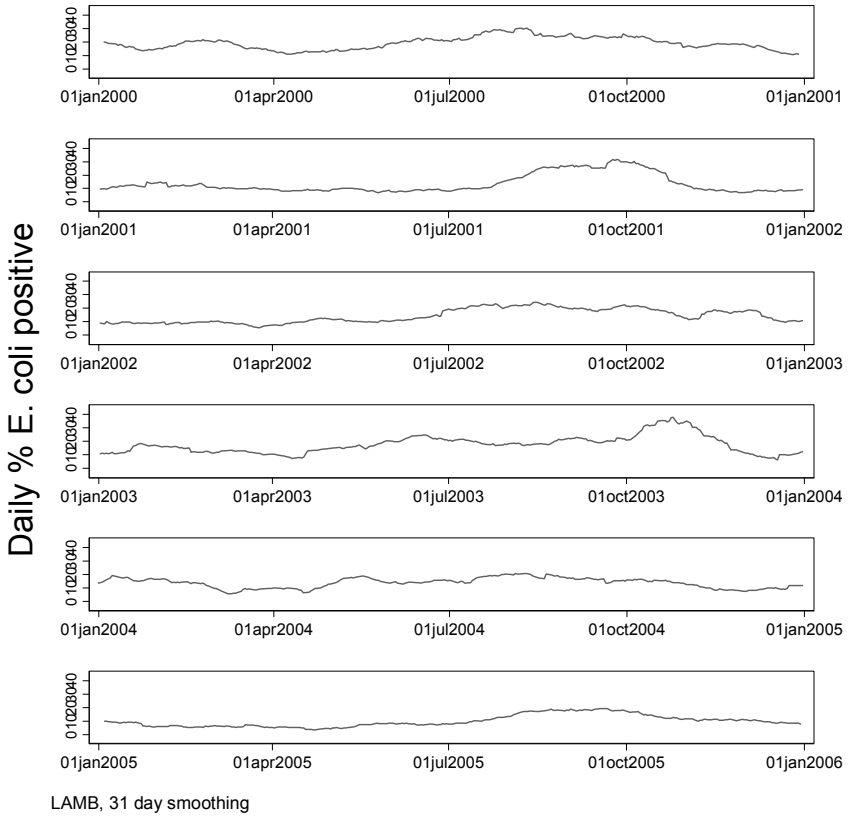

Figure 4.3k. Time series of the percentage of LAMB carcases test positive for *E. coli*, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 31 day moving average.

Interpretive notes: Similar to SHEEP carcases there is a distinct tendency for the frequency of positive tests for *E. coli* from LAMB carcases to be higher in the spring time. Further confirmation of the seasonal effect is sought in the following figure.

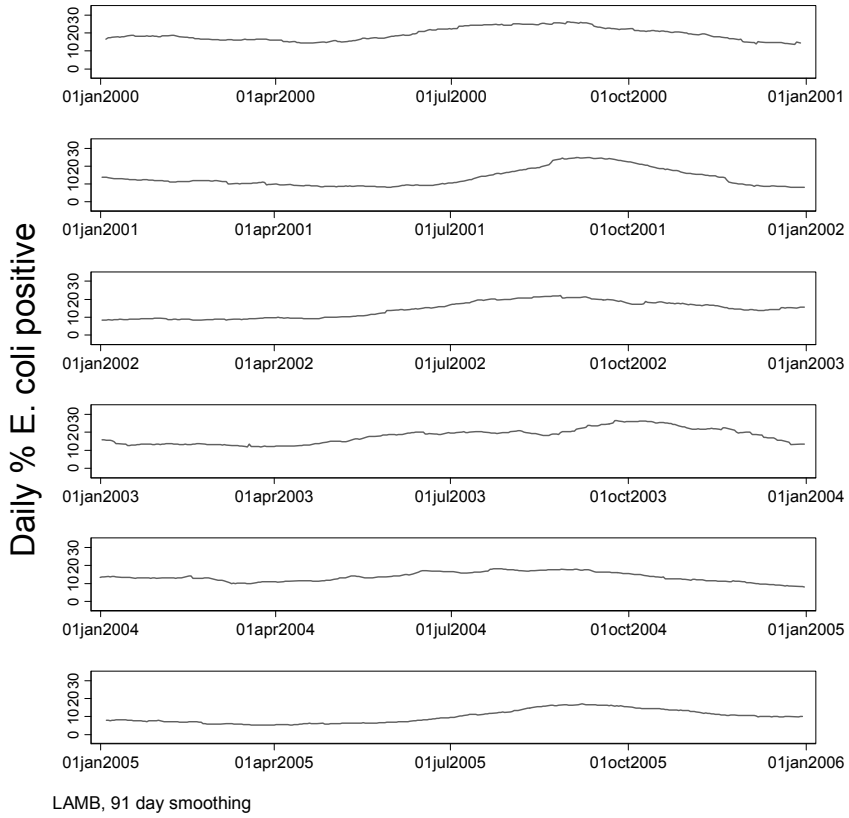

Figure 4.3l. Time series of the percentage of LAMB carcases test positive for E. coli, from 2000 to 2005 inclusive (one year per panel) with data smoothed using a 91 day moving average.

Interpretive notes: After applying the 91 day moving average smoothing filter, there is clear evidence of a winter-spring peak in frequency of positive tests for E. coli on lamb carcases.

Descriptive time series analysis of *Salmonella* detection by species

In this section we present findings from a similar analysis to the above but with the outcome being the proportion of tests for *Salmonella* that yield positive results. The data used for this is aggregated across all establishments to give a national picture of how the occurrence of *Salmonella* varies with time. Because *Salmonella* is comparatively rare compared to *E. coli* the entire study period is represented in a single plot, rather than being divided into a plot for each year. The data are smoothed using 11, 31 and 91 day moving averages (windows) to assist interpretation.

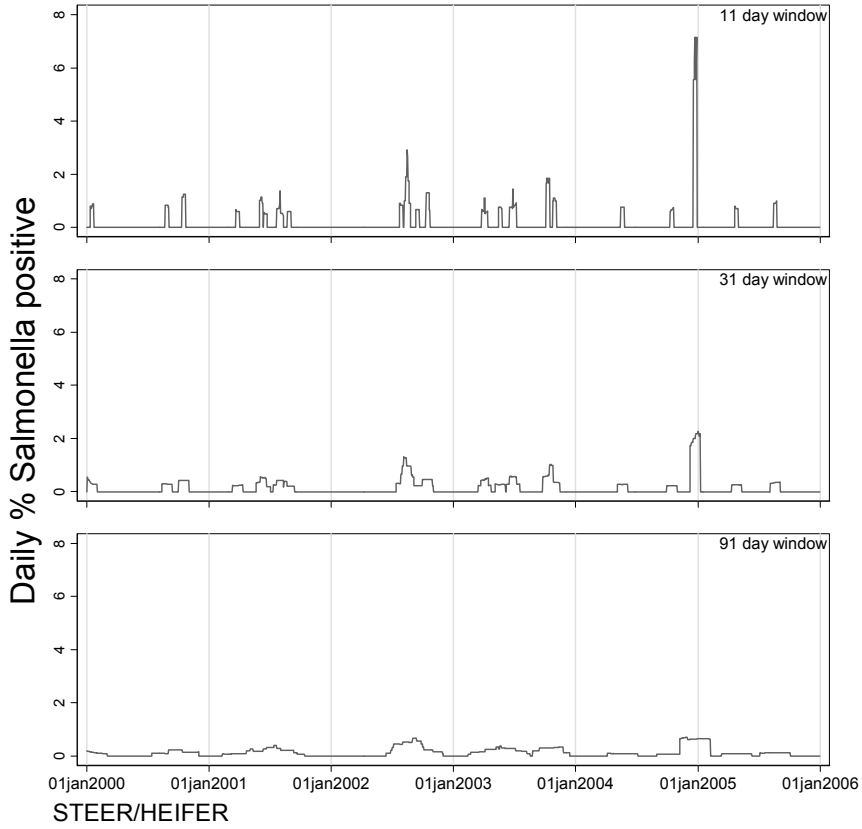

Figure 4.4a. Time series of Salmonella detection on STEER/HEIFER carcases for the entire study period with data aggregated from all establishments. Smoothing has been performed using 11, 31 and 91 day windows of moving average.

Interpretive notes: There is a suggestion of a seasonal effect with Salmonella being detected more often in the cooler months, although January 2005 is an exception.

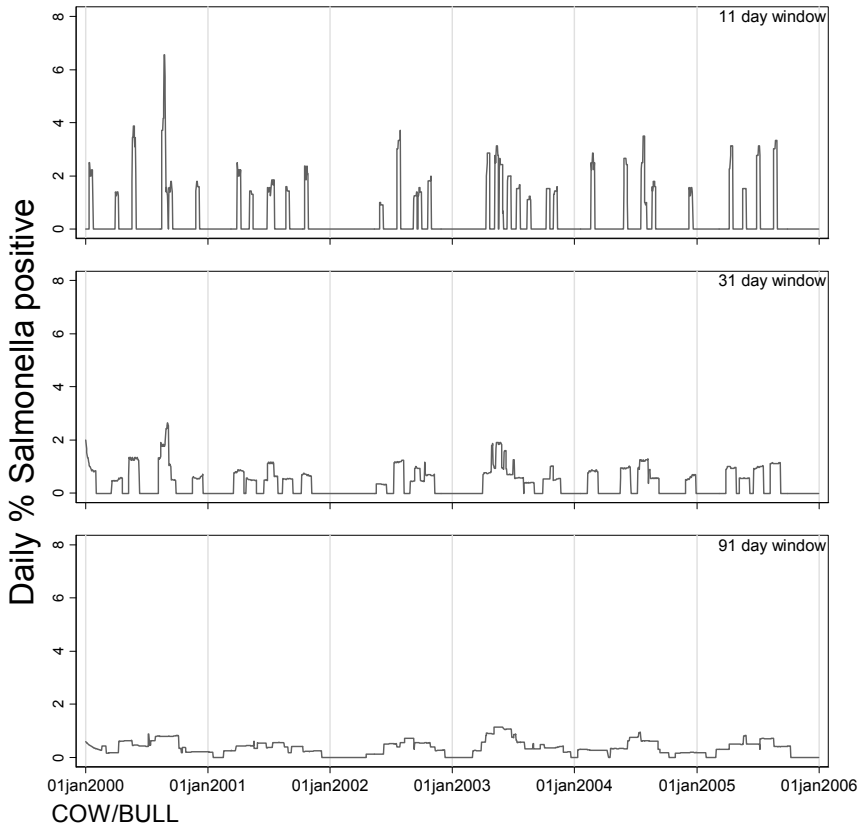

Figure 4.4b. Time series of *Salmonella* detection on COW/BULL carcases for the entire study period with data aggregated from all establishments. Smoothing has been performed using 11, 31 and 91 day windows of moving average.

Interpretive notes: There is evidence of a seasonal effect with *Salmonella* being detected more often in the cooler months. The effect with COW/Bull carcases is more marked than with STEER/HEIFER and presumably reflects the higher degree of microbial contamination as measured by indicator groups.

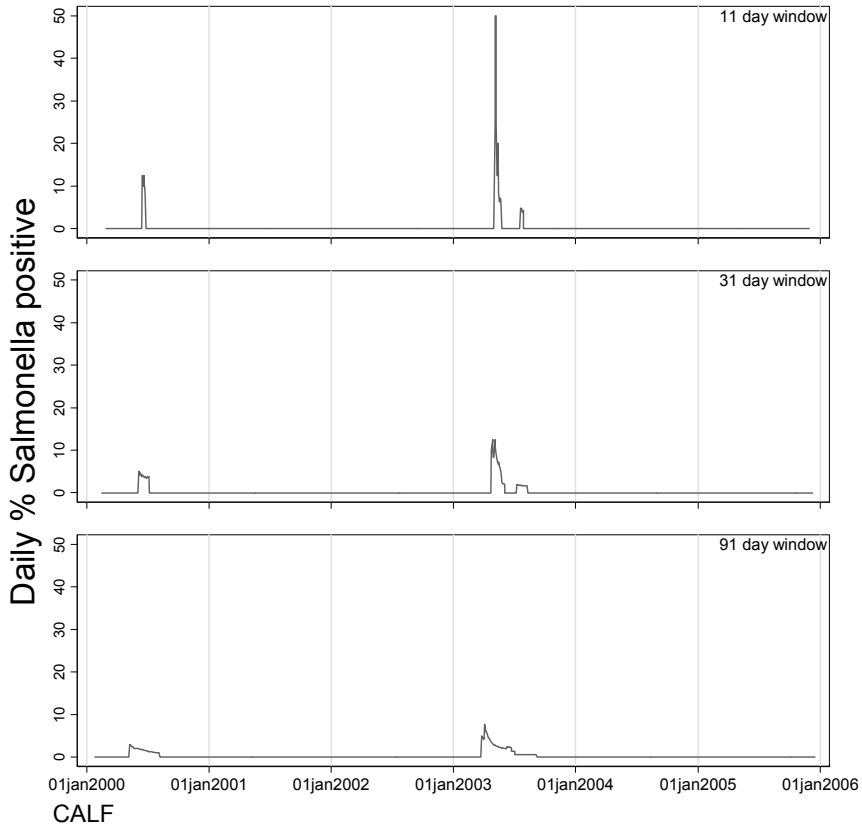

Figure 4.4c Time series of Salmonella detection on CALF carcases for the entire study period with data aggregated from all establishments. Smoothing has been performed using 11, 31 and 91 day windows of moving average.

Interpretive notes: Salmonella is detected too infrequently on CALF carcases to comment decisively about seasonality of detection. However, the observed data are consistent with the Salmonella being detected more frequently in cooler months.

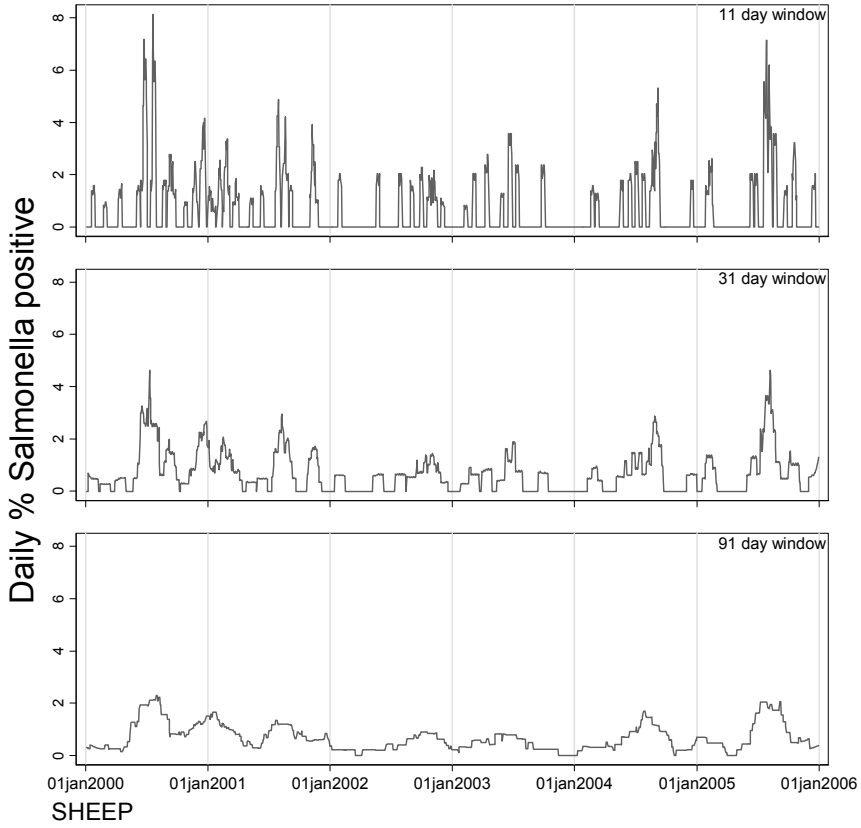

Figure 4.4d. Time series of Salmonella detection on SHEEP carcases for the entire study period with data aggregated from all establishments. Smoothing has been performed using 11, 31 and 91 day windows of moving average.

Interpretive notes: Similar to COW/BULL and STEER/HEIFER carcases there is evidence of a seasonal effect with Salmonella being detected more often in the cooler months. This seasonal Salmonella effect is more pronounced with SHEEP carcases than with other classes of carcase.

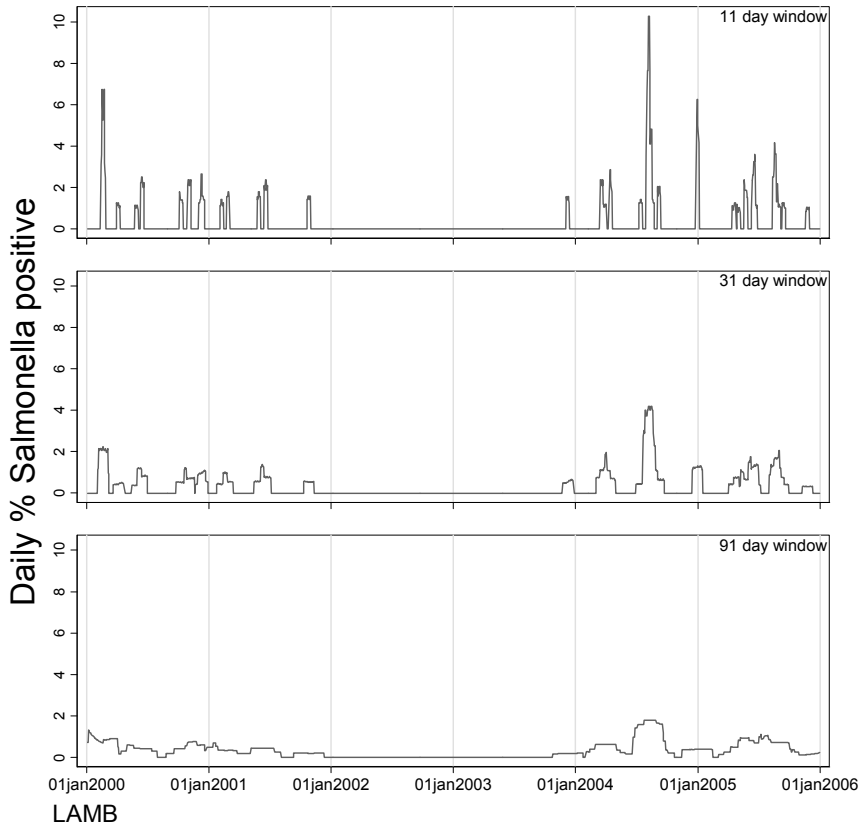

Figure 4.4e. Time series of *Salmonella* detection on LAMB carcases for the entire study period with data aggregated from all establishments. Smoothing has been performed using 11, 31 and 91 day windows of moving average.

Interpretive notes: Again there is evidence of a seasonal effect with Salmonella being detected more often in the cooler months. The sparsity of positive results for years 2002 and 2003 make this effect less pronounced for LAMB carcases compared to SHEEP carcases.

4.4 Discussion

From the results it can be seen that the ESAM outcome providing the greatest information in variation in carcase hygiene is TVC, this being similar to previous baseline studies (8-11). For this reason log TVC.cm-2 is well suited to time series analysis both at the aggregate and individual establishment levels. However, the currently available data on TVC does not appear suitable for aggregation and analysis by time series due to issues with data quality mentioned earlier in this report. Consequently, the results for time series of TVC data are restricted to an example plot for sheep to demonstrate the utility of the TVC data. An improved quality of TVC data can be expected in the future and so analyses that eventually follow this report will be able to place greater emphasis on TVC data.

The most important features of the data describing the presence or absence of E. coli on carcases, when summarised as a percentage of positive tests and on a national basis are:

Short term variation in E. coli: There is substantial day to day variation in the frequency of positive E. coli tests, even in the species of carcases with the lowest rate of detection of E. coli (STEER/HEIFER). This is despite the outcome being a national average. This variability represents the net accumulated effect of livestock factors, climatic factors, geographic factors, processing factors, testing factors etc. that occur across a large industry that is geographically dispersed. It seems unlikely that any single factor (or a small number of factors) could explain the amount of short term variation in the data. Most of this variation should be regarded as random noise. However, because of the extent of variation that occurs in the short term any attempt to assess carcase hygiene (or the impact of measures on carcase hygiene) needs to occur over a sufficiently long period to avoid the inaccuracy introduced by the noise in the data.

Seasonal variation in E. coli: In SHEEP and LAMB carcases there is clear tendency for a higher frequency of positive E. coli tests in the mid-year period. The data do not provide a basis for explaining the cause of this seasonal effect. However, a number of causes can be suggested based on events occurring during the annual cycle of the production of sheep meat. One such possible cause is the seasonal pasture flush that occurs throughout much of southern Australia (where most of the sheep exist) and that gives rise to feed intake that is highly digestible and of high water content. This dietary change can be followed by an increase in the amount of faecal matter attached to the fleece at slaughter. As well, exposure of sheep to internal parasites (adult and larval forms) generally increases from autumn to spring and can result in diarrhoea and accumulation of faecal matter on parts of the fleece. Collectively, the nutritional, parasitic and other causes of diarrhoea at this time are referred to as ‘winter scours’(7). A second hypothesised cause also relates to climate. In southern Australia the peak period of rainfall and period of lowest evaporation is during winter-spring. Wetting of sheep prior to slaughter has been identified in New Zealand as a factor leading to increased microbial contamination of carcases(2).

Long term variation in E. coli: In some instances long term trends are discernable by visual inspection of the data. However, simpler evidence on long term trends in E. coli detection on carcases at the national level is provided elsewhere in this work.

With respect to the analysis of Salmonella by time-series the most important outcomes are:

Rarity of Salmonella: The infrequent occurrence of Salmonella in most classes of carcase make it a poor tool to use for monitoring processing performance at individual establishments that already have good process control. However, when the data from all establishments are aggregated to form a national picture the data are more useful.

Winter dominance of Salmonella detections: Most classes of carcase were more likely to yield positive results for Salmonella in winter months. Importantly, this is opposite to the marked summer-dominant pattern of cases of human salmonellosis notified to health authorities in Australia (and other developed countries). This difference in seasonal patterns between livestock carcases and human cases suggests that contamination of red-meat carcases with Salmonella per se is unlikely to be responsible for a large proportion of human salmonellosis in Australia.

5 Analysis of individual establishments

5.1 Introduction

When the ESAM data is aggregated at the national level it potentially provides a useful picture of trends and developments in carcase hygiene in the recent past that might be of interest to industry advisors, AQIS and trading partners. However, perhaps the greatest potential benefit is for ESAM data to be analysed on an establishment-by-establishment basis and for the results to be used as a tool for improving meat hygiene and quality assurance. Such an analysis would not necessarily be sophisticated and could convey in a simple, graphical fashion the performance of an individual establishment over time using the most recently available data.
The first aim of this section was to analyse a selection of individual establishments with the results being provided back to quality assurance and management at each of these establishments on a confidential basis (to preserve confidentiality the results are not reported here). This activity is a key step in receiving feed-back from industry for defining a standard format future analysis of ESAM data. A second aim of this section was to produce simple and descriptive time-series analysis of E. coli (presence-absence data) for a limited number of individual establishments over the entire study period. The purpose of this second activity was to further demonstrate potential output for use by establishments in managing carcase hygiene and quality. A third aim of this section was to demonstrate output from a more complex analysis referred to as 'time series decomposition'. This was performed using log TVC cfu.cm-2 data from a small number of establishments.

5.2 Methods

Descriptive analysis of a group of selected establishments
As part of this project the investigators performed a confidential analyses for six different establishments. In each case the data for each establishment were extracted from the ESAM data and the following statistical tools were used:

For log total viable count (log TVC cfu.cm^{-2}):

- Time series graph of median daily count
- Time series graph of median daily count with smoothing to appraise seasonal trends
- Box plots by month and presented in yearly panels, panels arranged vertically to appraise seasonal trends
- Box plots by month
- Box plots by year

For *E. coli* (presence/absence):

- Time series of percentage of tests positive on each day
- Bar charts of percentage tests positive for each year

For Salmonella:

- No analysis performed because positive tests are too infrequent, simple percentages suffice.

Results are not presented for the above analyses because they were performed in confidence.

Example of quarterly % detection of E. coli as a time series

These plots are simple summaries of quarterly rates of the percentage of tests positive for *E. coli* at an individual establishment presented as a time series. Six examples of establishments processing cattle carcases and six that process sheep carcases are provided.

Time series decompositions of log TVC

More powerful statistical techniques exist to examine time series data than the simple descriptive techniques and smoothing techniques used elsewhere in this report. Here we use the technique of time-series decomposition to break down the observations made at any point in time to components attributable to day, month, season and random (error) effects. Motivation for this is to provide an additional example of possible analysis that industry or individual establishments could undertake. There are more advanced techniques that could possibly be applied that in addition account for some of the shortfalls of the TVC data including the discrete nature of observations at lower levels of TVC (causing the banding of observations) and the sometimes censored nature of observations at the upper end of concentration (causing a ceiling effect in some establishments). However, these latter techniques are beyond the scope of the current project. The time series decomposition of log TVC data performed here is an intensive analysis and so is only performed for several individual establishments (a beef processor and two sheep and lamb processors). In each case the decomposition analysis is preceded by a descriptive analysis to define the hygienic performance of this plant in a manner similar to earlier parts of this report. The establishments were chosen on the basis of having TVC data across the entire six years of the study period and with minimal interruptions due to missing data.

For these individual establishments the time series decomposition is performed by assuming the data can be modelled as:

$$Y = T + S + E$$

Where 'Y' is the log TVC cfu.cm^{-2}, where 'T' is the trend, where 'S' is the seasonal change and 'E' represents the random and independent error. In this analysis 'T' is further broken down into a linear component and a 'smooth trend' component represented by a flexible curve over the whole of the observation period. 'S' is further broken down into 'month' (of observation) and 'weekday' (of observation) components. The final model for fitting to the data is:

Y = *a* + *b* x day + *s*(day) + month + weekday + error

Where:

- *a* is a constant (part of the trend component)
- *b* is a constant (part of the trend)
- day is the sequential day number of each data point within the study period
- *s* is a smoothing function (part of the trend), effectively a series of simple curves joined together to provide a complex curve. Each simple curve is defined by a cubic polynomial and fitted over a 20 day interval of data.
- month is an effect due the calendar month of observation
- weekday is an effect due to the day of week of observation

This above formulation for decomposing sources of variation using smoothing curves is similar to the approach described by Verbyla et al.(14).

Estimates for the coefficients (*a* and *b*) and the smoothing function (*s*) in this model are obtained by an mathematical procedure known as restricted maximum likelihood estimation (REML). REML effectively conducts an iterative search for the unknown values of the model that best fit the data of the establishment being studied. REML was performed using the S-Plus statistical analysis package combined with the ASREML add-on (5, 6).

5.3 Results

Descriptive analysis of selected establishments

The results for the descriptive component performed for particular establishments are confidential and so are not provided in this report. The findings have been provided in reports to individual establishments and the investigators have discussed the suitability of the analysis and

graphical formats with quality assurance personnel and management in these establishments. In lieu of this, Appendix 1 provides a selection of graphs (for an anonymous establishment) that show how ESAM data could possibly be presented back to individual establishments.

Examples of individual establishment analysis

Figures 5.1a and 5.1b provide examples of time-series plots for the detection of *E. coli* in cattle and sheep carcases respectively. Other than noting the extent of variation between establishments and the range of results, these plots are difficult to interpret without specific knowledge about the operating conditions in each establishment for these periods. These plots are merely presented to illustrate the type of information that could be collected by establishments to assist in management of carcase hygiene.

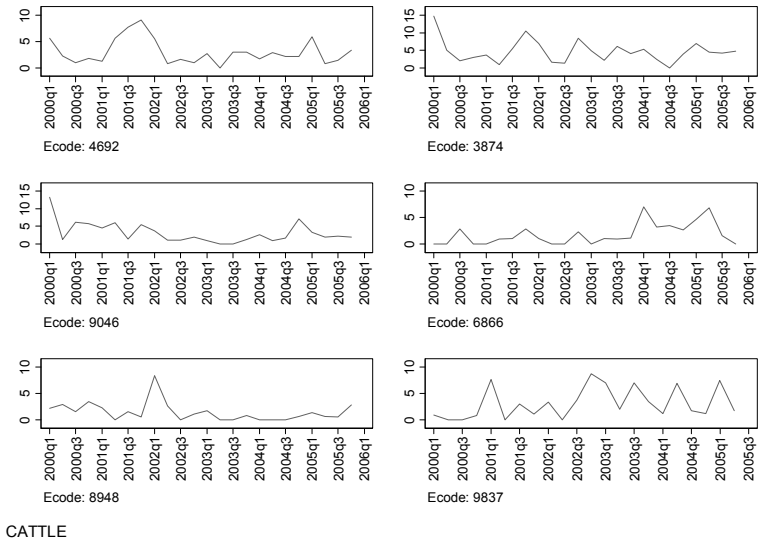

Figure 5.1a. Six anonymous examples of time series plots for percent detection of E. coli for individual establishments processing STEER/HEIFER or COW/BULL carcases. Each data point summarises the results for each quarter.

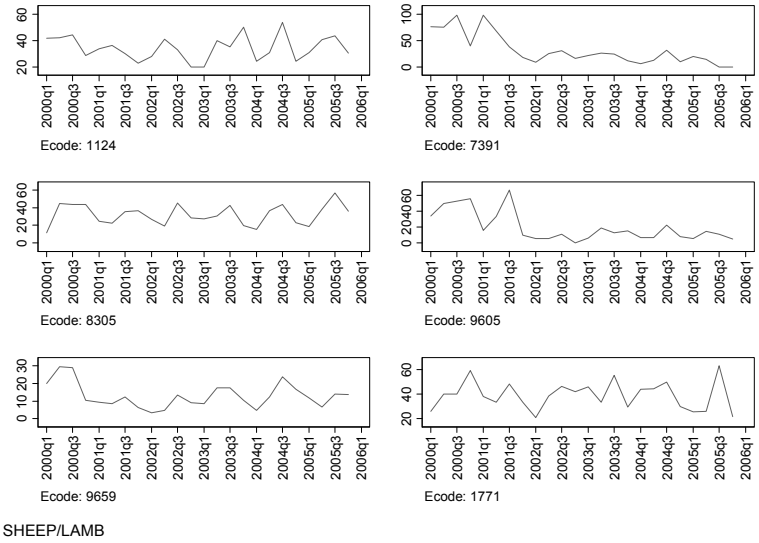

Figure 5.1b. Six anonymous examples of time series plots for percent detection of E. coli for individual establishments processing SHEEP or LAMB carcases. Each data point summarises the results for each quarter.

Example time series decomposition of log TVC – beef establishment
Descriptive analysis

The results for the preliminary descriptive analysis of log TVC for an anonymous establishment producing beef carcases are shown in Figures 5.2, 5.3, 5.4, 5.5 and 5.6. These figures are equivalent to a 'univariate analysis' in that observations are the result of the combined effect of the variable of interest in each figure and any additional effect arising from other variables not represented in the figure. Note that the quality of TVC data is not ideal, due to a 'ceiling effect' (right censoring) and banding (Figure 5.2).

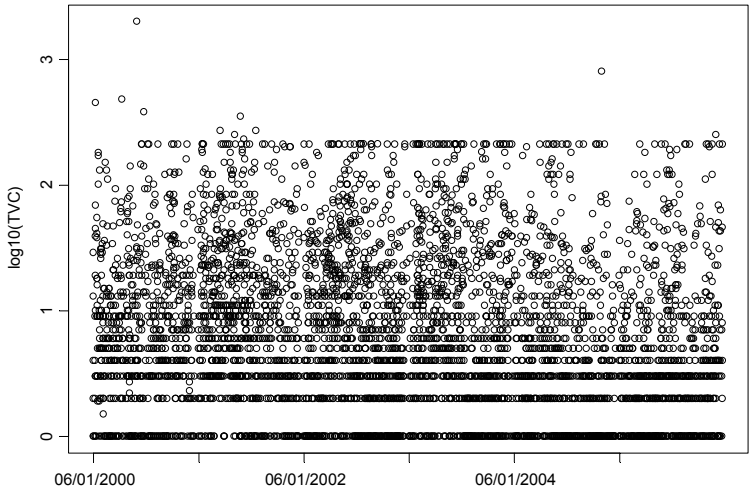

Figure 5.2. Observed log TVC cfu.cm^{-2} for the example beef establishment. This is a further example of 'banding' and 'ceiling' effects in the data.

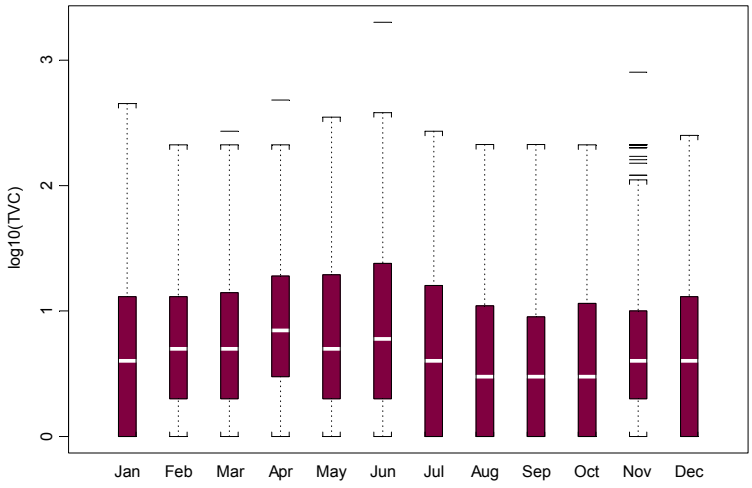

Figure 5.3. Descriptive summary of the log TVC.cm^{-2} measurements made from beef carcase surfaces grouped by month of sampling within the study period.

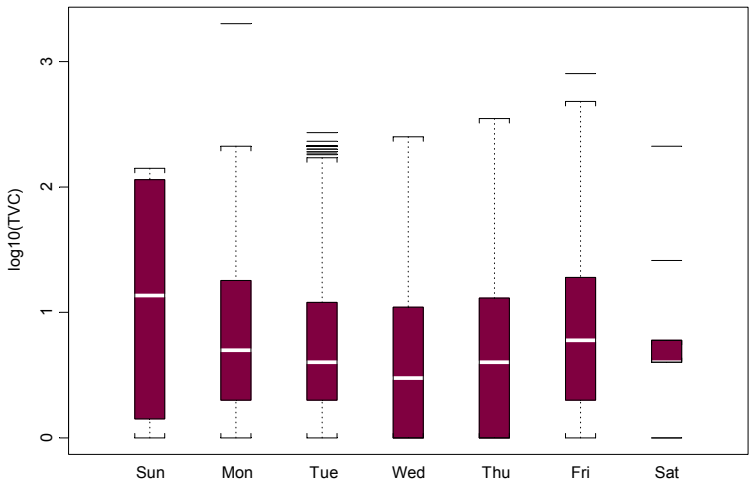

Figure 5.4. Descriptive summary of the log TVC.cm^{-2} measurements made from beef carcase surfaces grouped by day of week of sampling within the study period.

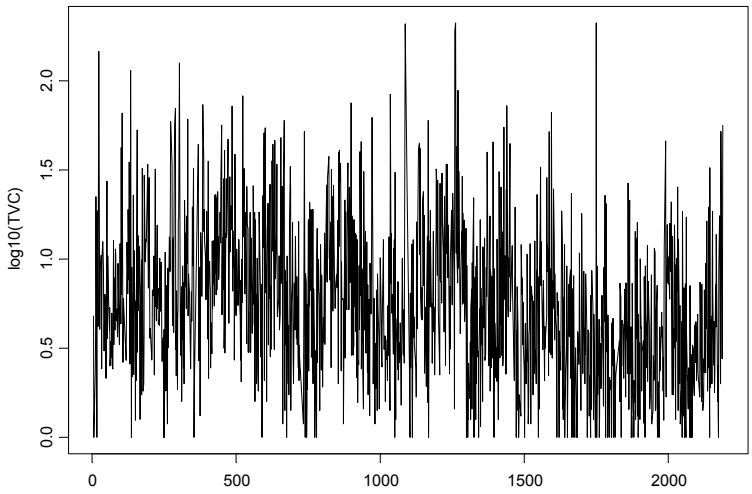

Figure 5.5. Mean of the log TVC.cm^{-2} for each day of the study period, compressed time scale.

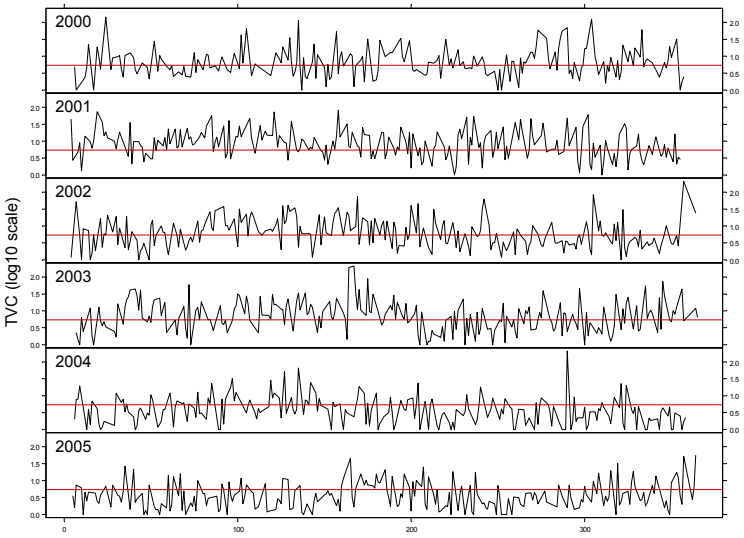

Figure 5.6. Beef example. Mean of the log.TVC.cm^{-2} for each day of the study period on an expanded time scale. The horizontal line shows the average result for the duration of the study period.

Model predictions

Figures 5.7 to 5.12 are predictions from the time series decomposition model. It is clear from comparing Figure 5.8 and Figure 5.10 that the compression of the X (time) axis influences the ability to interpret the predictions. The sum of all the components excluding the "error" component is displayed in Figure 5.7. By comparison with the raw data displayed previously, Figure 5.7 shows a distinct downward trend in TVC over the observation period although the narrower range of values (0.4-1.2 in the smoothed data compared to 0-2 in the raw data) indicates that "error" was a substantial component of the data.

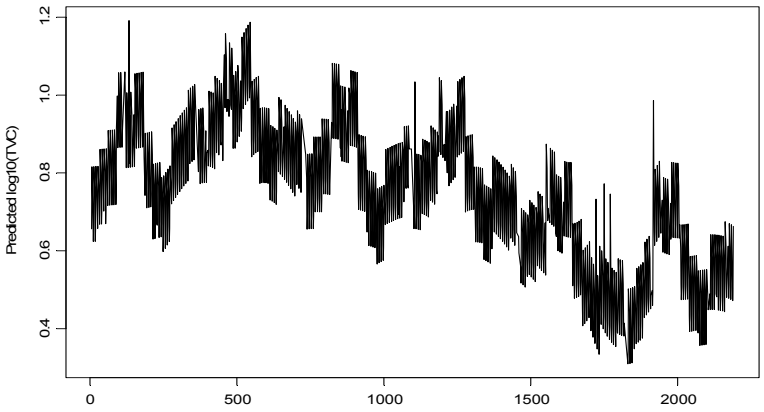

Figure 5.7. Beef example. Predictions from the time series decomposition model of mean daily log TVC.cm^{-2} , compressed time scale.

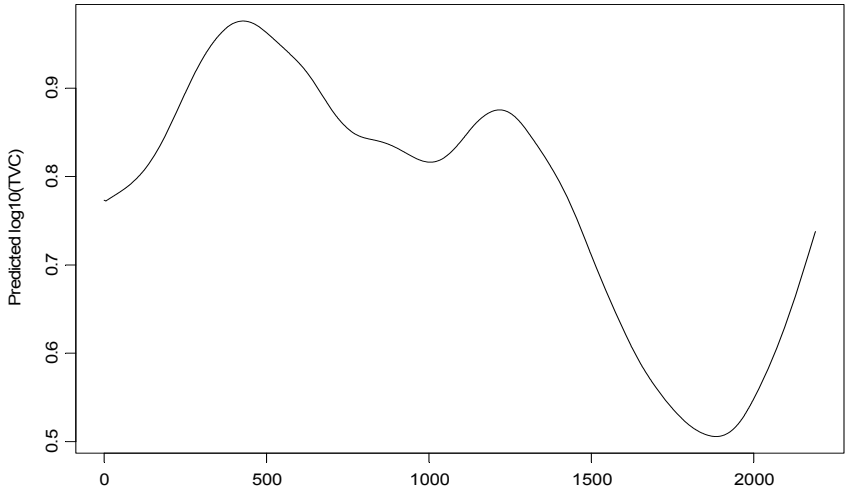

Figure 5.8. Beef example. Smoothed predictions from the time series decomposition model of mean daily log TVC.cm^{-2}, compressed time scale. Smoothing achieved by removal of month and day effects to show the overall trend over the study period (measured in days).

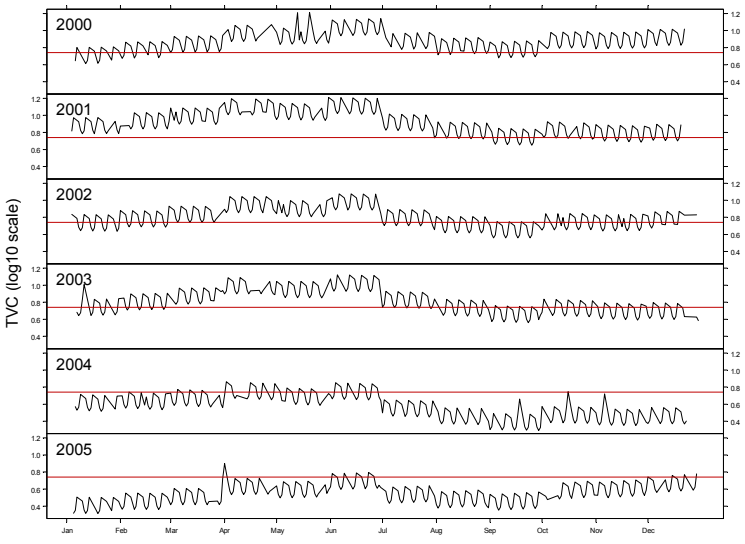

Figure 5.9. Beef example. Predictions from the time series decomposition model of mean daily log TVC.cm^{-2} expanded time scale. Panels representing years are arranged vertically to show seasonal effects. The short term variation resembling saw teeth is weekly variation.

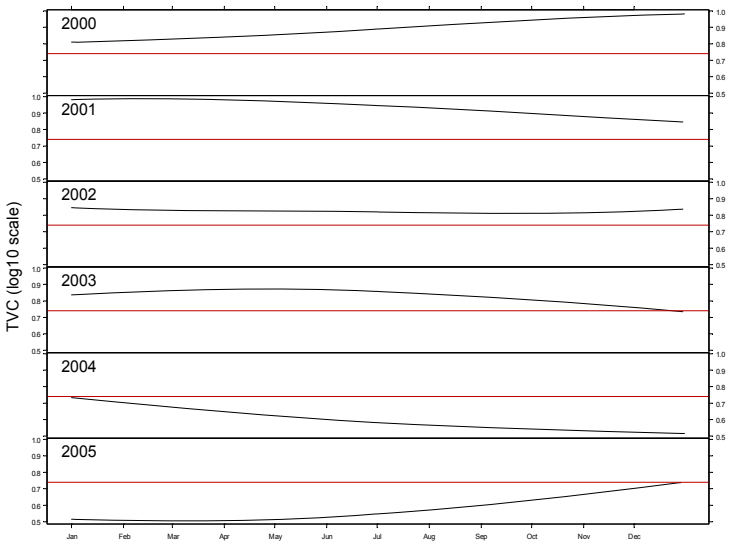

Figure 5.10. Beef example. Smoothed predictions from the time series decomposition model of mean daily log TVC.cm^{-2} for a beef establishment, expanded time scale.

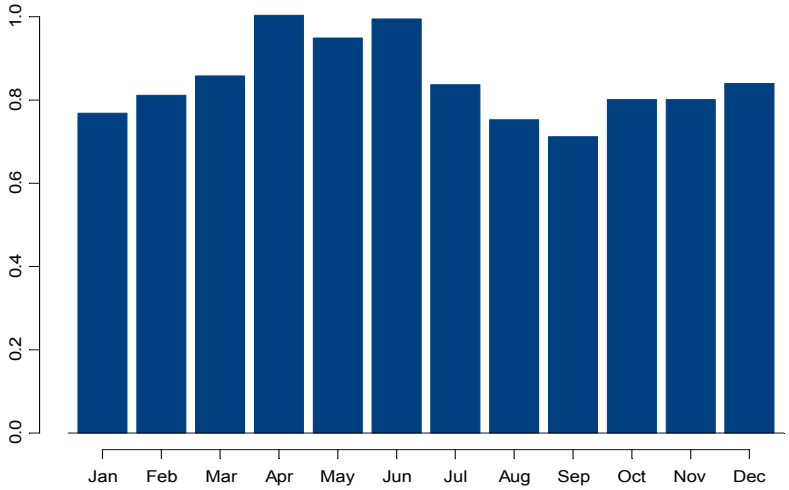

Figure 5.11. Beef example. Predicted effect of month of year on the contribution to mean daily log TVC.cm^{-2}.

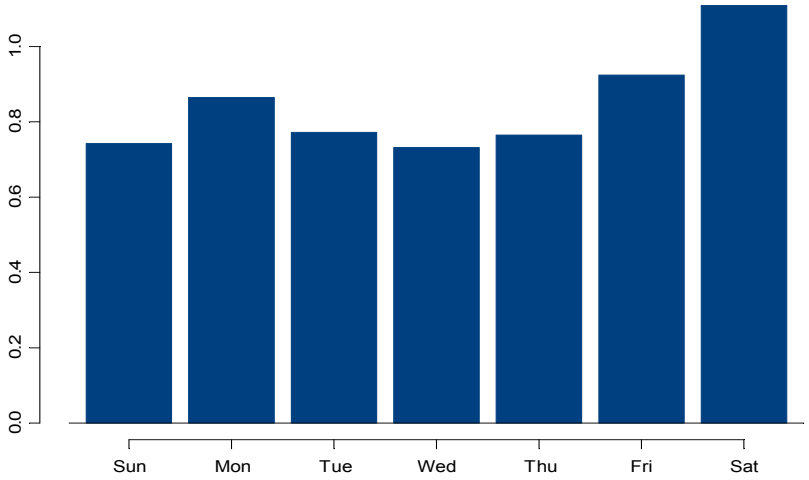

Figure 5.12. Beef example. Predicted effect of day of week on the contribution to mean daily log TVC.cm^{-2}.

Example time series decomposition of log TVC – sheep and lamb establishment 1

Descriptive analysis

The results for decomposition of 'sheep and lamb establishment 1' follow. These are presented in the same format as the previous example, first beginning with a descriptive analysis Figures 5.13 to 5.18 and then the time series decomposition analysis (Figures 5.19 to 5.23). The log TVC values are higher for this establishment as is generally the case with sheep carcases when compared to cattle carcases. Data quality issues exist with the TVC data (Figure 5.13) but are not as marked as the previous example.

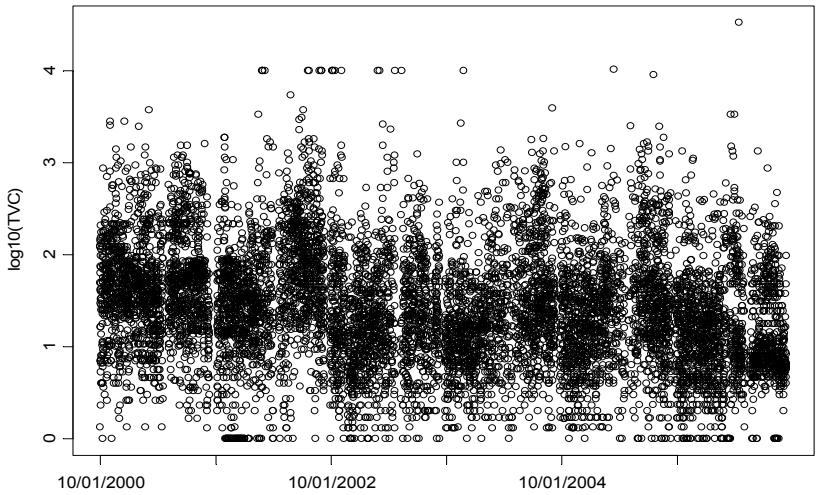

Figure 5.13. Sheep/lamb example 1. Scatter plot of log TVC.cm^{-2} over time.

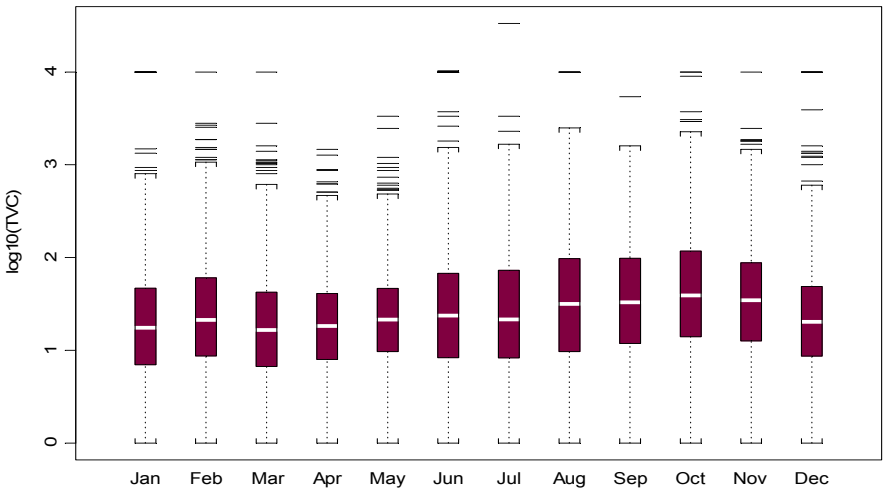

Figure 5.14. Sheep/lamb example 1. Descriptive summary of the log TVC.cm^{-2} measurements grouped month of year of sampling within the study period.

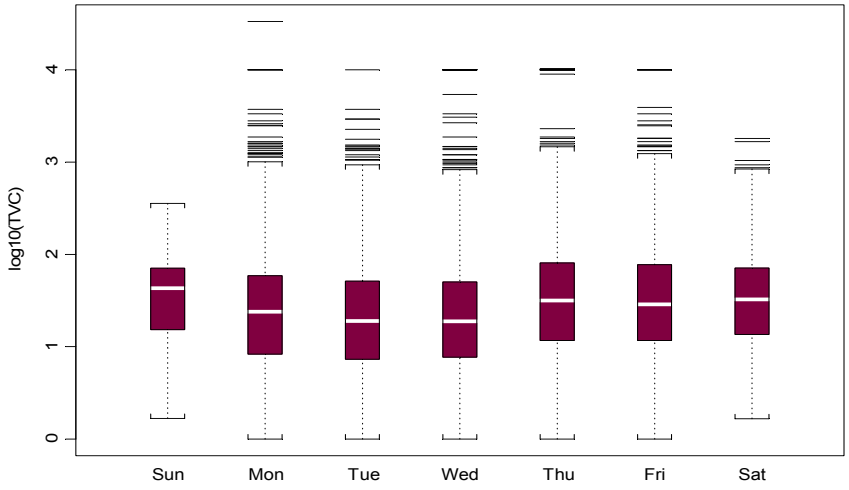

Figure 5.15. Sheep/lamb example 1. Descriptive summary of the log TVC.cm^{-2} measurements grouped by day of week of sampling within the study period.

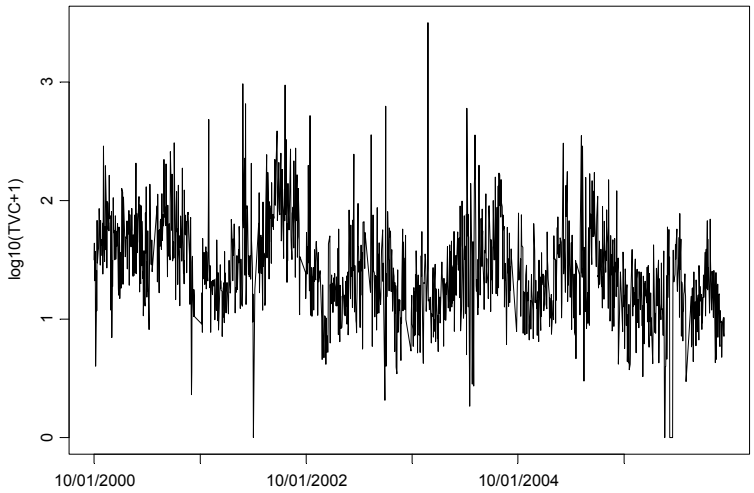

Figure 5.16. Sheep/lamb example 1. Mean of the log TVC.cm^{-2} for each day of the study period, compressed time scale.

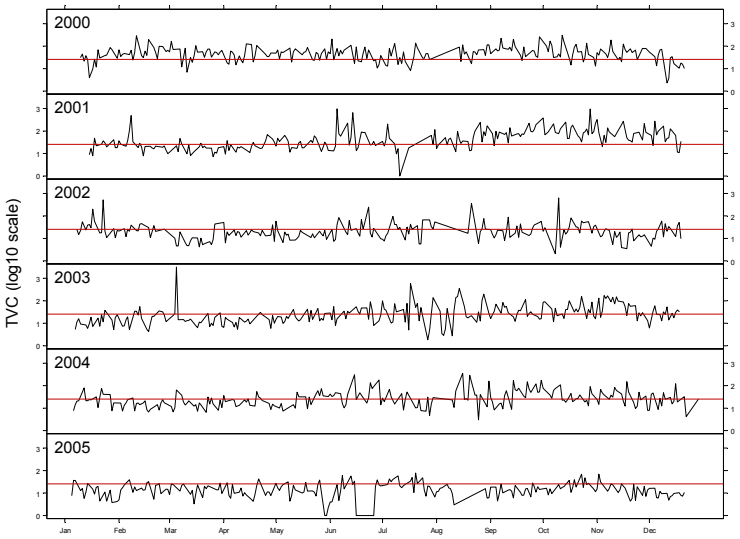

Figure 5.17. Sheep/lamb example 1. Time series plot of the mean of the log.TVC.cm^{-2} for each day of the study period on an expanded time scale. The horizontal line shows the average result for the duration of the study period.

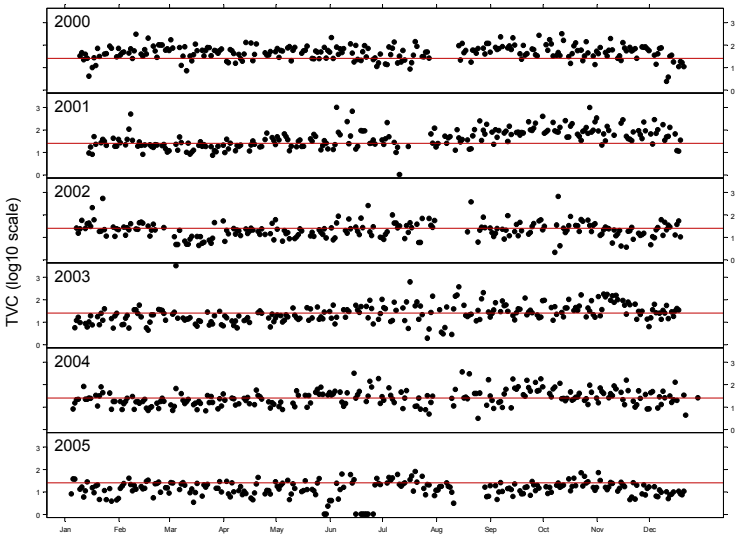

Figure 5.18. Sheep/lamb example 1. Scatter plot of the mean of the log.TVC.cm^{-2} for each day of the study period on an expanded time scale. The horizontal line shows the average result for the duration of the study period.

Model predictions

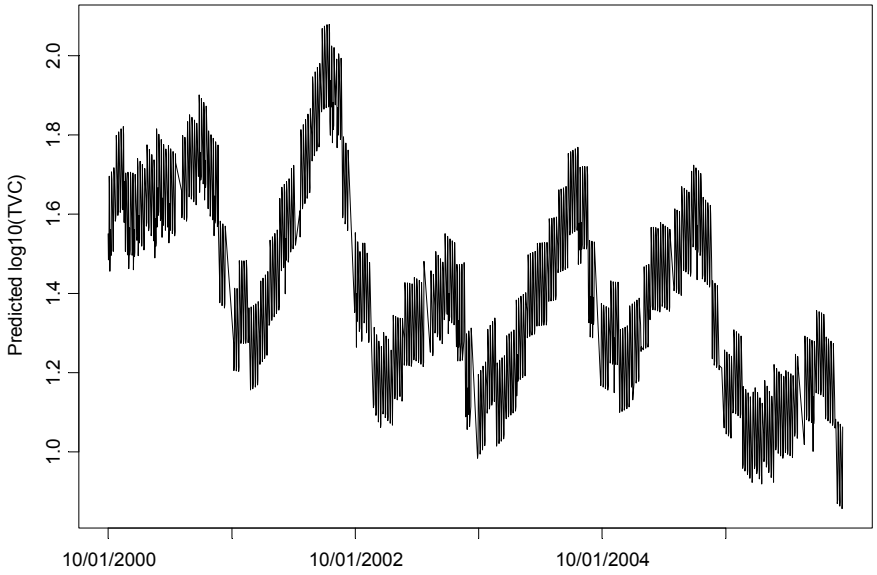

Figure 5.19. Sheep/lamb example 1. Predictions from the time series decomposition model of mean daily log TVC.cm^{-2} , compressed time scale.

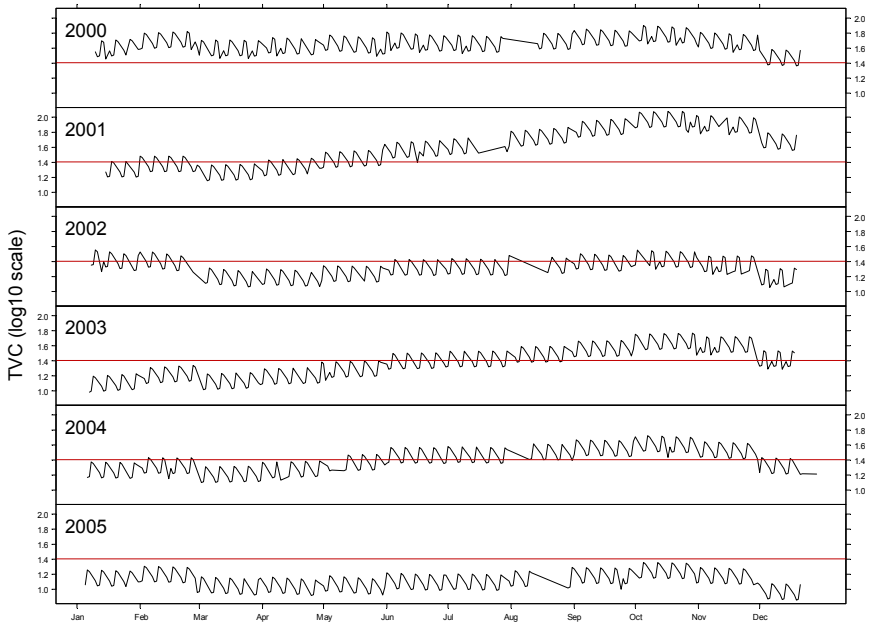

Figure 5.20. Sheep/lamb example 1. Predictions from the time series decomposition model of mean daily log TVC.cm^{-2} expanded time scale. Panels representing years are

arranged vertically to show seasonal effects. The short term variation resembling saw teeth is weekly variation.

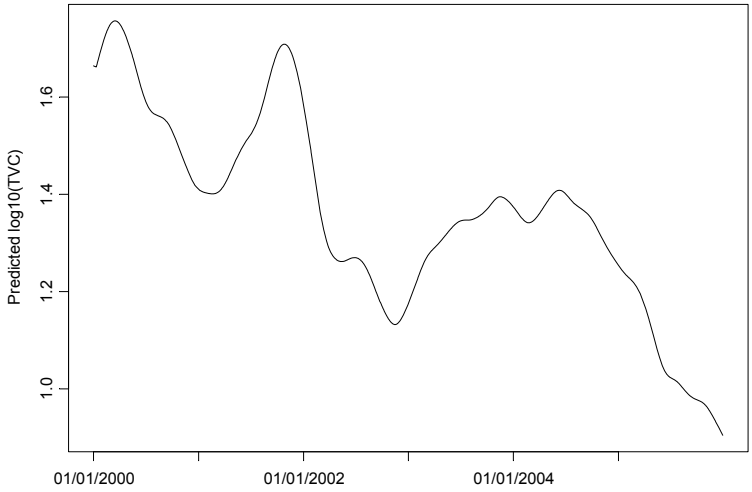

Figure 5.21. Sheep/lamb example 1. Smoothed predictions from the time series decomposition model of mean daily log TVC.cm^{-2}, compressed time scale. Smoothing achieved by removal of month and day effects to show the overall trend over the study period (measured in days).

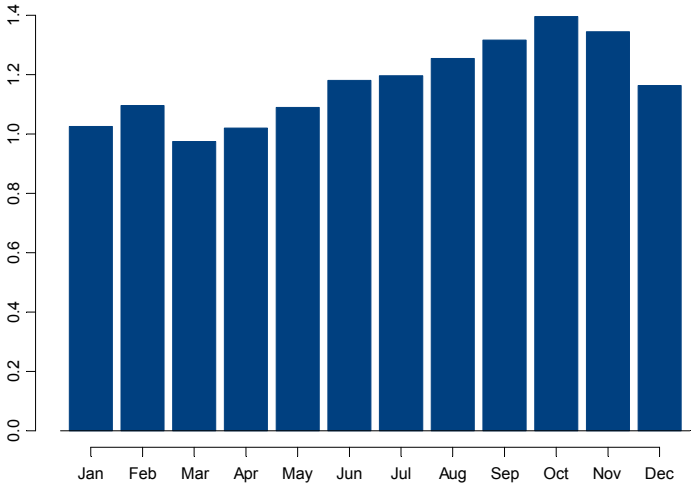

Figure 5.22. Sheep/lamb example 1. Predicted effect of month of year on the contribution to mean daily log TVC.cm^{-2}.

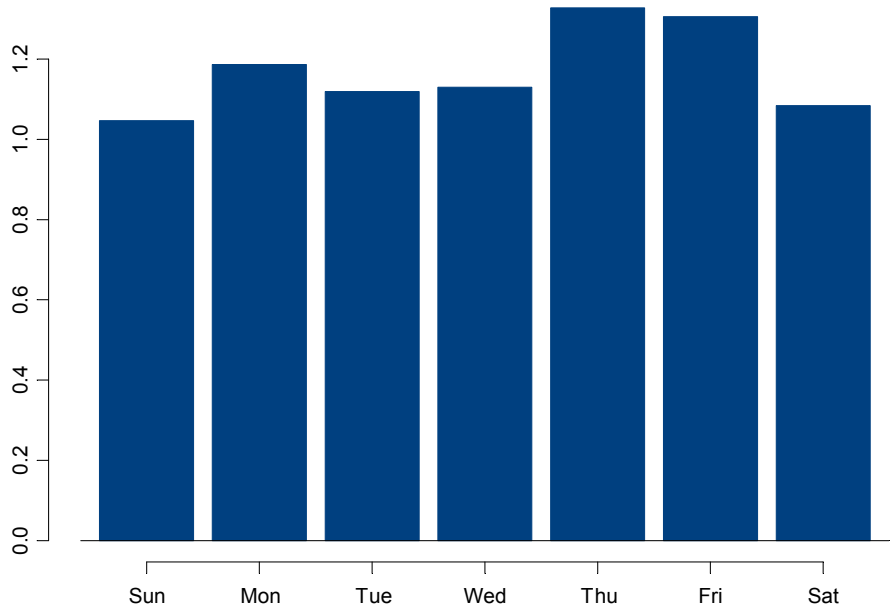

Figure 5.23. Sheep/lamb example 1. Predicted effect of day of week on the contribution to mean daily log TVC.cm^{-2}.

The results for the analysis of sheep and lamb establishment 1 show that log TVC.cm-2 has declined by about 0.5 log over the period of the study. However, this decline has not been in a uniform fashion, there being periods during the study period when log TVC.cm-2 has increased. As well, there is a noticeable increase in log TVC.cm-2 in the spring months, although this effect only amounts to about 0.4 log TVC.cm-2. Within a working week within this establishment, Mondays and particularly Thursdays and Fridays are associated with higher counts than other days, the maximum difference between days of the week being about 0.4 log TVC.cm-2. There are possibly some biases introduced into these findings by the quality of TVC data however they are likely to be small relative to those for other plants.

Example time series decomposition of log TVC – sheep and lamb establishment 2

Descriptive analysis

The results for decomposition of 'sheep and lamb establishment 2' follow and are again presented in the same format as the previous examples. Descriptive analysis appear in Figures 5.24 to 5.29 and then the time series decomposition analysis in Figures 5.30 to 5.34. The log TVC values are higher for this establishment as is generally the case with sheep carcases when compared to cattle carcases. While there is no clear ceiling effect for this data there are infrequent bands at the low end of concentration of TVC (Figure 5.24)

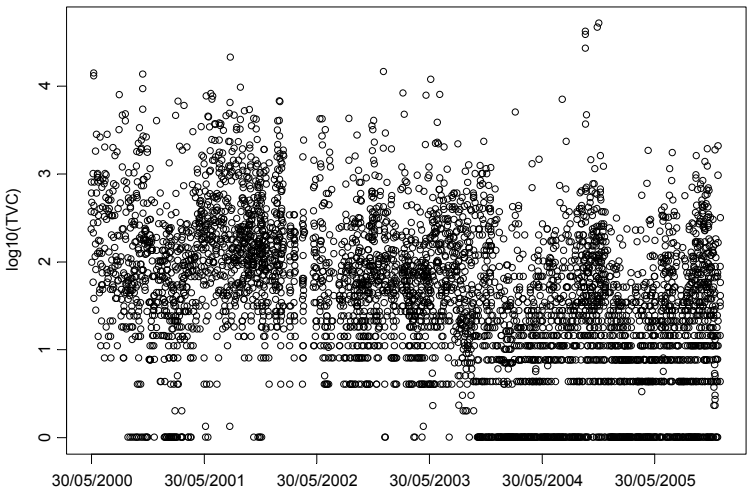

Figure 5.24. Sheep/lamb example 2. Scatter plot of log TVC.cm^{-2} over time.

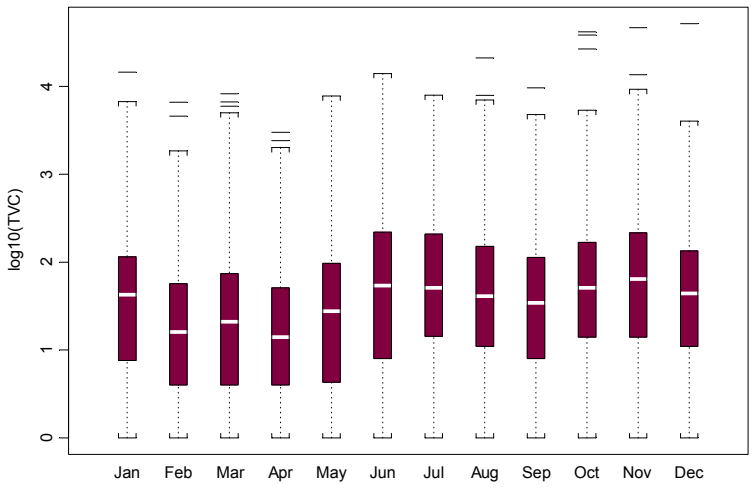

Figure 5.25. Sheep/lamb example 2. Descriptive summary of the log TVC.cm^{-2} measurements grouped month of year of sampling within the study period.

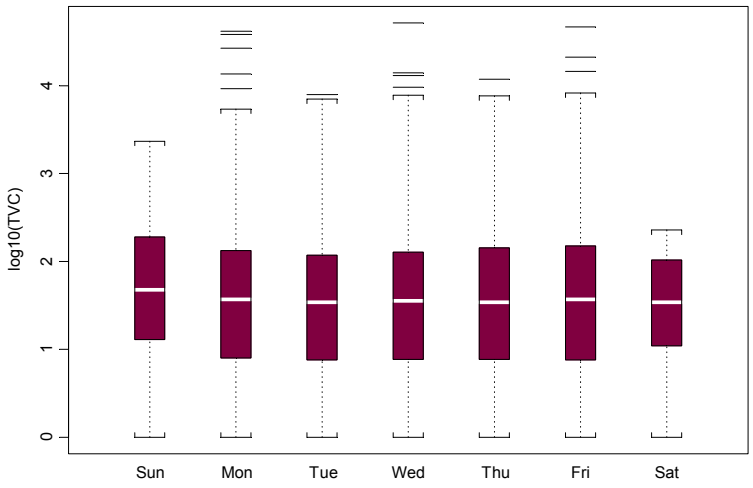

Figure 5.26. Sheep/lamb example 2. Descriptive summary of the log TVC.cm^{-2} measurements grouped by day of week of sampling within the study period.

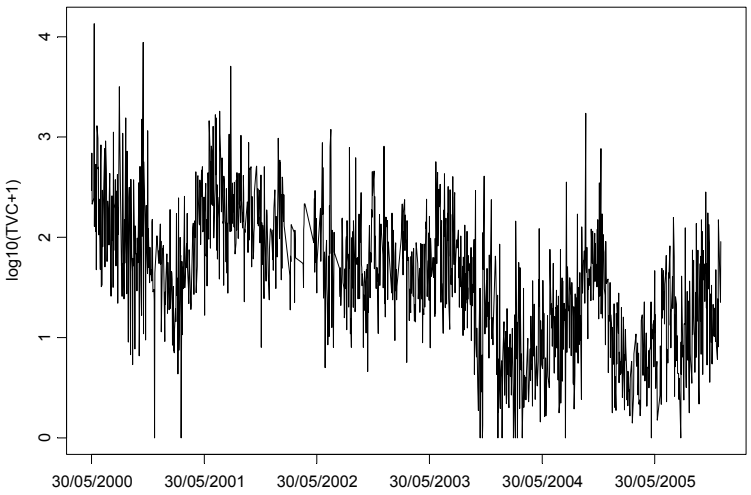

Figure 5.27. Sheep/lamb example 2. Mean of the log TVC.cm^{-2} for each day of the study period, compressed time scale.

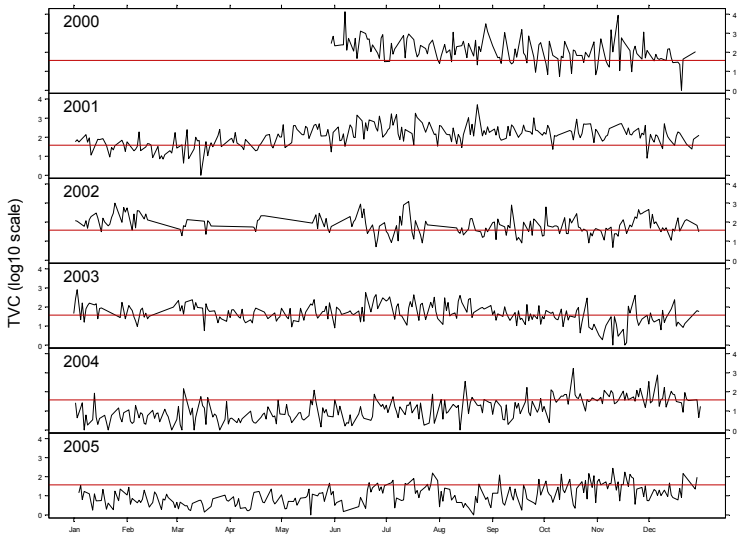

Figure 5.28. Sheep/lamb example 2. Time series plot of the mean of the log.TVC.cm^{-2} for each day of the study period on an expanded time scale. The horizontal line shows the average result for the duration of the study period.

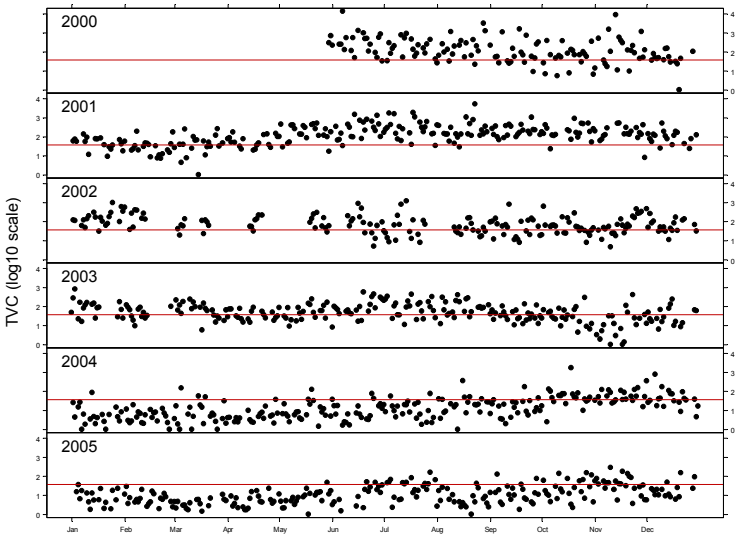

Figure 5.29. Sheep/lamb example 2. Scatter plot of the mean of the log.TVC.cm^{-2} for each day of the study period on an expanded time scale. The horizontal line shows the average result for the duration of the study period.

Model predictions

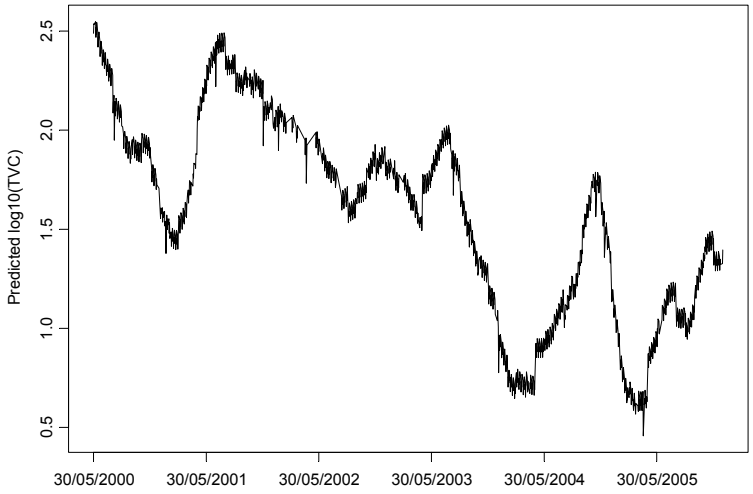

Figure 5.30. Sheep/lamb example 2. Predictions from the time series decomposition model of mean daily log TVC.cm^{-2} , compressed time scale.

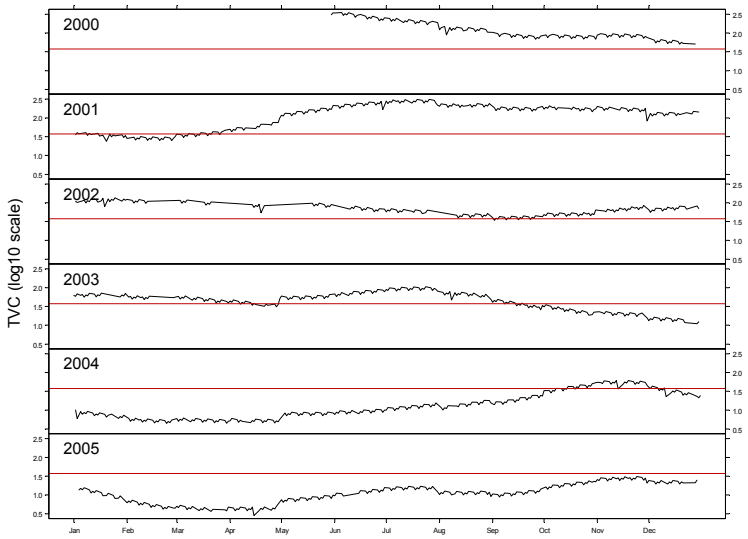

Figure 5.31. Sheep/lamb example 2. Predictions from the time series decomposition model of mean daily log TVC.cm^{-2} expanded time scale. Panels representing years are arranged vertically to show seasonal effects. The short term variation resembling saw teeth is weekly variation.

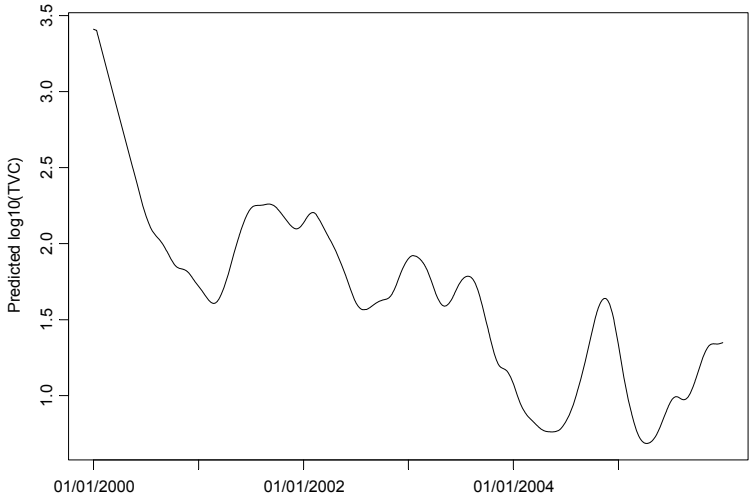

Figure 5.32. Sheep/lamb example 2. Smoothed predictions from the time series decomposition model of mean daily log TVC.cm^{-2}, compressed time scale. Smoothing achieved by removal of month and day effects to show the overall trend over the study period (measured in days).

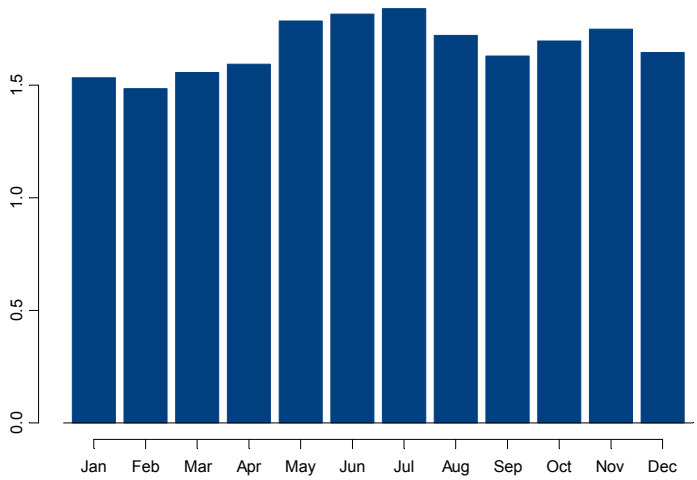

Figure 5.33. Sheep/lamb example 2. Predicted effect of month of year on the contribution to mean daily log TVC.cm^{-2}.

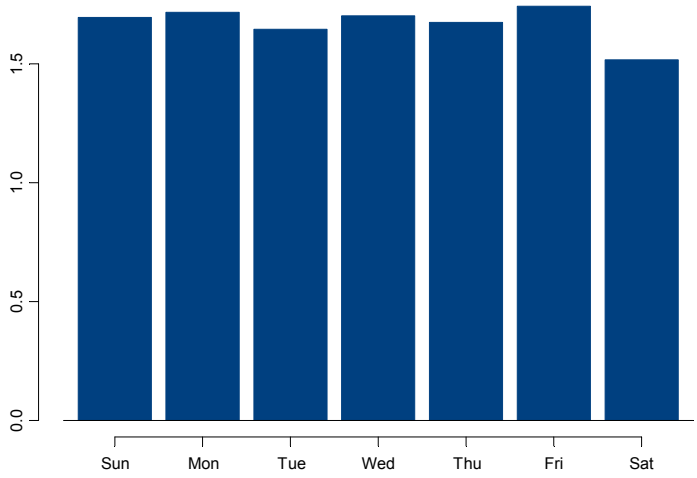

Figure 5.34. Sheep/lamb example 2. Predicted effect of day of week on the contribution to mean daily log TVC.cm^{-2}.

In similarity with the previous example, the log TVC cfu.cm^{-2} from carcases at sheep and lamb establishment number two also show a marked decline over the period of study. As in the previous example, this decline does not occur at a steady rate even when weekly and monthly sources of variation are accounted for. Another similarity is that there is a seasonal effect although in this example the peak levels of log TVC cfu.cm^{-2} are occurring in the spring rather than mid-winter period (compare with the previous example). Unlike the previous example there is a much smaller variation in this establishment between the counts obtained on different days of the week.

5.4 Discussion

The purpose of this aspect of the project was to define possible ways of presenting an analysis of ESAM data on a regular basis. The methodology was chosen so to exploit on a range of techniques of varying complexity and producing a range of outputs of differing format. Visual examination of the output by a range of individuals with experience and interests in meat hygiene will be necessary to decide on an approach for periodic analysis of the data.
Conduct of the descriptive analysis and discussion with interested parties has revealed a list of questions to be answered before defining the type of ongoing (periodic) analysis:

- How often should the data be analysed?
- What analysis should be performed for TVC?
- What analyses should be performed for *E. coli*?
- What analyses should be performed for *Salmonella*?
- Who will receive the results of an analysis?
- Who will manage the conduct of the analysis?
- Why will parties be interested in the results of the analysis?
- How will parties use the results of the analysis?

With respect to the analysis of data from individual establishments, key issues arising from this include:
Presentation of the data on E. coli: If analysing the data as a time-series with the proportion of swabs (carcases) positive for *E. coli* then the interval over which the data are summarised is an important choice. In most instances, plotting the data on a weekly basis is not informative because there are typically zero or very few detections in a single week. Hence in this analysis the data were summarised quarterly to provide a response that has sufficient variation to be of use in assessing the impact of livestock and processing factors on hygiene outcomes.

Format for periodic presentation of data on E. coli: If producing regular reports on hygienic performance over a shorter time period (e.g. quarterly or half yearly) then summarising on a monthly basis would be adequate for most establishments.

Interpretation of data on E. coli: Because of the very large number of establishments we only produce a sample of example plots. Each plot requires individual interpretation and it is presently unrealistic to expect that many establishments have the technical expertise to utilise the output from this analysis. Nevertheless, the first step in developing such expertise is for individuals involved in quality assurance to be exposed to the type of data that is available. The results here can serve that purpose.

Decomposition analysis for TVC. The findings from decomposition of TVC data in individual establishments do demonstrate how a more detailed explanation of the causes of variation in hygienic measurements can be obtained. However, for this analysis it was necessary to ‘hand pick’ the individual establishments to minimise interpretation difficulties related to the quality of TVC data. If sophisticated statistical analyses of this type are to be conducted in the future then it will be necessary to increase the number of establishments collecting good quality data on TVC. The data on E. coli cfu.cm-2, while generally of higher quality than the TVC data, is not very suitable for this purpose because for most classes of carcase the prevalence of detection is too low to result in useful information.

Some specific remarks can be made about each of the establishments used as an example in the time series decomposition of TVC data:

Beef example: The results for this establishment need to be interpreted in the light of the banding and ceiling effects that are present in the data. The ceiling effect leads to a truncation of the values at the upper end of the distribution of TVC concentrations and could effectively

introduce a bias into the analysis. It is possible that some of the month and day of week effects could be greater than that estimated here if the ceiling effect was removed. Nevertheless, the time series decomposition revealed that TVC readings declined over the study period although in the final year (2005) an increasing trend was detected. In general, TVC readings were higher over the late autumn to early winter months (April, May, June) and were lower in the mid week period.

Sheep and lamb example 1: After removal of variation due to week, month and error it was evident that TVC readings showed a consistent decline over the study period for this observation. Counts of TVC are seasonally higher in the months of late winter and spring.
Sheep and lamb example 2: TVC reading showed a general decline over the period of observation. TVC readings tended to be higher in the latter half of the 2004 and 2005 seasons. Variations in TVC reading due to days of the week were not as evident at this plant compared to other plants.

Further information on the decomposition of TVC counts is inhibited by lack of knowledge about conditions at the establishments when the data were collected. This highlights the need for such analysis to be performed in collaboration with each processing establishment if the maximum benefit is to be gained from the findings.

6 Evaluation of attribute sampling plans for *Escherichia coli* detection

6.1 Introduction

Attribute sampling plans are used to decide whether batches of product items should be accepted or rejected based on traits that measure quality. This approach to quality assurance has been widely adopted in food production and is a prominent tool in the evaluation and regulation of microbiological characteristics (most notably E. coli) of meat carcases.

Two class attribute sampling is where a group of items in a batch (consignment, carton, herd, etc) contains N product items, and from this n are selected for testing. The test applied to each item provides a dichotomous result (acceptable or not acceptable) either as positive or negative or as below or above an acceptable concentration of hazard. If the number of positive individual units in a batch exceeds some integer value (c) then the entire batch is classified positive (rejected). This type of attribute sampling is relatively simple to study because each plan is specified by a limited number of parameters that can be conveniently modelled using binomial and hypergeometric probability theory. Two class attribute sampling is relevant as the precursor to three class variants and has been used for monitoring Salmonella in the Australian meat industry(1)

Three class attribute sampling plans are encountered when monitoring E. coli during the production of meat carcases(1, 4). They work by separating each of the n individual items (carcases) that are tested into three classifications (acceptable, marginal and unacceptable) based on the strength of test reading (concentration, ELISA OD etc.). This is achieved by defining two interpretation points along the scale of the test's response (thus dividing the test scale into three categories of classification). Items with a test reading less than or equal to m are classified as acceptable. Items with a test reading greater than m but less than or equal to M are classified as marginal. Items with a test reading greater than M are classified as unacceptable. A batch is positive if one or more individual items is unacceptable, or, if the number of individual items classified as marginal exceeds a specified integer value (c). The parameters and definitions of attribute sampling plans are summarised in Table 6.1.

Table 6.1. Parameters, corresponding terminology and definitions used in conventional three class attribute sampling plans.

Parameter	Terminology	Definition
N	Batch size	Integer number of individual product items within a specified aggregate of interest (carton, consignment, shipment, window etc.)
n	Sample size	Number of individual product items selected from the batch for testing.
m	Low cut point value	Value of the test result along a continuos or discreet scale. Product items with a test result equal to or below this value are classified as acceptable.
M	High cut point value	Value of the test result along a continuos or discreet scale above which all product items are classified as unacceptable.
c	Tolerable number of marginals	The maximum number of product items amongst the *n* tested that can be classified as marginal without the batch being classified as having failed.
	Acceptable individual item	An item that has a test reading below or equal to *m*.
	Marginal individual item	An item that has a test reading greater than *m* but less than or equal to *M*.
	Unacceptable individual item	An item that has a test reading greater than *M*.
	Batch failing *M*	A batch that is classified as failed because it has one or more individual items with a test result that is unacceptable.
	Batch failing *c*	A batch that is classified as failed because it has more than *c* individual items with a marginal test result.

Applications of attribute sampling to meat carcase hygiene

In the production of meat carcases the definition of 'batch' and the interpretation of 'batch results' for attribute sampling has evolved into several variants. As well, some manifestations of attribute sampling encountered in carcase production have embraced aspects of statistical quality control such that it resembles a rolling mean or cumulative sum approach. One possible reason why attribute sampling plans have diverged from the traditional format is because the sequence of production of units (carcases) is known and this allows interventions to be applied as soon as deviation from the target level of hygiene is detected. Under the traditional approach to attribute sampling the position of each carcase in the production sequence would not be relevant. If an attempt is made to apply standard attribute sampling nomenclature to the production of carcases then a 'batch' must be implicitly re-defined as a consecutive group of carcases emerging from the production chain and the term 'window' replaces the term 'batch'. A single window consists of an integer number of carcases sequentially emerging from a processing chain. The window has a starting point followed by a finishing point, both of these denoted by integer numbers defining the position (sequence number) of carcases in the output que. At least in Australia, testing is performed at a set interval along the production sequence. For example, in establishments that slaughter adult cattle there are 300 carcases separating each carcase that is tested. In this system a window includes a maximum of 15 tests. Thus, n = 15 and by analogy with traditional attribute sampling, the results are (nominally) used to make inferences about the fitness of all 4,500 carcases (300 tested and 4,200 not tested) in the window (i.e. 4500 consecutively produced carcases = 300 x 15 = 4500).

With the above terminology and description it is possible to explain how attribute sampling plans for the management of microbiological contamination of carcases have diverged from the traditional format. At least five variants have been identified (possibly more exist) and these differ in the way windows are opened and closed as described under each heading below:

1. *Jumping window without reset (JUMPWIN)*: corresponds to traditional three class attribute sampling where a consecutive group of carcases defined by n consecutive carcase tests is regarded as the window (equivalent of batch). The window 'jumps' because the position of the start of each window is moved along the que of product items multiple (n) places at a time. Characteristics: windows do not overlap along the sequence of carcases being produced, windows are always of equal size. Example: equivalent to traditional, three-class attribute sampling plans (12)
2. *Jumping window with reset (JUMPWIN_R):* modification of conventional three class attribute sampling plans described by Vanderlinde et al.(13) in their study of *E. coli* testing in the Australian red meat industry. Characteristics: windows do not overlap, windows are not necessarily of the same size, a window is forced to close as soon as failure conditions are met, after failure a new window opens at the next test. Windows not closed by failure are open for n tests. Example: Vanderlinde et. al (13)
3. *Sliding window without reset (SLIDEWIN)*: Here each item being tested represents the start of a new window. This is an approach consistent with USDA Food Safety Inspection Service regulations for *E. coli* testing of meat carcases (4). The window 'slides' because the position of the start of each window moves along the product que only one position at a time. Characteristics: there are multiple windows open (n in number) at each single point of the production process, a window does not close immediately failure conditions occur but remains open for a total of n tests. Example FSIS performance criteria for *E. coli* on carcases (4)
4. *Sliding window with reset (SLIDEWIN_R)*: A modification of the SLIDEWIN variant that is officially used in the Australian meat industry for *E. coli* testing (AQIS meat notices 2003 (1)). Characteristics: A window is opened with each test, multiple windows are open simultaneously, all windows are closed when any single window meets failure

conditions, unless closed by failure conditions a window closes after *n* tests have been performed. Example: AQIS performance criteria for *E. coli* on carcases (1)

5. *Conditional opening window (CONDWIN)*: A version of this is used for monitoring *Salmonella* test results in the Australian meat industry(1). Characteristics: A window is only opened by a test positive event (marginal or unacceptable individual item), once the window is opened it is not closed until either failure conditions are met or *n* tests have been conducted, whichever comes first. Example: AQIS performance criteria for *Salmonella* on carcases (1).

Attribute sampling plans for monitoring E. coli in the Australian meat industry

The official procedure for monitoring the occurrence of E. coli on Australian meat carcases is based on a 'sliding window with reset' (SLIDEWIN_R) applied to the data collected as part of the ESAM program. For each class of carcases produced a specific combination of attribute sampling parameters is applied (see Appendix 1, AQIS meat notice 2003/6(1)). For example, for the carcases of steers and heifers (considered together) n = 15, c = 3, m = 0 and M = 20. These parameters are derived from a study that applied historical data from ESAM to a computer algorithm on attribute sampling. However, the algorithm that was applied in this work was 'the jumping window with reset' (JUMPWIN_R) approach rather than the 'sliding window with reset' (SLIDEWIN_R). A feature of both of the sliding window protocols is there is one window for each test observation and it can become difficult to interpret rates of failure when derived on a per window basis. For example, if SLIDEWIN is applied to 1,000 tests then 1,000 windows will be opened overall and at any one time 15 windows will be open. If SLIDEWIN_R is used then some of these windows will be closed early due to 'reset'. Under both SLIDEWIN and SLIDEWIN_R the overlapping of windows that occurs means that the same period of production is being evaluated multiple times. In the case of SLIDEWIN it is possible to have alternating periods of acceptance and rejection. From a practical perspective it is unclear whether this type of information has any advantages as a quality control tool compared to simply assessing the prevalence of positive tests. The availability of six years of ESAM data provided an opportunity to evaluate the performance of each sampling plan by assessing the frequency of occurrence of failures.

6.2 Methods

To understand the performance of different three class attribute sampling plans in the meat industry a series of five computer algorithms (one for each of the previously described attribute sampling plans) were developed in the statistical programming language Stata version 9.2 (Stata Corporation, College Station, TX, USA). Algorithms were designed to perform a retrospective analysis by applying the particular sampling plan to any amount of historical data that contains information on the amount of hazard and the sequence in which tests for hazard were performed. All algorithms were specified by the input parameters n, c, m and M (defined above).

Each algorithm was embedded in a test program that generated dummy data to mimic a sequence of negative tests randomly interspersed with positive tests (using a Bernoulli random variate) the latter being assigned with concentrations randomly drawn from a log normal probability distribution. The parameter p for the Bernoulli distribution and parameters μ and σ for the normal distribution giving rise to lognormal random variates were arbitrarily defined to give a pattern of test results that allows scrutiny of the performance of the algorithms (we used $p = 0.3$, $\mu = 0.4$ and $\sigma = 1$). The output from the test program was formatted so that it could be visually scrutinised to verify the correct functioning of each of the five attribute sampling algorithms, and to demonstrate the behaviour of the different algorithms when applied to identical data. To increase certainty of the correctness of algorithms the evaluation could be repeated after

changing the sequence of simulated data supplying a different random number seed for generating random variates, or by changing the parameters of the random variates (p, μ and σ). Additional algorithms were devised for analysing data from multiple processing establishments (referred to as 'grouped algorithms'). The grouped algorithms managed analysis on an industry level and operated by separating out the data belonging to each individual establishment (group) then calling the specified attribute sampling algorithm as a subroutine for that subset of data. On completion, the establishment-specific results were combined and summarised to provide an industry overview of the performance of the selected attribute sampling plan. When comparing the performance of algorithms at the industry (national) level it was necessary to avoid using the 'number of windows' as denominator because the number of windows under the different algorithms can vary substantially. Instead, performance of the algorithms at the level of the establishment was measured as the number of failures per thousand processed (fptp) and performance at the industry (national) level was measured as the number of failures per million carcases produced (abbreviated as fpmp) in the time period of interest. To demonstrate the grouped algorithm it was applied as the SLIDEWIN_R version to data on E. coli tests performed on STEER/HEIFER carcases to provide detailed output for each establishment for each year of the available data. Data on missing values for the variable 'boning method' were tabulated to assist in explaining the results.

Finally, for the purpose of comparing the behaviour of algorithms, the ESAM data describing the occurrence of E. coli on meat carcases for the period 1 January 2000 to 31 December 2006 were loaded into Stata. The variables for identifying the processing establishment, E. coli test result (in cfu.cm-2) and the testing sequence were provided as inputs to each of the grouped algorithms along with the input parameters: n, c, m and M set at those levels in official use by AQIS. Also supplied as input were the appropriate test intervals defining the number of carcases between tests (hence providing a basis for estimating fptp and fpmp). Data for each major class of livestock carcase were evaluated using these algorithms, with the analysis stratified by year. Because of the extent of missing values describing the 'boning method' for STEER/HEIFER and COW/BULL the latter carcase groups were considered twice, first disregarding the value of the 'boning method' variable and second by only including chilled carcases.

6.3 Results

Algorithm definition, verification and demonstration
A summary of the computer algorithms and test programs developed for this work and forming the basis of the results is given in Table 6.2. The programming code for the demonstration program (simattribsam) which includes the code for the individual algorithms is provided in Appendix 2.

Table 6.2. Programs derived for the analysis of data by application of attribute testing algorithms.

File	File type	Purpose
jumpwin.ado	Stata ado file	Sub-routine for evaluation of data using the JUMPWIN algorithm
jumpwin_r.ado	Stata ado file	Sub-routine for evaluation of data using the JUMPWIN algorithm.
slidewin.ado	Stata ado file	Sub-routine for evaluation of data using the SLIDEWIN algorithm.
slidewin_r.ado	Stata ado file	Sub-routine for evaluation of data using the SLIDEWIN_R algorithm.
condwin.ado	Stata ado file	Sub-routine for evaluation of data using the

		CONDWIN algorithm.
group_jumpwin.ado	Stata ado file	Evaluation of data from multiple establishments using JUMPWIN
group_jumpwin_r.ado	Stata ado file	Evaluation of data from multiple establishments using JUMPWIN_R
group_slidewin.ado	Stata ado file	Evaluation of data from multiple establishments using SLIDEWIN
group_slidewin_r.ado	Sata ado file	Evaluation of data from multiple establishments using SLIDEWIN_R
group_condwin.ado	Stata ado file	Evaluation of data from multiple establishments using CONDWIN
simattribsam	Stata do file	Demonstration program that simulates data and then applies each individual attribute sampling algorithm

A demonstration of the behaviour of different attribute sampling algorithms is shown in Table 6.3. The data show simulated observations made in a hypothetical setting and the corresponding events occurring within each sampling plan. It is evident from the application of the algorithms to this very small amount of ‘dummy’ data that each attribute sampling plans has its own behaviours, producing distinctively different rates of failure and varying in levels of complexity with respect to interpretation. It is also evident that comparison of the algorithms on the basis of number of windows failing divided by the total number of windows may not be wise because both the numerator and denominator vary.

Table 6.3. Extract of simulated data representing the concentration of hazard in 45 individual and consecutively produced items. The events occurring within each of five different attribute sampling plan algorithms are shown in columns to the right of the data. Events are abbreviated: O = opening of window, M = window closing with failure due to *M*, *C* = window closing with failure due to *c*, P = window closing with a pass result, R = the opening of a window that is then discarded due to window reset. Input parameters for each algorithm were: *n* = 15, *c* = 5, *m* = 0 and *M* = 20.

		Attribute sampling plan				
Sequence	Hazard	jumpwin	jumpwin_r	slidewin	slidewin_r	condwin
1	20.36908	O	OM	O	OM	OM
2	0	.	O	O	O	.
3	0	.	.	O	O	.
4	14.22834	.	.	O	O	O
5	0	.	.	O	O	.
6	0	.	.	O	R	.
7	0	.	.	O	R	.
8	0	.	.	O	R	.
9	0	.	.	O	R	.
10	0	.	.	O	R	.
11	0	.	.	O	R	.
12	0	.	.	O	R	.
13	0	.	.	O	R	.
14	1.111934	.	.	O	R	.
15	0	M	.	MO	R	.
16	0	O	P	PO	PR	.
17	0	.	O	PO	PR	.
18	0	.	.	PO	PR	P
19	574.2026	.	M	MO	MR	OM
20	0	.	O	MO	O	.
21	.3551186	.	.	MO	R	O
22	0	.	.	MO	R	.
23	13.65688	.	.	MO	R	.
24	.2523068	.	.	MO	R	.
25	0	.	.	MO	R	.
26	0	.	.	MO	R	.
27	.1446482	.	C	MO	CR	C
28	7.315565	.	O	MO	O	O
29	1.042152	.	.	MO	R	.
30	0	M	.	MO	R	.
31	0	O	.	MO	R	.
32	0	.	.	MO	R	.
33	0	.	.	MO	R	.
34	0	.	.	CO	R	.
35	0	.	.	CO	R	.
36	0	.	.	CO	R	.
37	0	.	.	CO	R	.
38	1.103882	.	.	CO	R	.
39	0	.	.	CO	R	.
40	0	.	.	CO	R	.
41	.6288582	.	C	CO	CR	C
42	.4327957	.	O	CO	O	O

43	0	.	.	CO	O	.
44	0	.	.	PO	O	.
45	0	P	P	PO	PR	P

Industry wide analysis of STEER/HEIFER using SLIDEWIN_R

Tables 4a to 4f show detailed (by establishment) results of the industry wide analysis of STEER/HEIFER data for *E. coli* from ESAM for the years 2000 to 2005 inclusive. This demonstration analysis was performed using the SLIDEWIN_R algorithm, the same algorithm applied by AQIS in monitoring quality assurance in Australian export establishments. Parameters for SLIDEWIN_R were input as n = 15, c = 3, m = 0 and M = 20. In each table, the establishments are listed in descending order of the prevalence of positive tests for that year. Establishments are identified by randomly allocated and unique four digit codes having no relationship to official identity numbers used by AQIS. For reasons of preserving anonymity the number of tests performed by each establishment has been deleted from the output.

Table 6.4a. Industry wide analysis of STEER/HEIFER data for *E. coli* on chilled carcases for the year 2000 using the attribute sampling plan algorithm SLWIN_R. Parameters were set at results for n = 15, c = 3, m = 0, M = 20, test interval = 300. Establishments listed in descending order of % positive tests.

#	Estab	%Pos	Failc	FailM	TotFail	FPTP
1	6826	31.73	7	0	7	0.22436
2	3012	22.22	0	0	0	0.00000
3	1771	22.22	1	1	2	0.24691
4	8233	12.77	4	0	4	0.07092
5	8305	12.50	1	0	1	0.10417
6	4018	11.54	0	0	0	0.00000
7	9870	10.17	0	0	0	0.00000
8	9539	8.57	0	0	0	0.00000
9	2721	5.92	0	0	0	0.00000
10	9034	5.00	0	0	0	0.00000
11	5399	4.94	0	0	0	0.00000
12	9185	4.76	0	0	0	0.00000
13	3874	4.35	0	0	0	0.00000
14	9046	4.17	0	0	0	0.00000
15	6267	4.08	0	0	0	0.00000
16	1691	2.89	0	0	0	0.00000
17	5031	2.78	0	0	0	0.00000
18	4478	2.54	0	0	0	0.00000
19	5289	1.72	0	0	0	0.00000
20	9286	1.69	0	0	0	0.00000
21	8948	1.64	0	0	0	0.00000
22	4892	1.61	0	0	0	0.00000
23	9837	1.30	0	0	0	0.00000
24	6216	1.25	0	0	0	0.00000
25	9322	0.92	0	0	0	0.00000
26	1042	0.83	0	0	0	0.00000
27	5851	0.80	0	0	0	0.00000
28	7938	0.00	0	0	0	0.00000
29	6866	0.00	0	0	0	0.00000
30	6842	0.00	0	0	0	0.00000
31	6357	0.00	0	0	0	0.00000
32	6051	0.00	0	0	0	0.00000
33	4974	0.00	0	0	0	0.00000
34	4969	0.00	0	0	0	0.00000
35	4692	0.00	0	0	0	0.00000
36	1405	0.00	0	0	0	0.00000
37	1294	0.00	0	0	0	0.00000

Total number of establishments with at least one failure in this time period = 4
Proportion of establishments with at least one failure in this time period = 0.1081
2000 fpmp: 14.9957

Table 6.4b. Industry wide analysis of STEER/HEIFER data for *E. coli* on chilled carcases for the year 2001 using the attribute sampling plan algorithm SLWIN_R. Parameters were set at results for n = 15, c = 3, m = 0, M = 20, test interval = 300. Establishments listed in descending order of % positive tests.

#	Estab	%Pos	Failc	FailM	TotFail	FPTP
1	2918	17.07	1	1	2	0.16260
2	9034	16.90	2	0	2	0.09390
3	1771	15.15	3	0	3	0.07576
4	3012	10.70	2	0	2	0.02743
5	9355	10.09	6	0	6	0.05935
6	5851	6.81	1	1	2	0.02837
7	4692	5.75	0	0	0	0.00000
8	8305	5.65	1	0	1	0.01449
9	9185	5.24	0	1	1	0.00831
10	1294	4.94	0	0	0	0.00000
11	5031	4.86	0	0	0	0.00000
12	4892	4.76	1	0	1	0.00835
13	9539	4.57	1	0	1	0.01522
14	5399	4.39	0	0	0	0.00000
15	6826	4.11	1	0	1	0.00623
16	8233	3.84	0	0	0	0.00000
17	6267	3.67	2	1	3	0.02825
18	9286	3.40	0	0	0	0.00000
19	1042	3.08	1	0	1	0.00734
20	4974	3.08	0	0	0	0.00000
21	6357	2.99	0	0	0	0.00000
22	4478	2.81	1	0	1	0.00669
23	2721	2.50	0	0	0	0.00000
24	5289	2.26	0	2	2	0.00942
25	9870	1.89	0	0	0	0.00000
26	9046	1.89	0	0	0	0.00000
27	7938	1.79	0	0	0	0.00000
28	4969	1.24	0	0	0	0.00000
29	4018	1.20	0	0	0	0.00000
30	8948	1.15	0	0	0	0.00000
31	3874	1.13	0	0	0	0.00000
32	9837	1.09	0	0	0	0.00000
33	1691	0.89	0	0	0	0.00000
34	6842	0.56	0	0	0	0.00000
35	1405	0.44	0	0	0	0.00000
36	6216	0.41	0	0	0	0.00000
37	9198	0.00	0	0	0	0.00000
38	8923	0.00	0	0	0	0.00000
39	8415	0.00	0	0	0	0.00000
40	6866	0.00	0	0	0	0.00000
41	6463	0.00	0	0	0	0.00000

Total number of establishments with at least one failure in this time period = 15
Proportion of establishments with at least one failure in this time period = 0.3659
2001 fpmp: 6.7984

Table 6.4c. Industry wide analysis of STEER/HEIFER data for *E. coli* on chilled carcases for the year 2002 using the attribute sampling plan algorithm SLWIN_R. Parameters were set at results for n = 15, c = 3, m = 0, M = 20, test interval = 300. Establishments listed in descending order of % positive tests.

#	Estab	%Pos	Failc	FailM	TotFail	FPTP
1	1771	18.80	3	1	4	0.10025
2	3012	17.84	6	1	7	0.09682
3	9198	10.81	1	0	1	0.09009
4	9355	10.45	7	0	7	0.03296
5	8520	9.09	0	0	0	0.00000
6	4749	7.41	1	0	1	0.01764
7	1294	6.48	0	0	0	0.00000
8	6826	6.07	5	0	5	0.03163
9	6357	6.06	0	0	0	0.00000
10	9034	5.56	0	0	0	0.00000
11	2721	4.80	0	0	0	0.00000
12	6267	4.33	0	0	0	0.00000
13	9046	4.07	0	0	0	0.00000
14	1042	3.95	1	0	1	0.00693
15	4892	3.67	0	0	0	0.00000
16	5289	3.49	0	0	0	0.00000
17	9539	3.33	0	0	0	0.00000
18	9286	3.24	0	0	0	0.00000
19	4974	3.08	0	0	0	0.00000
20	1405	3.04	1	0	1	0.00921
21	9185	3.03	0	0	0	0.00000
22	4018	2.80	0	0	0	0.00000
23	5031	2.68	0	0	0	0.00000
24	3874	2.58	1	0	1	0.00478
25	4478	2.40	0	1	1	0.00799
26	7938	2.00	0	0	0	0.00000
27	5399	1.95	0	0	0	0.00000
28	8923	1.80	0	0	0	0.00000
29	8305	1.71	0	0	0	0.00000
30	8233	1.66	0	0	0	0.00000
31	4692	1.55	0	0	0	0.00000
32	6842	1.40	0	0	0	0.00000
33	8948	1.24	0	0	0	0.00000
34	4969	0.75	0	0	0	0.00000
35	9870	0.75	0	0	0	0.00000
36	8415	0.45	0	0	0	0.00000
37	9837	0.26	0	0	0	0.00000
38	1691	0.25	0	0	0	0.00000
39	6216	0.21	0	0	0	0.00000
40	8352	0.00	0	0	0	0.00000
41	6866	0.00	0	0	0	0.00000
42	6463	0.00	0	0	0	0.00000
43	2918	0.00	0	0	0	0.00000

Total number of establishments with at least one failure in this time period =10
Proportion of establishments with at least one failure in this time period =0.2326
2002 fpmp: 6.6483

Table 6.4d. Industry wide analysis of STEER/HEIFER data for *E. coli* on chilled carcases for the year 2003 using the attribute sampling plan algorithm SLWIN_R. Parameters were set at results for n = 15, c = 3, m = 0, M = 20, test interval = 300. Establishments listed in descending order of % positive tests.

#	Estab	%Pos	Failc	FailM	TotFail	FPTP
1	2360	33.33	0	0	0	0.00000
2	3012	22.57	7	2	9	0.13274
3	9198	13.73	0	1	1	0.06536
4	6357	13.73	1	0	1	0.06536
5	8520	10.53	0	0	0	0.00000
6	9355	8.85	5	0	5	0.02234
7	1294	8.68	1	0	1	0.01522
8	6267	8.33	1	1	2	0.05051
9	1771	8.28	1	0	1	0.02299
10	4974	8.22	0	0	0	0.00000
11	2721	5.50	2	1	3	0.01410
12	9286	5.48	0	0	0	0.00000
13	9034	5.38	0	0	0	0.00000
14	1042	4.95	1	0	1	0.00868
15	9185	4.57	1	0	1	0.00952
16	4892	4.38	1	0	1	0.00913
17	8923	3.33	0	0	0	0.00000
18	9539	2.76	1	0	1	0.01312
19	6826	2.74	1	0	1	0.00652
20	5031	2.60	0	0	0	0.00000
21	4478	2.48	0	0	0	0.00000
22	4749	2.47	0	0	0	0.00000
23	7938	2.33	0	0	0	0.00000
24	4692	2.12	0	0	0	0.00000
25	8233	2.05	0	0	0	0.00000
26	8948	1.71	0	0	0	0.00000
27	4018	1.18	0	1	1	0.01972
28	6842	1.11	0	0	0	0.00000
29	1405	0.94	0	0	0	0.00000
30	4969	0.77	0	0	0	0.00000
31	3417	0.72	0	0	0	0.00000
32	3874	0.72	0	0	0	0.00000
33	5399	0.68	0	0	0	0.00000
34	8305	0.52	0	0	0	0.00000
35	1691	0.51	0	0	0	0.00000
36	9046	0.50	0	0	0	0.00000
37	9837	0.46	0	0	0	0.00000
38	9870	0.40	0	0	0	0.00000
39	6216	0.19	0	0	0	0.00000
40	8415	0.00	0	0	0	0.00000
41	8352	0.00	0	0	0	0.00000
42	6866	0.00	0	0	0	0.00000
43	6691	0.00	0	0	0	0.00000
44	6463	0.00	0	0	0	0.00000
45	1124	0.00	0	0	0	0.00000

Total number of establishments with at least one failure in this time period = 14
Proportion of establishments with at least one failure in this time period = 0.3111
2003 fpmp: 7.0756

Table 6.4e. Industry wide analysis of STEER/HEIFER data for *E. coli* on chilled carcases for the year 2004 using the attribute sampling plan algorithm SLWIN_R. Parameters were set at results for n = 15, c = 3, m = 0, M = 20, test interval = 300. Establishments listed in descending order of % positive tests.

#	Estab	%Pos	Failc	FailM	TotFail	FPTP
1	2360	25.00	0	0	0	0.00000
2	3012	14.88	4	0	4	0.05510
3	1771	12.20	0	0	0	0.00000
4	9034	9.16	2	0	2	0.05089
5	5851	9.00	3	0	3	0.03215
6	2067	8.33	0	0	0	0.00000
7	9355	8.31	3	0	3	0.01385
8	2721	7.59	3	0	3	0.01264
9	9928	7.14	0	0	0	0.00000
10	5289	6.13	0	0	0	0.00000
11	1294	5.45	0	0	0	0.00000
12	9870	4.83	1	0	1	0.00894
13	6267	4.44	0	1	1	0.01852
14	8923	4.20	0	0	0	0.00000
15	9185	4.19	0	0	0	0.00000
16	4969	3.92	0	0	0	0.00000
17	4749	3.76	0	0	0	0.00000
18	6357	3.45	0	0	0	0.00000
19	9198	3.33	0	0	0	0.00000
20	6826	3.13	1	0	1	0.00652
21	5399	2.76	0	0	0	0.00000
22	1042	2.70	0	0	0	0.00000
23	4974	2.60	0	0	0	0.00000
24	4018	2.36	0	0	0	0.00000
25	4692	2.33	0	0	0	0.00000
26	7938	1.94	0	0	0	0.00000
27	4892	1.75	0	0	0	0.00000
28	4478	1.56	0	0	0	0.00000
29	5031	1.34	0	0	0	0.00000
30	8233	1.30	0	0	0	0.00000
31	9046	1.24	0	0	0	0.00000
32	8415	1.16	0	1	1	0.01292
33	8948	1.06	0	0	0	0.00000
34	9539	0.78	0	0	0	0.00000
35	6842	0.75	0	0	0	0.00000
36	3417	0.45	0	0	0	0.00000
37	9837	0.28	0	0	0	0.00000
38	3874	0.17	0	0	0	0.00000
39	6216	0.07	0	0	0	0.00000
40	8352	0.00	0	0	0	0.00000
41	8305	0.00	0	0	0	0.00000
42	6866	0.00	0	0	0	0.00000
43	1691	0.00	0	0	0	0.00000

Total number of establishments with at least one failure in this time period = 9
Proportion of establishments with at least one failure in this time period = 0.2093
2004 fpmp: 4.2369

Table 6.4f. Industry wide analysis of STEER/HEIFER data for *E. coli* on chilled carcases for the year 2005 using the attribute sampling plan algorithm SLWIN_R. Parameters were set at results for n = 15, c = 3, m = 0, M = 20, test interval = 300. Establishments listed in descending order of % positive tests.

#	Estab	%Pos	Failc	FailM	TotFail	FPTP
1	1124	20.00	0	0	0	0.00000
2	1205	18.52	0	1	1	0.12346
3	3710	16.67	0	0	0	0.00000
4	2360	12.82	1	0	1	0.08547
5	6267	10.56	1	1	2	0.04141
6	9355	9.18	5	0	5	0.02318
7	1771	8.77	0	0	0	0.00000
8	5289	8.61	3	0	3	0.01511
9	9034	6.94	1	0	1	0.02315
10	9870	6.14	0	0	0	0.00000
11	9185	5.63	0	0	0	0.00000
12	2721	5.57	1	0	1	0.00422
13	3012	5.42	1	1	2	0.04016
14	4974	4.88	0	0	0	0.00000
15	1042	4.84	1	0	1	0.02688
16	9046	4.64	0	0	0	0.00000
17	6357	4.35	0	0	0	0.00000
18	6826	3.96	1	0	1	0.00660
19	4969	3.77	0	1	1	0.01142
20	1691	3.15	2	0	2	0.02625
21	1294	2.80	0	0	0	0.00000
22	4892	2.76	0	0	0	0.00000
23	5399	2.40	0	0	0	0.00000
24	4692	2.35	0	0	0	0.00000
25	2067	2.30	0	0	0	0.00000
26	8415	2.11	0	1	1	0.01406
27	8233	2.00	0	0	0	0.00000
28	9928	1.93	0	0	0	0.00000
29	9539	1.93	0	0	0	0.00000
30	5031	1.75	0	0	0	0.00000
31	7938	1.72	0	0	0	0.00000
32	6842	1.53	0	0	0	0.00000
33	5851	1.38	1	0	1	0.00577
34	9837	1.32	0	0	0	0.00000
35	3874	1.29	0	0	0	0.00000
36	4478	1.23	0	0	0	0.00000
37	8948	0.91	0	0	0	0.00000
38	4018	0.57	0	0	0	0.00000
39	8305	0.20	0	0	0	0.00000
40	8923	0.00	0	0	0	0.00000
41	6866	0.00	0	0	0	0.00000
42	6216	0.00	0	0	0	0.00000
43	6051	0.00	0	0	0	0.00000
44	3417	0.00	0	0	0	0.00000

Total number of establishments with at least one failure in this time period = 14
Proportion of establishments with at least one failure in this time period = 0.3182
2005 fpmp: 5.0682

Table 6.5. Distribution of data including missing data on hot and cold boning method applied to STEER/HEIFER carcases for each year of the study. Hot boned carcases are excluded from Tables 4a-4f. There are a substantial proportion of missing values in year 2000.

		Boning method		
Year	Missing value	Cold	Hot	Total
2000	12,148	3,272	44	15,464
2001	490	15,875	157	16,522
2002	418	16,935	258	17,611
2003	531	15,936	254	16,721
2004	456	17,365	493	18,314
2005	524	17,602	661	18,787
Total	14,567	86,985	1,867	103,419

Performance of algorithms by carcase type and year

When ESAM data for individual species of livestock carcases were analysed using the different algorithms for consecutive years the number of failures per unit output varied substantially as shown in Figure 1 for STEER/HEIFER data (all algorithms operating on the attribute sampling plan parameters in use under AQIS meat notice 2003/6). Despite the large absolute differences between results from each algorithm, the ranking of the performance of each year of processing was similar across algorithms. Note that when assessing the data for chilled beef carcases in year 2000 (Figures 2 and 4) that these years are based on much smaller numbers of observations than other years because of the amount of missing data on ‘boningmethod’ (Table 6.5).

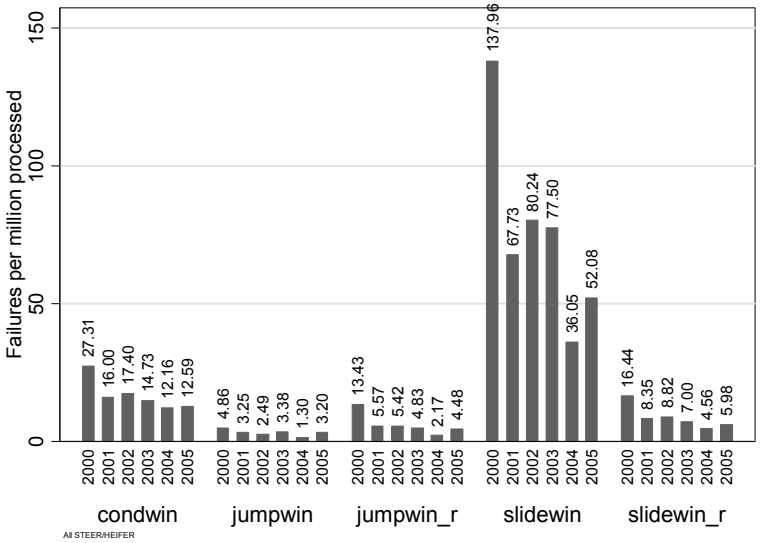

Figure6.1. Analysis of *E. coli* cfu.cm^{-2} data from cold boned and hot boned STEER/HEIFER carcases (sampled pre and post chilling) for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 3, m = 0, M = 20).

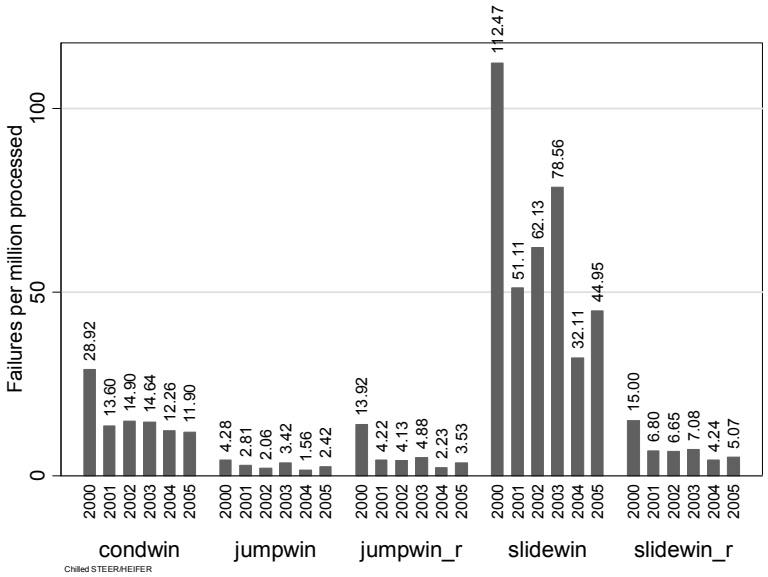

Figure 6.2. Analysis of *E. coli* cfu.cm^{-2} data from cold-boned STEER/HEIFER carcases (sampled post chilling) for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 3, m = 0, M = 20).

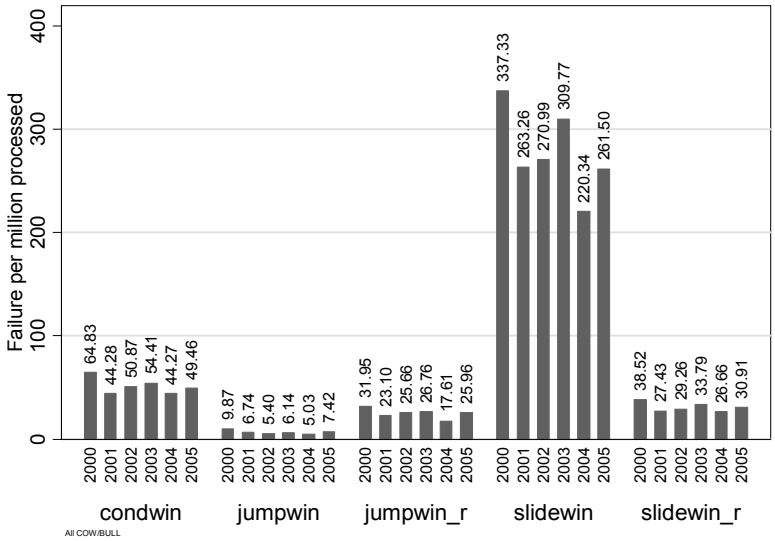

Figure 6.3. Analysis of *E. coli* cfu.cm^{-2} data from all COW/BULL carcases (sampled pre and post chilling) for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 3, m = 0, M=20).

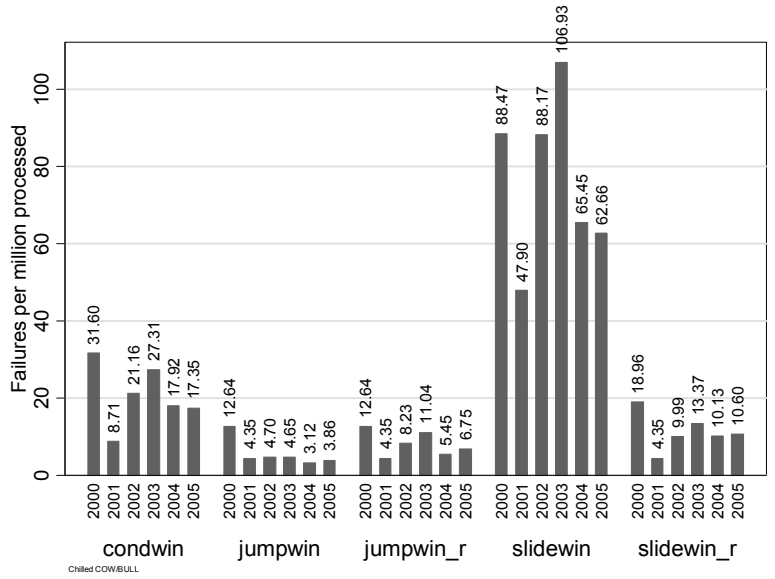

Figure 6.4. Analysis of *E. coli* cfu.cm^{-2} data from cold-boned COW/BULL carcases (sampled post chilling) for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 3, m = 0, M = 20).

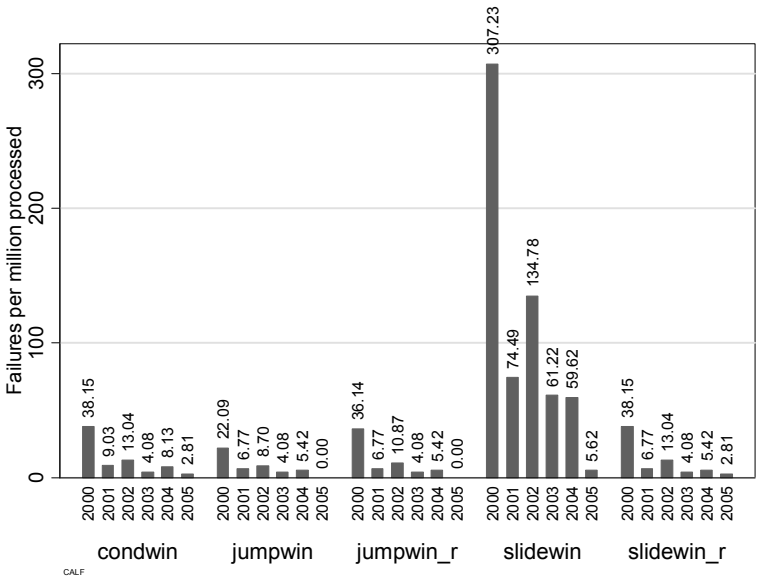

Figure 6.5. Analysis of *E. coli* cfu.cm^{-2} data from CALF carcases for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 7, m = 5, M = 100).

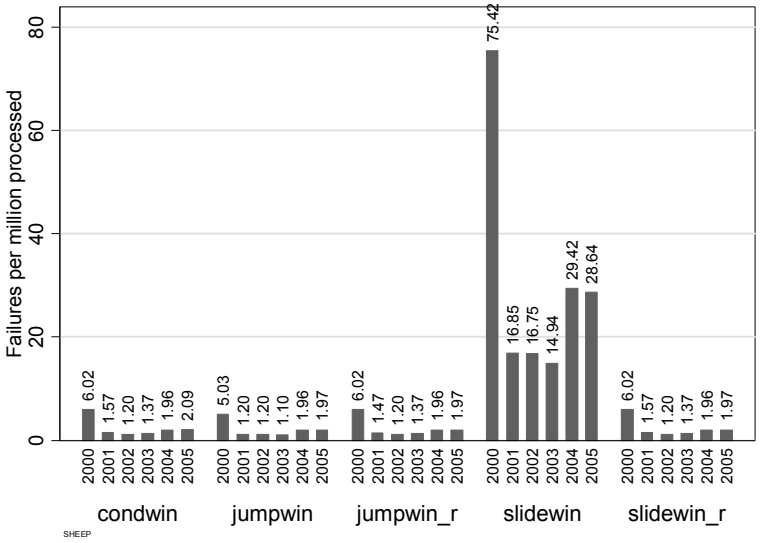

Figure 6.6. Analysis of *E. coli* cfu.cm^{-2} data from SHEEP carcases for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 7, m = 5, M =100).

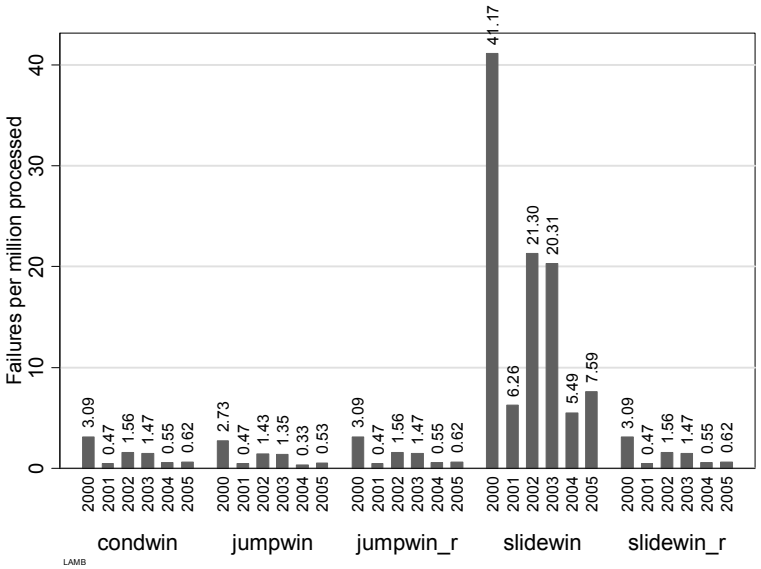

Figure 6.7. Analysis of *E. coli* cfu.cm^{-2} data from LAMB carcases for years 2000 to 2005 on an industry (national) basis using each of the attribute sampling algorithms (each applied with identical parameters of: n = 15, c = 7, m = 5, M = 100).

6.4 Discussion

Issues arising from this work that are relevant to the Australian Meat Industry are:

- Attribute sampling plans used in meat processing now appear to be more complex and diverse than previously described. They have evolved into multiple distinct forms characterised by the way each interpret the data in order to define whether windows are open or closed and whether pass or fail conditions are met. The new variations of attribute sampling are substantially dissimilar to traditional attribute sampling schemes. These developments appear to have occurred arbitrarily as a process of evolution to meet regulatory and trade needs of different jurisdictions rather than an as logical extension of the traditional approach based on statistical theory, microbiological theory or both.

- Assessing a population of processing establishments with respect to the proportion of windows passing or failing the attribute sampling classification appears inappropriate if it is possible that there is variation in the number and size of windows between establishments and sampling periods. This possibility exists when reset type algorithms are used (JUMPWIN_R or SLIDEWIN_R). As well, sliding window algorithms appear overly complex to interpret because each test causes the creation of a new window and there are multiple and overlapping windows open and being assessed at any one time. Comparisons between establishments, species and time periods and any summaries thereof appear more informative when the outcome is the number of failures per thousand carcases processed (establishment level) or number of failures per million carcases processed (national or industry level). It only appears to be appropriate to use the proportion of windows passing attribute test criteria when the sampling plan is traditional (i.e. JUMPWIN).

- When evaluated against historical data for *E. coli* concentrations on carcases the different algorithms in use all provide different failure rates (sometimes markedly different). Most notably the failure rate for SLIDEWIN is substantially higher than all of the other algorithms which reflects the combination off multiple, overlapping windows and no reset. However, the relative ranking of each year of production according to failure rates when examined on a national level is similar regardless of which attribute sampling plan is used.

- Sliding windows that are in use in processing in Australia (SLIDEWIN_R) and the U.S.A. (SLIDEWIN) provide overly complex output when applied to historical data because each piece of information is analysed on multiple occasions and (when resetting occurs) windows of different size are evaluated (SLIDEWIN_R). Output that is more convenient to interpret is produced by algorithms that do not have overlapping windows (JUMPWIN and JUMPWIN_R).

There is a difference between retrospective evaluation of sampling schemes (this work) and prospective interpretation of carcase microbiology data as soon as it is received from the laboratory in an industry (or regulatory) setting. Simplicity of interpretation is likely to be important in the prospective practical setting and so those approaches based on a sliding window may possibly be more prone to misinterpretation due to their greater complexity.

- Values of n, c, m and M used in interpretation of attribute sampling plans for *E. coli* on carcases (in Australia and elsewhere) appear to not have a defensible basis. However, it does appear as though the current values can be retained and used as a benchmark standard for assessing industry-wide progress with hygiene.

- The benefit of information arising from attribute sampling schemes is limited by the weaknesses of carcase swabs for defining hygienic status of a single carcase or group of carcases (similar limitations also apply to excision samples).

- The evolution of attribute sampling plans as they are applied to meat carcases seems to have been based on arbitrary decisions or decisions that do not have an objective basis, or which are related to risk to public health or adverse commercial outcomes. The developments have occurred on an ad-hoc basis and a long-term aim should be to improve the relevance of attribute sampling to the needs of commercial trade in meat products and public health.

7 References

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8 Appendices

8.1 Appendix 1: Periodic analysis of ESAM data – example plots

The following plot is one of the few approaches available for representing *E. coli* data (detection).

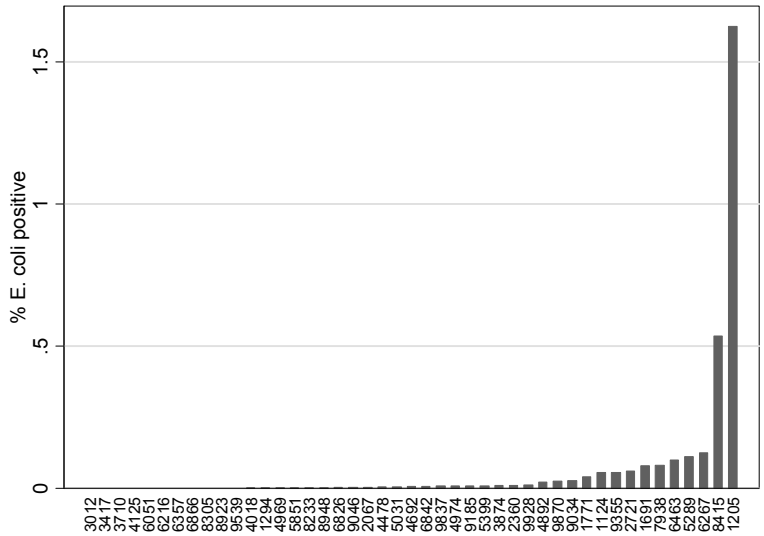

Figure A1.1. Percentage of *E. coli* positive test results for each individual establishment in ascending order. Establishments are identified by confidential numerical codes (x axis labels).

The following plots (Figures A1.2 to A1.) are produced as examples of how log TVC cfu.cm-2 data from particular establishments could be presented back to those establishments. The data is from an anonymous establishment and only considers a single six month period. Some plots include an industry wide comparison.

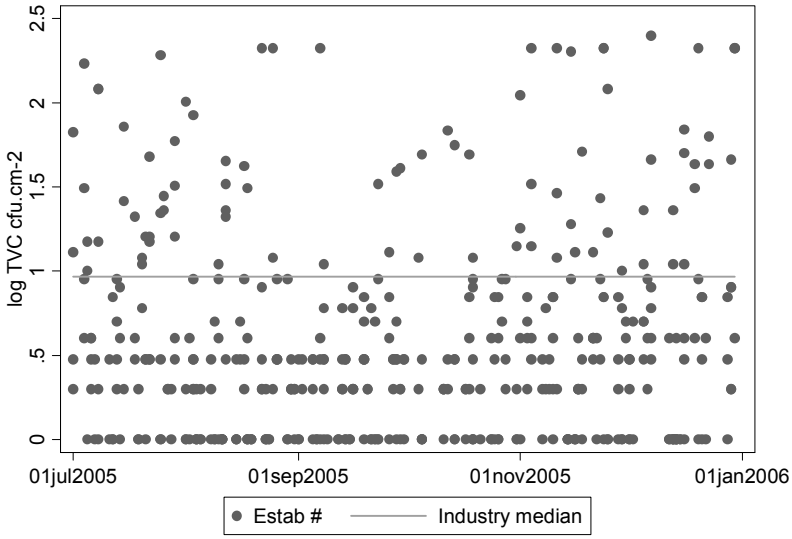

Figure A1.1. Example plot for periodic distribution to establishments. This is a scatter plot of six months of log TVC cfu.cm^{-2} from a single establishment and includes a line representing the industry median for the same period.

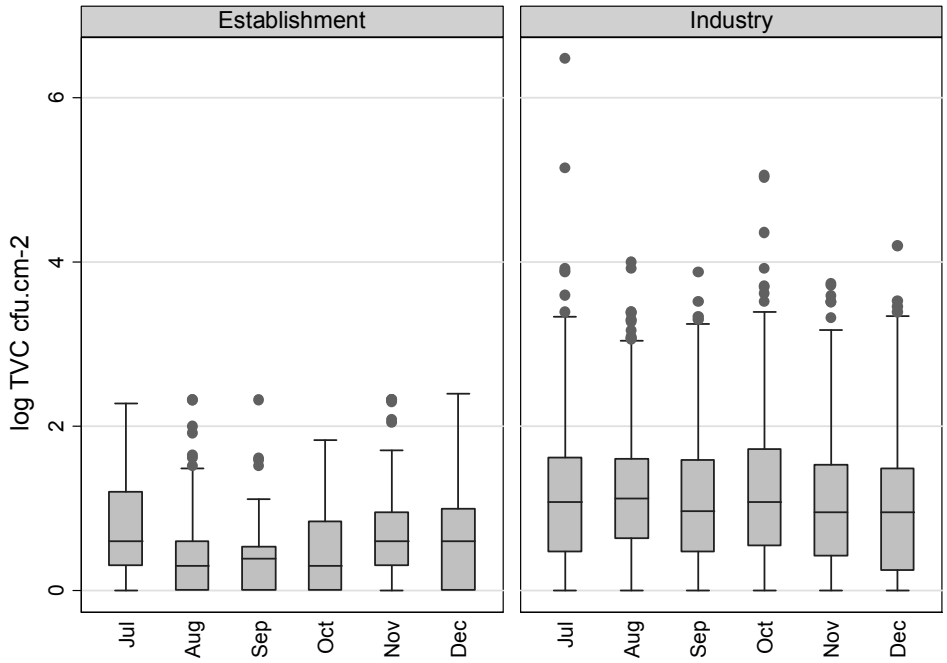

Figure A1.2. Example plot for periodic distribution to establishments. This plot consists of two panels of box plots. Within each panel are summarised log TVC cfu.cm^{-2} for the period of interest. The panel on the left is specific for the establishment the panel on the right is an industry wide summary.

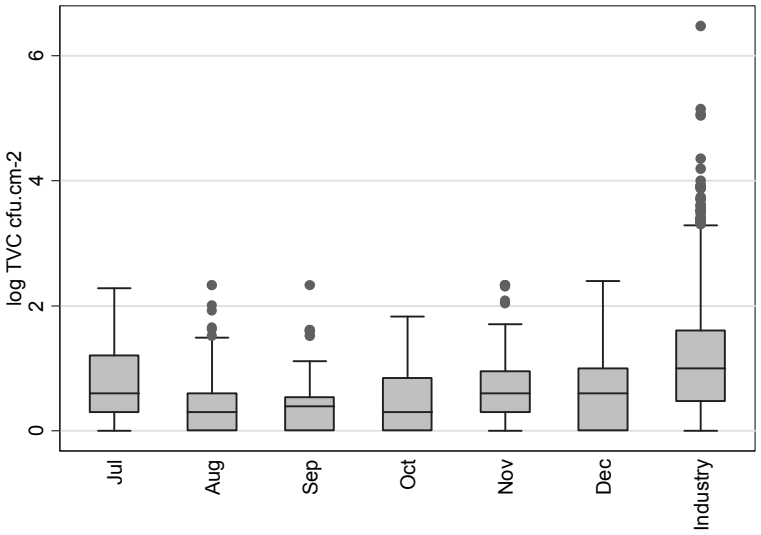

Figure A1.3. Example plot for periodic distribution to establishments. This plot consists of a summary of log TVC cfu.cm^{-2} for the period of interest for the establishment plus a separate box summarising the industry performance over the entire time period.

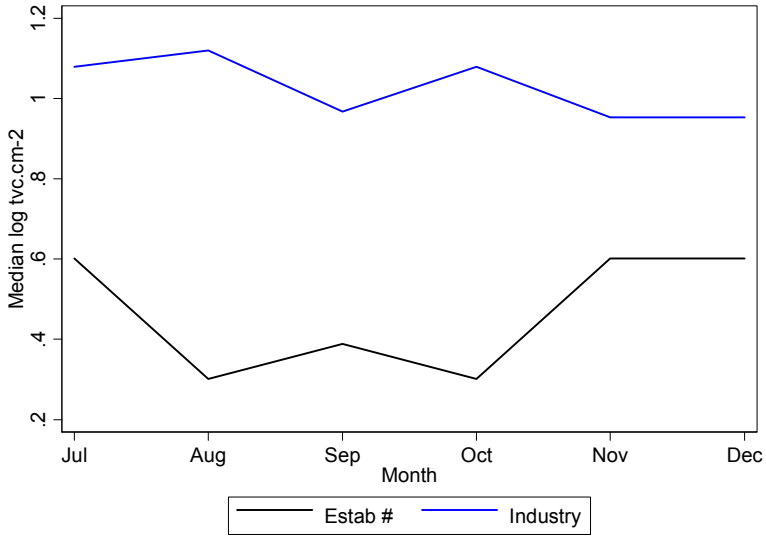

Figure A1.4. Example plot for periodic distribution to establishments. This plot consists of a time series plot of the median log TVC cfu.cm^{-2} for each month of the time period of interest. Separate lines are provided for the establishment of interest and the industry summary.

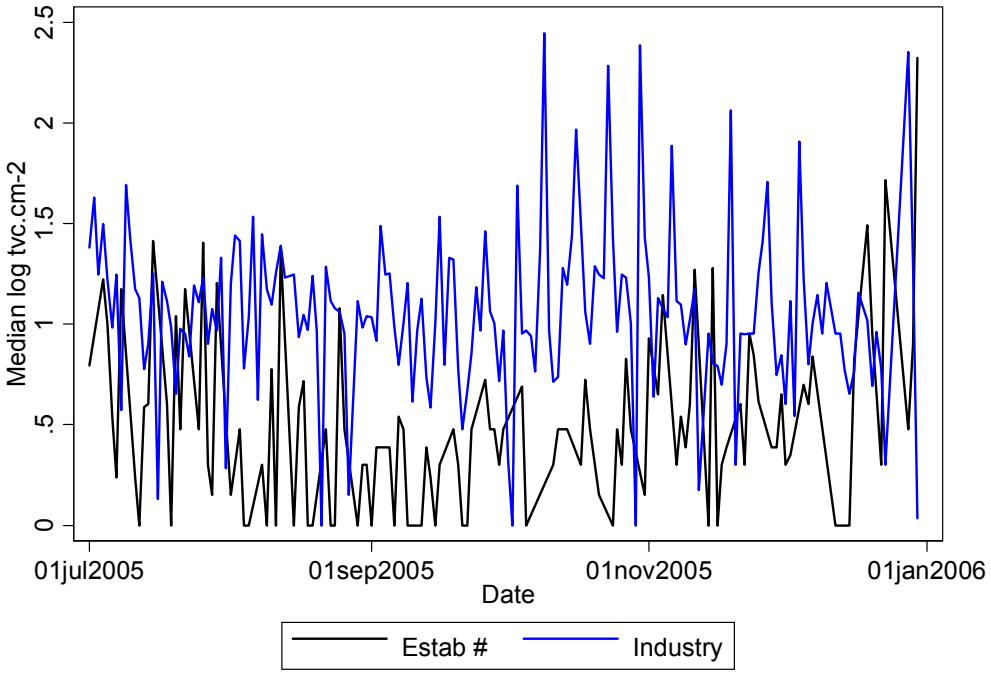

Figure A1.5. Example plot for periodic distribution to establishments. This plot consists of a time series plot of the daily median log TVC cfu.cm^{-2} over the time period of interest. Separate lines are provided for the establishment of interest and the industry summary.

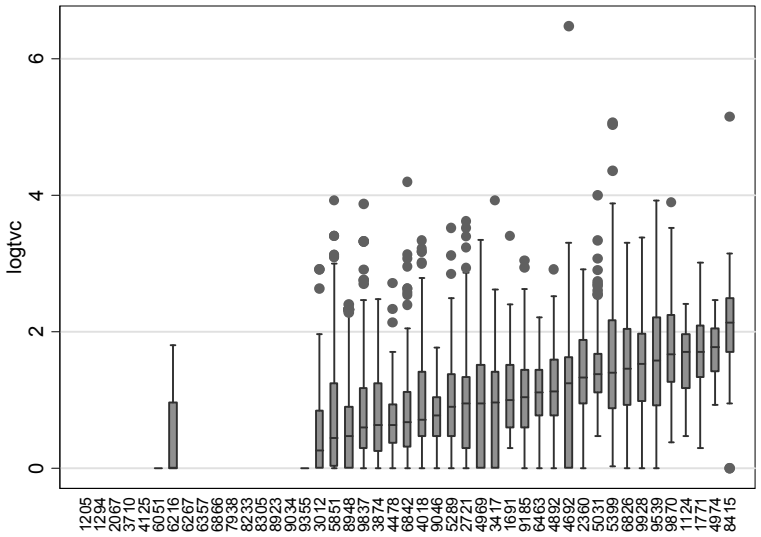

Figure A1.6. Example plot for periodic distribution to establishments. This plot enables a detailed comparison of the performance of each establishment over the six month period. Establishments can only be identified by a confidential numerical code (x axis labels).

8.2 Appendix 2: Stata programs for simulation and demonstration of attribute sampling plans

```
* Filename SimAttribSam
// Simulation of attribute testing
// Demonstration of attribute testing algorithms
// STATA version 9.2 program written for Meat and Livestock Australia
// Program produced for PRMS.02
// 3rd November 2006
// Author David Jordan, NSW Department of Primary Industries, Wollongbar, NSW, Australia

version 9.2
capture log close
clear
set more off

program drop _all

program define jumpwin, rclass sortpreserve
// One of serveral algorithms modelling attribute sampling plans
// This version has non-overlapping windows hence called a jumping window
// A window only closes after all testing has been performed (doesn't reset on failure)
// Overall classified as a jumping window without reset
// Author David Jordan, NSW Department of Primary Industries, Wollongbar, NSW, Australia

version 9.2
syntax varlist (min=2 max=2 numeric) [if] [in] , n(integer) c(integer) small_m(real) big_M(real)
gettoken hazard seq: varlist
display as res "JUMPWIN ALGORITHM"
display as res "Attribute sampling results for n = "`n' ", c = "`c' ", m = "`small_m' ", M =
"`big_M'
display

display as res "Tests performed                                                fail c
                    fail M"
display as res "-------------------------------------------------------------"
if "`if'"!="" | "`in'"!=""{
       quietly keep `if' `in'
}
// Seq to represent the order of observations
sort `seq'
// Use the variable y to represent a test result
quietly gen y = 2     if `hazard' < .
quietly replace y = 1 if `hazard' <= `big_M'
quietly replace y = 0 if `hazard' <= `small_m'
quietly gen jmpwin = ""
local wincount = 0
local c_fail = 0
local M_fail = 0
local i = 1
while `i' <= _N {
   local wincount = `wincount' + 1
   local endwin = `i'+`n'-1
   if `endwin' > _N {
      local endwin = _N
        }
        local k = `i'
        local c_count = 0
        local thiswinfail = 0
        quietly replace jmpwin = jmpwin+"O" if _n == `k'
        while `k' <=`endwin' {
               local x = y in `k'
               if `x' == 2 {
                      // Window failure due to M fail
                      if `thiswinfail' == 0 {
                             local thiswinfail = 2
                      }
                      local k = `k'+1
               }
               else if `x' < 2 {
                      local c_count = `c_count'+`x'
                      if `c_count' > `c' {
```

```
                        // Window failure due to c fail
                        if `thiswinfail' == 0 {
                                local thiswinfail = 1
                        }
                }
                local k = `k'+1
        }
} // end of while k loop
if `thiswinfail' == 2 {
        quietly replace jmpwin = jmpwin + "M" if _n == `k'-1
        local M_fail = `M_fail'+1
}
if `thiswinfail' == 1 {
        local c_fail = `C_fail'+1
        quietly replace jmpwin = jmpwin + "C" if _n == `k'-1
}
if `thiswinfail' == 0 {
        quietly replace jmpwin = jmpwin + "P" if _n == `k'-1
}
local i = `k'
}       // end of while i loop
drop y
quietly count if `hazard' < .
local totaltests = r(N)
display as res %10.0f `totaltests' %24.0f `c_fail' %20.0f `M_fail'
return scalar tt = `totaltests'
return scalar smallm = `c_fail'
return scalar bigm = `M_fail'
return scalar numwindows = `wincount'
end



program define jumpwin_r, rclass sortpreserve
// One of serveral algorithms modelling attribute sampling plans
// This version has non-overlapping windows hence called a jumping window
// This version closes a window as soon as a failure occurs hence has a reset window feature
// Overall classified as a jumping window with reset
// Author David Jordan, NSW Department of Primary Industries, Wollongbar, NSW, Australia

version 9.1
syntax varlist (min=2 max=2 numeric) [if] [in] , n(integer) c(integer) small_m(real) big_M(real)
gettoken hazard seq: varlist
display
display as res "Attribute sampling results for n = "`n' ", c = "`c' ", m = "`small_m' ", M =
"`big_M'
display as res "JUMPWIN_R ALGORITHM"
display as res "Tests performed                                              fail c
                  fail M"
display as res "-------------------------------------------------------------"
if "`if'"!="" | "`in'"!=""{
        quietly keep `if' `in'
}
// Seq to represent the order of observations
sort `seq'
// Use the variable y to represent a test result
quietly gen y = 2      if `hazard' < .
quietly replace y = 1 if `hazard' <= `big_M'
quietly replace y = 0 if `hazard' <= `small_m'
quietly gen jmpwin_r = ""
local wincount = 0
local c_fail = 0
local M_fail = 0
local i = 1
while `i' <= _N {
        local wincount = `wincount' + 1
        local endwin = `i'+`n'-1
        if `endwin' > _N {
                local endwin = _N
        }
        local k = `i'
        local c_count = 0
        local thiswindow = 0
```

```
        quietly replace jmpwin_r = jmpwin_r+"O" if _n == `k'
        while `k' <=`endwin' & `thiswindow' == 0 {
                local x = y in `k'
                if `x' == 2 {
                        // Window failure due to M fail
                        local M_fail = `M_fail'+1
                        local thiswindow = 2
                        quietly replace jmpwin_r = jmpwin_r+"M" if _n == `k'
                }
                if `x' == 1 {
                        local c_count = `c_count'+`x'
                        if `c_count' > `c' {
                                // Window failure due to c fail
                                local c_fail = `c_fail'+1
                                local thiswindow = 1
                                quietly replace jmpwin_r = jmpwin_r + "C" if _n == `k'
                        }
                }
                local k = `k'+1
        } // end of while k loop
        if `thiswindow' == 0 {
                quietly replace jmpwin_r = jmpwin_r + "P" if _n == `k'-1
        }
        local i = `k'
}        // end of while i loop
drop y
quietly count if `hazard' < .
local totaltests = r(N)
display as res %10.0f `totaltests' %24.0f `c_fail' %20.0f `M_fail'
return scalar tt = `totaltests'
return scalar smallm = `c_fail'
return scalar bigm = `M_fail'
return scalar numwindows = `wincount'
end



program define slidewin, rclass sortpreserve
// One of serveral algorithms modelling attribute sampling plans
// This version has overlapping windows hence called a sliding window
// This version only closes a window after n tests, it has no reset feature
// Overall classified as a sliding window without reset
// Author David Jordan, NSW Department of Primary Industries, Wollongbar, NSW, Australia

version 9.1
syntax varlist (min=2 max=2 numeric) [if] [in] , n(integer) c(integer) small_m(real) big_M(real)
gettoken hazard seq: varlist
display
display as res "Attribute sampling results for n = "`n' ", c = "`c' ", m = "`small_m' ", M =
"`big_M'
display as res "SLIDEWIN ALGORITHM"
display as res "Tests performed                                              fail c
                        fail M"
display as res "-------------------------------------------------------------"
if "`if'"!="" | "`in'"!=""{
        quietly keep `if' `in'
}
// Use the variable seq to represent the sequence number of the observation
sort `seq'
// Use the variable y to represent a test result
gen y = 2
quietly replace y = 1 if `hazard' <= `big_M'
quietly replace y = 0 if `hazard' <= `small_m'
quietly gen slwin = ""
// Set up variables for counting results and positions
local failM = 0
local failc = 0
local i = 0
while `i' < _N {
        // Start window evaluation
        local k = `i'
        quietly replace slwin = slwin+"O" if _n == `i'+1
        local ccount = 0
```

```
        local endwin = `k'+`n'
        local thiswindow = 0
        if `endwin' > _N {
                local endwin = _N
        }
        while (`k'<`endwin') {
                local k = `k'+1
                local x = y in `k'
                if `x' == 2 {
                        if `thiswindow' == 0 {
                                local thiswindow = 2
                        }
                }
                if `x' == 1 {
                        local ccount = `ccount'+1
                        if `ccount' > `c' {
                                if `thiswindow' == 0 {
                                        local thiswindow = 1
                                }
                        }
                }
                if `k' == `endwin' {
                        if `thiswindow' == 0 {
                                quietly replace slwin = slwin+"P" if _n == `k'
                        }
                        if `thiswindow' == 1 {
                                quietly replace slwin = slwin+"C" if _n == `k'
                                local failc = `failc'+1
                        }
                        if `thiswindow' == 2 {
                                quietly replace slwin = slwin+"M" if _n == `k'
                                local failM = `failM'+1
                        }
                }
        }       // end of while k
        local i = `i'+1
}        // end while i
quietly count
local totaltests = r(N)
display as res %10.0f `totaltests' %24.0f `failc' %20.0f `failM'
return scalar tt = `totaltests'
return scalar smallm = `failc'
return scalar bigm = `failM'
drop y
end



program define slidewin_r, rclass sortpreserve
// One of serveral algorithms modelling attribute sampling plans
// This version has overlapping windows hence called a sliding window
// This version closes a window as soon as a failure occurs hence has a reset window feature
// Overall classified as a sliding window with reset
// Author David Jordan, NSW Department of Primary Industries, Wollongbar, NSW, Australia

version 9.1
syntax varlist (min=2 max=2 numeric) [if] [in] , n(integer) c(integer) small_m(real) big_M(real)
gettoken hazard seq: varlist
display
display as res "Attribute sampling results for n = "`n' ", c = "`c' ", m = "`small_m' ", M =
"`big_M'
display as res "SLIDEWIN_R ALGORITHM"
display as res "Tests performed                                              fail c
                 fail M"
display as res "-------------------------------------------------------------"
if "`if'"!="" | "`in'"!=""{
        quietly keep `if' `in'
}
// Use the variable seq to represent the sequence number of the observation
sort `seq'
// Use the variable y to represent a test result
gen y = 2
quietly replace y = 1 if `hazard' <= `big_M'
```

```
quietly replace y = 0 if `hazard' <= `small_m'
quietly gen slwin_r = ""
// Set up variables for counting results and positions
local failM = 0
local failc = 0
local i = 0
while `i' < _N {
	// Start window evaluation
	local k = `i'
	quietly replace slwin_r = slwin_r+"O" if _n == `i'+1
	local ccount = 0
	local failposn = 0
	local endwin = `k'+`n'
	if `endwin' > _N {
		local endwin = _N
	}
	while ((`k'<`endwin') & (`failposn'==0)) {
		local k = `k'+1
		//display as text %8.0f `i' %8.0f `k'
		local x = y in `k'
		if `x' == 2 {
			local failM = `failM'+1
			local failposn = `k'
			quietly replace slwin_r = slwin_r+"M" if _n == `k'

		}
		if `x' == 1 {
			local ccount = `ccount'+1
			if `ccount' > `c' {
				local failc = `failc'+1
				local failposn = `k'
				quietly replace slwin_r = slwin_r+"C" if _n == `k'
			}
		}
		if `k' == `endwin' & `failposn' == 0 {
			quietly replace slwin_r = slwin_r+"P" if _n == `k'
		}
	}	// end of while k, failposn
	if `failposn' > 0 {
		if `failposn' != `i'+1 {
			local startreset = min(`i'+2, _N)
			quietly replace slwin_r = slwin_r+"R" in `startreset'/`failposn'
		}
		local i = `failposn'
		set trace off
	} // end if
	else {
		local i = `i'+1
	}
}	 // end while i
quietly count
local totaltests = r(N)
display as res %10.0f `totaltests' %24.0f `failc' %20.0f `failM'
return scalar tt = `totaltests'
return scalar smallm = `failc'
return scalar bigm = `failM'
drop y
end



program define condwin, rclass sortpreserve
// One of serveral algorithms modelling attribute sampling plans
// This version has non-overlapping windows hence called a jumping window
// This version only opens on detection of an unacceptable result. Hence conditional opening
feature.
// This version closes a window as soon as a failure occurs hence has a reset window feature
// Overall classified as a conditional opening, jumping window with reset.
// Author David Jordan, NSW Department of Primary Industries, Wollongbar, NSW, Australia

version 9.1
syntax varlist (min=2 max=2 numeric) [if] [in] , n(integer) c(integer) small_m(real) big_M(real)
gettoken hazard seq: varlist
```

```
display
display as res "Attribute sampling results for n = "`n' ", c = "`c' ", m = "`small_m' ", M =
"`big_M'
display as res "CONDWIN ALGORITHM"
display as res "Tests performed                                              fail c
                    fail M"
display as res "-------------------------------------------------------------"
if "`if'"!="" | "`in'"!=""{
       quietly keep `if' `in'
}
sort `seq'
gen y = 2      if `hazard' < .
quietly replace y = 1 if `hazard' <= `big_M'
quietly replace y = 0 if `hazard' <= `small_m'
quietly gen cowin = ""
local wincount = 0
local c_fail = 0
local M_fail = 0
local i = 1
while `i' <= _N {
       local x = y in `i'
       if `x' > 0 {    // Window only begins with a positive result
              local wincount = `wincount' + 1
              quietly replace cowin = cowin + "O" if _n ==`i'
              local endwin = `i'+`n'-1
              if `endwin' > _N {
                     local endwin = _N
              }
              local k = `i'
       local c_count = 0
              local thiswindow = 0
              while `k' <=`endwin' & `thiswindow'== 0 {
                     local x = y in `k'
                     if `x' == 2 {
                            // Window failure due to M fail
                            local M_fail = `M_fail'+1
                            local thiswindow = 2
                            quietly replace cowin = cowin + "M" if _n == `k'
                            local k = `k'+1
                     }
                     else if `x' < 2 {
                            local c_count = `c_count'+`x'
                            if `c_count' > `c' {
                                   // Window failure due to c fail
                                   local c_fail = `c_fail'+1
                                   quietly replace cowin = cowin + "C" if _n == `k'
                                   local thiswindow = 1
                            }
                            local k = `k'+1
                     }
              } // end of while k loop
              if `thiswindow' == 0 {
                     quietly replace cowin = cowin + "P" if _n == `k'-1
              }
              local i = `k'
       }       // end if loop
       else {
              local i = `i'+1
       }
}       // end of while i loop
quietly count if `hazard' < .
local totaltests = r(N)
display as res %10.0f `totaltests' %24.0f `c_fail' %20.0f `M_fail'
return scalar tt = `totaltests'
return scalar smallm = `c_fail'
return scalar bigm = `M_fail'
return scalar numwindows = `wincount'
drop y
end

//*********************************************************************
//Main program including simulation of data and application of algorithms
//*********************************************************************
```

```
// Define simulation settings
set obs 1000
set seed 111567
// Define common attribute sampling parameters
local xn = 15
local xc = 3
local xm = 0
local xM = 20
// Define Bernoulli p for prevalence of positive samples
local prev = 0.3
// Define parameters of a log normal distribution for the concentration of hazard
//       in positive samples
local hazmean = 0.4
local hazsd     = 1
//Begin simulation
gen hazpos = 1 if uniform() < `prev'
replace hazpos = 0 if hazpos == .
gen haz = 10^(invnorm(uniform())*`hazsd'+`hazmean')
gen test = _n
replace haz = 0 if hazpos == 0
drop hazpos
order test haz
//Perform each type of attribute sampling
jumpwin haz test, n(`xn') c(`xc') small_m(0) big_M(20)
//return list
jumpwin_r haz test, n(`xn') c(`xc') small_m(`xm') big_M(`xM')
//return list
slidewin haz test, n(`xn') c(`xc') small_m(`xm') big_M(`xM')
//return list
slidewin_r haz test, n(`xn') c(`xc') small_m(`xm') big_M(`xM')
//return list
condwin haz test, n(`xn') c(`xc') small_m(`xm') big_M(`xM')
// return list
// Improve presentation of data when listed
replace jmpwin = "." if jmpwin == ""
replace jmpwin_r = "." if jmpwin_r == ""
replace slwin = "." if slwin == ""
replace slwin_r = "." if slwin_r == ""
replace cowin = "." if cowin == ""
// tidy up last entry in slwin and slwin_r
local endfix = slwin[_N]
if      length("`endfix'") > 2 {
        local endfix = substr("`endfix'", -2, 2)+"*"
        local lastobs = _N
        replace slwin = "`endfix'" in `lastobs'
}
local endfix = slwin_r[_N]
if      length("`endfix'") > 2 {
        local endfix = substr("`endfix'", -2, 2)+"*"
        local lastobs = _N
        replace slwin_r = "`endfix'" in `lastobs'
}
set more on
```

8.3 Appendix 3. Detection and concentration of *E. coli* and detection of *Salmonella* in red meat

(Tables produced to enable direct comparison with the 2004 Baseline Study)
NOTES: Mean, standard deviation and quantiles of log transformed E. coli counts refer to the sub-set of the samples in which E. coli was detected. Units of counts are $log_{10}cfu.cm^{-2}$.

```
-> species = COW/BULL, year = 2000
   Number of valid E. coli obs      7095
           E. coli % detection    8.1325
           Mean of log10 count    0.2101
            Standard deviation    0.3101
                       Minimum    0.0334
                        Median    0.0934
                    75th pctle    0.2625
                    90th pctle    0.4771
                    95th pctle    0.8451
                    99th pctle    1.7076
                       Maximum    2.4800
Number of valid Salmonella obs      1401
      Number of Salmonella +ve         8
        Salmonella % detection  0.571021
----------------------------
-> species = COW/BULL, year = 2001
   Number of valid E. coli obs      6926
           E. coli % detection    6.1507
           Mean of log10 count    0.1739
            Standard deviation    0.2641
                       Minimum    0.0334
                        Median    0.0806
                    75th pctle    0.1987
                    90th pctle    0.3802
                    95th pctle    0.5441
                    99th pctle    1.5911
                       Maximum    2.1909
Number of valid Salmonella obs      1491
      Number of Salmonella +ve         6
        Salmonella % detection  0.402414
----------------------------
-> species = COW/BULL, year = 2002
   Number of valid E. coli obs      7405
           E. coli % detection    6.5496
           Mean of log10 count    0.1893
            Standard deviation    0.2859
                       Minimum    0.0334
                        Median    0.0682
                    75th pctle    0.2201
                    90th pctle    0.5119
                    95th pctle    0.7559
                    99th pctle    1.3424
                       Maximum    2.6201
Number of valid Salmonella obs      1663
      Number of Salmonella +ve         5
        Salmonella % detection  0.300661
----------------------------
-> species = COW/BULL, year = 2003
   Number of valid E. coli obs      7597
           E. coli % detection    7.1739
           Mean of log10 count    0.1514
            Standard deviation    0.2428
                       Minimum    0.0170
                        Median    0.0645
                    75th pctle    0.1703
                    90th pctle    0.3181
                    95th pctle    0.6021
                    99th pctle    1.1996
                       Maximum    2.4786
Number of valid Salmonella obs      1826
      Number of Salmonella +ve        10
        Salmonella % detection  0.547645
----------------------------
```

NOTES: Mean, standard deviation and quantiles of log transformed E. coli counts refer to the subset of the samples in which E. coli was detected. Units of counts are $log_{10}cfu.cm^{-2}$.

```
-> species = COW/BULL, year = 2004
   Number of valid E. coli obs      6626
           E. coli % detection    6.7462
           Mean of log10 count    0.1473
            Standard deviation    0.2405
                       Minimum    0.0334
                        Median    0.0645
                   75th pctle    0.1461
                   90th pctle    0.3579
                   95th pctle    0.6180
                   99th pctle    1.1139
                       Maximum    2.4900
Number of valid Salmonella obs      1468
      Number of Salmonella +ve         7
        Salmonella % detection  0.476839

----------------------------
-> species = COW/BULL, year = 2005
   Number of valid E. coli obs      5392
           E. coli % detection    6.8620
           Mean of log10 count    0.1480
            Standard deviation    0.2294
                       Minimum    0.0334
                        Median    0.0667
                   75th pctle    0.1523
                   90th pctle    0.3159
                   95th pctle    0.5105
                   99th pctle    1.1303
                       Maximum    2.3226
Number of valid Salmonella obs      1206
      Number of Salmonella +ve         4
        Salmonella % detection  0.331675

----------------------------
-> species = LAMB, year = 2000
   Number of valid E. coli obs      8428
           E. coli % detection   19.9573
           Mean of log10 count    0.4359
            Standard deviation    0.5110
                       Minimum    0.0645
                        Median    0.2227
                   75th pctle    0.5563
                   90th pctle    1.0000
                   95th pctle    1.3674
                   99th pctle    2.4928
                       Maximum    4.7243
Number of valid Salmonella obs      1687
      Number of Salmonella +ve        10
        Salmonella % detection  0.592768

----------------------------
-> species = LAMB, year = 2001
   Number of valid E. coli obs      8464
           E. coli % detection   13.2916
           Mean of log10 count    0.3337
            Standard deviation    0.3620
                       Minimum    0.0334
                        Median    0.2201
                   75th pctle    0.3655
                   90th pctle    0.7745
                   95th pctle    1.1810
                   99th pctle    1.7076
                       Maximum    3.1464
Number of valid Salmonella obs      1843
      Number of Salmonella +ve         5
        Salmonella % detection  0.271297

----------------------------
```

NOTES: Mean, standard deviation and quantiles of log transformed E. coli counts refer to the subset of the samples in which E. coli was detected. Units of counts are $log_{10}cfu.cm^{-2}$.

```
-> species = LAMB, year = 2002
   Number of valid E. coli obs      7701
           E. coli % detection   13.7255
           Mean of log10 count    0.3756
            Standard deviation    0.4010
                       Minimum    0.0414
                        Median    0.2201
                    75th pctle    0.4314
                    90th pctle    0.9031
                    95th pctle    1.1761
                    99th pctle    2.1061
                       Maximum    3.0004
Number of valid Salmonella obs      1523
      Number of Salmonella +ve         0
        Salmonella % detection  0.000000

----------------------------
-> species = LAMB, year = 2003
   Number of valid E. coli obs      8172
           E. coli % detection   16.3607
           Mean of log10 count    0.3282
            Standard deviation    0.3871
                       Minimum    0.0128
                        Median    0.1239
                    75th pctle    0.3655
                    90th pctle    0.7235
                    95th pctle    1.0504
                    99th pctle    1.9685
                       Maximum    5.3617
Number of valid Salmonella obs      1604
      Number of Salmonella +ve         1
        Salmonella % detection  0.062344

----------------------------
-> species = LAMB, year = 2004
   Number of valid E. coli obs      9104
           E. coli % detection   13.2030
           Mean of log10 count    0.3048
            Standard deviation    0.3805
                       Minimum    0.0334
                        Median    0.1239
                    75th pctle    0.3010
                    90th pctle    0.6955
                    95th pctle    1.0986
                    99th pctle    1.8710
                       Maximum    6.0000
Number of valid Salmonella obs      1927
      Number of Salmonella +ve        13
        Salmonella % detection  0.674624

----------------------------
-> species = LAMB, year = 2005
   Number of valid E. coli obs     11338
           E. coli % detection   11.1131
           Mean of log10 count    0.3862
            Standard deviation    0.3988
                       Minimum    0.0334
                        Median    0.2227
                    75th pctle    0.4771
                    90th pctle    0.9273
                    95th pctle    1.3287
                    99th pctle    1.8590
                       Maximum    2.6699
Number of valid Salmonella obs      2349
      Number of Salmonella +ve        12
        Salmonella % detection  0.510856

----------------------------
```

NOTES: Mean, standard deviation and quantiles of log transformed E. coli counts refer to the subset of the samples in which E. coli was detected. Units of counts are $log_{10}cfu.cm^{-2}$.

```
-> species = SHEEP, year = 2000
   Number of valid E. coli obs     11124
            E. coli % detection   32.4434
            Mean of log10 count    0.5007
             Standard deviation    0.4996
                        Minimum    0.0645
                         Median    0.3010
                     75th pctle    0.6335
                     90th pctle    1.0792
                     95th pctle    1.4890
                     99th pctle    2.5611
                        Maximum    4.0000
Number of valid Salmonella obs      2377
      Number of Salmonella +ve        23
        Salmonella % detection  0.967606

----------------------------
-> species = SHEEP, year = 2001
   Number of valid E. coli obs     10860
            E. coli % detection   25.2302
            Mean of log10 count    0.3825
             Standard deviation    0.3864
                        Minimum    0.0334
                         Median    0.2989
                     75th pctle    0.4771
                     90th pctle    0.8615
                     95th pctle    1.1761
                     99th pctle    1.8261
                        Maximum    3.5053
Number of valid Salmonella obs      2643
      Number of Salmonella +ve        25
        Salmonella % detection  0.945895

----------------------------
-> species = SHEEP, year = 2002
   Number of valid E. coli obs     10867
            E. coli % detection   33.0174
            Mean of log10 count    0.3167
             Standard deviation    0.3439
                        Minimum    0.0128
                         Median    0.1239
                     75th pctle    0.3674
                     90th pctle    0.7528
                     95th pctle    1.0374
                     99th pctle    1.6532
                        Maximum    4.0000
Number of valid Salmonella obs      2282
      Number of Salmonella +ve        11
        Salmonella % detection  0.482033

----------------------------
-> species = SHEEP, year = 2003
   Number of valid E. coli obs      7297
            E. coli % detection   35.9189
            Mean of log10 count    0.3516
             Standard deviation    0.3672
                        Minimum    0.0128
                         Median    0.2201
                     75th pctle    0.4265
                     90th pctle    0.8014
                     95th pctle    1.1139
                     99th pctle    1.7076
                        Maximum    4.7270
Number of valid Salmonella obs      1663
      Number of Salmonella +ve         7
        Salmonella % detection  0.420926

----------------------------
```

NOTES: Mean, standard deviation and quantiles of log transformed E. coli counts refer to the subset of the samples in which E. coli was detected. Units of counts are $log_{10}cfu.cm^{-2}$.

```
-> species = SHEEP, year = 2004
   Number of valid E. coli obs      8157
           E. coli % detection   26.5907
           Mean of log10 count    0.3890
            Standard deviation    0.3887
                       Minimum    0.0334
                        Median    0.2989
                    75th pctle    0.4742
                    90th pctle    0.8842
                    95th pctle    1.1523
                    99th pctle    1.8510
                       Maximum    4.0000
Number of valid Salmonella obs      1931
      Number of Salmonella +ve        12
        Salmonella % detection  0.621440

----------------------------
-> species = SHEEP, year = 2005
   Number of valid E. coli obs      8623
           E. coli % detection   25.2116
           Mean of log10 count    0.3910
            Standard deviation    0.3750
                       Minimum    0.0334
                        Median    0.3010
                    75th pctle    0.4742
                    90th pctle    0.8808
                    95th pctle    1.2263
                    99th pctle    1.8325
                       Maximum    2.6730
Number of valid Salmonella obs      2163
      Number of Salmonella +ve        15
        Salmonella % detection  0.693481

----------------------------
-> species = STEER/HEIFER, year = 2000
   Number of valid E. coli obs     14400
           E. coli % detection    4.3472
           Mean of log10 count    0.2122
            Standard deviation    0.3397
                       Minimum    0.0334
                        Median    0.0792
                    75th pctle    0.1987
                    90th pctle    0.5740
                    95th pctle    0.9117
                    99th pctle    1.8084
                       Maximum    3.2433
Number of valid Salmonella obs      2933
      Number of Salmonella +ve         4
        Salmonella % detection  0.136379

----------------------------
-> species = STEER/HEIFER, year = 2001
   Number of valid E. coli obs     14371
           E. coli % detection    3.1452
           Mean of log10 count    0.2133
            Standard deviation    0.3443
                       Minimum    0.0334
                        Median    0.0682
                    75th pctle    0.2214
                    90th pctle    0.5740
                    95th pctle    0.9385
                    99th pctle    1.8513
                       Maximum    2.8831
Number of valid Salmonella obs      3090
      Number of Salmonella +ve         6
        Salmonella % detection  0.194175

----------------------------
```

NOTES: Mean, standard deviation and quantiles of log transformed E. coli counts refer to the subset of the samples in which E. coli was detected. Units of counts are $log_{10}cfu.cm^{-2}$.

```
-> species = STEER/HEIFER, year = 2002
   Number of valid E. coli obs     14747
           E. coli % detection    3.3024
           Mean of log10 count    0.1781
            Standard deviation    0.2579
                       Minimum    0.0170
                        Median    0.0682
                   75th pctle    0.1875
                   90th pctle    0.4116
                   95th pctle    0.7853
                   99th pctle    1.2788
                       Maximum    1.6301
Number of valid Salmonella obs      3207
      Number of Salmonella +ve         7
        Salmonella % detection  0.218273

----------------------------
-> species = STEER/HEIFER, year = 2003
   Number of valid E. coli obs     13807
           E. coli % detection    3.0202
           Mean of log10 count    0.2077
            Standard deviation    0.3602
                       Minimum    0.0035
                        Median    0.0682
                   75th pctle    0.2430
                   90th pctle    0.5933
                   95th pctle    0.8573
                   99th pctle    1.4510
                       Maximum    3.9191
Number of valid Salmonella obs      3010
      Number of Salmonella +ve         7
        Salmonella % detection  0.232558

----------------------------
-> species = STEER/HEIFER, year = 2004
   Number of valid E. coli obs     15349

           E. coli % detection    2.9057
           Mean of log10 count    0.1688
            Standard deviation    0.2458
                       Minimum    0.0334
                        Median    0.0682
                   75th pctle    0.1523
                   90th pctle    0.4771
                   95th pctle    0.6721
                   99th pctle    1.1287
                       Maximum    1.5357
Number of valid Salmonella obs      3120
      Number of Salmonella +ve         3
        Salmonella % detection  0.096154

----------------------------
-> species = STEER/HEIFER, year = 2005
   Number of valid E. coli obs     15618
           E. coli % detection    3.1054
           Mean of log10 count    0.1697
            Standard deviation    0.3009
                       Minimum    0.0334
                        Median    0.0645
                   75th pctle    0.1761
                   90th pctle    0.4330
                   95th pctle    0.6021
                   99th pctle    1.5315
                       Maximum    3.5856
Number of valid Salmonella obs      3181
      Number of Salmonella +ve         2
        Salmonella % detection  0.062873
```