SEROANALYST: A PROGRAM TO ASSIST WITH THE INTERPRETATION OF SERIAL SEROLOGICAL RESULTS FROM SENTINEL HERDS.

Cameron AR

AusVet Animal Health Services, 140 Falls Road, Wentworth Falls, Australia, 2782

Sentinel flocks or herds are able to provide valuable information about the exposure of individual animals to various pathogens, and form an integral part of many disease surveillance systems. Typically, animals in a sentinel herd are sampled at regular intervals, and tested with one or more tests for evidence of exposure to one or more pathogens. A range of tests may be used, including antigen detection, viral isolation etc, but antibody detection tests are most common.

Interpretation of antibody test results from sentinel herds involves identifying the first test upon which an animal became antibody positive (seroconverted). With a perfect test, this would pose little problem, but in reality, many commonly used tests produce occasional false positive or negative results, which complicate the analysis. When young sentinel animals are used, analysis may be further complicated by the presence of maternal antibodies. The duration of persistence of antibodies and immunity to repeat infection is another factor that needs to be considered. It is therefore often necessary to examine a series of test results from an individual animal over time, and to use a certain degree of judgement based on experience, in order to reliably identify the time of seroconversion.

The task of assembling and analysing results from sentinel herds can be laborious and time consuming. Many laboratories maintain computerised databases of test results, but these results need to be first grouped by sentinel herd, sorted in date order for each individual animal, and then compared over time. This paper describes a software program to assist with the interpretation of results from sentinel herds.

The program was developed as part of Australia's ongoing livestock arbovirus surveillance – the National Arbovirus Monitoring Program (NAMP), but may be used to interpret any data from sentinel herds. The program was developed using Delphi version 4[1] and is designed to run on a PC under the Windows operating system. It currently accepts input data files in dBASE format.

Input data is derived from a laboratory diagnostic database, and must include at least fields for site identifier (location of herd), animal identifier, sampling date, test type and test result. Additional optional fields include a herd identifier, age, and age units.

When using the program, the data file is first loaded, and the names of the appropriate fields identified. The program then determines the number and identifier for separate herds included in the data file. The user then has the option of selecting a number of herds to analyse.

The analysis of data involves identifying seroconversions in individual animals. Results for the nominated herd are scanned to examine what tests have been used, and what results were obtained. Where multiple tests have been used and the results are not the same, or where non-standard results codes are used, the user is presented with the results and has the option of designating it as positive, negative, suspect or no result. Once a certain combination of tests and results has been interpreted, the system remembers the interpretation and will not ask again.

Once results have been interpreted, seroconversions are identified. Where seroconversions are unequivocal, the program identifies them automatically. However in many cases, determination of the date of seroconversion will require user input. To achieve this, the data for the current herd is displayed in a grid, using symbols to display current test result, and colour coding to show serological status. Each row of the grid represents an individual animal, and each column a test date for that herd. Each cell in the grid will be either blank (no test performed for that animal on that date) or have a symbol +, - or ? indicating positive, negative or suspect. Serological status values indicated by colours are white (susceptible), green (seroconversion), blue (non-susceptible) or red (recruitment). The first in a series of tests performed on an animal is designated the recruitment bleed. It is impossible to determine if seroconversion has occurred at this bleed as it is not known if the animal was seronegative before the bleed.

Serological status colour codes are automatically applied by the computer where possible. The user is then able to modify the codes using the right and left mouse buttons to indicate seroconversions, immune status or recruitment bleeds. When analysis has been completed, the data is saved to an output file, and the next herd is analysed. Figure 1 shows the display during data analysis.

The output file contains fields indicating the herd identifier, the pathogen for which the herd is being tested, and then, for each sampling date, the total number of animals sampled, the number of animals at risk of seroconverting at that sampling date, and the number of animals that actually did seroconvert at that date. This data can be used to calculate prevalence or incidence estimates or for the production of summary reports.

Discussion
This program provides an example of a simple tool that has potential to provide significant assistance in the task of analysing serological results from sentinel herds.

Figure 1 SeroAnalyst data analysis grid

To further enhance the level of integration with existing systems, one possible future enhancement of the program may be to enable direct SQL access to existing databases.

The increasing use of digital data processing systems within veterinary diagnostic laboratories has opened up the opportunity to increase the efficiency and accuracy with which epidemiological data is processed and analysed. However in many situations, researchers have yet to take advantage of the potential of these improved data management systems. This results in time consuming manual transcription or re-entering of results, with the danger of introducing transcription errors. The problem facing researchers is that the types of analysis required are often very specialised, and existing software packages are unable to meet their needs. There is therefore a need for the development of programs, such as the one described, which are able to mesh with existing data management systems, and allow researchers to reap the benefits of improvements in data management technology.

Reference
[1] Inprise Corporation 1998. Borland Delphi Professional version 4 (software program)