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APPLICATION OF THE SYSTEMS APPROACH
TO EPIDEMIOLOGIC AND ECONOMIC ANALYSIS OF DISEASE
IN DYNAMIC POPULATIONS

presented by

Howard Scott Hurd

has been accepted towards fulfillment
of the requirements for

Ph.D. degree in Lg. Animal Clin. Sci.

John B. Kaneene
Major professor

Date 5/18/90

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**APPLICATION OF THE SYSTEMS APPROACH
TO EPIDEMIOLOGIC AND ECONOMIC ANALYSIS OF DISEASE
IN DYNAMIC POPULATIONS**

By

Howard Scott Hurd

A DISSERTATION

**Submitted to
Michigan State University
in partial fulfillment of the requirements
for the degree of**

DOCTOR OF PHILOSOPHY

Department of Large Animal Clinical Sciences

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ABSTRACT

APPLICATION OF THE SYSTEMS APPROACH TO EPIDEMIOLOGIC AND ECONOMIC ANALYSIS OF DISEASE IN DYNAMIC POPULATIONS

By

Howard Scott Hurd

This dissertation is directed towards the development of methodologies in analytical epidemiology and animal health economics. The system to which these methods were applied is the National Animal Health Monitoring System, and disease frequency and cost estimation in Michigan dairy cattle. Stratified random sampling of dairy herds, with prospective observation of one year was implemented. Methodological issues in the computation of disease frequencies and their variance were addressed and a standard method proposed. Issues relating to the estimation of the costs of disease were discussed, and shortcomings in the standard NAHMS methods noted.

Simulation modelling in epidemiology was reviewed for the purpose of evaluating alternative modelling strategies to be implemented in the context of NAHMS. A comprehensive classification scheme for epidemiologic simulation models was proposed. A risk assessment analysis was performed using conditional logistic regression. The type of maternity facilities had a significant effect on the incidence of respiratory disease in calves. The proportion of on farm labor that was hired had an effect of disease in adult cows, but not in calves. If calves were born in multianimal maternity facilities their odds of having respiratory disease were 10.6 time greater ($p < .1$). Estimates of the effects of various risk factors on the occurrence of Clinical Respiratory Disease were to be

incorporated into the simulation models of Chapter 7 and 8.

The properties of a distributed delay for modelling infectious disease epidemics were compared to a stochastic Reed-Frost model. The distributions were similar and it was possible to achieve comparable average attack rates. This model is proposed for use in modelling a variety of infectious and noninfectious diseases. The model was applied, to Clinical Respiratory disease in dairy cattle. The model was approximately predict the observed annual incidence density for example herds from the database. Many specifics about the herds were not available to the model, which decreased its precision. The simulation model was a useful tool for evaluating the long term economic impact of disease on the farms gross margin of Dairy Income minus Disease Influenced Variable costs. Many different scenarios could be evaluated with this model. An 80 cow dairy averaging 15,000 (6818 kg) pounds of milk per cow per year was simulated over 5 years with different levels of respiratory disease and compared to a non disease run. The average, endemic, level of disease cost \$121,720. Moderate increases in disease cost \$125,986 over 5 years. If the case fatality rate was increased to 50% in an epidemic situation the discounted cost of disease was \$160,442 over a 5 year period.

DEDICATION

To Susan

**An excellent wife who can find?
For her worth is far above jewels.
The heart of her husband trusts in her,
and he will have no lack of gain....
Her children rise up and bless her;
her husband also saying
"Many daughters have done nobly,
but you excel them all."
Proverbs 31:10-11,28-29**

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Special thanks and accolades go to my major advisor, John B. Kaneene (Fearless Leader), for his enthusiasm, encouragement, trust and technical expertise. Other members of my committee are to be thanked for their encouragement and input, Stephen Harsh, Stuart Gage, Brad Thacker, and Tal Holms. One of my biggest regrets is that there was not time to interact much more with all of these talented individuals.

I have been blessed with a family that has provided indescribable support in every area. I thank my parents for sacrificing and investing in my education as a youth, and for teaching me it's value. I thank my in-laws for their support, especially C. D. VanHouweling D.V.M. for his model as a professional and constant encouragement.

There is not gratitude enough available to fully thank my wife for all her life that she has poured into mine and into this third college degree that we have earned together.

Mostly, I thank my God and Father of the Lord Jesus Christ. ("Let him who boasts, boast in the Lord" II Corinthians 10:17)

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INTRODUCTION

SYSTEMS APPROACH

A variety of definitions might be used to describe the systems approach. For this student, the definition, represents an amalgamation of input from a variety of different disciplines, from electrical engineering, entomology, economics, and epidemiology. The consistencies in the various definitions are distilled into the following essential features:

1) a methodology for solving unstructured problems 2) that begins with a defined set of needs, 3) moves to a description of the whole system as it currently exists, 4) generates alternatives for meeting the expressed needs, 5) evaluates those alternatives with various modelling techniques, and 6) designs and 7) implements the policies found most capable of meeting the needs (Checkland, 1981:161-191; Manetsch and Park, 1982:8-15).

The procedural steps, of the Systems Approach, outlined by Kitching (1983) provide the outline for this dissertation and the course pursued in completing this work, those steps are: 1) problem definition, 2) system identification, 3) decisions on model type, 4) mathematical formulation, 5) decisions on computing methods, 6) programming, 7) parameter estimation, 8) validation, 9) experimentation. It should be noted that model building is only a part of the Systems Approach and a computer simulation model is a byproduct or tool of the effort.

NEEDS ANALYSIS

The National Animal Health Monitoring System (NAHMS) was initiated in order to address the problem of "substantial losses" in the United States livestock industry as a result of endemic disease and other animal health problems. The USDA's Animal Plant Health Inspection Service (APHIS) became the lead agency in a "comprehensive effort to develop methodology for securing information on disease prevalence, incidence, and economic costs" (King, 1983). Michigan was one of the original pilot project states involved in this methods development effort (Kaneene and Hurd, 1986). The needs of the NAHMS, as stated by Dr. King, form a basis for a large portion of the problem formulation for this dissertation; "we need new techniques for evaluating the causes, interactions, and economic consequences of complex disease syndromes on a national level."

Specifically, most modern livestock diseases are multifactorial problems, with multiple risk factors associated with their occurrence. Interaction and synergism is often suggested between factors, and the effect of a causal factor may change over time. Current experimental and analytical methods aimed at addressing the above issues have certain disadvantages. For example, results from experimental and laboratory methods are not readily generalized and have low external validity, and can only study one or two risk factors at a time. However, they have the advantage of good control over extraneous variables. Observational field studies are often expensive and time consuming, difficult to replicate, and it is impossible to hold all other variables constant while changing only one. Multivariate statistical models cannot measure the effect of changes

in population structure as it relates to disease occurrence, and they assume that causal interactions should be controlled or transformed away (Koopman, 1987). Most procedures fit a model by variance relationships versus biologically plausible pathways, and have difficulty dealing with the effects of time (MacVean, 1986; Altman, 1988). Simulation models in epidemiology often ignore different levels of structure within a population, such as age groups, (Bailey, 1975), and are often mathematical modelling exercises versus byproducts of a problem solving methodology. Models for evaluating the economics of disease control are usually based on static estimates of disease, or predetermined costs, and cannot model changes in rates of disease or costs due to changes in the population structure, ie. feedback (Willadsen, 1977).

PROBLEM STATEMENT

Analytic epidemiological methods need to be developed that can use observations from field studies of animal populations, particularly the National Animal Health Monitoring System, to quantitate the relative and economic effect of various risk factors on the occurrence of multifactorial diseases in dynamic populations and to predict the effects of disease control strategies over time.

OBJECTIVES

The general objective of this dissertation is to apply the Systems Approach to the unstructured problems of multifactorial disease analysis. The specific objectives are 1) to describe the system in question; including disease frequencies, cost estimates, statistical

properties of the frequency measures used, and factors associated with the occurrence of clinical respiratory disease; 2) to develop a generic epidemiologic simulation model for the dairy herd that will provide the realism, and flexibility to address the multifactorial dynamic disease analysis problems; and 3) to quantitatively determine the effects of changes in the level of various management characteristics on the economics of clinical respiratory disease syndrome.

OVERVIEW

An overview of the entire work is present here to facilitate cohesiveness. Chapters 1-3 are not focussed on specifically on respiratory disease but present the methodology relating to sampling and data collection procedures. They should be considered as the System Identification phase of the project. Chapter 2 was required in order to define the exact methods to be used for the computation of disease frequencies used throughout the project. This represents a unique contribution, as this methodology had apparently not been developed, for prospective monitoring systems with sampling of multiple populations. Chapter 3 describes the gross, short term costs of common clinical diseases. This chapter also discusses some of the shortcomings of the economic methods and suggests ways to improve the cost estimates. Chapter 4 describes the current state of applied simulation modelling in human and veterinary epidemiology. Chapter 4 is part of the alternative model evaluation phase of the Systems Approach. Chapters 5-8 represent the modelling phase of the Systems Approach. Chapter 5 is an application of the "standard" epidemiologic statistical (associative) models, the conditional logistic

regression, and linear regression with categorical and continuous independent variables, the intent of this analysis was to provide information as to important variables to be included in the simulation model of Chapter 7 and 8. Chapter 6 proposes a generic type of disease process model to be used for infectious and non infectious diseases, and serves as a form of validation for the main theoretical subunit to be used in the applied model of Chapters 7 and 8. Chapter 7 applies the model of chapter 6 to Clinical Respiratory Disease in 3 ages of dairy cattle. Chapter 8 demonstrates the utility of the model, from Chapter 7, for improving the cost estimates and economic evaluations of disease control.

It was necessary to expedite publication of the findings. For this reason, each chapter of this dissertation was written as an individual paper for publication. Therefore each chapter has its own set of objectives, literature review, material and methods, and summary section.

CHAPTER 1

The National Animal Health Monitoring System in Michigan I. Design, data, and frequencies of selected dairy cattle diseases.

ABSTRACT

A National Animal Health Monitoring System (NAHMS) in Michigan was started in 1986 to develop statistically valid data for use in estimating disease frequencies and associated costs in dairy cattle. The objectives of this chapter are to: 1) describe what was done to implement and maintain the system in Michigan, 2) present selected disease frequencies, 3) and discuss the epidemiological considerations of what was done with implications for the results obtained. Veterinary medical officers (VMOs, veterinarians from the university, state and federal governments) served as data collectors. Following several sessions of training in current disease and management problems of dairy cattle, interview techniques, sampling methods, and data collection instruments, the VMOs participated in selection of the sample herds and data gathering. Sixty ($n=60$) of 6,012 dairy herds were randomly selected and the VMOs visited the farms once a month for 12 months to collect management, disease, inventory, production, preventive treatment, financial and any other relevant data. Strict data quality control devices were used. Specific feedback and morale boosting techniques were developed for the producers and data collectors.

Of the three age groups studied, cows had the greatest number of disease problems. The top six disorders found more frequently were (from highest to lowest) breeding problems, clinical mastitis, birth problems, metabolic problems, gastrointestinal problems, and lameness. In young stock, respiratory, multiple system, breeding problems, gastrointestinal, lameness, and birth problems were the major problems, while in calves gastrointestinal, respiratory, multiple system, lameness, Metabolic/nutritional, and urogenital were the major problem.

INTRODUCTION

Numerous systems of disease monitoring/surveillance have been reported. These systems vary in five basic ways: 1) sampling design, 2) frequency of data collection, 3) mechanisms of data collection, 4) measure of disease frequencies, and 5) purpose or anticipated use of the data. Some monitoring systems have been developed to estimate prevalence and/or incidence of a single infection/disease. For example, the brucella milk ring test (USDA Uniform Rules and Methods, 1986) and the market cattle test (Beal, 1977) are strictly for brucellosis in the USA, and the tuberculosis program in the USA is primarily for bovine tuberculosis (Poppensick and Budd, 1966).

Various monitoring systems are designed to estimate disease frequencies of more than one disease, but the place of observation and type of measure of disease may vary. Slaughterhouse based monitoring systems, for instance, have been designed primarily to measure prevalence of disease conditions as detected at slaughter (Willeburg, 1978; Lloyd and Schwab, 1987; and the USDA national residue monitoring, 1985).

Some monitoring systems combine information from slaughterhouses and reports from the farms. These include the disease reports by the Food and Agricultural Organization and the International Office for Epizootics in France (FAO/IDE, 1975) and the Inter-American Institute for Cooperation on Agriculture. In the IOE and IICA monitoring systems, data are obtained from various ministries/departments of agriculture/animal industry. These two are passive monitoring systems and, for most times, the numbers of animals at risk are not known and true rates of diseases cannot be estimated. In addition, data relating to management, production and cost of disease are not collected. Furthermore, the sampling and criteria used for data collection are not very clear. For their intended use, however, these systems provide valuable disease information on the global and/or regional level.

The Minnesota disease reporting system for food producing animals (Diesch and Martin, 1979; Diesch, 1983) was an active monitoring system where farm level data were collected. The herds were selected using proper sampling procedures and the results, therefore, could be extrapolated to the rest of the state. The animals at risk in

most cases were known, so that rates of disease could be computed. In the Minnesota system, however, management, production, and cost data were not collected.

Since the Minnesota disease program, many farm level monitoring systems have been developed where multiple diseases, production and management factors were estimated (Riemann, 1982; Stephens et al.; Bartlett et al., 1986; Dohoo and Stahlbaum, 1986; and Bigras-Poulin and Harvey, 1986). While these monitoring systems included production, management and cost data, the results obtained may not be generalizable to the original reference populations due to the type of sampling used. More comprehensive monitoring systems that involve frequencies of various diseases, management, production, environment, soil type and social environment of the farms have been reported (Barnouin and Brochart, 1986; Barnouin, 1986; and Barnouin et al., 1986). These systems offer variable information on diseases of ruminants and the effects of environment, and production on observed disease frequencies.

In the USA, a National Animal Health Monitoring System (NAHMS) was started in 1983; the system was originally called the National Animal Disease Surveillance System. The NAHMS is a farm level active surveillance system whose goal is to generate data for statistically valid estimates of incidence and prevalence rates, and costs of various diseases of livestock and poultry.

A branch of the NAHMS as initiated in the state of Michigan during the 1986/87 calendar year. The objective of the program, in Michigan, was to generate statistically valid data about dairy cattle health related events, for use in computing national and state estimates of incidence rates and costs of these animal events. The objectives of this chapter are to: 1) describe what was done to implement and maintain the system in Michigan, 2) present selected results, and 3) discuss epidemiological consideration of what was done with implications for interpretation of the results.

MATERIALS AND METHODS

Initiation

Preparatory steps for initiation of the program started approximately one year in advance and involved the formation of interdisciplinary planning and management committees. The committees secured support for the program from: The Michigan Veterinary Medical Association, Michigan State University (MSU), Michigan Department of Agriculture (MDA), the U.S. Department of Agriculture (USDA/APHIS/VS) office in Michigan, Michigan Dairy Herd Improvement Association (DHIA), and several producer groups. The planning committee, which dealt with policy matters, and met monthly, was composed of the State veterinarian, the Director of Animal Industry in the state, the federal veterinarian in charge of Michigan, and an epidemiologist from the University. The management committee was composed of one professor of epidemiology, one PhD student in epidemiology, and one veterinarian from the State Department of Agriculture. This committee coordinated the everyday activities of the program, including data collection, management and processing.

Design of Sample

Sixty of the 6,012 available dairy herds were to be selected for participation in the project. Specific counties, areas within these counties, and the number of herds in each herd size category to be included in the sample were identified. Herd size data and maps from the National Agricultural Statistical Service (NASS) and Michigan Crop Reporting Service (MCRS) were obtained. Using these data, the state was stratified into the 6 geographical (agricultural) districts and animal density strata. Herds were stratified according to the number of adult cows available into four size strata - 10-49, 50-99, 100-199, and >200. Because the NASS lists tend to overlook small herds, a List Frame Selection (LAS) alone would not be appropriate. On the other hand, the use of an Area Frame Selection (AFS) would pick up the small herds that may not appear on the NASS list. Using the AFS alone, however, was not viewed as an efficient approach, since too much time would be needed for the VMOs to physically locate herds. Because of the aforementioned reasons, both the LAS and AFS methods were used. As a result, a

sample of 60 herds, based upon probability proportional to animal numbers, was obtained. Detailed maps with AFS or LAS guidelines and selections were prepared for use in training of the data collectors and the actual selection of the sample herds.

A total of fifteen veterinary medical officers (VMOs) from the College of Veterinary Medicine, State and Federal Departments of Agriculture served as data collectors. The VMOs attended a training session (lasting two days) where interview techniques, current management practices and common dairy disease problems were reviewed. Two additional training sessions (each lasting one day) were held. These two sessions covered: the forms to be used for data collection, the need for probability based random sampling, the use of area and list frames, and the steps to be followed in selecting the participating producers.

Selection of the 60 sample herds

Each VMO was assigned 2-5 herds, no VMO had more than five. The VMOs were asked to use the following procedures for the final selection of the herds: 1) contact the milk inspectors and dairy extension agents in the selected areas to explain the program, 2) visit with the milk inspectors and dairy extension agents to seek their help in locating the herds in the specified areas (using the list or area frame methods as indicated on the maps), 3) confirm the herd sizes with the milk inspector and dairy extension specialist, 4) write names and addresses of the eligible producers in notebook, and 5) number the producers serially, i.e., from 1-n. Each VMO then called the university epidemiologist to confirm the herd size category and the number of available herds in that size category. Using a simple random procedure and the information provided by the VMO, the university epidemiologist selected which particular producer(s) would be included in the sample. To save time, but at the same time assuring that every individual producer had an equal chance of being selected, 3-5 numbers were selected and the order in which herds were to be approached was given. The VMO would go to the first randomly-selected producer and ask him to participate in the program. If the producer refused, the VMO wrote down the reason for refusal and approached the next randomly-selected producer.

Maintenance of the System

All producers who agreed to participate in the program signed an agreement to keep records for twelve months which assured them of complete confidentiality of their records. Each producer was paid \$25.00 for every month he participated. The VMOs collected data at the beginning of the program using the initial visit form (Form 1) and provided the farmer with forms (Producer's Daily Log) to record animal events during the time between visits. All data collection forms are shown in Appendix A. The VMO visited the farm monthly and interviewed the producer regarding any animal events that occurred during the previous month. Data relating to inventory and disease prevention activities were recorded on Form 2. Data relating to disease (cases, actions taken to correct them, and consequences of the disease) were recorded on another form, Form 3. In Michigan, individual cow identification (IDs) were maintained. To maximize the availability of these individual IDs, a special worksheet (NAHMS VMO worksheet) was developed. This worksheet was produced for each farm every month. It listed all the cows on the farm, their most recent calving dates, and any diseases/conditions that were reported during the previous month. These computer-generated worksheets were sent to the VMO before the next data collection visit. The VMO worksheets enabled the VMO to gather data on a case-by-case basis for each individual cow, which should have improved the ability to identify new cases. Data for completing the aforementioned forms were extracted from the interviews, producer daily logs, other sources such as bills, milk receipts, and conversations with the producer's veterinarian.

All forms were mailed to the Division of Epidemiology at MSU where they were checked for errors, missing values, proper disease codes, and changes in inventories. The checking of data was accomplished by veterinary students, graduate students and faculty in the Division of Epidemiology. Data were entered in microcomputers using the R:Base System V data base management program. Checks were built in the data entry process to avoid errors of entry. These check devices would not permit, for instance, entry of improper disease codes, drug codes, ID, producer code, or wrong month. After correction for errors on microcomputers, data were copied into files and

transmitted to an IBM 3090-180 mainframe computer for storage and analysis.

A monthly report was sent to producers. The report included risk rates of diseases reported the previous month in the given herd and means of risk rates of the same diseases observed in the their herd-size stratum. A six-month report, primarily in graphics, was provided to the producers. This report included one-month risk estimates of disease comparing the producer's herd to the stratum average. A twelve-month (final) report was given to the producer and this report contained all major findings in that herd, including estimates of risks of disease, costs of diseases and costs of preventive measures. A monthly newsletter was used to communicate with VMOs on various issues of the project, particularly data-quality issues. Examples of the producer reports and monthly newsletters can found in Kaneene and Hurd, 1987.

Computation of Disease Frequencies in a Herd

The incidence density (ID) method was used as a measure of disease frequency for the individual herd for one month (Meittinen, 1976). This method was employed since there may be a high turnover of animals during a month, since multiple cases can occur in the same animal within a month and no individual animal data were utilized. This method is a modified version of the actuarial method discussed by Elandt-Johnson (1977) (equation 1.1). For this chapter the monthly incidence densities were summarized into an annual figure (aID_{ij}) for each herd as shown in equation 1.2.

$$ID_{ijm} = \frac{\text{\# cases}}{\text{animal months}} \quad (1.1)$$

$$ID_{ijm} = \frac{\text{\# cases of disease (X) during current month}}{\text{\# of animals at risk at end of previous month} - 1/2 \text{ withdrawals} + 1/2 \text{ additions}}$$

$$\begin{aligned} \text{withdrawals} = & \text{\# sold} + \text{\# died due to } \underline{\text{other}} \text{ disease} \\ & + \text{\# transferred to different age group.} \end{aligned}$$

additions = # purchased + # transferred in from
other age groups.

$$\begin{aligned}
 aID_{ij} &= \text{"annual" incidence density for the } i^{\text{th}} \text{ herd in the } j^{\text{th}} \text{ stratum, expressed per 100 cow years} & (12) \\
 &= \frac{\sum_{m=1}^{12} \text{cases}}{\sum_{m=1}^{12} \text{animal months}} / 12 * 100
 \end{aligned}$$

Computation of the mean "annual" incidence density for a stratum is shown in equation

13. Procedures for computation of the variances are discussed in Chapter 2.

$$\overline{aID}_j = \text{estimate of the "annual" incidence density for the } j^{\text{th}} \text{ herd size stratum} \quad (13)$$

$$= \sum_{i=1}^n W_{ij} aID_{ij}$$

where:

$$W_{ij} = \frac{aNAR_{ij}}{\sum_{i=1}^n aNAR_{ij}}$$

aNAR = average annual herd size

RESULTS

Sample characteristics of the herds selected are presented in Table 1.1. Seven of the producers contacted (10.76%) refused to participate for three reasons:

- 1) too much work involved in keeping the required data (large herds),
- 2) lack of interest
- 3) and family illness.

Table 11 Projected and achieved Michigan sample characteristics of dairy herds in round I.

Herd size	No. of cattle	% of cattle	No. of herds	Projected no. of herds in sample	Achieved # herds	Projected (achieved) no. of herds represented by each herd in sample
10-49	93,692	27.2	3,283	16	19	205 (173)
50-99	125,353	36.3	1,870	22	18	85 (104)
100-199	94,923	27.5	750	16	12	47 (62)
200+	31,021	9.0	109	6	5	18 (22)
Total	344,989	100	6,012	60	54	

Of the three age groups, cows¹ had the greatest number of disease problems (Table 12). Calves² were second in numbers of disease problems (Table 13) and the young stock³ had the least disease problems (Table 14). Many of the specific diseases reported were somewhat similar, such as pneumonia and respiratory disease. For this reason many of the similar disease syndromes were grouped together. The composition of disease groups are presented in Appendix B. There was noticeable seasonal variation in disease frequencies, particularly in respiratory and birth problems.

¹Lactating and dry females after first parturition

²Male or female animals from birth to weaning off liquid ration

³Male or female animals from weaning to first calving (females) or first use for breeding purposes (males).

Table 12 Most frequently reported disease problems in Cows, expressed as mean incidence densities (one standard deviation) per 100 cow years.

Disease group	Strata 1	Strata 2	Strata 3	Strata 4	All strata
Breeding problems	48.98 (4.18)	41.12 (4.27)	27.90 (2.42)	82.63 (5.49)	49.85 (2.28)
Mastitis	32.71 (3.99)	32.84 (3.32)	34.65 (2.25)	31.98 (3.38)	33.05 (1.64)
Birth problems	9.22 (1.86)	17.08 (2.57)	11.51 (1.65)	14.37 (2.37)	13.80 (0.79)
Metabolic/nutrition	7.21 (1.66)	7.54 (1.59)	4.96 (1.13)	20.37 (2.84)	10.21 (0.89)
Gastrointestinal	12.91 (2.08)	4.95 (1.74)	4.76 (1.12)	9.42 (1.88)	7.26 (1.23)
Lameness	4.36 (1.70)	10.28 (1.85)	5.06 (1.00)	4.66 (1.51)	6.61 (0.39)
Multiple system	5.87 (1.63)	6.06 (1.95)	5.56 (1.36)	3.90 (1.24)	5.34 (0.85)
Urogenital system	6.87 (2.04)	7.69 (2.02)	1.68 (.87)	3.04 (1.07)	4.84 (0.81)
Respiratory	4.02 (1.66)	1.33 (1.09)	1.68 (.83)	1.52 (.74)	1.87 (0.74)

Table 13 Most frequently reported disease problems in Calves, expressed as mean incidence densities (one standard deviation) per 100 animal years.

Disease group	Strata 1	Strata 2	Strata 3	Strata 4	All strata
Gastrointestinal	40.88 (3.88)	61.18 (5.42)	31.65 (5.52)	230.76 (11.76)	79.74 (4.76)
Respiratory	40.88 (2.48)	42.03 (4.76)	28.39 (3.45)	67.69 (5.10)	42.40 (2.66)
Multiple system	24.84 (4.91)	12.07 (2.72)	5.12 (2.05)	6.92 (1.72)	11.27 (1.74)
Lameness	0.0 (0.0)	.41 (0.57)	0.0 (0.0)	.76 (0.69)	0.28 (0.26)
Metabolic/nutrition	0.80 (0.88)	.42 (1.18)	0.0 (0.0)	0.0 (0.0)	0.28 (0.45)
Urogenital	0.0 (0.0)	0.0 (0.0)	.46 (0.67)	0.0 (0.0)	0.14 (0.13)

Table 14 Most frequently reported disease problems in Young Stock, expressed as mean incidence densities (one standard deviation) per 100 animal years.

Disease group	Strata 1	Strata 2	Strata 3	Strata 4	All strata
Respiratory	0.66 (0.65)	8.21 (2.86)	3.70 (1.75)	6.20 (1.99)	5.55 (0.79)
Multiple system	2.65 (1.36)	1.76 (1.26)	0.13 (0.38)	2.12 (0.61)	1.60 .61
Breeding problems	0.88 (0.87)	0.83 (0.74)	0.53 (0.41)	2.00 (1.09)	1.09 (0.39)
Gastrointestinal	3.10 (1.49)	0.58 (0.85)	0.13 (0.24)	0.0 (0.0)	0.66 (0.65)
Lameness	0.66 (0.65)	0.33 (0.48)	0.0 (0.0)	0.22 (0.33)	0.27 (0.28)
Birth problems	0.0 (0.0)	0.08 (0.30)	0.0 (0.0)	0.11 (0.27)	0.06 (0.00)
Mastitis	0.0 (0.0)	0.0 (0.0)	0.13 (0.24)	0.0 (0.0)	0.03 (0.07)

DISCUSSION

Preparatory steps taken during the initiation phase seemed to have been useful in obtaining industry, professional, and political support within the state. Such support minimized the logistics of implementation and maintenance of the system and would appear to be mandatory for any state wanting to implement NAHMS. All the groups contacted during the preparatory phase wanted to know if there was a real need for a NAHMS and how they would benefit from such a system. The herd statistics from both the NASS and MCRS seemed to have been satisfactory for use in the design of the sample, particularly when both list and area frames were used. However, to maintain a random sample based upon probability proportioned to animal numbers it was essential for the VMOs to confirm location and sizes of herds. This is because size of herds change from time to time. The fact that one person picked the final herds (as opposed to each VMO picking their own) produced consistency, and helped to maintain randomness.

Feedback from all the VMOs indicated that the training received was essential and should be an ongoing program within NAHMS. It was through repeated training that the need for random sampling, minimizing information bias (and other biases), and understanding the data collection instruments was appreciated. The VMO worksheet (as determined by a percentage of corrections made) was a very useful instrument for cross-checking with data recorded on the general NAHMS forms. Additionally, it enabled the VMO to prompt the producer to remember specific events on specific cows, since this worksheet had individual cow identification. Data quality has and will always be an important issue in field studies (Anderson, 1982). In the Michigan experience, data quality was a function of confidentiality assurance to the producers, feedback information to producers, morale of the VMOs, and critical checking of the data. Because producers were assured confidentiality of their records, most producers were willing to record various events on the farm, including drugs used and financial aspects of their farms. All VMOs indicated that the monthly and semi-annual reports

encouraged the producers to record events on their farms. The producers particularly liked comparing themselves to other herds of the same herd-size stratum. These reports to the producers, however, should be as simple as possible and mostly in graphics. The VMOs had a very delicate role in that they had to sell the program to the producer, probe the producer for data and clarifications, record the data accurately, interact with the producer's veterinarian and interpret the monthly, semi-annual and annual producer reports. It was, therefore, essential for them to be motivated. The morale-boosting mechanisms used (see Material and Methods section) were effective in maintaining and/or increasing the VMOs' morale. Of particular value (according to the VMOs assessment) were the group sessions held. These resulted in open discussion. Additionally, the VMOs indicated that seeing the monthly, bi-annual and annual producer reports boosted their morale. They could see the results of their efforts, the scientific value of the data, and had tangible products to show to their producers.

The availability of individual cow identifications was helpful in confirming new cases. These data will be helpful when we examine the relationships of various risk factors to specific disease frequencies. In an active surveillance like this one where all producers are asked to record all possible disease conditions, it is efficient to report disease frequencies in terms of groups of disease entities. Since definitions of disease entities may vary from system to system, results reported in this chapter may not be directly comparable to those reported elsewhere. Several methodological issues regarding computation of disease frequencies were raised in Michigan. Since these issues may be of great value to NAHMS as a whole and to epidemiologists in general, the second chapter of this dissertation addresses these issues.

CHAPTER 2

The National Animal Health Monitoring System in Michigan II: Methodological issues in the estimation of frequencies of disease in a prospective study of multiple dynamic populations.

ABSTRACT

Procedures for the computation of disease frequency measures and their associated variances from data collected through prospective study of multiple dynamic cohorts (herds) with a National Animal Health Monitoring System, are proposed. Estimates of the annual incidence density for a group of herds or the one month risk of disease can be calculated from the same within herd measure of monthly incidence density.

It is proposed that the choices regarding which measure to be estimated depends on the intended use of the information. Risk estimates are appropriate for producers and clinical health professional making decisions at the animal or herd level. Incidence density measures are appropriate for purposes of extrapolation to populations for state and regional level decision making.

INTRODUCTION

Disease monitoring activities in livestock populations can take on a variety of forms, with a variety of goals and users (Beal, 1983). Some activities observe prevalent cases of disease at slaughter (Willeburg, 1978, Lloyd and Schwab, 1987) or upon submission to a diagnostic laboratory (Davies, 1978). Other activities might observe disease occurrences as a result of ongoing herd management and disease control programs (Stephens, et al., 1982, Bartlett, et al., 1986, Dohoo and Stahlbaum, 1986). The shortcomings of these activities for gaining estimates of disease frequency that are statistically valid, hence useful for extrapolation to a source population, have been

discussed (Beal, 1983). Efforts to overcome these shortcomings have resulted in the antecedent Minnesota Food Animal Disease Reporting System (Diesch, 1983) and the present National Animal Health Monitoring System. These projects are unique in that herds are purposefully selected for follow-up. In these situations, multiple cohorts (herds) are repeatedly observed in a prospective longitudinal study for the purpose of obtaining a sample estimate of disease frequency that can be extrapolated, with defined confidence limits, to a reference population at the state, regional, or national level.

By comparison, most follow-up studies in human epidemiology involve observations on only one or two cohorts of individuals. The purpose of these studies is usually hypothesis testing about the effect of an exposure or risk factor on the occurrence of disease in an individual, not the estimation of a population parameter (Kleinbaum, et al., 1982, Susser, 1985). Consequently, most statistical procedures have been developed around estimation and variance calculations of these effect measures, such as the risk ratio, odds ratio, and the risk difference. (Fliess et al.; 1976, Rothman, 1986). In animal populations some work has been done in regards to estimating the prevalence of disease (Beal, 1985; Farver et al., 1985); however, this may not be directly applicable to incidence data from follow-up studies (Chiang, 1961).

Estimation procedures, that can be consistently applied to estimate the frequency of disease in a population consisting of multiple dynamic subpopulations (herds or cohorts), need to be documented. Since NAHMS is a national effort in the United States, it is important that these and other methodologies be standardized in order to provide for comparability between states. The objectives of this chapter are to: 1) raise the issues involved with disease frequency estimation, 2) propose a criterion for determining the appropriate disease frequency measure to be estimated, and 3) propose methods for computing sample estimates and variances of these frequency measures.

METHODS

Herd selection and data collection

Sixty (60) of the 6,012 dairy cattle herds in Michigan were randomly selected for one year of follow-up. A detailed account of the selection of these herds, data collection tools, and the data collected are presented in Chapter 1. Individual animal information, such as calving date and age were collected in the Michigan project. However, since this information is not usually collected in the standard NAHMS design, it will not be considered in this chapter.

End product to be estimated

Two general types of disease frequency have been recognized, the risk rate and the true rate or incidence density (Martin, et al. 1987; Bendixen, 1987b; Klienbaum et al., 1982). We propose that choices regarding the type of measure, to be estimated from a NAHMS, depend on the intended use of the estimates, with constraints based on the type of data available. Incidence densities are useful for population estimates and macro decision making by state and national level policy makers. The risk rate is useful for selecting appropriate treatments, and for personal decisions regarding health related behaviors, in other words, micro level decision making by producers and clinically concerned health professionals.

The incidence density is a meaningful measure of the experience of the population group (Chiang, 1961), and as such is more appropriate for extrapolation (Alderink, 1986). Leech (1971), when discussing disease monitoring systems in Britain, comments that incidence density measures are more meaningful than risk estimates. The animal disease surveillance program in Minnesota estimated disease frequency as incidence densities (Diesch, 1983), and incidence densities of mastitis have been reported by Bendixen (1988). However, the incidence density has no application at the individual animal level, and is not very useful to a producer or clinical epidemiologist (Miettinen, 1976, Bendixen, 1987b). The exception to this statement is when incidence density measures are used to determine the relative risk of a given exposure. Morgenstern et al. (1980) defined risk as the conditional, a priori, probability of disease occurrence in an

individual. Risk estimates of common dairy cattle diseases have been reported by many investigators (Bartlett, et al., 1986; Bendixen, 1987a; Curtis et al., 1988; Dohoo et al., 1983; Erb, 1984; Martin et al., 1975; Simensen, 1982; Waltner-Toews, 1986). Although some of these reports may use the term "incidence rate", examination of the calculations show that the measure is actually a risk. These reports are generally aimed at the producer or the clinician and relate to the question of how individual factors may affect an animal's risk of disease. These risk estimates might be useful for decisions regarding the implementation of some intervention, such as a vaccination program, which must include consideration of the expected probability (ie. the risk) that an animal and/or herd will be infected.

Bendixen (1987b) discusses how the type of data constrains the choice of measure to be estimated. The risk, or cumulative incidence is appropriate for fixed populations and some dynamic populations if the risk period is well defined. The incidence density is appropriate for dynamic populations when disease occurrence is not restricted to a specific time. The latter applies to data from the NAHMS.

Herd calculation of disease frequency

Calculation of the frequency of disease in a given herd, for a given month can be implemented in a variety of ways, depending on whether the population at risk is assumed to be of fixed size during the observation interval or of changing size. If the population is fixed or animals are at risk for a definable time period or proportion of animals affected, the risk can be calculated (Klienbaum et al., 1982; Elandt-Johnson, 1975). This number represents the risk of disease for a given time period. The risk is conditional on new animals not entering the population and that only one occurrence of the disease per animal is being considered.

In a situation, such as NAHMS, the population size may change dramatically during the observation period, and animals can be affected more than once. The former instance was particularly true for calves in the Michigan experience. In this situation, the incidence density is recommended (Bendixen, 1987b; Kleinbaum et al., 1982; Miettinen, 1976; Rothman, 1986). Also in cases where individual animal data are not available, it is

not possible to calculate measures such as the lactational incidence rate or periparturient risk rates, as it is not possible to determine which animals have recently calved and are at risk. The formula for the incidence density (ID_{ijm}) for one disease, for one month, for the i^{th} herd, in the j^{th} stratum is shown in equation 21. This is a modified version of the actuarial method as shown by Elandt-Johnson (1977).

Incidence densities for some diseases may be biased downward due to the inclusion of animals in the denominator that are no longer at risk for that particular disease. Due to the nature of the data collected, all animals in the herd, in a given age group, contribute to calculation of the animal months. Collection of individual information, for all age groups would allow for better estimation of frequencies as well as providing better data for research applications such as identification of important individual risk factors.

$$ID_{ijm} = \frac{\# \text{ cases}}{\text{animal months}} \quad (21)$$

$$ID_{ijm} = \frac{\# \text{ cases of disease (X) during current month}}{\# \text{ of animals at risk at end of previous month} - 1/2 \text{ withdrawals} + 1/2 \text{ additions}}$$

$$\text{withdrawals} = \# \text{ sold} + \# \text{ died due to other disease} + \# \text{ transferred to different age group.}$$

$$\text{additions} = \# \text{ purchased} + \# \text{ transferred in from other age groups.}$$

Population estimates of annual incidence

Since it has been proposed that the incidence density (true rate) is the most meaningful expression of disease frequency for macro level decision making, the calculation of a population estimate of this measure will be discussed. For population estimates of disease, it may be reasonable to aggregate the results of monthly observations into one annual figure for each herd. The monthly incidence densities (ID_{ijm}) are easily aggregated as shown in equation 22 (Rothman, 1986). This term will

be referred to as the "annual" incidence density (aID_{ij}) which is not as accurate as calling it the incidence density expressed in terms of animal years, but is more convenient. This annual incidence density (aID_{ij}) represents the average force of morbidity observed over one year of repeated monthly observations. It assumes a constant rate of disease for the entire year, hence seasonal fluctuations are ignored. This may present a problem as some diseases did exhibit noticeable seasonal fluctuations (Kaneene and Hurd, 1989).

$$\begin{aligned}
 aID_{ij} &= \text{"annual" incidence density for the } i^{\text{th}} \text{ herd in the } j^{\text{th}} \text{ stratum, expressed per 100 cow years} & (22) \\
 &= \frac{\sum_{m=1}^{12} \text{cases}}{\sum_{m=1}^{12} \text{animal months}} / 12 * 100
 \end{aligned}$$

If the annual incidence density (aID_{ij}) represents the unit of measure for one herd, then a summarization of the frequency for many herds is required in order to estimate the rate for a population. It is proposed that the data should be stratified according to herd size (Beal, 1985), since this is assumed to affect management and comparability of disease rates. For this reason, discussion of the summarization of rates will not proceed beyond the herd size stratum (j) level, although an overall frequency estimate is estimable if desired. The average stratum specific annual incidence density (aID_j) is computed as in equation 2.3. It is the weighted average of the herd specific annual ID's (aID_{ij}). The weights are those used in standard sampling theory for estimation of proportions (Cochran, 1977; Levy and Lemeshow, 1980). Other weights could be considered, (such as the inverse of the variance) since the incidence density is not a binomial proportion (Klienbaum, 1982; Rothman, 1986). It is also reasonable that a finite population correction factor (n_j/N_j), for the herd sampling, should be considered; however, this was dropped since the number of herds sampled (n_j) was relatively small compared to the number of herds in the state (N_j). This also simplifies the equations

for discussion.

$\overline{aID}_j$ = estimate of the "annual" incidence density for the j^{th} herd(23)
size stratum

$$= \sum_{i=1}^n W_{ij} aID_{ij}$$

where:

$$W_{ij} = \frac{aNAR_{ij}}{\sum_{i=1}^n aNAR_{ij}}$$

n = number of herds in j^{th} stratum

$aNAR_{ij}$ = number of animal years = $\frac{\sum \text{animal months}}{12}$

Variance estimates of annual incidence

If one views the multistage sampling procedure as a cluster sample, where herds are the clusters, then variation will be contributed from within herds and between herds (Alderink, 1986; Beal, 1985; Farver, 1987). However, it might be argued that, since we are observing all the animals within the herd for disease, there will be no within herd variance in the aID_{ij} . This is equivalent to saying that we have perfect knowledge of the rate of disease in that herd and that it is not subject to any random variation. Chiang (1961) suggests that we are considering a stochastic phenomenon (disease) which is subject to chance and as such a within herd variance should be considered.

Since the incidence density (aID_{ij}) is not a binomial proportion, nor is it a probability function, its variance must be approximated by its relationship to the probability (risk) of disease in a given herd. The relationship of incidence density to risk for a given period has been described as shown in equation 24 (Morgenstern *et al.* 1980). Application of this functional relationship results in a variance estimator for aID_{ij} as shown in equation 25. Annual number at risk (aNAR) represents the average number of animals in the herd for the year. The variance of the average annual incidence

density $S(aID_j)$ for the j^{th} stratum is a function of the weighted individual herd variances $S(aID_{ij})$ and the between herd variances as shown in equation 2.6.

$$\text{Risk} = 1 - \exp(-ID) \quad (2.4)$$

$$S^2(aID_{ij}) = \frac{aID_{ij} [1 - (1 - \exp(-aID_{ij}))]}{aNAR} \quad (2.5)$$

= Sample estimate of the variance of the "annual" incidence density for i^{th} herd in j^{th} stratum

$$aNAR_{ij} = \text{number of animal years} = \frac{\sum \text{animal months}}{12}$$

$$S^2(\bar{aID}_j) = \frac{\sum_{i=1}^n (aID_{ij} - \bar{aID}_j)^2 + \sum_{i=1}^n W_{ij}^2 S^2(aID_{ij})}{n_j} \quad (2.6)$$

= sample estimate of the variance of the "annual" incidence density

Where:

$$n_j = \# \text{ of herds in } j^{\text{th}} \text{ stratum}$$

Risk estimation

An estimate of the probability of occurrence of a disease on a farm should aid producers in planning health care and other management changes. The risk estimate must be defined for a specific time period, for example the one month risk of disease, the one year risk, or the lactational risk. For some diseases the one month risk (R_{ijm}) will vary seasonally. Since these risk estimates were reported to the participating NAHMS producers they were not aggregated over time. Therefore, equations shown are for stratum estimates of the one month risk (R_{jm}) and its variance.

The one month risk (R_{ijm}) for a given herd can be approximated from the incidence density for one month. If the ID_{ijm} is less than 0.10 and the time period is short, the risk and ID can be assumed to be equal (Klienbaum, et al., 1982; Erb, 1984).

If these assumptions do not hold, the risk can be approximated using equation 24. In most cases, in Michigan, these assumptions held true, but occasional outbreaks of diarrhea and respiratory disease in calves did result in large ID's some greater than 1.0, which is acceptable for the incidence density measure (Rothman, 1986). Therefore the conversion in equation 24 is recommended as a routine procedure for NAHMS. An estimate of the stratum one month risk (R_{ijm}) and its variance ($S^2(R_{ijm})$) can proceed, as in equations 27-2.10, treating the risk as a binomial proportion (Elandt-Johnson, 1977; Martin, 1987). Use of the cluster method for computing a variance should be considered (Beal, 1985), but one is then forced to assume that R_{ijm} represents an observed number of positive cases out of an observed number of sampled cases.

$$R_{ijm} = 1 - \exp(-ID_{ijm}) \quad (27)$$

R_{ijm} = one month risk of disease (X) for the i^{th} herd in the j^{th} stratum, for the m^{th} month

Where: ID_{ijm} same as equation 2.1

$$S^2(R_{ijm}) = \frac{R_{ijm}(1 - R_{ijm})}{m_{ijm} - 1} \quad (28)$$

$S^2(R_{ijm})$ = sample estimate of the variance of the risk from the i^{th} herd in the j^{th} stratum for the m^{th} month.

Where:

m_{ijm} = hypothetical number of animals at risk in the i^{th} herd in the j^{th} stratum for the m^{th} month.

$$R_{jm} = \frac{\sum_{i=1}^n W_{ijm} R_{ijm}}{n} \quad (29)$$

= mean one month risk of disease (X) for the j^{th} stratum for the m^{th} month only

Where:

$$W_{ijm} = \frac{m_{ijm}}{\sum_{i=1}^n m_{ijm}}$$

$i = 1-n$; n = number of herds in the j^{th} stratum

$$S^2(R_{jm}) = \frac{\sum_{i=1}^n (R_{ijm} - R_{jm})^2 + \sum_{i=1}^n W_{ij}^2 S^2(R_{ijm})}{n_j} \quad (210)$$

= sample estimate of the variance of R_{jm}

n_j = # of herds in j^{th} stratum

Further summarization of the stratum risk (R_{jm}) estimates, could be accomplished in two separate ways: computation of a mean one month risk for 12 months of observations (R_j), and computation of an annual risk of disease (annR). The mean monthly risk for one year of observation could be computed as the sum of all the weighted mean risk estimates (R_{jm}) divided by the number of months of observation. This will represent the average one month risk of disease; it's value may be limited as this measure tends to ignore the fact that multiple cases of disease can occur in the same animal and that the occurrence of disease in an animal or risk (R_{ijm}) for a herd may not be independent from one month to the next. Computation of a variance for these risk estimates is not meaningful since the risk is likely to vary significantly within that 12 months of observation due to seasonal effects, versus random variation.

The annual risk of disease (annR), which could be a valuable measure, would be computed according to equation 211 (Kleinbaum, et al, 1982). This measure is only appropriate if animals are at risk for the entire 12 month period. This does not apply for calves which mature into different age category, or for periparturient cow diseases. For diseases with a limited risk period, the annual risk (annR) will probably be an inaccurate since the model assumes animals are at risk for the full 12 months and the risks are derived from IDs which are biased downward for these diseases.

$$\text{annR} = 1 - \prod_{m=1}^{12} (1 - R_{jm}) \quad (211)$$

CONCLUSIONS

The choice of the most appropriate disease frequency measure to be estimated from a National Animal Health Monitoring System is primarily user dependent. A set of calculations have been proposed in order to provide for standardization of frequency computations. All the various estimators are derived from the incidence densities calculated from a from herds randomly selected and observed monthly for a period of time, in this case, one year. The progression of each of these measures from the incidence density (ID_{ijm}), is in shown in figure 21. Suggested uses of each measure are also shown. Other progressions could be considered, but these were chosen based on their anticipated use and approximatable statistics. Further work is needed in the areas of 1) improved ways to calculate the ID_{ijm} so as to remove bias, 2) determining the most appropriate weighting term for stratum estimates, and 3) calculation of the variances.

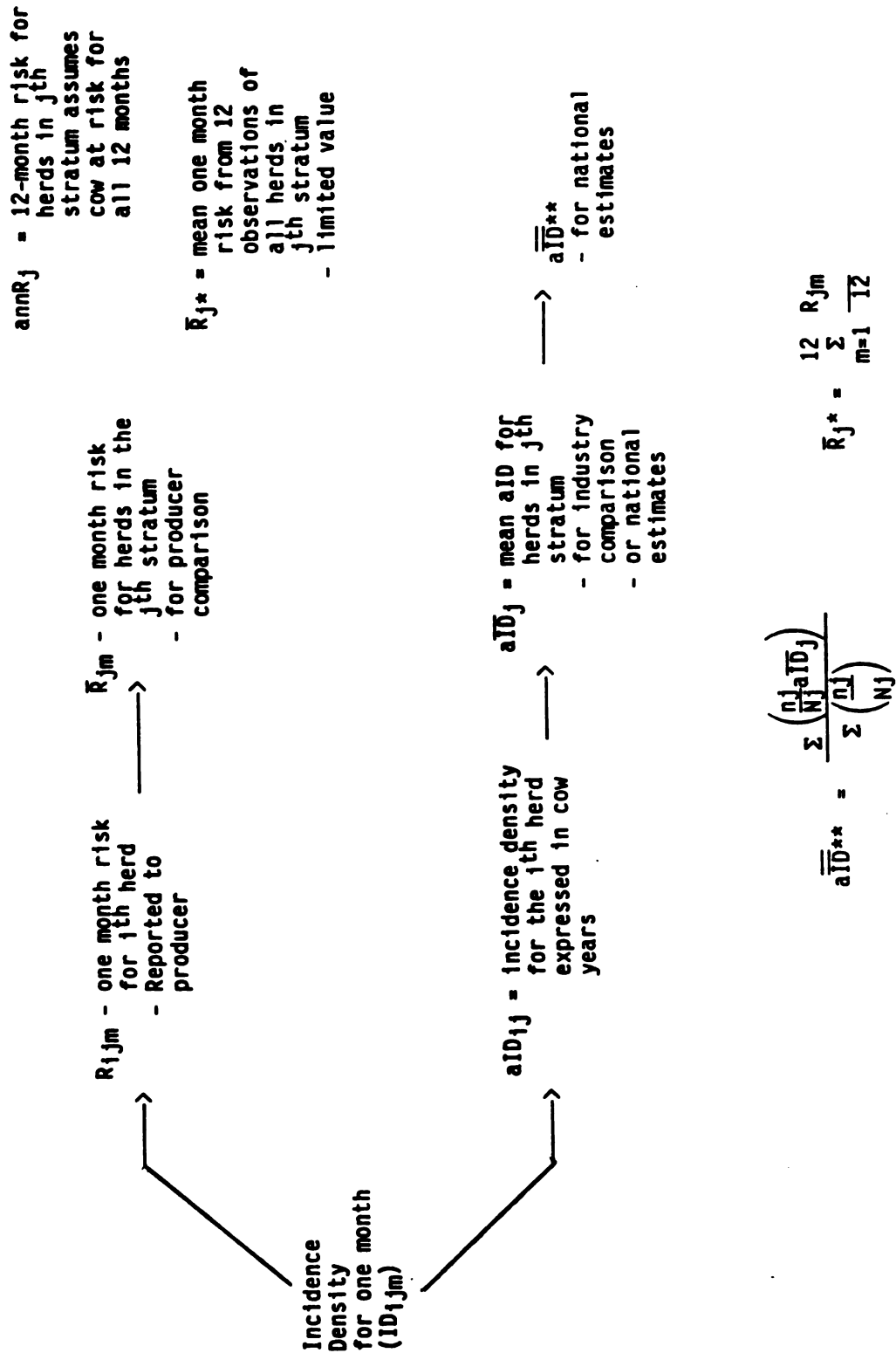


Figure 21 - Flow chart of various disease frequency measures proposed, with definition and expected use.

CHAPTER 3

The National Animal Health Monitoring System in Michigan III. Cost estimates of selected dairy cattle diseases

ABSTRACT

A study was conducted to estimate costs of major dairy cattle diseases. Sixty (n = 60) of the 6,012 dairy herds in Michigan were stratified and randomly selected for participation in the National Animal Health Monitoring System in Michigan. Government and university veterinarians visited each herd once a month for a total period of 12 months. At each visit data relating to diseases, production, management, finance, treatments, preventive activities, animal events, and any other relevant events were collected.

Monthly and annual cost estimates of disease treatments were computed in each herd and stratum. Similarly, monthly and annual estimated preventive costs were estimated. Results were expressed as cost per head and given separately for cows, young stock, and calves. In cows, the most expensive seven disease entities were: 1) clinical mastitis, 2) breeding problems, 3) gastrointestinal problems, 4) birth problems, 5) multi-system, 6) lameness, and 7) metabolic/ nutritional diseases (1 being the highest and 7 the lowest). In terms of estimated annual preventive cost, however, the ranking of the seven disease entities were (from highest to lowest): 1) Mastitis, 2) breeding problems, 3) lameness, 4) birth problems, 5) multi-system, 6) gastrointestinal disease, and 7) metabolic/nutritional problems.

In young stock, the mostly costly diseases were the multiple system problems, breeding problems, respiratory disease, birth problems, gastrointestinal, and lameness. In calves, the most costly disease problems were gastrointestinal problems, respiratory diseases, multiple systems, birth problems, metabolic diseases, and lameness. Methodo-

logical issues, as they relate to data collection and estimation of costs as well as suggestions for improving the accuracy of these estimates, are discussed.

INTRODUCTION

In Chapter 1, the National Animal Health Monitoring System (NAHMS) in Michigan was described in relation to the design of the project, data collection and observed frequencies of dairy cattle disease. In Chapter 2 methodological issues in the estimation of frequencies of diseases in a prospective study of multiple dynamic populations were discussed. In the present chapter, cost estimates of dairy cattle disease observed in a 12 month period will be discussed.

Interest in the economic effects of diseases and the related control/prevention activities has been increasing in the last 15 years. Many studies have focused on the economic effect of one disease entity. These have included: mastitis (Janzen, 1970; Pilchard, 1972; Natzke, 1976; Dobbins, 1977; Blosser, 1979; Fetrow et al., 1980, 1987; and Kirk and Bartlett, 1988), reproductive problems (Speicher and Meadows, 1967; Louca and Legates, 1968; Pelissier, 1972; Esslemont, 1974; Olds et al., 1979; James and Esslemont, 1979; Holmann et al., 1984; Dijkhuizen et al., 1985(a), 1985(b); Bartlett et al., 1985, 1986(a), 1986(b); Slenning, 1986; and Marsh et al., 1987). Some studies have reported on the economics of a single agent caused disease (Goodger and Skirrow, 1986; Kliebenstein et al., 1986; Hallam et al., 1986). Only limited reports on economics of disease control and prevention have been found in the literature (Grunsell et al., 1969; Barfoot et al., 1971; Morris, 1971; James and Ellis, 1979; Goodger and Kushman, 1984/85; Ellis, 1986; Alderink, 1986; Hallam, et al., 1986; Alderink and Kaneene, 1987).

The literature, however, is virtually devoid of reports where costs of production diseases (non-regulatory) were estimated using data from an active surveillance program like NAHMS. The objective of this chapter, therefore, is to report on cost estimates of production diseases. Specific aims of the chapter are to: 1) describe the methods used

in estimating costs of diseases, 2) critically evaluate the results in relation to the data and methods used in the cost estimates, and 3) offer some suggestions for improving the accuracy of the cost estimates.

MATERIALS AND METHODS

Design, data collection and data quality control techniques

The design, coordination, data collection, and data quality techniques used were described in the first chapter. Briefly, 60 dairy cattle herds were randomly selected to participate in the program. Veterinary medical officers (veterinarians from the university, state and federal departments of agriculture) visited the herds once a month and collected data for a period of 12 months. The forms used to collect preventive measure costs and to collect other disease related costs are shown in appendix A.

Estimation of monthly cost of a disease in a herd

Assume that the disease in question was X in a herd i, stratum j for the month m. The monthly total cost $TC(X)_{ijm}$ was then estimated using equation 3.1.

$$TC(X)_{ijm} = \text{Drug}(X) + \text{Vet}(X) + \text{Labor}(X) + \text{Cull}(X) + \text{Dead}(X) + \text{Dead calf}(X) + \text{Milk loss}(X) \quad (3.1)$$

Where:

Drug(X)	= Drug cost of disease (X) treatment
Vet(X)	= Veterinary expenses for disease (X) treatment
Labor(X)	= Hours spent treating the disease (X) multiplied by a standard wage of \$5.50 (Nott <i>et al</i> , 1986)
Cull(X)	= Net cull costs for disease (X) Net cull cost = Replacement value -net salvage value Replacement = Replacement cost for an animal of same age and genetic potential Net salvage = Salvage price less transportation and any other related expenses
Dead (X)	= Replacement cost (as defined Cull) plus disposal fees
Dead calf(X)	= Value (as reported by producers) of calves born dead due to the disease (X) in the dam (This figure did not include calves that were affected with the disease and died. These figures were reported separately)
Milk loss(X)	= (lbs loss x price per month) - (lbs loss x % fed to calves) x (replacer price)

Preventive(X) = Monthly cost for preventing disease (Computed as annual total for each herd then divided by number of months to give a monthly cost.

Estimation of weighted mean monthly cost of a disease

This estimate was computed in two steps. The first step was to determine the cost of a disease per head, for one month, in a given herd using equation 3.2. This included preventive and treatment costs.

$$C_{ijm} = \frac{TC(X)_{ijm}}{\frac{\# \text{ of animals at risk at end of previous month} + \# \text{ of animals at risk at end of this month}}{2}} \quad (3.2)$$

Where:

$TC(X)_{ijm}$ = the new dollars incurred from incident and prevalent cases

C_{ijm} = cost per head in the i^{th} herd in the j^{th} stratum for the m^{th} month

"at risk" = all animals of the specific age group minus nonrecovered cases from the previous month

The next step was to use the values estimated in equation 3.2 and estimate a weighted monthly mean cost of a disease per head using equation 3.3.

$$C_{jm} = \frac{\sum_{i=1}^n (C_{ijm} \cdot m_{ijm})}{\sum_{i=1}^n m_{ijm}} \quad (3.3)$$

Where: m_{ijm} = Number of animals at risk in the i^{th} herd in the j^{th} stratum for the m^{th} month estimated from the denominator of equation 3.2, $i = 1$ to n ,
 n = number of herds in the j^{th} stratum

Annual disease costs for a given disease

This figure was the sum of all the monthly means and was expressed on a per head basis.

$$\text{Annual costs} = \sum_{m=1}^{12} C_{jm} \quad (3.4)$$

Annual preventive costs

The annual costs of preventing disease (X) were computed for each herd by taking the total expenditures for one year preventive measures. This includes activities such as dry treatment, vaccination, and associated labor.

RESULTS

The disease/problems were grouped for expressing and comparing results, and these groupings are presented in Appendix B. The estimated annual costs of disease in Cows, Calves, and Young Stock are presented in Tables 3.1, 3.2 and 3.3, respectively. Similarly, the estimated annual costs of prevention in the three groups are presented in Tables 3.4, 3.5 and 3.6.

Table 3.1 Total dollar cost of disease per COW per year (including cost of prevention)

Disease Group	<u>Herd Size Strata</u>				Overall
	Stratum 1	Stratum 2	Stratum 3	Stratum 4	
Mastitis	38.22 (0.00-124.60)*	39.29 (5.65-68.19)	28.72 (1.77-154.85)	35.73 (5.29-54.94)	35.54 (0.00-154.85)
Breed	24.98 (0.00-66.13)	26.46 (4.02-61.66)	21.25 (2.30-31.67)	24.70 (0.97-33.72)	24.46 (0.00-66.13)
GI	23.23 (0.00-36.70)	6.28 (0.00-18.35)	8.09 (0.43-19.57)	13.40 (0.02-24.58)	11.13 (0.00-36.70)
Birth	10.29 (0.00-43.66)	14.92 (0.07-42.53)	1.75 (0.00-13.55)	9.89 (1.72-14.76)	9.60 (0.00-43.66)
Multi	14.55 (0.00-67.83)	7.72 (0.00-30.78)	4.46 (0.28-26.39)	8.09 (0.20-19.82)	8.01 (0.00-67.83)
Lameness	9.00 (0.00-18.22)	9.79 (0.00-30.88)	0.10 (0.00-18.41)	8.18 (0.00-14.45)	6.81 (0.00-30.88)
MetaNutr	8.27 (0.00-19.57)	6.82 (0.00-21.38)	3.12 (0.30-26.64)	6.53 (1.49-10.75)	6.03 (0.00-26.64)
Resp	2.36 (0.00-24.03)	1.65 (0.00-7.42)	10.45 (0.00-4.12)	1.56 (0.16-4.57)	3.95 (0.00-24.03)
UroGen	6.89 (0.00-38.41)	3.94 (0.00-13.12)	0.04 (0.00-48.36)	1.65 (0.05-3.97)	2.80 (0.00-48.36)

* = Minimum and maximum values.

Table 32 Total dollar cost of disease per CALF per year (including cost of prevention).

Disease Group	<u>Herd Size Strata</u>				Overall
	Stratum 1	Stratum 2	Stratum 3	Stratum 4	
Mastitis	24.92 (0.00-100.00)*	38.32 (0.00-261.53)	8.09 (0.00-150.00)	74.60 (18.01-345.92)	33.46 (0.00-345.92)
Resp	17.41 (0.00-117.00)	10.64 (0.00-119.16)	10.45 (0.00-114.86)	26.67 (0.00-36.71)	14.71 (0.00-119.16)
Multi	29.11 (0.00-236.22)	14.46 (0.00-73.88)	4.46 (0.00-20.57)	3.52 (0.00-23.78)	11.15 (0.00-236.22)
Birth	5.41 (0.00-13.53)	4.18 (0.00-12.31)	1.75 (0.00-16.03)	1.52 (0.00-11.42)	3.17 (0.00-16.03)
MetaNutr	0.13 (0.00-1.84)	0.70 (0.00-4.08)	0.08 (0.00-0.60)	6.05 (0.00-26.46)	1.39 (0.00-26.46)
Lameness	0.00	0.02 (0.00-0.17)	0.10 (0.00-1.14)	0.08 (0.00-0.44)	.05 (0.00-1.14)
Urogen	0.00	0.04 (0.00-0.93)	0.04 (0.00-0.27)	0.00	0.01 (0.00-0.93)

* = Minimum and maximum values.

Table 33 Total dollar cost of disease per YOUNG STOCK per year (including cost of prevention).

Disease Group	<u>Herd Size Strata</u>				Overall
	Stratum 1	Stratum 2	Stratum 3	Stratum 4	
Multi	5.91 (0.00-24.45)*	3.33 (0.00-41.40)	0.93 (0.00-11.25)	4.49 (0.00-14.52)	3.45 (0.00-41.40)
Breed	1.88 (0.00-20.84)	1.07 (0.00-3.86)	2.02 (0.00-5.03)	4.78 (0.00-11.90)	2.41 (0.00-20.84)
Resp	1.21 (0.00-4.69)	0.90 (0.00-4.94)	1.65 (0.00-3.35)	3.98 (0.70-9.25)	1.95 (0.00-9.25)
Birth	1.41 (0.00-5.56)	1.20 (0.00-2.73)	1.10 (0.00-19.06)	2.07 (0.24-5.73)	3.17 (0.00-19.06)
GI	1.21 (0.00-16.46)	0.65 (0.00-8.48)	1.14 (0.00-4.15)	0.17 (0.00-0.78)	0.71 (0.00-16.46)
Lameness	0.31 (0.00-3.21)	0.05 (0.00-0.64)	0.03 (0.00-0.14)	0.02 (0.00-0.04)	0.08 (0.00-3.21)
MetaNutr	0.01 (0.00-0.18)	0.03 (0.00-0.45)	0.02 (0.00-1.68)	0.00	0.02 (0.00-1.68)
Mastitis	0.01 (0.00-0.23)	0.03 (0.00-0.45)	>0.00 (0.00-0.02)	0.00	0.01 (0.00-0.45)

* = Minimum and maximum values.

**Table 3.4 Annual cost of preventive measures of the top 10 disease problems of COWS
(expressed as mean U.S. dollars per cow)**

Disease Group	<u>Herd Size Strata</u>				Overall
	10-49	50-99	100-199	200+	
Mastitis	2.45 (0.00-13.04)*	6.50 (0.99-28.13)	3.31 (0.19-8.70)	4.45 (1.34-6.79)	4.56 (0.00-28.13)
Breed	3.11 (0.00-15.84)	4.36 (0.00-12.86)	3.70 (0.43-6.53)	3.97 (0.00-5.92)	3.91 (0.00-15.84)
Lameness	1.38 (0.00-12.20)	1.45 (0.00-6.32)	0.64 (0.00-3.81)	4.37 (0.00-10.56)	2.00 (0.00-12.20)
Birth prob	0.47 (0.00-6.69)	1.36 (0.00-16.86)	0.28 (0.00-1.38)	0.30 (0.00-0.71)	0.68 (0.00-16.86)
Multi system	0.17 (0.00-2.79)	0.17 (0.00-1.08)	1.10 (0.00-9.91)	0.13 (0.00-0.55)	0.39 (0.00-9.91)
GI	0.43 (0.00-5.78)	0.22 (0.00-1.24)	0.15 (0.00-0.84)	0.75 (0.00-1.40)	0.38 (0.00-5.78)
MetaNutr	0.44 (0.00-2.81)	0.43 (0.00-5.88)	0.11 (0.00-0.44)	0.49 (0.00-1.85)	0.37 (0.00-5.88)
Resp	0.35 (0.00-4.45)	0.32 (0.00-1.47)	0.42 (0.00-2.61)	0.36 (0.16-1.00)	0.36 (0.00-4.45)
Integ	0.26 (0.00-2.33)	0.50 (0.00-6.32)	0.00	0.00	0.21 (0.00-6.32)
UroGen	0.14 (0.00-1.12)	0.00	0.00	0.00	0.02 (0.00-1.12)

* = Minimum and maximum values.

Table 3.5 Annual cost of preventive measures of the top 8 disease problems of CALVES (expressed as mean U.S. dollars per calf).

Disease Group	<u>Herd Size Strata</u>				Overall
	10-49	50-99	100-199	200+	
GI	0.96 (0.00-4.95)*	3.67 (0.00-23.37)	1.85 (0.00-27.03)	5.29 (0.00-28.04)	2.94 (0.00-28.04)
Birth	1.84 (0.00-8.73)	2.70 (0.00-10.65)	1.04 (0.00-2.74)	1.47 (0.00-8.36)	1.82 (0.00-10.65)
Resp	1.13 (0.00-10.69)	0.07 (0.00-2.53)	2.23 (0.00-9.14)	4.08 (0.00-11.40)	1.64 (0.00-11.40)
MetaNutr	0.04 (0.00-0.67)	0.37 (0.00-4.08)	0.08 (0.00-0.60)	5.34 (0.00-19.16)	1.14 (0.00-19.16)
Multi	0.55 (0.00-12.97)	0.56 (0.00-10.80)	1.69 (0.00-6.93)	0.09 (0.00-0.39)	0.82 (0.00-12.97)
Integ	0.00	0.09 (0.00-1.39)	0.00	0.02 (0.00-0.08)	0.03 (0.00-1.39)
Lameness	0.00	0.00	0.07 (0.00-0.40)	0.00	0.02 (0.00-0.40)
Urogen	0.00	0.04 (0.00-0.93)	0.00	0.00	0.01 (0.00-0.93)

* = Minimum and maximum values.

Table 3.6 Annual cost of preventive measures of the top 8 disease problems of YOUNG STOCK (expressed as mean U.S. dollars per animal).

Disease Group	<u>Herd Size Strata</u>				Overall
	10-49	50-99	100-199	200+	
Birth	0.90 (0.00-5.56)*	1.20 (0.00-2.73)	0.48 (0.25-1.17)	0.68 (0.00-1.13)	0.86 (0.00-5.56)
GI	0.31 (0.00-1.68)	0.53 (0.00-3.40)	0.33 (0.00-1.40)	0.20 (0.00-0.78)	0.36 (0.00-3.40)

Resp	0.37 (0.00-2.82)	0.24 (0.00-0.92)	0.30 (0.00-2.25)	0.22 (0.00-0.75)	0.27 (0.00-2.82)
Multi	0.21 (0.00-1.42)	0.41 (0.00-2.75)	0.35 (0.00-2.21)	0.00	0.26 (0.00-2.75)
Breed	0.24 (0.00-2.46)	0.24 (0.00-1.37)	0.10 (0.00-0.97)	0.10 (0.00-0.38)	0.17 (0.00-2.46)
Integ	0.01 (0.00-0.25)	0.13 (0.00-1.10)	0.00	<0.01 (0.00-0.02)	0.05 (0.00-1.10)
Lameness	0.12 (0.00-2.42)	0.00	0.00	0.01 (0.00-0.04)	0.02 (0.00-2.42)
Mastitis	0.01 (0.00-0.23)	0.03 (0.00-0.45)	0.00	0.00	0.01 (0.00-0.45)

* = Minimum and maximum values.

DISCUSSION

Cost, defined as a measure of an amount of value released in the acquisition or creation of economic resources in production (Hepp, 1985), is made up of two components. One component is that cost measured in terms of money spent while the other is the lost potential. Presently, NAHMS data can only be used to estimate dollars spent.

Cost computation

The denominator of equation 3.2 represents the average number of animals at risk of disease during a month. This is in contrast to most economic reports that calculate the mean cost per case of disease. The cost per head figures reported in this chapter represent the mean cost per case plus the mean risk of disease occurrence. This figure is valuable as it conveys the expected probability of disease occurrence and the expected cost from incident and prevalent cases.

Comments on various data sets for cost estimation

The drug and veterinary cost data sets were fairly accurate, since they were substantiated (for the most part) by invoices from the producer's veterinarian and/or supplier. In the future, efforts should be made to differentiate between drugs administered under the supervision of a veterinarian and those administered strictly at

the discretion of the producer.

There were many omissions of these labor data by the producer. Efforts should be directed toward educating the producers to record the time spent on various aspects of their operations. The time spent performing a task should be recorded instead of monetary figures, since labor wages fluctuate. The time spent then can be converted into monetary terms using an accepted labor wage factor. The figures used for the replacement value of an animal were those as given by the producer. These figures were assumed to be fairly accurate since the producer would know the genetic potential of the animal and current market price. It was difficult, however, to assess the accuracy of these figures. An alternative way of collecting these data has been suggested, which would involve collecting information about the animal and then using accepted standards to estimate a replacement value for the animal in question. Another problem associated with computing net cull cost was the fact that it was not possible to adjust the net cull cost to include the probability that the animal would have been soon culled regardless of her disease status. In other words, a cow may have had other problems which when combined with disease, resulted in a culling decision. It may not be reasonable to charge the entire cost of culling to disease X. Further reports should focus on methods for addressing this issue.

The figures used for the value of dead calves were those given by the producer. This can cause problems as seen in Table 3.2 for gastrointestinal disease in calves in stratum four. For reasons mentioned under the cull and death data section, the use of a standard value for deacon⁴ calves has been suggested as an alternative. In these results, the milk loss estimated was that discarded due to treatment. In some limited instances, it also included milk production lost due to an acute disease. In such cases the loss was the producer's estimate of the difference between what the cow was producing before and during the illness. These estimates of milk loss must be evaluated very cautiously. First, all discarded milk should not be assumed to be a loss. This is because

⁴Deacon calves = Calves sold under seven days old

some milk is fed to calves, in which case some money (approximately \$7.00 per cwt)⁵ would be saved in buying milk replacers. To correct for this discrepancy, the estimates were adjusted to account for the discarded milk fed to calves. The producers reported the percentage of discard milk fed to calves. Second, subclinical effects of disease on milk production could not be estimated with data from the conventional NAHMS data collection procedures where individual cow IDs are not available. Also, a decrease in milk production will cause a decrease in feed intake with a corresponding decrease in cost (savings). Further studies were conducted to improve these estimates in NAHMS, and are reported in Chapter 8.

It is felt that preventive cost figures were underestimated. There was great difficulty in recording bulk purchases and it was not always possible for the Veterinary Medical Officer (VMO) to know if individual doses of drugs recorded in the current month might have been recorded as a bulk purchase in a previous month. Bulk purchases may not have been recorded as the VMO was anticipating collection of those costs at time of administration to the animal. Another problem in the preventive data relates to which disease should be charged for a certain preventive measure. In case of a multivalent vaccine against Infectious Bovine Rhinotracheitis, Bovine Viral Diarrhea, and five strains of Leptospirosis, it was difficult to determine which disease was being prevented. Thus, the cost to vaccinate against one of these diseases was estimated as the total cost of the vaccine divided by the number of disease entities or the cost was attributed to the syndrome the producer was concerned about preventing. The merit of this approach may be questionable, and some standardized procedure should be agreed upon.

Specific comments on the results

Due to the grouping of disease problems used, the dollar values in this chapter may not be directly compared to other reports in the literature, even if values from those reports were to be adjusted to current monetary values. At this point, it is not

⁵Price of reconstituted milk replacer based on a sample (n=4) of Michigan feed suppliers, October 1987

possible to generalize the monetary figures reported and conclude that a given amount of money could be saved on a given farm by preventing disease (X). This is true for 3 reasons: 1) some disease is unpreventable and this cost never can be recovered; 2) as discussed, current cost estimations are incomplete and should be used with caution; 3) whereas application of standards may improve cost estimations for extrapolation to a reference population, use of standards or population estimates on a given farm may be fraught with hazards (Lloyd, et al., 1987). The cost estimates reported here might be called gross, short term costs of clinical disease. They are gross because revenue increasing effects of disease, such as the savings in feed costs due to the animal being off feed, were not included. It should also be noted that gross costs overestimate the true net costs of disease. The costs are considered short term since the chronic and long term effects of disease (e.g., those on reproductive efficiency) were not included. Even though occasionally some registered cattle might have been overvalued, we feel that many gross costs were underestimated or omitted. The costs reported in this chapter, therefore, should be considered as the lower bound of the gross costs associated with disease occurrence and prevention.

Suggestions for improving the accuracy of cost estimates

Future efforts need to focus on methodologies for estimating costs associated with lost potential due to diseases within the NAHMS program. To be able to estimate costs of lost potential associated with disease, it is essential to have individual identification of animals and the NAHMS program should strive to achieve such status. Alternative methods for estimating the value of the animal, as opposed to accepting the farmer's figures, should be explored. More rigorous quantitative methods of estimating costs associated with diseases, using data from an observational prospective study of multiple dynamic populations, like the NAHMS, should be applied.

CHAPTER 4

The Application of simulation models and systems analysis in Epidemiology: A review

ABSTRACT

A method for classifying epidemiologic process models is presented along with a brief history of epidemiologic modelling. Epidemiologic models are distinguished as being associative or process models. Associative models attempt to establish etiology by observing the associations of various risk factors with the occurrence of disease. Process models attempt to quantitatively describe the course of disease in a dynamic population, beginning with hypotheses about the underlying structural processes involved. A process model can be further classified according to: 1) how it models the effect of chance, 2) it's application perspective, 3) the mathematical treatment of time, 4) the computational treatment of individuals, and 5) the method for determining a solution.

The literature was reviewed for examples of applied epidemiologic process models. Examples are cited and classified according to the proposed classification method. Suggestions for further research are made.

INTRODUCTION

It has long been recognized that the occurrence of disease is a result of interactions between components of the famous agent, host, environment complex. The discipline of epidemiology has developed as a result of efforts to unravel the mysteries of this complex. A survey of current epidemiologic literature (Susser, 1985) shows most of the mathematical and quantitative work in epidemiology has resulted in what King and Soskolne (1988) have termed associative models. These are models that attempt to establish etiology by observing the associations of various risk factors with the occurrence of disease. This approach has been very fruitful and has resulted in a variety of health recommendations, particularly with reference to individual risk factors for

chronic and noninfectious disease.

However, these associative models generally overlook the fact that interactions in this famous complex are dynamic and relationships change over time, as do the populations in which these interactions are occurring (Anderson and May, 1985; Catalano and Serxner, 1987). Efforts to address this issue of dynamic interactions in epidemiology have resulted in what are best termed process models (King and Soskolne, 1988). Process models attempt to quantitatively describe the course of disease in a population, so that state of the population, in terms of number infected, susceptible, etc. can be expressed over time. The goal of this paper is to focus on this latter type of modelling. The objectives are: 1) to present a brief perspective on the development, past and present, of epidemiologic process models, 2) to offer a method for classification of these process models, and 3) to classify specific applied models, with their application in veterinary or human epidemiology.

HISTORY

It is interesting that some of the earliest epidemiologists were process modelers (Susser, 1985). Early workers such as William Farr in 1840, Brownlee, Greenwood, Kermack, and McKendrick, observed the consistent patterns of the occurrence of epidemics and developed mathematical representations of these patterns with the hopes of predicting the course of epidemics, a priori. One of the first and few "successful" attempts at modelling was on a veterinary problem. In a letter to the London Times in 1865, W. Farr used an equation of second and third ratios to predict the outcome of a rinderpest epidemic in England. This success was not often repeated but it encouraged workers like Brownlee who persisted in the attempt to fit epidemic curves to variations of the normal curve (Fine, 1979). Bailey (1975) mentions the work of Greenwood, Kermack and McKendrick along with Hamer, Soper and Ross who developed versions of what would later be called mass action models. Wade Hampton Frost, the first chair of epidemiology at The Johns Hopkins School of Hygiene and Public Health, was the originator of the Reed-Frost model of epidemics which still finds wide applicability

today (Abbey, 1952; Ackerman *et al.*, 1984).

Given the illustrious beginnings of early process modelling, one might well ask, why is this not an important part of epidemiology today? A further look at the history of epidemiology and process modelling might offer some possible explanation. As the early 20th century progressed, epidemiology and process modelling were cooperative partners in addressing disease control problems such as malaria and helminth infections in humans, particularly schistosomiasis (Fine, *et al.*, 1982; Hethcote and Yorke, 1984; Anderson and May, 1985; Dietz and Schenzle, 1985). This assessment, of cooperative partnership, is based on the observations from these reviews, and others (Bailey, 1982; Koopman, 1987), showing mathematical development concurrent with data collection and disease control policy recommendations resulting from models. Nobel laureate, Sir Ronald Ross, derived the first threshold theorem from a differential equation model (Ross, 1911). This model determined that there was a threshold density of man and mosquitoes below which malaria would not be able to maintain itself. George MacDonald's (1956) conclusions, that control of adult mosquitoes by residual insecticides is more effective than larval control, is considered, by some, as "the single most important insight into public health planning from modelling" (Dietz and Schenzle, 1985). MacDonald (1965) also published an important paper on the dynamics of schistosome infections and humans that has spawned a great deal of mathematical development in parasitology, this is thoroughly discussed in Anderson and May (1985).

After this time, however, one can see a divergence between applied epidemiology and mathematical modelling (Bailey, 1975, Thrusfield, 1986). Bailey (1975) suggests this point of divergence occurred around 1957. Susser (1985) infers the change began after World War II. During this period it is possible to perceive two responsible forces. First, epidemiologists are beginning to be more concerned with chronic, noninfectious diseases (Susser, 1985; King and Sorkolne, 1988), which tend to focus on individual risk factors versus population dynamics, and find more use for associative (statistical) models than for process models. Secondly, the limiting assumptions of the early mathematical models, the mass action and chain binomial, began to impinge on their practical

applicability. These limiting assumptions will be discussed briefly later. As a result, the models were not able to describe recurrent cycles of disease and fell out of use by many epidemiologists (King and Soskolne, 1988).

The net result of these phenomenon can be expressed by the nursery rhyme bemoaning the fact that "the dish (epidemiologist) ran away with the spoon" (statistician), and left the cow (mathematician) to more esoteric pursuits, such as "jumping over the moon". This observation has been echoed by the mathematicians themselves (Bailey, 1982; Bart *et al.*, 1983). One leader in the field of measles and helminth modelling has noted: "some of the mathematical literature has taken on a life of its own, free from data and full of elegant theorems in hopeful search of a disease" (May, 1982). The modelling literature that occurs after this time is largely theoretical (Wickwire, 1977; Mollison, 1977; Dietz and Schenzle, 1985; Isham, 1988) and difficult for the non-mathematician (Koopman, 1987; King and Soskolne, 1988).

Unfortunately, a great deal of this rich theory has been overlooked by most epidemiologists. This is particularly a handicap for the veterinary epidemiologist, who in the majority of cases, is dealing with disease in dynamic populations. It may also be a fair assumption that he or she is often dealing with infectious disease or parasitic disease with which almost all of the process model development has dealt.

During this same post-war period, separate from epidemiology, the theory and practice of systems analysis begins to develop (Chestnut, 1965). This methodology has enjoyed a very fruitful tenure with a wide variety of applications to industrial processing (Law and Kelton, 1982), management and social sciences (Sutherland, 1975), ecology and entomology (Kitching, 1983). Before the late 1970's only a few apparent applications of this theory to epidemiology can be found (Waler *et al.*, 1962; Brogger, 1967; Waler, 1968; ReVelle *et al.*, 1969). The count is increased if one includes the few health care management applications (Farrow *et al.*, 1971; Bailey and Thompson, 1975).

In the late 1970's and early 1980's one can see signs that the once separated fields of dynamic mathematics and epidemiology are beginning to reunite (Nokes and Anderson, 1988). Epidemiology is bringing along the more fully developed field of

statistics, and dynamic mathematical disease models have been enhanced by computer simulation. Simulation allows for relaxation of some of the assumptions, while decreasing the need for rigorous mathematics and closed form analytical solutions. This approach can more effectively deal with nonlinearities, time dependence and various forms of feedback (Habtemariam *et al.*, 1982b; Angulo, 1987). The possibility that systems science will begin to contribute to epidemiology is suggested by Bailey (1982), Koopman (1987), and some examples in the current literature which will be discussed below. Koopman (1987) calls for a science of transmission systems analysis which merges the mathematical theory of dynamic populations, with simulation modelling, as in Ackerman *et al.* (1984), with a constant eye to statistical interpretation of real world data, as in Haber, Longini, and Cotsonis (1988). Stimulated by the current epidemic of human immunodeficiency virus (HIV) infections and the call for more production and economically oriented veterinary medicine, it is anticipated that this science of transmission systems analysis, or the systems approach will gain an increased role in epidemiology.

CLASSIFICATION

Any new methodology or discipline seems to suffer from an ambiguity of terminology and lack of a unified classification scheme. This ambiguity seems to exist in epidemiologic process modelling. The result is an increase in the amount of words required to communicate the essential features of a model, miscommunication and an overall decrease in the rate of new developments. Based on the writings of various authors, a means of describing and hence classify current process models is presented in this paper. It is hoped that all current models can be described in terms of these various characteristics. Specific applied models published since 1970 are then characterized along with their apparent application. An effort has been made to include only papers that are considered to be applied and epidemiologic in nature. The determination of the whether a paper is applied or theoretical is not always clear. Applied papers are those that were deemed to be attempting to answer a specific

epidemiologic question, using data that is current enough to be considered useful. It is not necessary that the data be collected primarily for the model, as most models depend heavily on literature for estimates of many parameters. Some models were considered theoretical, and excluded even though they employ current data. The reason being it was perceived, by the authors, that the purpose of the data was only to evaluate behavior of the model versus make disease control recommendations. Epidemiologic papers are those that relate to control of disease in animals or humans. Agricultural production models (Jenkins and Halter, 1963; Oltenacu *et al.*, 1980 and 1981;) and statistical simulation models (Lemeshow *et al.*, 1985; Suttmoller, 1986; and Akhtar *et al.*, 1988), along with econometric simulations (McCauley, *et al.*, 1977) were generally excluded. No attempt has been made to evaluate the usefulness or quality of the specific models included, or the validity of their conclusions.

Secondly, three general types of models are identified and described. These genera seem to represent most models that have been presented to date. Identification of a model's genera along with its specific classification will convey most of the important information on a model's technicalities.

Classification method

The classification of epidemiologic models might best be achieved by the application of 6 characteristics that would express most of a model's salient features (Figure 4.1). These characteristics are: 1) the model's causal perspective, 2) how it models the effect of chance, 3) its application perspective, 4) the mathematical treatment of time, 5) the computational treatment of individuals, and 6) the method for determining a solution. Each of these characteristics are dichotomous, therefore for a given characteristic a model will generally have one or the other traits. This allows for flexibility in model characterization along with simplicity, since many types of models can result from various combinations of these traits.

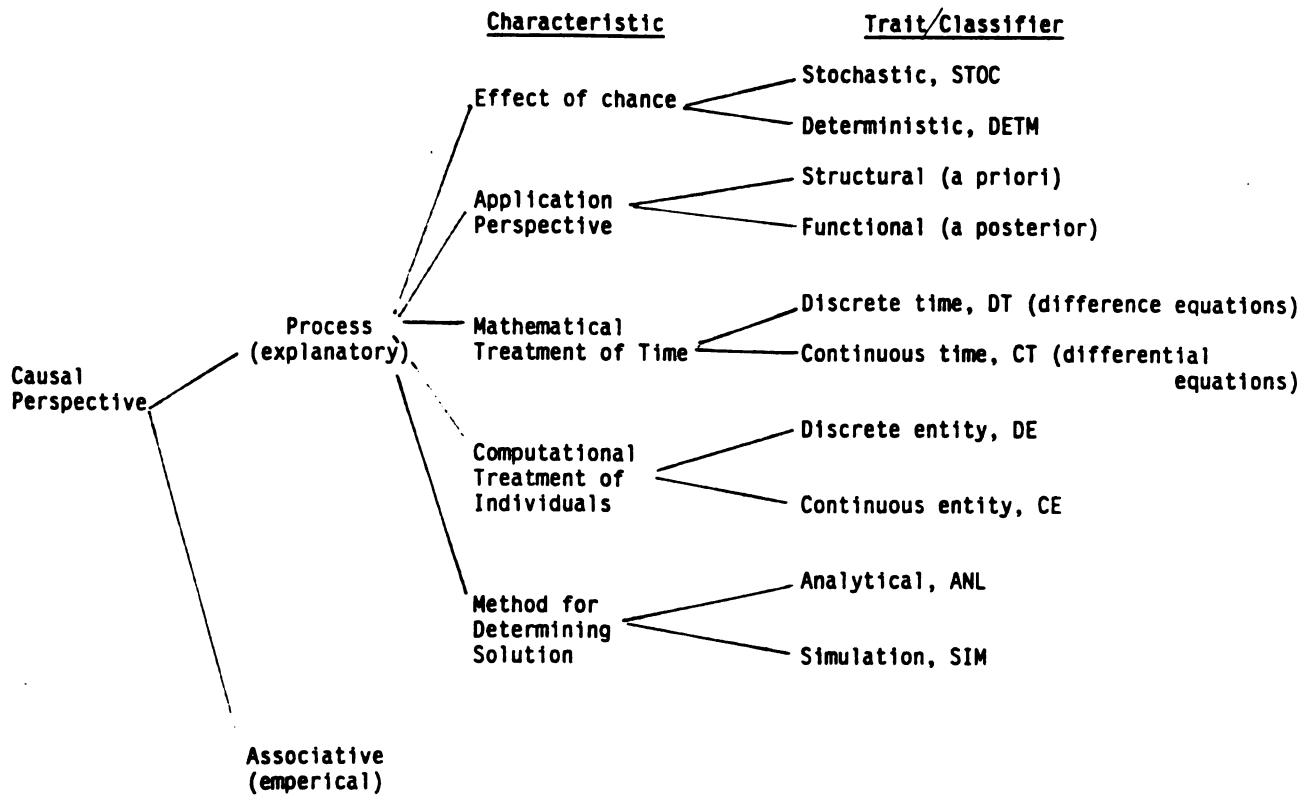


Figure 4.1 Proposed Classification Method for Process Epidemiologic Models

A model's causal perspective reflects the nature of the original hypotheses that an investigator may have been interested in. Associative models will infer causality without a knowledge of the pathways or processes leading to the observed phenomenon. Process models begin by defining hypothesized pathways and structural processes that may describe the system under investigation. As already stated, this paper is confined to process versus associative or statistical models. So our first characteristic is defined; a model is either associative or process. This distinction of associative versus process seems to be similar to Thrusfield's (1986) designation of empirical versus explanatory models.

Following King and Soskolne's (1988) hierarchy, we can distinguish the characteristic of how a model relates to the effects of chance. A model can be described as being stochastic (STOC) or deterministic (DETM). Stochastic models include elements

of random variation and chance. Fully stochastic models, if run repeatedly will lead to a distribution of epidemic sizes and durations (Ackerman *et al.*). These fully stochastic models are exhibiting the threshold theorem of epidemics (McKendrick, 1926). Other stochastic models, of non-infectious disease will include the random effects of certain variables, but will not exhibit the threshold phenomenon. Stochastic models have the advantage of reflecting the realistic aspects of chance and uncertainty in a model's behavior. The predictions can be expressed with confidence intervals and expected values instead of just point estimates. Deterministic models give the same result, every time they are run, and one can consistently determine the state of the model for any given set of initial starting values and parameters. Deterministic models are useful for determining the sensitivity of a system's behavior to changes in certain parameters.

The next level of classification is its application perspective. A model is either functional or structural (King and Soskolne, 1988). This is similar to Fine's (1982) distinction of descriptive (a posteriori) versus a priori, or dynamic models. Structural models attempt to portray the underlying mechanism of the disease transmission process for the purpose of making a priori predictions or exploring implications of assumptions and alternative assumptions. Most simulation models are of this type. On the other hand, functional models begin from the standpoint of modelling a process, but their goal is to quantitatively describe observed phenomenon, or to gain estimates of risk factors, with a statistical application to the process model. Functional models attempt to model a process and look backward in time, whereas structural models attempt to look forward in time and make predictions about future states of a population. These functional models are not the focus of this paper, but they represent a fascinating application of the interface between process modelling and statistics. An interesting example of functional modelling is a recent paper by Haber (Haber *et al.*, 1988) where a heterogeneous population model was used to assess the effects of various individual risk factors for influenza. The model used was previously developed by Longini and Koopman (Longini *et al.*, 1982, 1984b, 1988). These are applications of chain binomial models in a functional manner (Poku, 1979). Functional models would also include the

so called catalytic models (Muench, 1959). In these models prevalence data are fitted to differential equations to estimate the age specific force of infection in a population (Sundaresan and Assaad, 1973; Goldacre, 1977; Schenzle *et al.*, 1979; Fine and Clarkson, 1982; Remme *et al.*, 1984; Nokes *et al.*, 1986; McLean and Anderson, 1988). Box-Jenkins, autoregressive integrated moving average (ARIMA), and other time series types of analysis, might be classified as functional models (Angulo *et al.*, 1977; Choi and Thacker, 1981; Cliff and Haggett, 1982; Helfenstein, 1986; Catalano and Serxner, 1987). Markov models have also been used as functional models (Schwabe *et al.*, 1977; Leviton *et al.*, 1980). A simulation by Goodger *et al.* (1988) might be classified as a functional model, as simulation was used as tool for making statistical inferences about the difference in milk production in *Streptococcus agalactiae* infected cows that were treated versus not treated.

The next characteristic of a model relates to its mathematical treatment of time. A model will be discrete (DT) or continuous time (CT). Discrete time models divide time into units of equal duration and employ the algebra of finite difference equations. For example, the number of susceptibles at the next time period equals the number of susceptibles at this time period minus the number of new cases ($S_{t+1} = S_t - C_{t+1}$) (Fine, 1982). Continuous time models treat time as a continuous variable and use differential equations to express instantaneous rates of change. For example, the rate of change of new infections (ie. infection rate) might be a function of the number of susceptible (S), cases (C) and some contact parameter (b), ($dC/dt = S \cdot C \cdot b$). The number of cases at any given point in time is just the integral of this rate (Bailey, 1975).

For the computational treatment of individuals a model can be classified as discrete entity (DE) or continuous entity (CE). Discrete entity models will be defined as models that track one individual at a time through the simulation model. This individual is exposed to infectious individuals and any other experiences, such as calving, death, etc. The behavior of the system is the sum of the behavior of each individual. These types of models can get very complex, and this increases as the number of individuals in a population increases. This complexity has the disadvantage of increased

computer and programmer time and decreased intuitive appeal (Ackerman *et al.*, 1984). Continuous state (entity) models treat the number of individuals in any state as a real number, they can be computed in continuous or discrete time. Continuous entity models, or macro models (Ackerman *et al.*, 1984) tend to deal with homogeneously mixing populations. The homogeneous population assumption can be a disadvantage if one feels that interactions are not the same for each individual in the population. The advantage is that the size of the population being simulated will not effect the speed of computer processing for continuous entity models. It should be noted that if a model is mathematically defined in continuous time, ie. with differential equations, then it will a continuous entity model. However, the distinction blurs when a differntial equation model is simulated on a digital computer, since time is discretized into very small units for numerical integration (Law and Kelton, 1982).

In terms of how a model arrives at its solutions, one can classify a model as analytical versus simulation (Fine, 1982). Analytical models depend on mathematical manipulation alone to explore the relationships between variables, i.e. they seek a closed form solution to the state of the system at some equilibrium. There is an extremely large number of these types of epidemic models which are largely the domain of the mathematician (Bailey, 1982). The advantages are that, they can be rigorously evaluated and stability criterion determined. The disadvantages are that much realism is often assumed away in order to produce a more tractable model, and they are inaccessible to the non-mathematician. Simulation models depend on numerical substitution, according to model defined rules, to find the expected outcome of a mathematical formulation. (Fine, 1982; Ackerman *et al.*) The example models presented below are mostly simulation models.

In summary, 6 characteristics have been presented for classification of various epidemiologic models (see Figure 4.1). For each of these characteristics two possible traits exist: process versus associative, functional versus structural, stochastic versus deterministic, discrete time versus continuous time, discrete entity versus continuous entity, and analytical versus simulation.

General model types

When categorizing and classifying models, some authors have mentioned various types of models such as the mass action, the Reed-Frost, Markov models, network models, matrix models, systems models and others. It is useful if these various types are grouped into three genera: mass action models, chain binomial, and systems models (Table 4.1). Grouping the models in this manner conveys a sense of a model's assumptions and view of the system it is attempting to describe.

Mass action models refer to the phenomenon that infection is the result of the random and homogeneous mixing of infectious and susceptible individuals within a population (Fine, 1982). They can be deterministic or stochastic (Bartlett, 1953), and they can be discrete (Soper, 1929) or continuous time (Bailey, 1955). However mass action models are always continuous entity. Some of the limiting assumptions of these type of models are that they assume random and homogeneous mixing, and there is a linear relationship between the incidence rate and the number of cases (eg. $C_{t+1}/S_t = C_t * \beta$). This linear relationship makes it is possible to erroneously calculate more cases than there are susceptible, in a small population. Also, the epidemiologic meaning of the transmission coefficient (β), for mass action models, is not quite clear (Fine, 1982).

In order to overcome these limiting assumptions the chain binomial models were developed (Greenwood, 1946). In these models, new cases of disease occur in a series of stages. The number of cases at any stage will have a binomial distribution depending on the number of infectious and susceptible at the previous stage (Bailey, 1975). These models are fully stochastic, discrete time and continuous entity. These models assume the period of infectiousness is relatively short and of constant duration, there is a constant probability of infection in each serial interval. (Fine, 1982).

There are at least four types of chain binomial models, the Greenwood type (Greenwood, 1946), Reed-Frost, the Elveback type, and Markov models (Table 4.2). Markov models or chains are sometimes used for simulations. These are mathematically equivalent to chain binomial models with a finite state and discrete time parameter (Dietz, 1967).

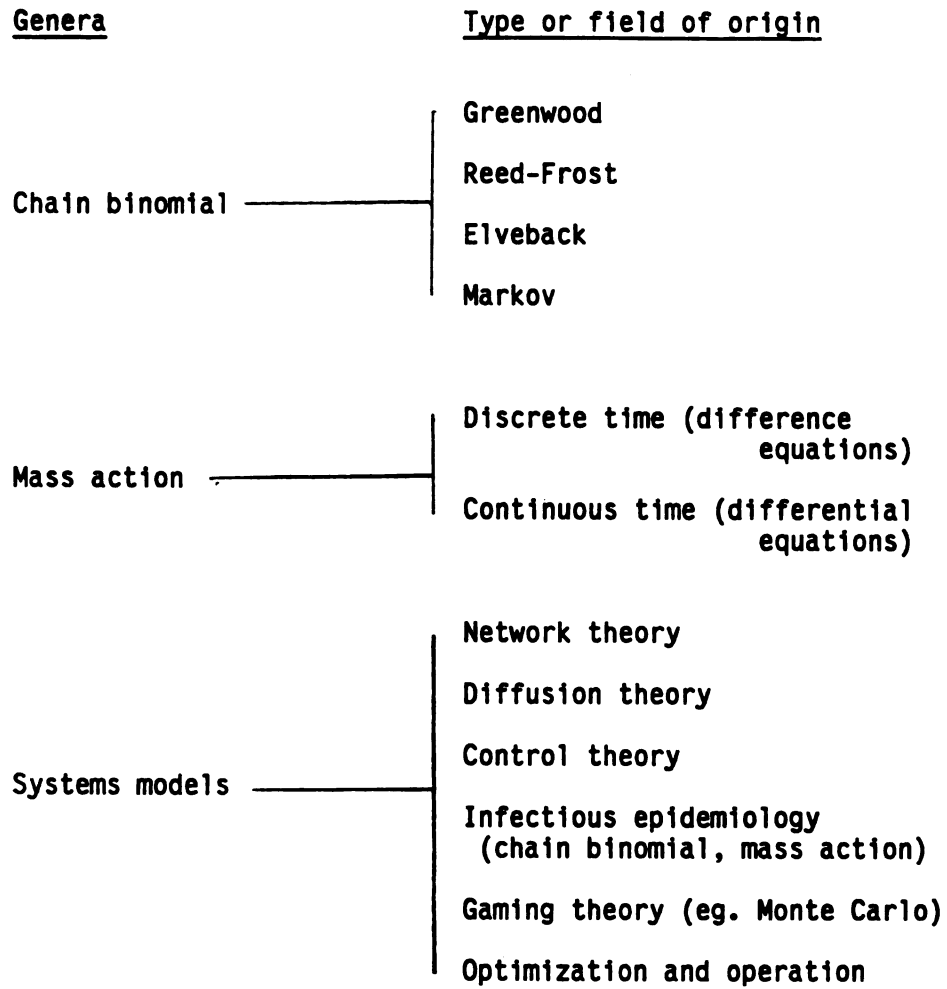


Figure 4.2 Genera of Epidemiologic Process Models

A special case of the chain binomial is the Reed-Frost model where the expected number of cases for the epidemic can be deterministically derived from the recursive formula shown in equation 5.1 (Ackerman *et al.*, 1984). This model is discrete time, and continuous entity. Mathematically it is deterministic but can be made stochastic with computer simulation. It still suffers from the assumption of random mixing, and short, constant length of infectious period.

$$C_{t+1} = S * (1-qC_t) \quad (5.1)$$

where: C = cases, S = susceptible
 $q = 1-p$, p = probability of effective contact

A discrete entity version of the Reed-Frost model resulted in what is often referred to as the Elveback type of model (Ackerman *et al.*, 1984). In this model one individual at a time is processed through a simulation model and randomly infected, with the probability of infection derived from the above equation. These models have the advantage of allowing for heterogeneity of contact and different infection probabilities for each individual. However, they soon become very complicated and computer intensive.

There exists a third genera of models that are not derived from any particular mathematical school of thought. These we might call systems models. These models use whatever mathematical or simulation techniques are necessary to describe the particular system of interest, i.e. whatever works. This may include differential equations (Thrusfield, 1986), Leslie matrices (Kitching, 1983), Monte Carlo theory, and network theory (Paton and Gettinby, 1983). Cohen (1977) calls them hybrid dynamic models when referring to the schistosomiasis models of Nasell (1976a; 1976b) and others (Nasell and Hirsch, 1973), which employ Markov laws along with differential equations. A variety of optimization techniques can also be included (Carpenter and Howitt, 1988). The mass action models and chain binomial models may often be the essential building blocks of the systems models, but modifications are made in order to move away from many of the limiting assumptions, and in order to represent the complexities of the whole system.

The definition of systems analysis or the systems approach may seem to be as broad as the problems it attempts to solve. However, certain consistencies in the various definitions can be found. The essential features are that it 1) is a methodology for solving unstructured problems 2) that begins with a defined set of needs, 3) moves to a description of the whole system as it currently exists, 4) generates alternatives for meeting the expressed needs, 5) evaluates those alternatives with various modelling techniques, and 6) designs and 7) implements the policies found most capable of meeting the needs (Checkland, 1981:161-191; Manetsch and Park, 1982:8-15). The two important attributes are that it "overtly seeks to include all factors which are important in arriving at a "good" solution, and it makes use of quantitative models and often computer simulation in making rational decisions." (Manetsch and Park, 1982:8). Simply put, it is a holistic approach (Martin *et al.*, 1987). Systems models offer the greatest potential for future use as they are not limited by the assumptions of basic infectious disease models (Bailey, 1982; Koopman, 1987). They are also very valuable tools for consideration of the economics of disease and disease control.

It is possible, in most cases, to apply the 6 classification criterion to systems model and thus aid in giving a better description of these systems models. This is important since these models do not easily fit into clear classes. An advantage of the proposed classification scheme is its ability to describe the wide range of models in existence. For example, models that use queuing theory might be described as discrete time, discrete entity, stochastic simulation models (Law and Kelton, 1982).

Classification of applied models

Shown in Table 4.2 is a listing of those publications that were chosen as applied epidemiologic models published since 1970. The table shows only models of the structural process type. The other important characteristics, for each model, are indicated, as well as its general type.

Of the over 200 simulation and mathematical articles reviewed for this paper, only 49 were considered as applied, epidemiologic, structural, process models. Of those, 19 seemed to represent enough complexity and holistic view to be classified as systems models. It is interesting that the majority of the systems type models dealt with veterinary or zoonotic disease problems. This reflects the importance that this approach has for veterinary epidemiology.

Table 4.2 Classification of applied epidemiologic structural process models

Reference	Application	Chance	Time	Entity	Method	Genera
Barret, 1988	hetersex spread of HIV in early epidemics	STOC	DT	DE	SIM	C.B.
Carpenter and Howitt, 1988	determine optimal downtime and head placement for a broiler operation	STOC	CT	DE	SIM	SAM
Dijkhuizen, 1988	evaluate economics of alternatives to vaccination for control of FMD	DETM	DT	CE	SIM	Markov
Oluokun and David West, 1988	evaluate factors controlling CALF MORTALITY in Nigeria, with economic effects	DETM	DT	DE	SIM	SAM
Sorensen, 1988	evaluate economic effects of PNEUMONIA levels in a dairy cattle herd	STOC	DT	DE	SIM	SAM
Tse vat, <u>et al.</u> , 1988	examine alternatives for prevention of TUBERCULOSIS with isoniazid	DETM	DT	DE	SIM	Markov
Anderson, <u>et al.</u> , 1987	evaluate impact of mass vacc. on incidences of MUMPS	DETM	CT	CE	SIM	M.A.
Carpenter, <u>et al.</u> , 1987	economics of control of BRUCELLA OVIS	DETM	DT	CE	SIM	R.F.
Sattenspiel, 1987	analyze spread of HEPATITIS A in day care centers	STOC	DT	DE	SIM	Elve.
Anderson and May, 1986	find important factors for future rends in the HIV epidemic	DETM	CT	CE	SIM	M.A.
Anderson and Greenfell, 1986	impact of vaccination strategy on CONGENITAL RUBELLA SYNDROME (CRS)	DETM	CT	CE	SIM	M.A.
Dijkhuizen, <u>et al.</u> , 1986	economics of culling and	STOC	DT	DE	SIM	SAM
Papoz, <u>et al.</u> , 1986	predict rates of sero-conversion to TOXOPLASMOSIS in a population	STOC	DT	CE	SIM	C.B.
Shonkwiler and Thompson, 1986	study outbreak of TOXOPLASMOSIS	STOC	DT	DE	SIM	SAM
Paton and Gittinby, 1985	evaluate control strategies for <u>OSTERTAGIA</u> in sheep	DETM	DT	CE	SIM	SAM
Longini, <u>et al.</u> , 1985	predict global spread of HONG KONG INFLUENZA	DETM	CT	CE	SIM	SAM

Table 4.2 (cont.)

Ackerman, <i>et al.</i> , 1984	many applied and theoretical models of POLIO and INFLUENZA	STOC	DT	DE,CE	SIM	C.B.
Levy, 1984	determine the effect of MEASLES vaccination program on number of susceptibles	DETM	CT	CE	ANL	M.A.
Anderson and May, 1983	examine impact of different vaccination policies on incidence of MEASLES and CRS	DETM	CT	CE	ANL	M.A.
Hethcote, 1983	cost-benefit analysis of vaccination strategies for MEASLES and CRS	DETM	CT	CE	ANL	M.A.
Smith, 1983	evaluate alternative control strategies for <u>BABESIA BOVIS</u>	DETM	DT	CE	SIM	SAM
Habtemariam and Cho, 1983	determine level of POULTRY INSPECTION for any given farm at slaughter house	DETM	DT	—	SIM	SAM
Paton and Gettinby, 1983	control of OSTERTAGIA in sheep	STOC	DT	CE	ANL	SAM
Croll, <i>et al.</i> , 1982	effectiveness of mass treatment for eradication of <u>ASCARIS LUMBRICOIDES</u>	DETM	CT	CE	SIM	M.A.
Cvjeticanovic, <i>et al.</i> , 1982	cost effectiveness analysis of vaccination programs, MEASLE and POLIO in USA	DETM	DT	CE	SIM	Matrix
Habtemariam, <i>et al.</i> , 1982a	benefit-cost analysis for control of TRYPANOSOMIASIS	DETM	ST	CE	SIM	Matrix
Habtemariam, <i>et al.</i> , 1982b	describe epidemic and endemic characteristics of TRYPANOSOMIASIS	STOC	CT	CE	SIM	SAM
Habtemariam, <i>et al.</i> , 1982c	evaluate disease and vector control strategy of TRYPANOSOMIASIS	STOC	CT	CE	SIM	SAM
Hethcote, <i>et al.</i> , 1982	evaluate 6 prevention methods GONORRHEA control	DETM	CT	CE	ANL	M.A.
Dietz, 1981	determine best method to compute cost for vaccination strategies of MEASLES control	DETM	CT	CE	ANL	M.A.
Kramer and Reynolds, 1981	evaluate 28 control programs for GONORRHEA	STOC	DT	DE	SIM	SAM
Meek and Morris, 1981	evaluate control programs for OVINE FASCIOLIASIS	STOC	DT	DE	SIM	SAM
Carpenter and Riemann, 1980	B/C for eradication of <u>Mycoplasma meleagridis</u>	DETM	DT	CE	SIM	Markov

Table 4.2 (cont.)

Harris, <i>et al.</i> , 1980	identify environmental variables important in the prevalence of HYDATID DISEASE	DETM	DTY	CE	SIM	?
Knox, 1980	predict effectiveness of alternative vaccination policies for CRS	DETM	DT	CE	SIM	SAM
MacDonald and Bacon, 1980	explore effect of vaccination of foxes for RABIES control	DETM	?	?	SIM	SAM
Longini, <i>et al.</i> , 1978	optimum INFLUENZA vaccine distribution among age groups	DETM	CT	CE	ANL	M.A.
Nasell, 1977	test efficiency of sanitation for control of SCHISTOSOMIASIS	DETM	CT	CE	ANL	M.A.
Elveback, <i>et al.</i> , 1976	effect of vaccination for INFLUENZA A in school children	STOC	DT	DE	SIM	Elve
Hugh-Jones, 1976	test effect of milk-lorry borne spread of FMD	STOC	DT	DE	SIM	SAM
Miller, 1976	simulate spread of FMD across the USA	DETM	DT	CE	SIM	Markov
Roe and Morris, 1976	BRUCELLOSIS control in Australia	STOC	DT	DE	SIM	Elve
Horwitz and Montgomery, 1974	effect of underreporting on alternative vaccination programs for MEASLES in USA	DETM	DT	CE	SIM	M.A.
Reynolds and Chan, 1974	evaluate control programs for GONORRHEA	DETM	CT	CE	SIM	SAM
Dietz, <i>et al.</i> , 1974	quantitate different interventions for MALARIA control	DETM	DT	CE	SIM	M.A.
Cvjetanovic <i>et al.</i> , 1973	B/C analysis of sanitation versus vaccination for CHOLERA	DETM	DT	CE	SIM	M.A.
Cvjetanovic, <i>et al.</i> , 1972	B/C analysis of different vaccination programs for TETANUS	DETM	DT	CE	SIM	M.A.
Cvjetanovic, <i>et al.</i> , 1971	B/C analysis of sanitation and mass vaccination for TYPHOID FEVER	DETM	CT	CE	SIM	M.A.
Elveback, <i>et al.</i> , 1971	effect of school closing and vaccination on spread of polio	STOC	DT	DE	SIM	Elve.

? = not enough information to classify

M.A. = mass action

C.B. = chain binomial

M.C. = Monte Carlo, chain binomial

R.F. = Reed-Frost

SAM = systems model

Elve. = Elveback type of chain binomial

HIV = human immunodeficiency virus

FMD = foot and mouth disease

CRS = congenital rubella syndrome

B/C = benefit-cost analysis

DISCUSSION

It is possible that some models considered not to be systems models should have been classified as such. These could be considered as systems models of a very narrow well defined system. For example Carpenter, *et al.* (1987), is a Reed-Frost model where the system might be defined as only the sheep in the simulated herd with the only inputs from the environment being vaccination and price information. As one can see, the differentiation of systems models from the other model types is somewhat debatable. It is however, still a useful distinction. This is particularly true if one considers the historical perspective from which the system modelling approach is derived, as opposed to the mass action and chain binomial models. These latter types of models are derived from models of the dynamics of interactions between individuals, with strict emphasis on the assumptions of infectious disease. By collecting the experiences of individuals they are able to describe a dynamic population. The systems models, on the other hand, begin from the top down in describing the behavior of an unstructured problem. A systems model will use any mathematical, computerized or symbolic means in order to describe the important phenomenon. If a systems model ends up using a mass action or chain binomial model, it is because it is thought to best represent the behavior of that system, although modifications are usually made to reduce the assumptions required. It is not being suggested that systems models have no assumptions, or that they will accurately predict reality. However, if assumptions are made it is because they are not considered to be important, or, lamentably, because the data are lacking. This is in contrast to the other model types which often make assumptions due to mathematical constraints of the base model.

In reference to whether a model should be considered as applied or theoretical the distinction was usually clear. Many articles concluded by saying that the model could be applied to a specific problem, implying that it had not been applied as yet. Some models were obviously theoretical, as they began with another author's model and made certain changes, testing the effects of those changes against an example dataset. There is a much smaller group of articles that seemed to have originated with the intent

of making some epidemiologic conclusions, however, due to lack of data, the authors were forced to conclude that the models could be more valuable, given the appropriate data. It is unfortunate that a great deal of excellent work was excluded with these criteria.

Further research

It is often the case that the modelling exercise brings to light important deficiencies in the available body of knowledge (Martin *et al.*, 1986). The model can be used to demonstrate the importance of the missing data and direct data collection efforts. Model building is an important means of generating and formalizing hypotheses. For this reason, preliminary work in population dynamics and dynamical disease control should begin with model building. This is in contrast to most experimental research that begins with a hypothesis and small data collection efforts (pilot studies), followed by larger efforts ending with analytical model building. A pilot study in population epidemiology should involve model building and testing.

There is need for more data collection efforts generated by systems modelling. Besides the above noted work that was excluded, by lack of data, some of the work cited in table 4.2, was lacking data in some areas. As a result, assumptions were often necessary, and parameter estimates were often extracted from the literature. Even when parameter estimates are available, from current data, they are often assumed to remain constant throughout the simulation period, and are not changed in response to changes in the system being modelled. Another weakness of many parameter estimates has been discussed by Lloyd, *et al.* (1987). This relates to that fact that standards are often used when making decision for a specific situation to which the standards may not apply. Modelling techniques to overcome these shortcomings and develop models that will adjust to specific application are being developed (Lloyd, 1989).

Given the value of systems modelling and the relative paucity of work in this area it is reasonable to conclude that a great deal more work needs to be done in terms of model development and application of current modelling types to specific veterinary problems (Riemann, 1988). It is likely that veterinary epidemiologists should be the

leaders in this area as they commonly deal with populations and the unit of concern is often the herd versus the individual. It is also notable that much of the work is related to the behavior of these populations within the context of the overall production system. Here one can see the need for the systems view of the interactions between the financial system, animal system, and, say, the crop production system. The systems approach is more than a modelling technique, it is a point of view that is essential for the modern practitioner of veterinary preventive medicine, and its development should be encouraged. It is also recommended in the educational curriculum of medical and public health practitioners (Nokes and Anderson, 1988).

CHAPTER 5

Risk factors associated with clinical respiratory disease in Michigan dairy cattle: Analysis of data from the National Animal Health Monitoring System

ABSTRACT

Data from round I of the National Animal Health Monitoring System in Michigan were analyzed with the objective of identification and estimation of the relative importance of various risk factors for clinical respiratory disease in 3 age groups of dairy cattle. A stratified random sample of 60 dairy herds was obtained. Herds were visited monthly to collect data on the incidence of various diseases including clinical respiratory disease. A management survey was completed at the end of the 12 month follow-up period. A general linear regression model was employed to determine variables associated with the incidence density of respiratory disease. A conditional logistic regression was used to estimate odds ratios, with adjustment for confounding and herd size effect. In calves the odds ratio for being born in a multi-animal maternity area was 10.6. Having sand for bedding in the maternity area gave an odds ratio of 2.8 and receiving colostrum through a tube feeding versus nursing resulted in an odds ratio of 1.45. Housing type had no effect in calves. In young stock, which are animals from weaning to first parturition, receiving hay that had been stored outside with no protection slightly increased the risk of disease. In cows the risk of disease was 1.8 times greater if more than 50% of the non-milking, non-field work labor was performed by hired personnel. For cows living in loose housing the risk was decreased.

INTRODUCTION

Respiratory disease plays a significant role in mortality and morbidity experiences of the United States dairy cattle farm (Martin and Wiggins, 1973, Oxender et al., 1973; Curtis et al., 1988a). Most work has focused on disease in calves less than 6 months of age, yet disease in older heifers and adults may still be important. For

example, in the 12 month period of June 1986-July 1987, the National Animal Health Monitoring System in Michigan estimated that approximately 32,000 out of 690,000 young stock, and 9,000 out of 345,000 cows were reported to have some form of respiratory disease or pneumonia (see Chapter 1). A plethora of experimental research data exists on the important factors affecting the physiology of this disease syndrome (Roy, 1979; Yates, 1982; Roth, 1983), and some data exist from cross-sectional study designs. However, only a few prospective, or longitudinal studies of northern dairy states have been conducted (Curtis et al., 1988a). The advantages and disadvantages of these differing study designs have been discussed elsewhere (Dohoo and Waltner-Toews, 1985; Waltner-Toews et al., 1986a).

Evidence from past research has implicated a set of risk factors for respiratory disease which might be classified into 5 general categories, 1) macro-environmental, 2) micro-environmental, or housing related, 3) nutritional, 4) immunological, and 5) management or people related. Macro-environmental factors include season of the year, local weather, and extremes of temperature and humidity. Season is generally thought to effect the incidence of respiratory disease (Martin et al., 1975b; MacVean et al., 1986; Waltner-Toews et al., 1986a; Waltner-Toews et al., 1986b; Curtis et al., 1988b; and others). The specific components of season that cause this effect are still in debate (Yorke et al., 1979). Much of the prior experimental work has been directed at determining the effects of factors such as environmental extremes of temperature and humidity (Elazhary and Derbyshire, 1979; Roy, 1979; Webster, 1981; Collier et al., 1982; Robinson et al., 1983; Jones and Webster, 1984; Dennis, 1986; MacVean et al., 1986; Jones 1987). In addition, MacVean et al. (1986) measured the effect of dust levels on respiratory disease incidence. Seasonal effects are important from an epidemiologic standpoint as possible confounding variables which are associated with the occurrence of disease and the hypothesized risk factors (Rothman, 1986). However, it is reported that the specific effects of weather are difficult to quantify due to the differences in housing effects and the ability of animals to acclimate (Miller et al., 1980).

Experimental studies tend to find housing patterns (micro-environmental) that

reduce weather extremes are generally beneficial (Roy, 1979; Collier *et al.*, 1982; Roe, 1982; Dennis, 1986). Yet the observational evidence is inconsistent as to the positive effects of these housing practices (Hartman *et al.*, 1974; Jenny *et al.*, 1981; Simensen, 1982; Waltner-Toews *et al.*, 1986c; Curtis *et al.*, 1988b). For example, Waltner-Toews *et al.* (1986c) showed that hutches reduced the risk of disease in calves by 25 times compared to those housed inside in individual pens, while Curtis *et al.* (1988b) found that, in the summer, calves housed in hutches had an increased risk of respiratory disease compared to those indoors in group pens.

Micro-environmental risk factors related to the mixing of animals have been implicated. These practices include crowding, and housing of susceptible animals with infected (Waltner-Toews *et al.*, 1986c); although this risk producing effect of the latter is not consistently observed (Hartman *et al.*, 1974; Simensen, 1982). The importance of ventilation has been investigated, with various results (Mihajlovic *et al.*, 1972; Donaldson, 1978; Pritchard *et al.*, 1981), as has the effect of bedding type (Martin *et al.*, 1980; Simensen, 1982; Curtis *et al.*, 1988b).

Of the important nutritional factors, colostrum intake has received the most attention (Gay, 1983). The amount fed and the postpartum time to feeding have been found to be significant (Jenny *et al.*, 1981; Mechor *et al.*, 1987). The most beneficial route of administration is still debatable (Withers, 1952; Speicher and Hepp, 1973; Ferris and Thomas, 1974; Waltner-Toews *et al.*, 1986c; Curtis *et al.*, 1988b). The risk of using milk replacer versus whole milk for calf feeding has received mixed reviews (Oxender *et al.*, 1973; Hartman *et al.*, 1974; Jenny *et al.*, 1981; Simensen, 1982; Waltner-Toews *et al.*, 1986c). Selenium deficiency was shown to have no effect experimentally (Phillippo *et al.*, 1987), but some effect in observational studies (Waltner-Toews *et al.*, 1986c).

Nutritional factors which affect older cattle have been evaluated in beef feedlots. In the feedlot studies, high levels of grain feeding (Wilson *et al.*, 1985), and high and early amounts of corn silage feeding (Martin *et al.*, 1980; Martin *et al.*, 1981; Hutchings and Martin, 1983) increase disease and mortality rates.

The effects of many of the aforementioned risk factors have been hypothesized

to have their effect through immunologic pathways (Roth, 1983). Other factors, such as vaccination, are directly implicated in reducing disease rates or, in some cases, increasing rates (Martin *et al.*, 1980; Martin *et al.*, 1981; Martin, 1983). Some viral pathogens have shown evidence of reducing immune responses (Roth, 1983; Wilke, 1983; Baker *et al.*, 1986; Brown, 1988). These phenomena have not been carefully assessed in field studies of dairy cattle populations.

Management, or people factors, represent effects of uncertain origin that are measured by proxy variables, such as years of dairy experience (Hird and Robinson, 1982), herd size (Martin *et al.*, 1975a; Jenny *et al.*, 1981), or person responsible for feeding calves (Speicher and Hepp, 1973; Simensen, 1982). The causal relationship of these variables to increased risk of respiratory disease is not clear.

The risk factors identified are hypothesized to represent biologically plausible pathways to disease. It is likely that important variables for the dairymen are those that are tangible and economically feasible to alter. Field studies that measure the effects of such factors in real world situations using statistical designs that allow for generalization to other "average" farms in the northern United States should be beneficial. The objective of this paper is to identify and estimate the relative importance of various risk factors for clinical respiratory disease in 3 age groups of dairy cattle using data collected through the National Animal Health Monitoring System in Michigan.

MATERIALS AND METHODS

Herd selection and data collection

As part of the National Animal Health Monitoring System in Michigan round I (1986/87), a random selection of all Michigan dairy herds was obtained for one year of follow-up. A detailed account of the selection of these herds, data collection tools, and the data collected is presented in Chapter 1.

The producer was responsible for most of the diagnoses of respiratory disease, although occasionally the diagnosis was confirmed by the local practitioner or rarely by a diagnostic laboratory. The definition of disease for this study includes cases of

pneumonia and respiratory diseases not otherwise specified.

At the end of the follow-up period an extensive management survey was conducted by a visiting veterinary medical officer (VMO). For many of the questions, the producers were allowed to provide more than one response, since it was likely that more than one type of management practice or housing system might exist on the same farm.

Statistical analysis

Two types of statistical models were employed. A general linear model (GLM) (SAS, 1985: GLM procedure, p. 433) was used where the dependent variable was the annual incidence density (ID) of respiratory disease. Secondly, a conditional logistic regression model (PHGLM, Harrell 1986) was used to estimate odds ratios for important variables determined from the general linear regression model. The odds ratio measures the strength of association between a factor and disease, or the probability of disease given a certain risk factor. For the logistic model the annual incidence density was dichotomized, for each of the 3 different age groups, according to table 5.1.

Table 5.1 Dichotomization of dependent variable (ID) for use in the conditional logistic regression, by age group.

Dependent variable name	Meaning	Age group tested in		
		Calves	Young stock	Cows
DPOS3	annual incidence density (ID) ≥ 3 per 100 animal years			
DPOS4	annual incidence density (ID) ≥ 4 per 100 animal years	+		
DPOS.1	annual incidence density (ID) ≥ 0.1 per 100 animal years		+	+
DPOS.2	annual incidence density (ID) ≥ 0.2 per 100 animal years		+	+

The model building process was a manual form of the stepwise backward elimination procedure. All variables were originally entered into the model. Variables with a high p value, ($P > 0.5$) with the F-test were considered for deletion. If the variable was not expected to be an important confounder, it was deleted. The model was then recalculated. If the p values of the reestimated model differed greatly from the previous model, then the most recently deleted variable was incorporated back to the model. The goal was a model with the fewest number of important variables, resulting in more precise estimates for the remaining variables (Kleinbaum *et al.*, 1982).

The odds ratios of significant variables, from the GLM, were then estimated with a conditional logistic regression model. The conditional estimates were implemented by application of a unique approach to the SAS proportional hazards model for survival analysis (Harrell, 1986). It was thought that this approach was more appropriate given the small sample size and large number of variables being tested (Kleinbaum *et al.*, 1982). The herds were "matched" for herd size stratum, so the results are adjusted for the effect of herd size. Conditional models contained only 2-3 variables; the variable of interest and one or two confounders. The confounders represented non-mutually exclusive responsive to questions that could be classified as one effect. For example, a herd could have calf hutches (HUTCHCAF) and calves in the cow barn (COWBNCAF). The odds ratios estimated for HUTCHCAF would adjust for the fact that the other category (COWBNCAF) may have also been checked on the management survey.

RESULTS

The overall mean unweighted annual incidence densities of respiratory disease for calves, young stock and cows was 3.12, .467, and .19 cases per 100 animal years, respectively. For calves the number of herds coded as DPOS3 (disease positive at ID ≥ 3 per 100) and DPOS4 (disease positive at ID ≥ 4 per 100) are 17 and 11 respectively. For young stock the number of herds coded as DPOS.1 (disease positive at ID ≥ 0.1 per 100) and DPOS.2 (disease positive at ID ≥ 0.2 per 100) were 18 and 10, respectively; for cows the numbers were 19 and 10 for DPOS.1 and DPOS.2.

The variables originally tested in the GLM models are shown in Tables 5.2 and 5.3. The frequency of positive responses to categorical variables and means for continuous variables are also shown in these tables.

Table 52 Variables tested in general linear model (GLM) for effect on the annual incidence density of respiratory disease in COWS and YOUNGSTOCK (number of positive responses, or mean).

Variable name	Meaning of the variable	Age grp. tested in	
		Cows	Young stock
STRAT*	herd size stratum, 1 = 10-49 cows(17), 2 = 50-99(19), 3 = 100-199(8), 4 = $\geq$ 200(4)	+	+
DAIRYEXP	total years of dairy experience of primary herdsman(27.4)	+	+
FARMPLAN*	plans for the farm in the next year, 1 = expand(9), 2 = stay same(33), 3 = decrease size(1), 4 = sell(1), 5 = other ownership transfer(4)	+	+
MHIREPOS*	$\geq$ 50% of milking is done by hired non-family labor (n = 9)	+	+
OHIREPOS*	$\geq$ 50% of non-field work is done by hired labor (n = 11)	+	+
CAVFAC*	type of calving facilities, 1 = multi animal maternity pen - MULTMATN only(22), 2 = individual calving pens = INDVSTAL only(19), 3 = both MULTMAIN and INDVSTAL(3), 4 = neither = calving with dry or lactating cows(4)	+	
HAYSTOROUT*	hay stored outside uncovered (n = 13)	+	+
HSTORIN*	hay stored inside (n = 37)	+	+
HAYSTORCOV*	hay stored outside but covered (n = 2)	+	+
HAYPROP	proportion of total forage fed on that farm that is dry hay (24%)		+
HLPROP	proportion of total forage that is haylage (42%)		+
SCPROP	proportion of total forage that is corn silage (33%)		+
STANCHCHL*	cows housed in stanchions(2)	+	
STANCHYS	young stock housed in stanchions(8)		+
LOOSECL*	cows housed in loose housing(9)	+	
LOOSEYS*	young stock housed in loose housing(22)		+
FSTALLCL*	cows housed in freestalls(25)	+	
FSTALLYS*	young stock housed in freestalls(9)		+

*Class variables.

Table 53 Variables tested in general linear model (GLM) for effects on the annual incidence density of respiratory disease in CALVES (number of positive responses, or means).

Variable	Meaning of the variable
STRAT*	herd size stratum, 1 = 10-49 cows(17), 2 = 50-99(19), 3 = 100-199(8), 4 = ≥ 200 (4)
DAIRYEXP	total years of dairy experience of primary herdsman(27.4)
FARMPLAN*	plans for the farm in the next year, 1 = expand(9), 2 = stay same(33), 3 = decrease size(1), 4 = sell(1), 5 = other ownership transfer(4)
MHIREPOS*	$\geq 50\%$ of the milking is done by hired non-family labor (n = 9)
OHIREPOS*	$\geq$ of non-milking, non-field work is done by hired labor (n = 11)
CAVFAC*	type of calving facilities, 1 = multianimal maternity MULTIMATN(22), 2 = individual calving pens INDVSTAL(19), 3 = both MULTIMATN and INDVSTAL(3), 4 = neither calving with dry or lactating cows(4)
BEFCAV*	cow stays in maternity area ≥ 3 days before calving (n = 16)
DISINF*	use of disinfectants to wash maternity area, for those that do wash the maternity area at least once per year (n = 13)
STRAWBED**	use of straw for bedding in maternity area (n = 40)
SANDBED*	use of sand for bedding in maternity area (n = 2)
CORNBED*	use of corn fodder for bedding in maternity area (n = 2)
SAWBED*	use of sawdust for bedding in maternity area (n = 13)
COLSBOTL*	first feeding of colostrum delivered by bottle feeding (n = 40)
COLSTUBE*	first feeding of colostrum delivered by tube feeding (n = 3)
COLSNURS**	first feeding of colostrum delivered by nursing dam (n = 23)
MILKREPL*	frequency of use of milk replacers versus whole milk 1 = $\leq 10\%$ of the time(16), 2 = 10-25%(1), 3 = 25-50(6), 4 = 50-75%(4), 5 = $> 75\%$ (19)
HUTCHCAF*	calves housed in individual hutches (n = 14)
COWBNCAF*	calves housed in same barn as cows (n = 17)
CAFBNCAF**	calves housed together in separate barn for calves only (n = 26)

*Class variables.

**Variable dropped from model to prevent singularity with remaining variables.

The variables in the final GLM model odds ratios for selected variables, are shown in Tables 5.4- 5.6. For those variables with estimated odds ratios, the variables that were included in the conditional logistic model are shown with their associated beta values and standard errors. These are shown so that an odds ratio could be estimated for a herd that was positive for the variable of interest as well as one of the confounders.

Table 5.4 Variables in the final GLM model for respiratory disease in CALVES.
Conditional odd ratios for interesting variables, adjusted for herd size strata.

Variables	F value (df)	Pr>F	Odds Ratio (CI*)	Confounding variables used when estimating OR****
STRAT	1.65 (3)	.198	NE**	
OHIREPOS	.34 (1)	.565	2.8 (.86, 9.0)	MHIREPOS ($\beta = .09$, SE = .88)
CAVFAC	6.32 (3)	.002		
MULTMATN only***	.18 (1)	.67	10.6 (1.98, 52.8)	INDVSTAL ($\beta = 1.04$, SE = .855)
INDVSTAL only***	9.44 (1)	.0044	2.8 (.70, 11.6)	
BEFCAV	1.02 (1)	.320	.32 (.09, 1.09)	MULTMATN ($\beta = 3.0$, SE = 1.2), INDVSTAL ($\beta = 1.28$, SE = .96)
HUTCHCAF	2.23 (1)	.145	1.85 (.61, 5.6)	COWBNCAF ($\beta = .54$, SE = .98)
COWBNCAF	2.53 (1)	.1217	.58 (.12, 2.9)	HUTCHCAF ($\beta = 0.6$, SE = .67)
SANDBED	16.77 (1)	.0003	2.8 (.49, 17.1)	none included
CORNBED	.03 (1)	.871	NE	
SAWBED	.52 (1)	.472	NE	
DISINF	4.73 (1)	.037	.37 (.063, 2.15)	none included
COLSBOTL	.6 (1)	.44	NE	
COLSTUBE	5.58 (1)	.0247	1.45 (.30, 7.0)	COLSBOTL ($\beta = .46$, SE = 1.08)

* 90% confidence interval.

** NE = not estimated.

*** the effect of that variable is contrasted against all others in the CAVFAC effect.

**** shown with associated coefficients (β) and standard errors (SE).

Table 5.5 Variables in the final GLM model for respiratory disease in YOUNG STOCK. Conditional odd ratios for interesting variables, adjusted for herd size strata.

Variables	F value (df)	Pr>F	Odds Ratio (CI*)	Confounding variables used when estimating OR***
STRAT	.83 (3)	.48	NE**	
HSTORIN	2.08 (1)	.16	NE	
HSTOROUT	3.53 (1)	.07	1.52 (.50, 4.6)	HSTORIN ($\beta = .12$, SE = .71)
HSTORCOV	1.92 (1)	.17	NE	
HLONLY	2.38 (1)	.13	NE	
STANCHYS	.40 (1)	.52	NE	
LOOSEYS	1.84 (1)	.18	.79 (.25, 2.4)	STANCH ($\beta = .32$, SE = .84), FSTALL ($\beta = .32$, SE = .86)
FSTALLYS	.91 (1)	.34		
OHIREPOS	1.11 (1)	.29		

* 90% confidence interval.

** NE = not estimated.

*** with associated betas (β) and standard errors (SE).

Table 56. Variables in the final GLM model for respiratory disease in COWS. Odds ratios for interesting variables, adjusted for herd size strata.

Variables	F valve (df)	Pr>F	Odds Ratio (CI*)	Confounding variables used when estimating OR****
STRAT	.94 (3)	.43	NE*	
CAVFAC	3.75 (3)	.02		
MULTMATN***	.94 (1)	.34	17 (.39, 7.3)	INDVSTAL ($\beta = 1.45$, SE = .97)
INDVSTAL***	.94 (1)	.34	4.3 (.86, 21.18)	MULTMATN ($\beta = .53$, SE = .88)
STANCH	1.98 (1)	.17	2.9 (.83, 10.3)	none included
LOOSE	2.92 (1)	.09	.87 (.22, 3.4)	none included
FSTALL	.02 (1)	.90	NE	none included
CSPROP	2.64 (1)	.11	NE	
OHIREPOS	6.61 (1)	.014	1.8 (.47, 1.9)	MHIREPOS ($\beta = 1.03$, SE = 1.18)
MHIREPOS	1.62 (1)	.21	NE	
DAIRYEXP	1.57 (1)	.22	NE	

* 90% confidence interval.

** NE = not estimated.

*** the effect of that variable is contrasted against all others in the CAVFAC effect.

**** with associated coefficients (β) and standard errors (SE).

DISCUSSION

It is difficult to compare the reported disease frequencies in this paper with previous reports as they represent a mean rate which may not be the best measure of central tendency for a skewed distribution (Curtis *et al.* 1988a). Also it is difficult to compare frequencies if they are computed in different manners. For example, Waltner-Toews *et al.* (1986a) reports the frequency of pneumonia to be 14%, this represents the risk per 100 live born calvings and not an incidence density. A more

comparable reporting of monthly incidence densities is reported as approximately 8% (Waltner-Toews *et al.*, 1986b). The rate of 7.4 reported by Curtis *et al.* (1988a) seems to represent a six month risk or the rate per 100 half years, since the denominator reflected the number of animals at risk during the designated 6 month season.

The effect of having hired personnel (OHIREPOS) caring for the animals had no significant impact on the occurrence of respiratory disease in calves (Table 5.1). This is somewhat of a contrast to previous reports; however, these reports were focusing on calf mortality versus incidence of respiratory disease (Withers, 1952; Oxender *et al.*, 1973; Hartman *et al.*, 1974). More recent reports from, prospective studies, have agreed with this paper and shown no effect of the person caring for calves (Simensen, 1982; Waltner-Toews *et al.*, 1986c). The effect of this factor in cows was significant ($p = .014$), but not in young stock. This factor has not been previously studied in animals older than calves.

The effect of type of calving facilities (CAVFAC) was important with respect to disease incidence in calves. This is not surprising, as it has been reported that cleanliness (Simensen, 1982) and the ability to receive adequate colostrum are important to calf health. The estimated odds ratio for multi-animal maternity facilities (MULTMATN) in calves was 10.6 (significant, $p < 0.1$). This risk enhancing effect of multi-animal or group calving pens has been observed elsewhere (Ferris and Thomas, 1974; Curtis *et al.*, 1988b). It is interesting that, in the GLM model, having individual calving stalls only (INDVSTAL) significantly reduced the rate of disease. In the logistic model, however, the variable INDVSTAL did not have an odds ratio significantly different than 1.0. The conclusions are the same with both models; that MULTMATN increase the risk of disease and INDVSTAL does not.

Whether or not MULTMATN produces a risk in adult cows is debatable (OR=1.7), however the variable CAVFAC (in GLM) did have a significant ($p = 0.02$) effect on the annual incidence density of disease in the cows.

The effects of housing are not conclusive for any of the three age groups, although some trends can be suggested. HUTCHCAF had some tendency to increase disease in

calves, and housing of calves with the cows seemed to prevent disease. Housing of calves in the stanchion with the cows has been reported to decrease mortality (Oxender *et al.*, 1973; Speicher and Hepp, 1973). Loose housing (LOOSE) had some effect at decreasing disease in cows. The reason is not clear since one might expect freestalls to be as well ventilated as loose housing.

In youngstock the variable HAYSTOROUT contributed significantly ($p = 0.07$) to variation in the incidence density and had an odds ratio of 1.52 with a confidence interval (.50, 4.6) that tended to be greater than 1.0. The hypothesis is that hay which is stored outside and is uncovered is of less nutrient value than protected hay, thereby increasing an animals risk for disease and might be more susceptible to molds. This should be investigated further.

In calves, it is interesting that DISINF tended to be protective for respiratory disease. It is not clear how occasional disinfection of the maternity area would prevent the spread of respiratory disease. Most likely, this variable reflects the overall quality of farm management which might tend to reduce disease. The pernicious effect of COLSTUBE in calves, which was shown here, has been reported elsewhere (Waltner-Toews *et al.*, 1986d).

Most of the odds ratios that were estimated had 90% confidence intervals that included 1.0. Some might judge these variables as "insignificant." However, it is possible that with a larger sample size, these variables would have become "significant." The fact that the variables were "significant" in the GLM model suggests that the estimated odds ratios are valuable but not as precise as could be estimated with more data.

The use of the general linear model, which is simply a linear regression that automatically creates dummy variables for categorical factors, is justified even though the dependent variable (ID) was not distributed normally. If distribution of the errors or residuals is normal, then the model is acceptable (Neter and Wasserman, 1974). The distribution of residuals was checked for all three final models, with PROC UNIVARIATE (SAS, 1985), and found not to be deviated from normality ($p < 0.02$).

The slightly different results obtained between the GLM and the conditional

odds ratio can be explained by differences in coding of the dependent variable. In GLM the dependent variable was continuous and as much information as possible is derived from any observation whereas dichotomization (DPOS) of the incidence rates tends to reduce the amount of information derived from an observation. Also the fact that the PHGLM used a data set that was assumed to be "matched" for herd-size strata, reduced the effective sample size and decreased the chances of finding a "significant" result.

The use of conditional estimation accounts for the fact that the small sample size and large number of variables precludes the use of parametric tests such as the Chi square. The procedure is an iterative maximum likelihood estimation that assumes the marginal totals are fixed for each stratum. This is similar to the Mantel-Haenszel procedure and gives asymptotically similar results. It is generally observed that unconditional estimates tend to overestimate the odds ratios for small sample sizes, compared to conditional (Kleinbaum et al., 1982:492-503). Therefore, the odds ratios reported in this paper may be smaller than those that would result with the use of unconditional estimation on a larger data set.

The NAHMS data are generally evaluated relative to the quality of the disease rates and costs that are estimated. If the purpose of the NAHMS is strictly estimation of the incidence and costs of endemic diseases, (Glosser, 1988) then these data, from the Michigan project, were relatively useful. However, for purposes of risk factor elucidation and estimation of the relative effect of various factors, some shortcomings were noted. A fairly large amount of data were collected on the dependent variable, incidence density of respiratory disease, but a limited amount of data were available for possible risk factors, or independent variables. The presence of most risk factors was determined by the one time management survey. In Michigan, individual cow data were available and could have been analyzed, but this was not available for calves and youngstock. Also, in this project, data on the occurrence of disease and animals inventories was collected monthly, but no monthly data were collected regarding the presence of possible risk factors. The sample size, of only 48 usable herds, resulted in estimates risk factors that appeared important, but were not statistically significant.

In order for the National Animal Health Monitoring System to provide a valid database for epidemiologic efforts beyond descriptive statistics (Farrar, 1988) some areas could be strengthened by: 1) beginning the project with a narrowly defined disease syndrome to be analyzed, and a clear set of hypotheses to be tested, 2) collecting input or risk factor data concurrently with output or disease frequency data, 3) providing for standardization of input, as well as output data, to allow for aggregation of data across states and data collection rounds, 4) considering individual animal identification where appropriate, and 5) developing dynamic analytical techniques to evaluate the implications of the project's findings in reference to disease control and economics (Riemann, 1988). All of these activities could still be implemented within the broad scope of disease frequency and cost estimation.

CHAPTER 6

A Stochastic distributed delay model of disease processes in dynamic populations

ABSTRACT

A simulation model that is applicable to infectious and noninfectious disease is proposed. The objectives of this paper are to describe a model for simulation of infectious and noninfectious disease processes in dynamic populations using a distributed delay (DDEL) approach, and to compare its behavior to a stochastic version of the Reed-Frost model, for a hypothetical infectious disease. This model represents the main theoretical subunit of an applied model to be discussed in a subsequent paper.

The distributed delay as an aggregate approximation of the transitions of individuals through multiple disease states. The average waiting time until disease occurrence and time to recovery from disease are the delay (DEL) parameters used in the model. The ability of the distributed delay to simulate the stochastic nature of these waiting times is investigated, and the epidemic threshold theorem is applied in the model.

Monte-Carlo simulations of both modeling approaches were run to produce epidemics of randomly determined sizes. Both models demonstrated the characteristic bimodal distributions of total number of cases per epidemic, although the shape of the distributions was slightly different.

INTRODUCTION

Epidemiologic simulation models can be generally categorized into mass action, chain binomial, and a general group of models resulting from the systems approach (Chapter 4). Most applications of simulation modeling of epidemiologic problems have been to project the course of infectious diseases. This is probably due to the fact that both the mass action and chain binomial models are based on the premise of

interactions between infectious and susceptible individuals being the driving force for dynamic phenomenon. The basic mass action equations for the susceptible, infected, recovered (SIR) model are shown in equations 6.1 - 6.3.

$$\frac{dS}{dt} = -\beta \cdot S \cdot I \quad (6.1)$$

$$\frac{dI}{dt} = \beta \cdot S \cdot I - \gamma \cdot I \quad (6.2)$$

$$\frac{dR}{dt} = \gamma \cdot I \quad (6.3)$$

where:

- S = # susceptible or nonclinical
- I = # infected or clinically ill
- R = # recovered
- β = infectivity parameter
- γ = recovery parameter

One can see that the incidence rate (dS/dt) is a function of some interaction, defined by β , between the infected and susceptible individuals. The exact epidemiological meaning of this β term is not clear (Fine, 1982). It has been called the "infectivity", the "transmission coefficient", and the "transmission rate", and the "force of infection". If one assumes completely random and homogeneous mixing between individuals, this β parameter reflects a characteristic of the disease agent regarding its ability to spread between individuals, with or without direct contact (Riley, et al., 1978).

A commonly employed type of chain binomial model, the Reed-Frost model, is shown in equation 6.4. The meaning of p , in this equation, represents the probability of effective contact. The assumption is that contact will always result in transmission of disease, hence it reflects two separate and unrelated phenomenon, the mixing characteristics of the population and the transmissibility

or infectivity of the organism. The Reed-Frost model also assumes that the infection duration is relatively short, one time period, and that a single attack of disease produces lasting immunity (Abbey, 1952).

$$I(t+1) = S(t) * [1 - (1-p)^{I(t)}] \quad (6.4)$$

where: p = probability of effective contact

S = # susceptible or nonclinical

I = # infected or clinically ill

A model applicable to infectious and noninfectious disease is proposed. The objectives, of this paper, are to use a distributed delay (DDEL) model for simulation of infectious and noninfectious disease processes in dynamic populations and to compare the model's behavior to a stochastic version of the Reed-Frost model, for a hypothetical infectious disease. This model represents the main theoretical subunit of an applied model to be discussed in Chapter 7.

MATERIALS AND METHODS

Disease process as a distributed delay

The process of disease occurrence for infectious disease, parasitic disease (Cohen, 1977), or for cancer, can be viewed as a set of multiple transitions from one state of development to the next. For example, cancer development, can be seen in terms of initial onset of disease resulting from some exposure, followed by progression to clinical manifestations, followed by death or recovery (Morrison, 1979). Infectious disease can be viewed as the movement from the state of susceptibility, to latency, to incubation, to clinical infection, to recovered, dead, or immune as shown in Figure 6.1 (Nokes and Anderson, 1988).

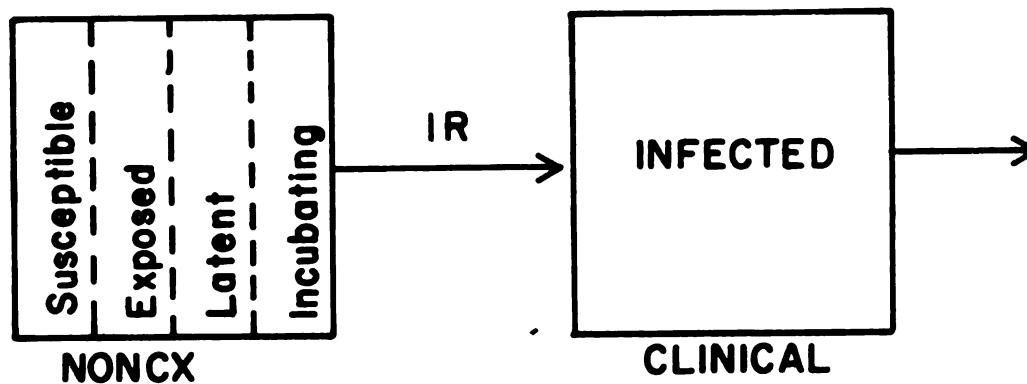


Figure 6.1 Infectious disease application of the proposed distributed delay model. NONCX = Nonclinical state, CLINICAL = diseased

These transitions can be observed within a population as various rates; for example, the clinical incidence rate (IR) represents the movement from the nonclinical state to the clinically affected state, the seroconversion rate represents movement from the latent to the immune state. The experiences of a single individual within this population can be represented as a queuing process where the transition from one state to the next is accomplished at some sort of a "server" (Ross, 1985). This is analogous to shopping in a supermarket, where an individual may go to a number of random servers such as the meat service counter, wait to be served, then move to the produce department, and finally the checkout stand. The time to exit from the store, or total shopping time, is the sum of the waiting and service times (random delays) at each server. If one is observing the exit rate of a large number of people from the shopping center, measurement of the exit rate represents an observation of the average shopping time for the average individual, which is the aggregate of a number of separate waiting and service times that occurred at each server. For an infectious disease, these transitions might involve the waiting time to exposure, the event of exposure, the time in the latent state, the incubation period, and finally transition or "exit" to the clinically infected state (Bartlett, 1953). The transition to clinically infected is termed an exit

because it is this transition that is readily observable in a population, ie the incidence rate of clinical disease. Commonly, the first set of transitions, before infection, is not observable and can be viewed as one aggregate state, like the shopping center.

Since the disease experience in a population can be viewed as a process of multiple individuals moving from server to server (state to state), a continuous time model which simulates this process should be beneficial. This model should adequately reflect the random process of delay at each server, for each individual, and the experience of movement through multiple servers. The distributed delay has been shown to be appropriate for representing a variety of aggregate stochastic processes (Manetsch, 1966). Given the probability density function and the average waiting time (DEL) for the aggregate process, we can simulate it with a distributed delay.

The distributed delay used in this simulation model is an Euler numerical integration (Hamming, 1962) of the k^{th} order differential equation shown in equation 6.5. The Quick Basic (Microsoft, 1988) subroutine for simulating this equation with time varying delay and proportional losses is shown in Appendix C. This model is useful for representing a wide variety of processes such as the maturation process (Plant and Wilson, 1986), diffusion of ideas (Manetsch, and Park, 1977), many entomology simulation models (Kitching, 1983), and transitions between different disease states. Many different delays can be linked together as long as there is information to parameterize them, ie to set the delay and the k .

$$a_k \frac{d^k y(t)}{dt^k} + a_{k-1} \frac{d^{k-1} y(t)}{dt^{k-1}} + \dots + a_1 \frac{dy(t)}{dt} + a_0 y(t) = x(t) \quad (6.5)$$

$x(t)$ = the input at time t
 $y(t)$ = the output at time t
 k = the order of the defining differential equation
 a_k = the k specific parameter defining the response of $y(t)$ to $x(t)$

The model proposed in this paper, consists of 2 distributed delays in series, (Figure 6.2). The first distributed delay, NONCX (nonclinical), represents

individuals in a population susceptible to clinical disease. The second distributed delay, CLINICAL, represents individuals diagnosed, by clinical signs, to have the disease. The rate of movement between the two populations is measured by the incidence rate (IR). After a certain amount of time in CLINICAL, individuals are removed from this state. At this time they may be immune, dead or susceptible again. These susceptible could cycle back into the first distributed delay and become repeat cases or go to other states. This option was not implemented in this chapter in order to provide a comparison to the Reed-Frost SIR (Susceptable, Infected, Recovered) model (Ackerman, *et al.*, 1984).

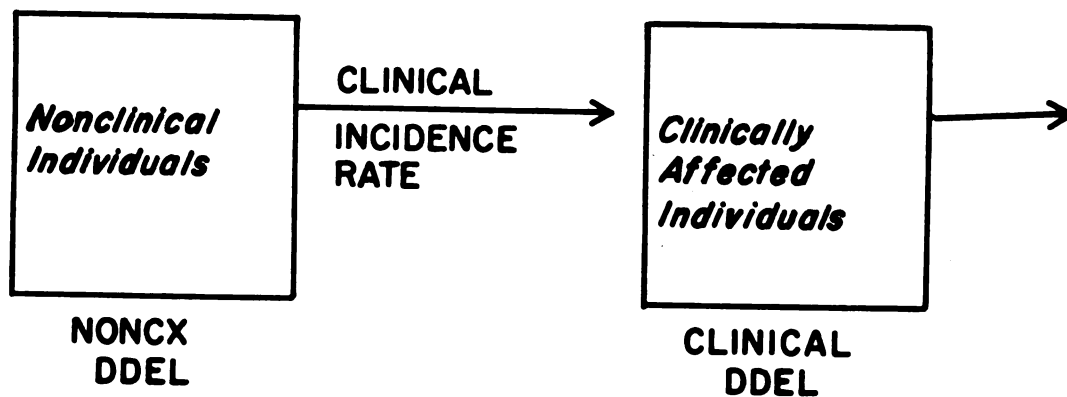


Figure 6.2 Schematic diagram of proposed distributed delay model for infectious and noninfectious diseases. NONCX = nonclinical

The average time individuals spend in CLINICAL is the average duration of disease (IDUR) which represents the delay (DEL) for that distributed delay. The average time in NONCX is the delay (DEL) for that state. Calculation of this DEL, for an infectious disease will be discussed.

The use of the distributed delay for the CLINICAL state has been proposed by others (Hethcote, *et al.*, 1981; Hethcote and Tudor, 1980), however its

application to the susceptible or nonclinical disease state (NONCX) has not been attempted. This application has the advantage of being useful for modelling infectious as well as noninfectious diseases in populations. This works even if the rate of transitions between various states, within NONCX, is not observable. The stochastic processes of multiple individuals moving through multiple states, or arriving at multiple servers can be realistically approximated by a distributed delay.

Estimation of the output distribution

The magnitude of k determines the distribution of the output. If, for example a group of individuals were simultaneously added to a distributed delay, the deterministic output for different values of k , but the same average delay (DEL) is shown in Figure 6.3 (Manetsch and Park, 1972). Figure 6.3 shows the family of Erlang distributions which can be represented by a distributed delay. Determination of the best value of k to use for a particular application can be a difficult issue, unless one can make observations on a number of individuals simultaneously entering NONCX, all of whom are known to be susceptible and in the same stage of disease development. The shape of the output for a constant DEL will indicate the best k to use.

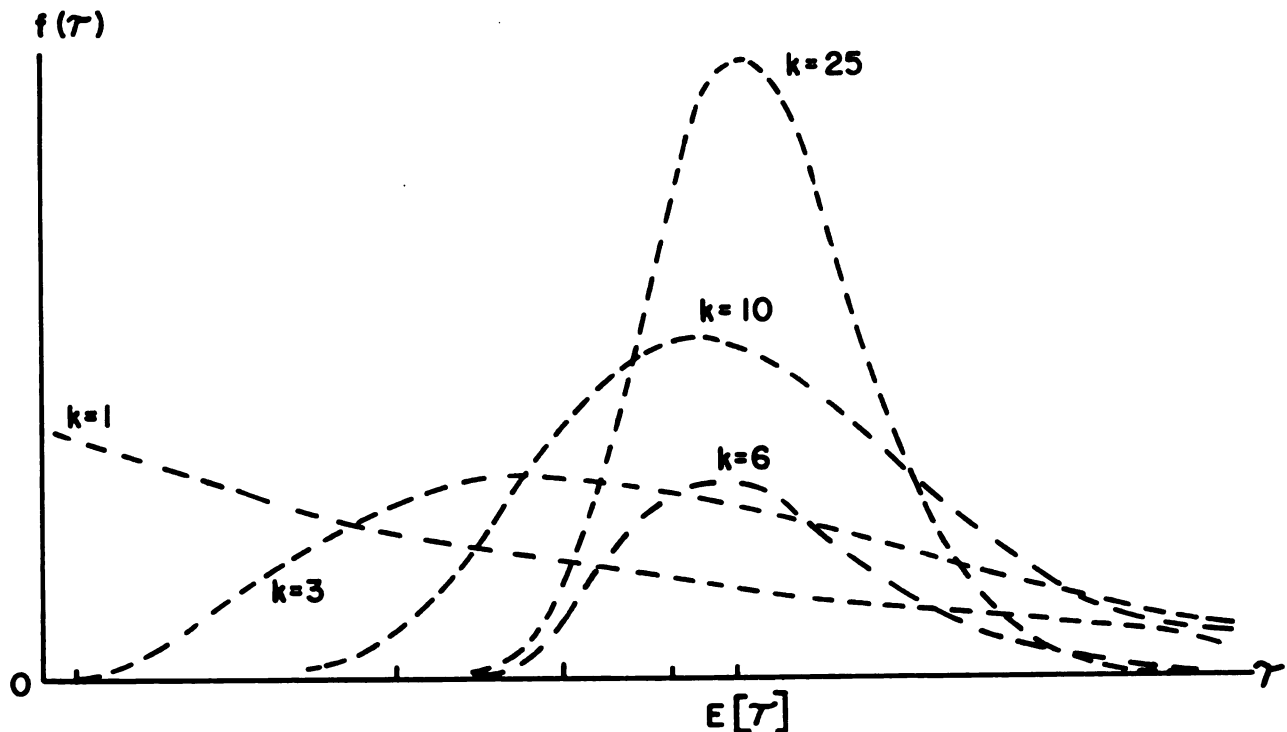


Figure 6.3 Family of Erlang distributions for waiting times to exit, which can be represented with a distributed delay. $E[\tau]$ = average waiting time to exit. (Manetsch, 1966)

For a hypothetical population of known healthy people, Rothman (1986) has shown that the time between deaths is exponentially distributed with mean $1/IR$ (IR = incidence rate). This is equivalent to a $k=1$ distributed delay, with unit input. This would be analogous to a single stage server where each person was assured the event, death, and the only thing that was random is the waiting time to exit. These waiting times, are generally assumed to be an exponentially distributed random variables (Ross, 1985). Most diseases usually involve multiple transitions, or visits to exponential servers, so that $k=1$ is not universally appropriate. The sum of multiple exponential distributions is an Erlang distribution, if all waiting times are equal (Law and Kelton, 1982), or gamma if the waiting times are different.

It should be noted that the distribution being approximated is not the epidemic curve, but the distribution of waiting times until exit from the NONCX state if

a number of individuals enter simultaneously.

For the second delay, CLINICAL, the distribution can be defined by estimating the shortest and the longest time that an individual might stay in this state given assumptions of the average infection duration. Three combinations of $k=1$, $k=6$, $k=20$ were evaluated, in the model, for each state CLINICAL and NONCX.

Estimation of DEL

The Incidence rate (IR) or density (ID) represents the average waiting time until disease occurrence, for a steady state dynamic population, or a fixed size population with complete follow-up (Morrison, 1979; Rothman, 1986). The ID is calculated as (sum of cases/ sum of observation time periods for all individuals). Therefore, the inverse of the IR, theoretically, will provide the needed DEL for the NONCX distributed delay. Since the units of the ID are the reciprocal of time, the delay is expressed in those time units. For example, if an IR is reported as cases per animal years, the DEL is expressed in average number of years an animal is expected to spend in the NONCX state. It is important that the method used to calculate the IR's are appropriate to the time frame of the model (Hurd and Kaneene, 1989a).

The mathematical relationship, between DEL for NONCX and the IR can be used to derive an equation to generate a time varying DEL for infectious disease models. In this case, the incidence rate, or number of new cases per time unit is defined by the relationship between the number of infectious individuals, and the infectivity (β) as in the mass action and chain-binomial models. For the distributed delay model proposed in this paper it is necessary to derive an equation for computing a DEL in the same manner. It is stated that for the mass action model $IR = \beta * S(t) * I(t)$, and for the Reed-Frost or binomial models $IR = C_t + 1/S(t) = 1 - (1-p)^{I(t)}$. For small values of p and/or large populations, the Reed-Frost and mass action models are essentially equivalent (Fine, 1982), but the Reed-Frost performs better for small populations ($n < 40$) (Bailey, 1955). Therefore we

can derive a method for computing the delay at time = t , $DEL(t)$, as a function of the number of infectives at time= t , $I(t)$, by using the Reed-Frost model. As shown in equation 6.6, the waiting time (DEL) will decrease as the number of infecteds increase, hence more individuals will get sick faster, producing the classic epidemic curve. The probability of effective contact (p), from the Reed-Frost model is not used in equation 6.6, as it is not clear that β has the same properties as p .

$$DEL(t) = \frac{1}{1-(1-\beta)^{I(t)}} \quad (6.6)$$

Epidemic threshold theorem applied

An important phenomenon of infectious disease process is the epidemic threshold theorem (McKendrick, 1926; Becker, 1979; Fine, 1982). This theorem states that for an epidemic to progress, the probability of infection must be greater than the probability of recovery, ie. the odds of a new case should be greater than 1. A certain number of suseptibles is required to meet this condition, this number, or threshold, is determined by the ratio of the recovery rate (γ) to the transmission factor (β) such that $S(t) < \gamma/\beta$, where the recovery rate (γ) is the inverse of the infection duration (IDUR). If γ and β are constant characteristics of the disease, the demise of an epidemic is the result of a decrease in the number of suseptibles, not in a decrease in number of infectives. This relates to the concept of herd immunity that suggests adequate vaccination should proceed to the point where the number of suseptibles is less than $1/\beta$ (Fox, et al., 1979). This threshold theorem has been shown to be applicable to continuous or discrete time mass action models (McKendrick, 1926; Fine, 1982) as well as non-Markovian and Markovian continuous time models (Becker, 1979).

Simulation of this phenomenon is straightforward with the Reed-Frost model. The computer program is equipped with a stopping rule that causes the process to stop if there are no new cases produced at time $t+1$, $C_{t+1} = 0$. For

continuous time mass action models the conditions for epidemic shut off have been mathematically established, but an equivalent expression is needed for the distributed delay model. Mathematically the continuous mass action model predicts an increase in the incidence as long as the $S(t) > \gamma/\beta$ (Fine, 1982). The determination of an equivalent expression, for this threshold, that is pertinent to the distributed delay model of disease is shown in equation 6.7.

$$\frac{dI}{dt} = 0, \text{ when } \beta \cdot S \cdot I = \gamma \cdot I \quad (6.7)$$

Introduction of stochasticity

Stochastic versions of both the mass action and chain binomial models have been studied (Bailey, 1975; Ackerman, et al., 1984). Most of the mass action stochastic models have studied the number infected or susceptible individual as the random variable and sought analytical solutions to the equations. The Reed-Frost simulation model used in this paper generates a uniformly distributed random number for each susceptible, at each iteration. This random number (RND) is then compared to the current probability of escape $q(t) = (1-p)^{I(t)}$. If RND is greater than $q(t)$ then a new case is added.

In the proposed distributed delay model, stochasticity is implemented by allowing the beta (β) to vary randomly. This represents the uncertainty in the value of β as well as the random error for any individual in a population. The model was run with a triangular distribution as shown in Figure 6.4 or an exponential distribution assigned to the β . The effects of different distributions on the number of infective contacts along with more rigorous mathematical theory are discussed elsewhere (Dietz and Schenzle, 1985).

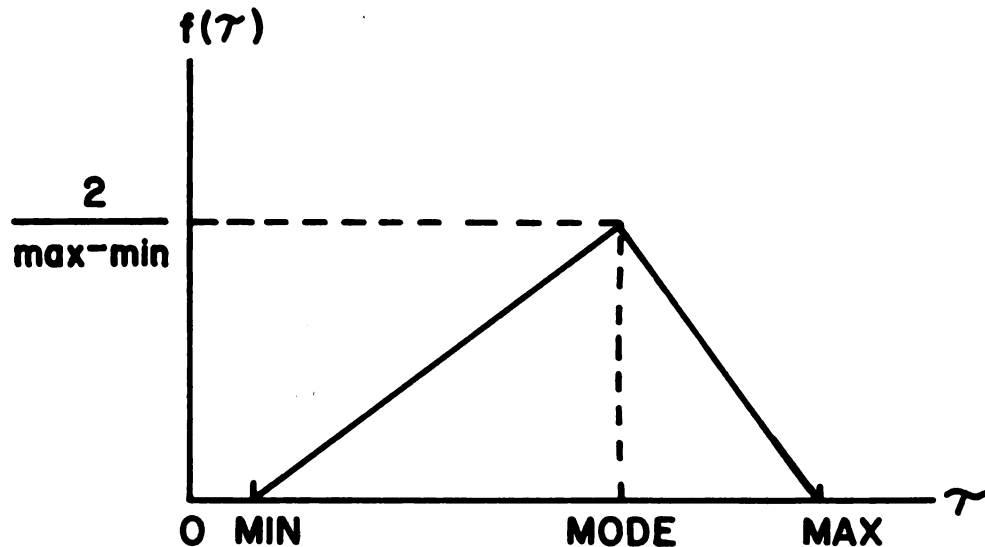


Figure 6.4 Triangular distribution assigned to β . The minimum (MIN), maximum (MAX), and MODE must be defined.

Model comparisons

The Reed-Frost computer model outlined in Ackerman, *et al.* (1984), page 34 was compared to the proposed distributed delay model. Monte-Carlo runs of the models were implemented for 100 epidemics. Different values for p , in the Reed-Frost, and distributions of β , for the distributed delay model were compared. The goal was to reproduce the characteristic frequency distributions of total number of cases per epidemic observed with the Reed-Frost model. Also the average attack rate for 100 runs was compared between models, where the per epidemic attack rate = sum cases/total population size.

Different settings for the k in NONCX and CLINICAL were evaluated and distributions compared to the Reed-Frost. All combinations of values of $k=1$, $k=6$, and $k=20$ were evaluated. Model runs were carried out on a microcomputer with Quick Basic (Microsoft, 1988) as the programming language for the distributed

delay and Pascal for the stochastic Reed-Frost model (Foster, 1984). All populations started with 1000 susceptible individuals and 2 infectives.

RESULTS

A comparison of average attack rates and number of epidemics with total cases less than fifty, for different parameter settings is shown in Table 6.1. Results of the average attack rates for the Reed-Frost are similar to those of the triangularly distributed β , for the same value of p or β . However, average attack rates from the exponentially distributed β were much higher, and the number of epidemics with less than 50 cases was lower than for comparable values of p or triangular β .

Table 6.1 Comparison of Reed-Frost and distributed delay stochastic models.

Reed-Frost			Distributed delay				
p	Average* attack rate	No. epidemics with <50 cases	B	Average attack rate		No. epidemics** with <50 cases	
				Expn	Tri	Expn	Tri
.0016	.58	10	.0016	.76	.57	8	19
.0012	.15	50	.0012	.60	.18	21	52
.001	.03	78	.001	.49	.03	33	86
.0008	.013	95	.0008	.39	.015	99	99
.0004	.005	100	.0006	.22		63	0

*Average attack rate = $\frac{\text{NRUN} \sum E}{1}$ cases/population size, NRUN = # of simulation runs

p = probability of effective contact for Reed-Frost S(0) = 1000, I(0) = 2

B = infectivity parameter for distributed delay

**Number of epidemics with less than 50 cases

Histograms comparing the frequency distributions for the Reed-Frost, DDEL with a triangularly distributed β and an exponentially distributed β are

shown in Figures 6.5 - 6.8. The values of $k = 6$ were used in the distributed delay simulations. Values of $k = 1$ did not display as pronounced of a bimodal distribution, and values of $k=20$ produced computational problems due to the lack of conservation of flow as a result of the random changes in the delay.

The histograms from the distributed delay model (exponential and triangular) show the desired bimodal distributions. The details of the DDEL plots do differ somewhat from the Reed-Frost model. For example, the triangular $\beta = .0016$, (Figure 6.5) the separation between the two peaks is not as great as the Reed-Frost. This not surprising since the distributed delay is continuous entity model, ie. it uses real numbers instead of integers, resulting in a smoother curve. For $\beta = .0012$, triangularly distributed (Figure 6.6) the tail is slightly more extended and there are more epidemics in the 50-100 case range, but the bimodal distribution is still evident. The exponentially distributed β also demonstrated the bimodal distribution (Figures 6.7-6.8, top graph). The spread between the two peaks is more pronounced than the triangularly distributed β and than the Reed-Frost. Figures 6.7 and 6.8 compare distributions between the two models that produced similar average attack rates (see also Table 6.1).

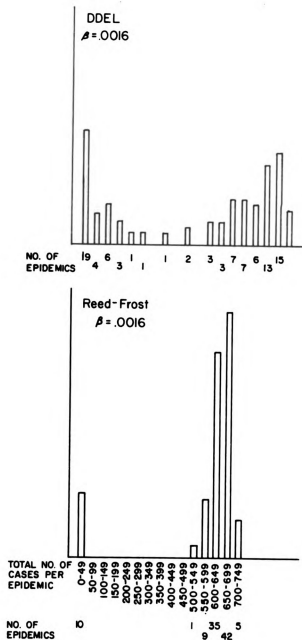


Figure 6.5 Frequency distributions (100 epidemics) of distributed delay (DDEL) (a) and Reed-Frost (b) stochastic disease models for $p = .0016$ and $\beta = .0016$, TRIANGULAR distribution

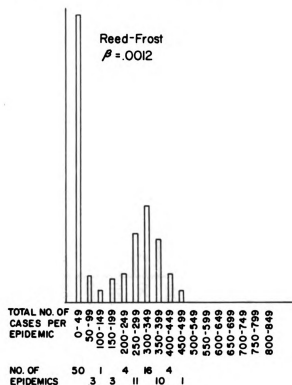
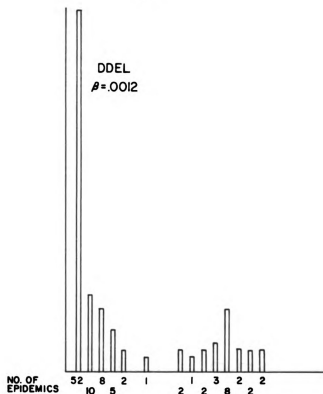


Figure 6.6 Frequency distributions (100 epidemics) of distributed delay (DDEL) (a) and Reed-Frost (b) stochastic disease models for $p = .0012$ and $\beta = .0012$, TRIANGULAR distribution.

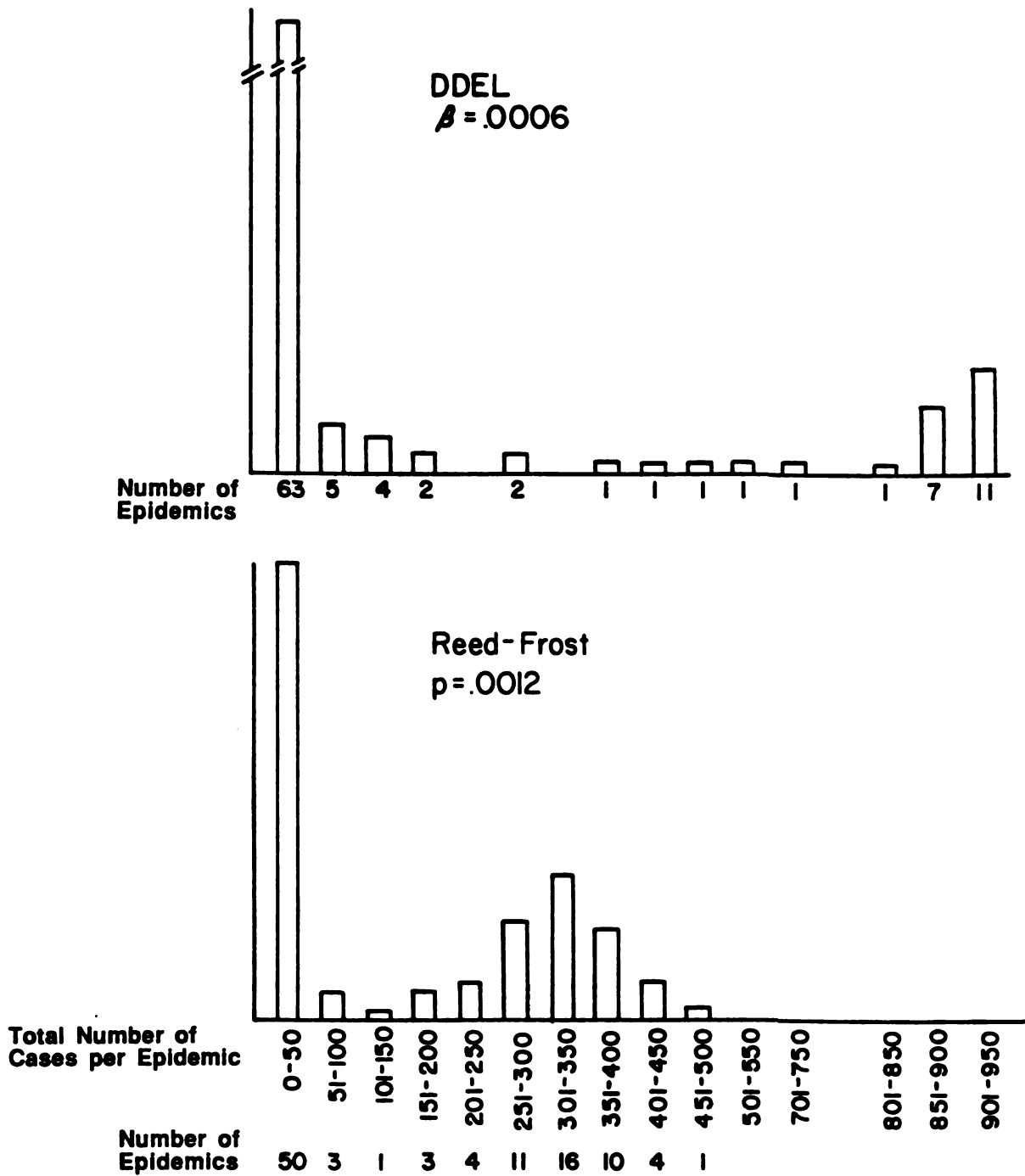


Figure 6.7 Frequency distributions (100 epidemics) of distributed delay (DDEL) with EXPONENTIAL distribution (a) and Reed-Frost (b) stochastic disease models for $p = .0012$, $\beta = .0006$.

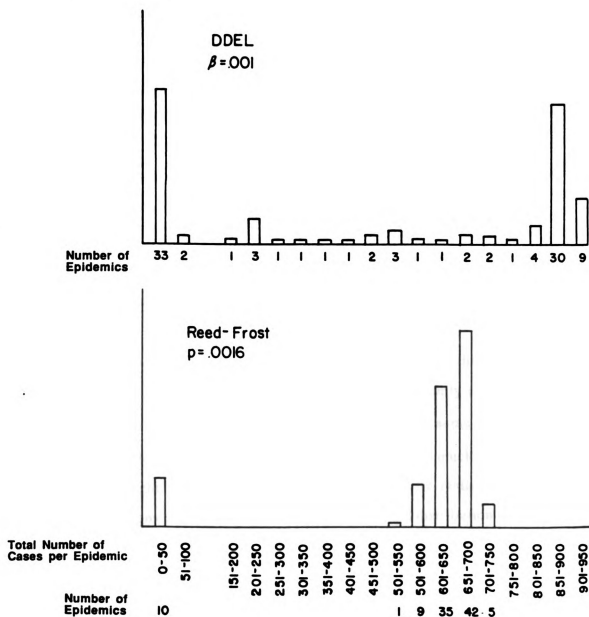


Figure 68 Frequency distributions (100 epidemics) of distributed delay (DDEL) with EXPONENTIAL distribution (a) and Reed-Frost (b) stochastic disease models for $p = .0016$, $\beta = .001$

DISCUSSION

It is not necessary that matching β and p should values should produce the same distribution, or same average attack rate, as the meaning of the two values is different. It might be expected that a value for β lower than p would be required to produce the same average attack rate since the distributed delay model tends to retain individuals in the infected state longer than the Reed-Frost model which assumes infectivity lasts one discrete time period. This was noted in the exponentially distributed delay. The triangular distribution was set with upper limits much lower than those permitted with the exponential distribution which theoretically has no upper limit. This explains the higher attack rates and wider spread to the bimodal frequency distribution observed with the exponential.

The best distribution to use for β should be determined by its distribution in the system which is being modelled, not by comparing it to another theoretical distribution. A definition and estimation of β and its distribution will be discussed in Chapter 7.

An advantage of a distributed delay model is shown in that, depending on the k , the infection duration (IDUR) can actually be randomly represented. For example, if the mean IDUR is 7 days ($E[\tau]=7$) and $k=6$, some individuals will start to leave the state in only 2 days and others will stay much longer (Figure 6.3). It is thought that these distributions allow for more realistic models than most mass actions models which assume an exponential distribution of IDUR, ie, $k=1$ (Bailey, 1975).

A disadvantage of the distributed delay may be that it is more computationally complex and stability criterion must be carefully monitored. As a continuous entity model there is some aggregation error, especially for small populations. That the output of the distributed delay are represented by the family of Erlang distributions assumes that the waiting times at all "servers" within

the state are equal. A gamma distribution might be more realistic, if the waiting times at each "server" were known to be different.

Other advantages are that it is useful for infectious or noninfectious diseases. It represents the stochastic nature of waiting times until disease occurrence and exit from the nonclinical state, and allows flexibility in defining the distribution of the outputs by altering the k value. It can realistically accommodate other vital dynamics, such as birth or migrations into the populations. The computational speed of the model is not affected by the number of individuals in the population as are other discrete entity models (Chapter 4).

That both models demonstrate the threshold phenomenon has ramifications for all epidemiologic studies of infectious disease. For example, statistical analysis of the effects of various factors on the incidence of disease between two populations could be biased by this threshold phenomenon, since the errors will not be distributed normally. For example, two populations with the same set of risk factors might have very different rates due just to chance, as each epidemic falls in a different peak of the bimodal distribution. The effects of this phenomenon on infectious disease analysis need further investigation.

It is hoped that this distributed delay model of disease processes will provide a generic model for simulation of disease processes in dynamic populations of a various types. The applicability of this model will be investigated in the next chapter.

CHAPTER 7

Application of a stochastic distributed delay simulation model to the epidemiology of clinical respiratory disease in a dairy cattle population.

INTRODUCTION

The various type of epidemiological simulation models have been described in Chapter 4. The data collection process, descriptive epidemiologic and economic statistics, along with a critique of data quality have been discussed in Chapters 1 and 3. A generic model for disease processes in dynamic populations has been described and tested in Chapter 6. The objectives of this chapter are to describe the application of the model in Chapter 6 to clinical respiratory disease in a typical Michigan dairy cattle herd. The predictive ability of the model will be tested against the database described in Chapter 1 and 3.

MATERIALS AND METHODS

Model description

According to the proposed epidemiologic model classification scheme in Chapter 4, this model can be classified as a stochastic structural process model with continuous time and entity computation by simulation.

The distributed delay model, proposed in Chapter 6, is applied in this model to represent the 3 age groups of cattle defined in the NAHMS database. Additional states of disease, such as IMMUNE and RECOVERED are defined along with the CLINICAL and NON-CLINICAL states. Most of the disease states are implemented with the time varying distributed delay of Chapter 6, however, the additional feature of proportional losses from the delay are included to allow for aging and losses from the populations (Manetsch, 1976). A detailed block diagram of the dairy herd, is shown in Figures 7.1 a-c. Each figure represents one age group, but the groups are interconnected so that

animals can grow into the next age group. The assumptions and definitions for each age group will be discussed below.

Calves are defined as animals from birth until weaning. Calves can fall into 4 disease states, CLINICAL and NON-CLINICAL, IMMUNE due to infection, and COLOSTRUM-IMMUNE due to intake of colostral antibodies. NON-CLINICAL Calves are assumed to be susceptible to disease (S), and are noninfectious. CLINICAL Calves are presenting overt signs of respiratory disease, such as coughing, runny noses, respiratory distress, or any other signs consistent with a diagnosis of upper or lower tract respiratory disease. CLINICAL Calves are spreading the disease to other animals in the herd, therefore are considered infective (I). IMMUNE Calves are those that have passed through the CLINICAL state and are resistant to reinfection. Some of these animals may have a decrease growth rate and will be weaned at a later age, these are classified as "poor doers". Since it is assumed that the duration of immunity (270 days) is longer than the time to weaning (90-140 days) these Calves will be weaned into the IMMUNE Young Stock state and do not have a chance to return to the susceptible state. The impartation of natural immunity from antibodies in colostrum is considered to play an important role in the epidemiology of respiratory disease (Miller, et.al, 1980). For this reason, the state of COLOSTRUM-IMMUNE was included to represent those animals born of IMMUNE or VACCINATED cows. The duration of this natural immunity is estimated from the literature to be 60 days (Radostitis and Blood, 1985). COLOSTRUM-IMMUNE Calves are moved into the NON-CLINICAL state after an average 60 days, and become susceptible to infection.

Calves are born into the NON-CLINICAL or COLOSTRUM-IMMUNE states at a daily rate determined by the number of cows present in the herd. Calves born of cows in the IMMUNE state go into the COLOSTRUM-IMMUNE state for Calves, and Calves born from CLINICAL and NON-CLINICAL cows go into the NON-CLINICAL state.

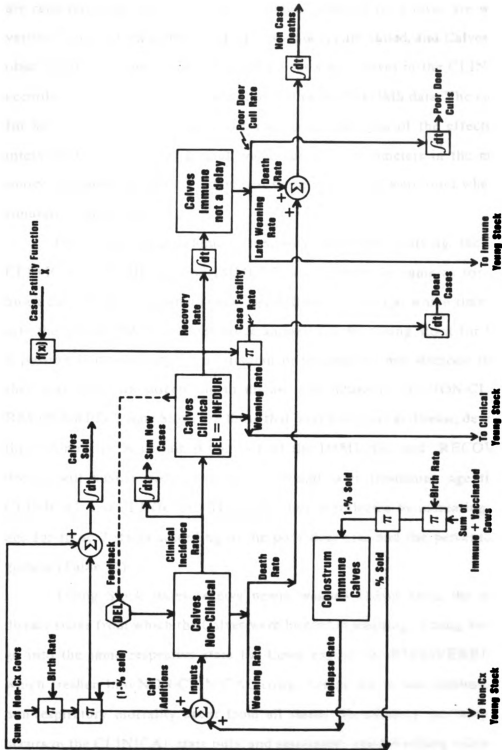


Figure 7.1a Epidemiologic simulation model of the Animal Population and Production System (APPS) for CALVES.

By application of the proportional loss feature of the distributed delay, animals are removed from each of the above states. Some of the Calves are weaned into the various Young Stock states, others die, poor doers are culled, and Calves are sold at the observed sell rate, which includes bull Calves sold. Calves in the CLINICAL state die according to the case fatality rate observed in the NAHMS data. The case fatality rate for all age groups can be altered for economic analysis of the effects of veterinary intervention (Chapter 8). Default values used for parameters in the model and their source are shown in Table 7.1. Some of these parameters were reset when herd specific simulations were run.

For Young Stock, animals from weaning to first calving, the 3 states, NON-CLINICAL, CLINICAL, and IMMUNE are defined the same as for Calves. Young Stock can also be vaccinated at any user defined age level, at which time they will move into the VACCINATED state. Since animals can be Young Stock for 19-25 months, it is possible that immunity from infection, or vaccination, may decrease to the point that they may be again susceptible to disease and return to the NON-CLINICAL state. RECOVERED Young Stock are those that have had clinical disease, developed, and lost their immunity. A certain proportion of the IMMUNE and RECOVERED ("poor doers") will have a reduced growth rate and later freshening age than the NON-CLINICAL and CLINICAL. This proportion is reflected by increasing the freshening age for those 2 states according to the poor doer rate and the percentage decrease in growth (Table 7.1).

Young Stock states receive newly weaned Calves from the same respective disease states from which the Calves were located at weaning. Young Stock that freshen go into the same respective state for Cows, except for RECOVERED Young Stock which freshen into NON-CLINICAL cows. Losses due to non respiratory culling, and non-respiratory mortality occur from all states. Respiratory mortality (case fatality) occurs in the CLINICAL state only, and respiratory related culling relates to poor doers in the RECOVERED and IMMUNE states (Table 7.1).

Legend

Σ = Summation, $+$ addition, $-$ subtraction

π = Multiplication

$\int dt$ = Integration with respect to dt , dt = computational time step

$f(x)$ = Function of various independent variables, x . Or manually altered

BEL = Time varying DELAY factor $\text{BEL} = \frac{1}{1 - (1-f)^i}$, $i = \#$ in infected state
 β = transmission coefficient, a random variable

$\square$ = A state variable = the number of designated individuals in a state or delay at any given time

$\int_{dt}$ = Integration with respect to dt over a 30 day period

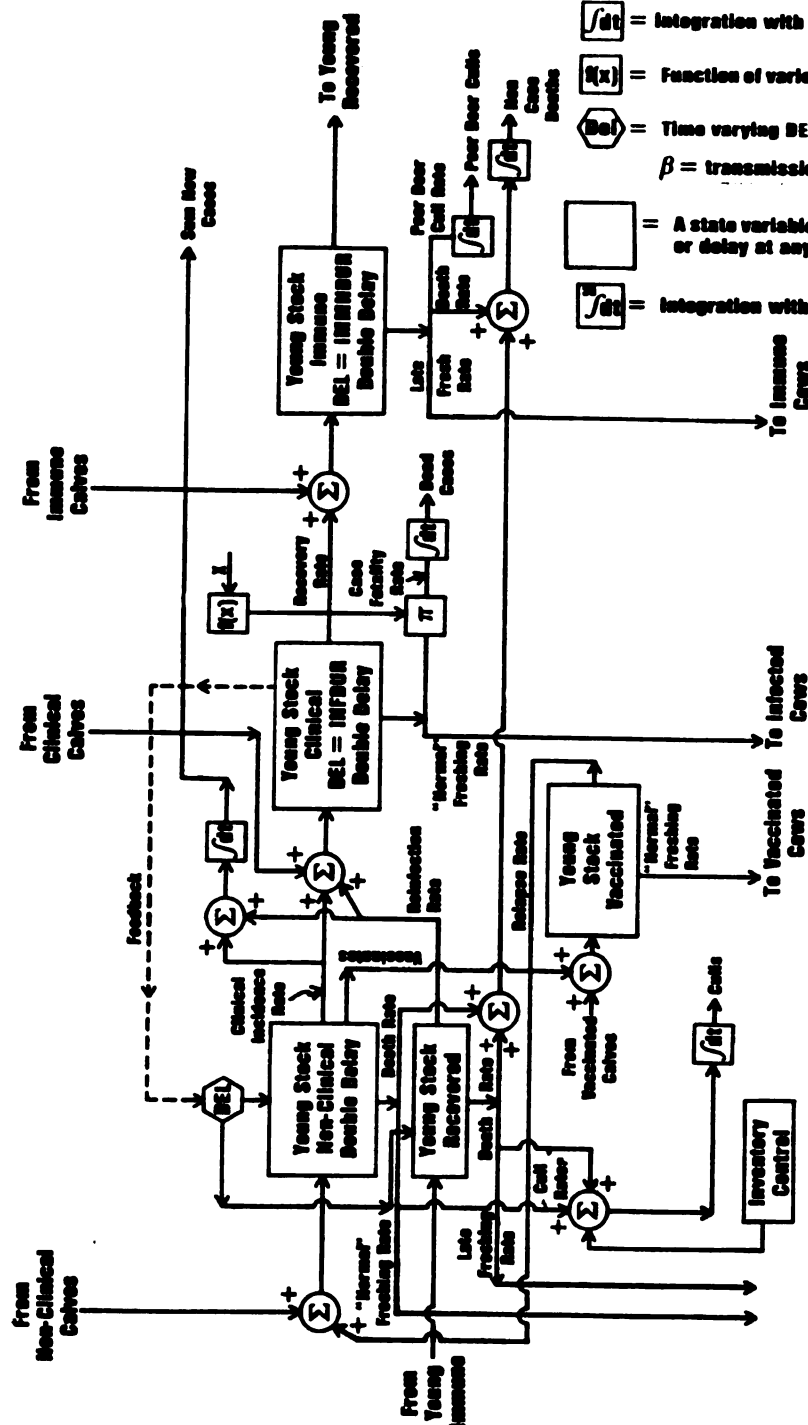


Figure 7.1b Epidemiologic simulation model of the Animal Population and Production System (APPS) for YOUNG STOCK.

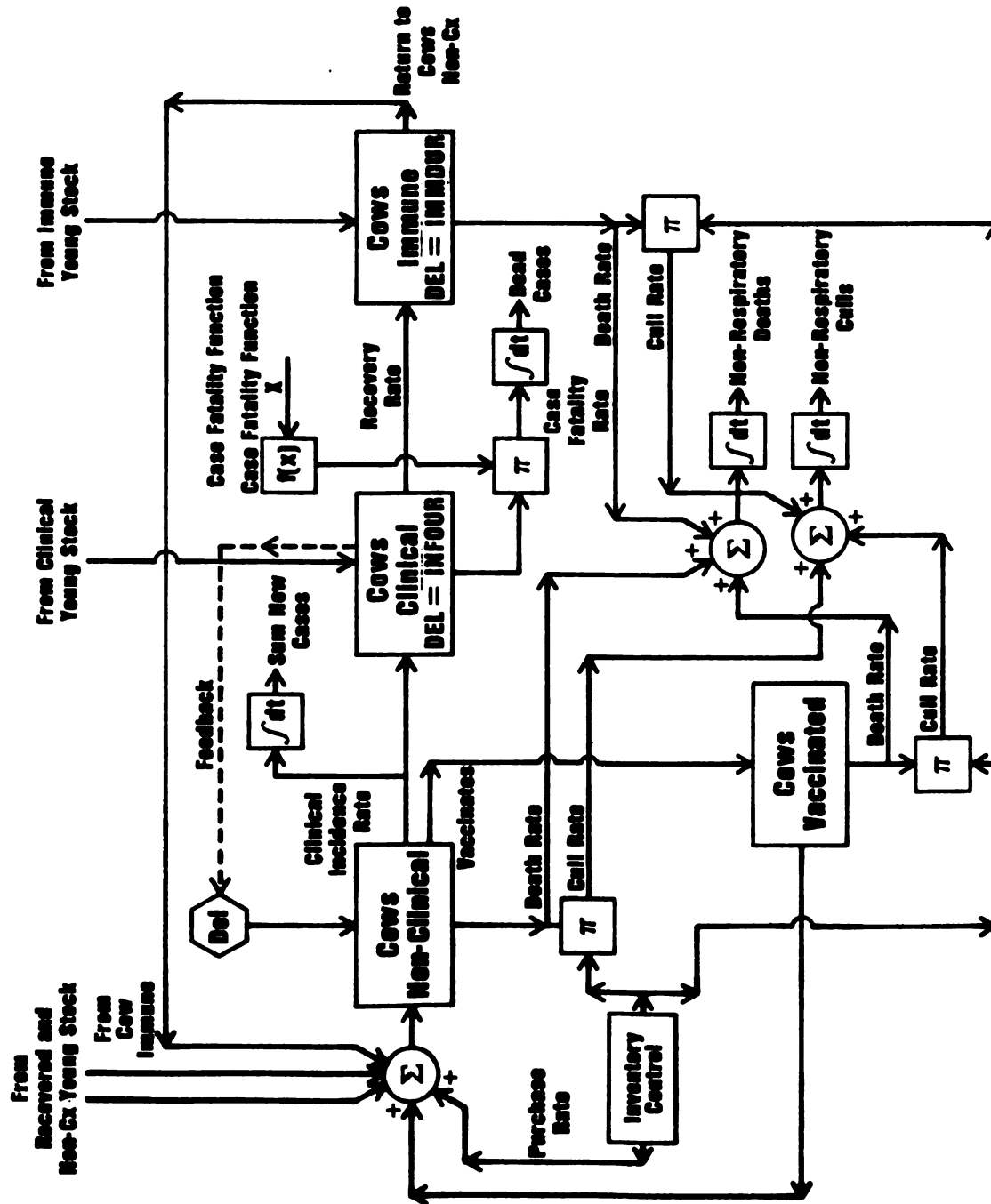


Figure 7.1c Epidemiologic simulation model of the Animal Population and Production System (APPS) for COWS.

In Cows, animals after first calving, the disease states are the same as in Young Stock with the exclusion of the RECOVERED state. It is assumed, based on the authors clinical experience, that most respiratory disease in adult dairy cattle does not impair long term performance, so the RECOVERED state was not needed. Animals in the NON-CLINICAL and IMMUNE states will produce milk at a user defined daily rate, and those in the CLINICAL state will produce milk at a decreased rate (Chapter 8).

For all 3 age groups the length of the delay in NON-CLINICAL is set at some starting level. This initial value can be set as a function of the observed annual incidence density or a prediction from the linear regression equation of Chapter 5. This delay is then altered as a function of the number of individuals in the CLINICAL state as described in Chapter 6 and equation 7.1. This in effect represents a feedback loop as shown in Figures 7.1a-c.

$$DEL(t) = \frac{1}{1-(1-\beta)^{I(t)}} \quad (7.1)$$

Computational methods

The early versions of the model were designed and tested on the Apple Macintosh SE with a graphic simulation software program (STELLA, 1987). Due to computational limitations of STELLA, the full model was implemented with Quick Basic (Microsoft, 1988). A 365 day run on a Compaq 386, 25 megahertz clock speed with a math coprocessor, took about 8 minutes. The delta time (dt), for numerical integration, was set at 0.1, so each day of simulation required 10 loops through the model.

The mathematics and behavior of the distributed delay is described in Chapter 6. However, for Young Stock, a unique modification was made to the distributed delay routine. This modification is called the double delay and its subroutine is shown in Appendix D. The double delay manipulates an array of animals each cell of the array designates a different KI stage of disease progression (Chapter 6) and KA level of

maturation. The number of animals in any cell is computed with Euler integration similar to the distributed delay. The subroutine allows for bilateral movement for animals, along the disease progression and maturation processes. It also allows for selective age level vaccination. The user can choose the age range at which Young Stock should be vaccinated and only those animals stored in the appropriate KA stage of the delay will be removed to the VACCINATED state. Since the transit time for an animal from a newly weaned calf to freshening heifer is fairly long (19-24 months) and variable, it seemed reasonable to allow this process to have the same distributed features as described for disease processes in Chapter 6. The maturation process is the most common application of the distributed delay (Plant and Wilson 1986).

Parameter estimation

A majority of the important model parameters were estimated from the NAHMS data, using average values from all 48 herds with useable data. Those that were not available were derived from the literature (Table 7.1). For those parameters, such as infection and immunity duration, which were estimated from the literature, averages were taken from various authors who were describing separate specific etiologies. For example, the infection duration for Parainfluenza 3 infection is reported to be 7-8 days (Gillespe and Timoney, 1981), and 3-5 days for Bovine Respiratory Syncytial Virus (Mathes and Axthelm, 1985). Duration of immunity was more variable it was reported as being short for BRSV (Gillespe and Timoney, 1981), and solid but indefinite for Bovine Virus Diarrhea (Blood, et al. 1985)

Table 7.1 Epidemiologic model parameters. Average daily rates from Michigan NAHMS Round I and literature.

Variable	Default	Units	Comment	Source
CALVES				
Non-resp mortality	.001	hd/day	3 per 100 calf months	Data
Non-resp cull rate	0.0	hd/day	assume not sold for dairy	Data
Resp cull rate	$6E^{-6}$	hd/day	.02 per 100 calf months	Data
Case fatality rate	.02	hd/day	15% over 7-day infection	Data
Weaning age	120	days		
Late weaning age	140	day	Due to a 2-7% decrease in daily gain	Thomas, 1973 Miller, 1980
CLOSDUR	60	day	Duration of natural immunity from colostrum	Radostits, 1985
Mean SAR	.106		Secondary attack rate	Data
Prob New	.15	%	Probability of new infective	Data
YOUNG STOCK				
Non-resp mortality	$2.4E^{-5}$	hd/day	7 per 10,000 animal months	Data
Non-resp cull rate	0.0^5	hd/day	6 per 10,000 animal months	Data
Resp cull rate	$8.3E^{-5}$	hd/day	From immune and recovered	Data
Case fatality rate	.013	hd/day	9% over 7-day infection	Data
Freshening age	27	months	Assume delay not due to respiratory disease	DHIA
Late freshening age	29	months	Based on a 5% decrease in weight gain	Miller, 1980
Mean SAR	.019		Secondary attack rate	Data
Prob New	.07		Probability of new infective	Data
COWS				
Purchase rate	variable	hd/day	Function of number in animal inventory	
Non-resp mortality	$1.06E^{-4}$	hd/day		Data
Non-resp cull rate	.0008	hd/day	Increase if number in animal inventory above starting level	
Resp cull rate	0	hd/day		
Case fatality rate	$2.8E^{-3}$	hd/day	2% over 7-day infection duration	Data
Mean SAR	.005		Secondary attack rate	Data
Prob New	.06	%	Probability of new infective	Data
ALL AGES				
Infection duration	7	days	Average time in CLINICAL	Literature
Immunity duration	360	days	After natural infection	
Vaccination duration	270	days		

Secondary Attack Rate

In other mass action models it is stated that the meaning of the β term, or infectivity parameter is not clear (Fine, 1982). For this model it will be defined as the classic Secondary Attack Rate (SAR) (Kemper, 1980) which is defined as the propensity of disease to spread within a population after the introduction of a single infective individual. This parameter can be estimated from any herd within the NAHMS database, for any month, as shown in equation 7.2. If one case of disease occurred within a month the SAR = 0 since this original case generated no new cases. If no cases of disease occurred the SAR was not estimable, as the lack of an initial case made it impossible to determine the propensity for disease to spread.

$$\text{SAR} = I - 1 / S - 1 \quad (7.2)$$

I = the number of new cases during the month
S = the number of animals at risk (Chapter 2)

The frequency distribution of the SAR's was simulated with exponential distribution so values for β were randomly generated from a subroutine (EXPON, Appendix D) with the mean SAR set at the beginning of the run. A new value for β was generated every 30 days from the exponential distribution. Since the SAR assumes that one infective is present in every population experiencing disease the model was altered from Chapter 6 to allow alteration of the delay, by feedback, only if the number in the CLINICAL state was greater than or equal to 10.

The model was usually initialize with one or two animals in the CLINICAL state, however once this infective recovered it was necessary to allow the introduction of new infective into the herd. This was accomplished, for each age group, by calculating the proportion of herd months that had at least one infection in the herd, and comparing that to a uniform random distribution generated every 30 simulation days. If the uniform random number was greater than the probability of infection, one individual was added to the CLINICAL state. In Calves, Young Stock, and cows the observed probabilities of a new infection were, .15, .07, and .06, respectively.

Testing of the model

In order to test the ability of the model to predict annual incidence densities (aID) of clinical respiratory disease, data from one herd in each herd-size stratum (Chapter 1) was compared to 365 day runs of the model. The number of animals in each age group was set to the average number observed in the herd. Random variation occurred in the SAR, and addition of new infective. It was necessary to use specific parameters of cull, mortality, and sell rates for each herd simulated (Table 7.2). This was done in order to model the population sizes observed in the data.

It is clear from Chapter 6 that the proportion of individuals in the susceptible and immune states of disease plays a very important role in determining the observed or simulated frequencies of disease. Unfortunately it was not possible to estimate this proportion in the herds observed in this project. Therefore when testing the model was necessary to evaluate different starting ratios of susceptibles (NON-CLINICAL) and IMMUNE. A 1:3, and 1:1, ratio was evaluated for each herd. Unlike the model of Chapter 6, no initial infective was added to the herd as the beginning of the run.

The model was run Monte Carlo for 50 runs of 365 day, for each of the two starting ratios. A 95% confidence interval was estimated on the aID's predicted from the model and this was compared to the observed annual incidence density (aIDobs) with the confidence interval test (Law and Kelton, 1982).

Table 7.2 Observed and simulated annual incidence densities (aID) for NAHMS herds. Herd specific sizes and loss rate used for each model run.

Age	Ave. Herd Size	Daily Loss rates					aIDobs	Susceptible/Immune	
		NRCull	RCull	NR Mort	R Mort	Sell		1:3	1:1
11:02									
1	33	0	0	8.3E ⁻⁵	8.3E ⁻⁵	.0043	.0044	.0089±.045*	.023±.076*
2	164	3.3E ⁻⁵	0	0	0	6.7E ⁻⁵	.0010	.0085±.015*	.012±.02*
3	143	0	0	1.5E ⁻⁴	0	f	.0011	.0023±.002*	.0036±.0026*
15:01									
1	4	0	0	.0048	.0008	.008	.02	.034±.035*	.054±.032
2	18	0	0	1.4E ⁻⁴	0	.00076	0.0	.0159±.009	.0211±.016
3	26	0	0	.0022	0	f	0.0	.0043±.0018	.0048±.002
15:02									
1	8.0	0	0	4.3E ⁻⁴	0	0	.044	.021±.016	.056±.04*
2	73	3.7E ⁻⁵	0	0	0	6.E ⁻⁴	.0057	.022±.018*	.05±.015*
3	49	4.5E ⁻⁴	0	1.1E ⁻⁴	0	f	0.0	.0008±.0023*	.0019±.003*

RESULTS * = observed annual incidence density fell within 95% confidence interval of simulated aID

The mean observed SAR for Calves, Young Stock and cows was 0.106, 0.019, and 0.005. Most herds had an SAR = 0 with a maximum in Calves = 2.0, Young Stock = .64, and cows = .43. These maxima were much higher than most of the other observations in the age group, and were considered outliers and deleted to compute the above means. The distributions of the observed SARs, minus the outliers, are shown in Figure 7.2. This was the reason for using the exponential distribution for the secondary attack rates.

Predicted versus simulated disease frequencies

The observed annual incidence density (aIDobs) for the 3 herds tested fell within the 95% confidence interval 6 of 9 times, for both ratios, which was not significantly ($p < .01$) different from expected of 9 of 9 times, with the Chi Square goodness of fit test. Producer 15:01 had the fewest number of accurate predictions. The 1:1 Susceptible to Immune ratio had generally higher predicted aID's, with wider confidence intervals.

Observations on model behavior

If the mean SAR for the random exponential distribution was set higher than the observed mean, then a herd might experience high rates of disease in one run of the model and low to zero rates in the next run. Thus the characteristic bimodal distribution was observed. The initial incidence density determined the endemic level of disease in a herd, for settings of the SAR at or below the mean. The SAR's modulated the epidemic potential, and the probability of a new infective reflected the effects of introduction of new infection from outside of the herd.

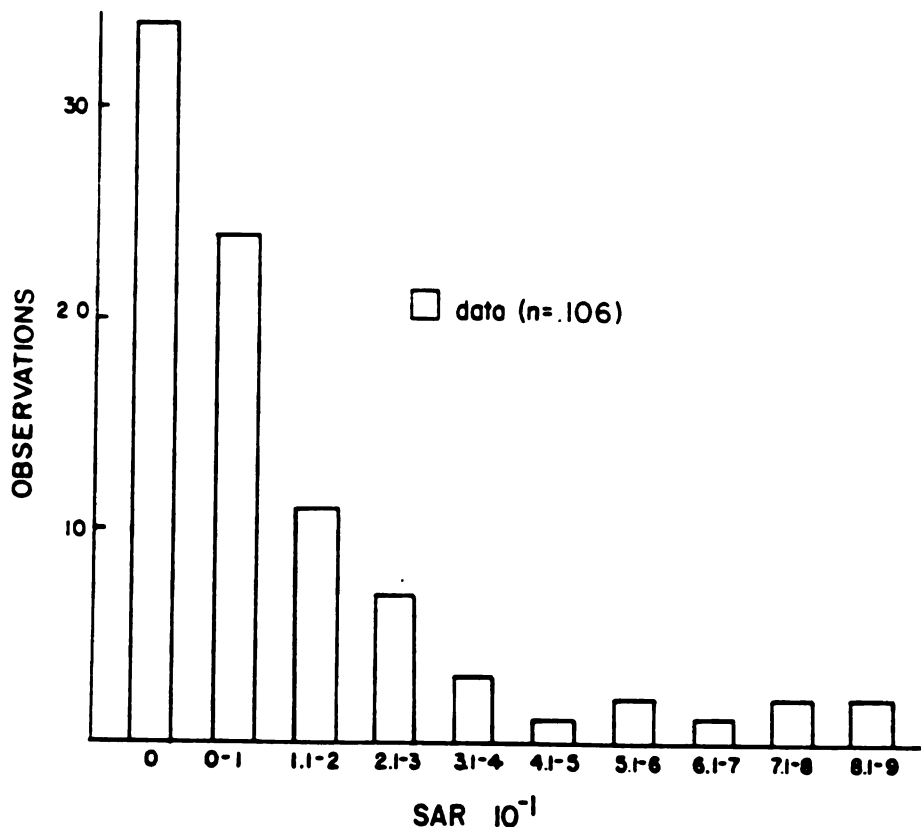


Figure 7.2 Observed distribution of Secondary Attack Rate in CALVES.

DISCUSSION

Herd 15:01 was the smallest herd and had the lowest success rate. This could be due to aggregation error or failure to include a particular specific herd phenomenon such as contact between age groups. The use of herd specific cull, mortality, and sell rates added as much specificity as the data would allow. More data were needed on the actual ratios of Susceptible to Immunes in a given herd.

It seems reasonable to expect that this model could accurately predict the rates of disease in a given herd, on a monthly basis, provided the appropriate herd specific data were available. Further statistical analysis that determined the effect of changes in monthly risk factors and seasonality on herd specific Secondary Attack Rates (SAR) would allow evaluation of the economic and epidemiologic effect of interventions to change the levels of risk factors. Analytical techniques that use a process model such as this one to isolate and estimate dynamic parameters such as the SAR, would be increase the utility of this model for purposes of risk factor analysis. The integration of stochastic SAR's, randomly generated new infective, and a baseline incidence density, allowed for modelling of the endemic characteristics of this disease while including the potential of epidemic occurrence.

Many of the parameters used in this model were derived from the original database to which the model applied. This has the advantage of giving a more accurate representation of the system in question. Since averages were used from all herds in the sample, and since the sample was randomly selected to represent the Michigan dairy population conclusions from the modelling exercise should apply to the "average" Michigan dairy herd. It was not the intent of this chapter to make conclusions about the epidemiology and control of respiratory disease in Michigan dairy herds. However, the following chapter will attempt to make some estimations of the economics of respiratory disease in Michigan.

For parameters not derived from the data, such as the average infection duration or duration of immunity, the literature was used to give estimates for what may be termed "generic" respiratory disease. The specifics of particular etiologic agents was overlooked since this accuracy of diagnosis was not available in the data. The implications of the accuracy of diagnosis for the decision maker are discussed in Chapter 1. The advantage of this model is that the epidemiology of specific agents can be addressed with the input of pertinent parameters, and little or no restructuring of the model.

The use of a continuous entity model may have some disadvantages in terms of aggregation error and lack of the ability to identify individual animal characteristics (Elveback *et al.*, 1984). However, this type of model is frequently employed in epidemiology (Chapter 4). It has the advantage of not being computationally slowed or complicated by the size of the population being modelled. It can readily accommodate the use of rates and proportions to describe the characteristics of movement, for example the SAR, culling and mortality rates, estimated from the NAHMS database. The use of a continuous entity model allows the employ of the distributed delay routine, which is an important feature in adding realism to the model. For example, the distributed delay applied to the CLINICAL state, removes a common assumption of other epidemiologic model, that of an exponential distribution for infection duration in the mass action model (Fine,1982) or the short and constant infection duration of the Reed-Frost model (Abbey, 1952, Chapter 4).

The use of the distributed delay for the NON-CLINICAL state has the advantage of being useful for modelling non-infectious disease. Since the delay time, or waiting time in NON-CLINICAL can be described to be a function of other factors within the herd, such as environment or management, it need not be driven by the number of individuals in the infected state as do the mass action and Reed-Frost type of models.

SUMMARY

Compared to other epidemiologic models (Chapter 4), this model contains the realistic representations of the dynamics of disease in a dairy herd. Few models found include more than one age group of animals, in combination with immigration and emigration and multiple states of disease susceptibility. The model's ability to approximate the endemic and epidemic potential of disease should make it useful for purposes of economic analysis of disease.

CHAPTER 8

Application of a stochastic distributed delay simulation model to economic analysis of Clinical Respiratory Disease in Michigan dairy cattle

INTRODUCTION

In Chapter 3 estimations of the "costs" of common dairy diseases were described. The methods used to define and calculate these costs were designed to meet the needs of all states participating in the National Animal Health Monitoring System. Certain shortcomings in the methods used in Chapter 3 were discussed. These include: 1) no estimation of the long term effects of disease due to lost animal potential, 2) no measurement of subclinical effects of decreased growth, 3) dependency on producer estimates of animal value, 4) lack of adjustment for revenue increasing effects of disease, and 5) milk loss estimates based on discarded milk only. The common assumption of the methods of Chapter 3 and other cost of disease estimates (Janzen, 1970; Natzke, 1976; Fetrow *et al.* 1987; Goodger and Skirrow, 1986) seems to be that the total of expenses associated with the occurrence of disease represents the true cost of the presence of that disease. The underlying premise is that a disease free alternative exists, and that the elimination of disease will result in an increase in profit equal to the total of expenses. These methods overlook savings due to disease and the effects of changes in population structure, due to disease that may effect the total economic picture. Also, since a disease free utopia is unlikely, it would be more appropriate, for the individual farm manager, to consider the economic impact of changes in disease level or management strategies that affect disease, versus the cost of disease.

The objectives of this chapter are 1) to apply the epidemiologic simulation model of Chapter 7 to economic analysis of Clinical Respiratory disease, 2) define and estimate the cost of respiratory disease in an "average" Michigan dairy herd, and 3) to determine the effects of changes in the level of various management characteristics on this cost.

MATERIALS AND METHODS

The epidemiologic model for simulation of a dairy herd has been described in Chapter 7. A subroutine was added to this model to compute dairy income and disease influenced variable costs. Revenue and expenses are computed on the basis of the number of individuals in any given disease state, in addition to animals sold. The block diagram for computation of dairy income and disease influenced variable costs for all animals not in the CLINICAL state is shown in Figure 8.1 a,b. This was implemented in order to include the economic effects of changes in population structure due to disease, but not directly observed as disease expenses. The costs and income generated by this portion of the model will differ as the level of disease in a herd changes. Income, costs, and disease associated expenses directly related to disease are computed according to Figure 8.2.

The sum of costs generated in Figures 8.1 and 8.2 are termed the Diseased Influenced Variable Costs. The Diseased Influenced Variable Costs include feed costs for Calves, Young Stock, and Cows, purchasing costs for replacement of Cows, variable costs of milk production, and disease associated expenses. Disease associated expenses were estimated from the NAHMS database and include veterinary fees, drugs administered, and labor for care and treatment (Figure 8.2). Variable costs of milk production include items such as hauling and advertising. Building depreciation, equipment repairs, and interest are not included in the analysis as they do not change with the frequency of disease. The tax effects of selling livestock was not addressed. Purchasing costs were modelled for Cows only. This was implemented by an inventory control routine that would initiate the purchase of cows, at a set price (Table 8.1), if the inventory, of cows, dropped below the starting level.

Feed costs, for all disease states, were modelled by assigning a daily intake rate, per head per day. Daily intakes and price per pound of feed (Table 8.1) were estimated from NRC (1987) recommendations and application of the Spartan ration balancer (MSU/CES, 1987) to generate a typical ration for each age of animal. It was assumed

Table 81 Economic parameters for the "average" dairy herd

Variable	Default	Units	Comments	Source
<u>CALVES</u>				
Female birth rate	0.43	hd/cow/yr		AEC 508
Male birth rate	0.43	hd/cow/yr	Sold at birth	AEC 508
Purchase rate	0			
Poor doer rate	10	%	% of past infected that perform poorly	
Cull value-non-resp	120	\$/hd	Assume these are same value as bulls	AEC 508
Cull value-poor doer	100	\$/hd	Assume 20% reduction in value	
Bull calf value	120	\$/hd		AEC 508
Drug Tx Expense	0.5	\$/case/day		Data
Labor Tx hours	0.33	hr/case/day		Data
Vet Tx Expense	0.05	\$/case/day		Data
Daily intake-non Cx	4	# feed/day	For 165 pound calf	NRC
Daily intake-poor	3.5	# feed/day	2-7% decrease with in gain, no change in feed conversion ratio	Miller, 1980
Daily intake-Cx	2	# feed/day	Maintenance only	
Price feed	0.05	\$/#	.07 \$/# for milk replacer, .04 \$/# for dry feed	Data
Discard milk to calves	50	%	% of milk discarded due to antibiotic treatment that is fed to calves	Data
<u>YOUNG STOCK</u>				
Poor doer rate	1	%	% of past infected that perform poorly	Blood and Henderson, 1985
Cull/sell value-non-resp	1000	\$/hd	Assume sold for dairy	
Cull value-poor doer	260	\$/hd	Assume 20% decrease in value	
Drug Tx expense	0.47	\$/case/day	\$3.28/case for 7 days	Data
Labor Tx hours	0.034	hr/case/day	.23 hr/case for 7 days	Data

Table 81 (cont'd.)

Vet Tx expense	0.03	\$/case/day	\$.21/case for 7 days	Data
Daily intake-non-Cx	16	# feed/day	Average 12-month-old heifer at 660 lbs	NRC, 1989
Daily intake-poor	14	# feed/days	2-7% decrease in decrease daily gain	Miller, 1980
Daily intake-Cx	8	# feed/day	Maintenance only	
Price feed	0.03	\$/#	4# Gnd shell corn, 12# alfalfa grass hay, 7# corn silage with vitamin premixes	MSU/CES, 1987

COWS

Milk production-non-Cx	41.7	#/day	Based on 15,000 # for 360 days	
Milk production-Cx	10	#/day		
Milk price	12	\$/cwt		
Poor doer rate	0	%	% of past infected that perform poorly assume no effect in adults	
Purchase price	1500	\$/hd	Price of replacement cow	
Cull value-non-resp	546	\$/hd	1300# @ \$.42/#	AEC 508
Drug Tx expense	1.8	\$/case/day	\$13/case for 7 days	Data
Labor Tx hours	0.08	\$/case/day	.5/case for 7 days	Data
Vet Tx expense	0.75	\$/case/day	5.30/case for 7 days	Data
Daily intake-maintenance	24	DM #/day	Based on feeding 60-month-old dry cow	MSU/CES, 1987
Daily intake/# milk	0.3	DM #/# milk		MSU/CES, 1987
Variable cost of milk hauling, etc.	.01/#	\$/# milk		For advertising AEC 508
Discard milk	50%	%	Assume 50% of sick cows are treated	
Price feed	0.03	\$/#		MSU/CES, 1987

ALL AGES

Discount rate	0.1	%/yr	Opportunity cost of intermediate term capital	
Wage rate	5.5	\$/hr		AEC 508
Infection duration	7	days	Average time in CLINICAL	Literature
Immunity duration	360	days	After natural infection	
Vaccination duration	270	days		

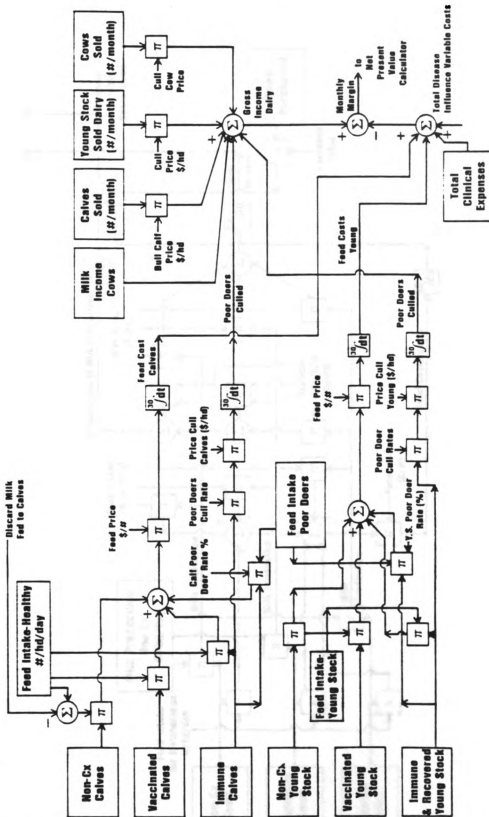


Figure 81a Dairy income and Disease influenced variables cost for CALVES and Young Stock. Block diagram

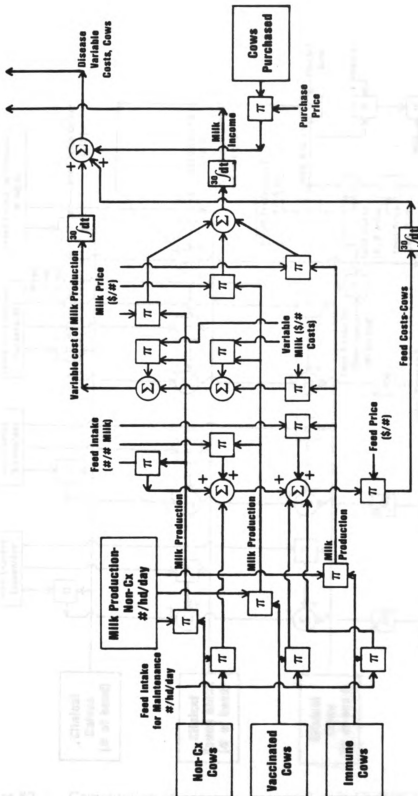


Figure 8.1b Dairy income and disease influenced variable cost for COWS

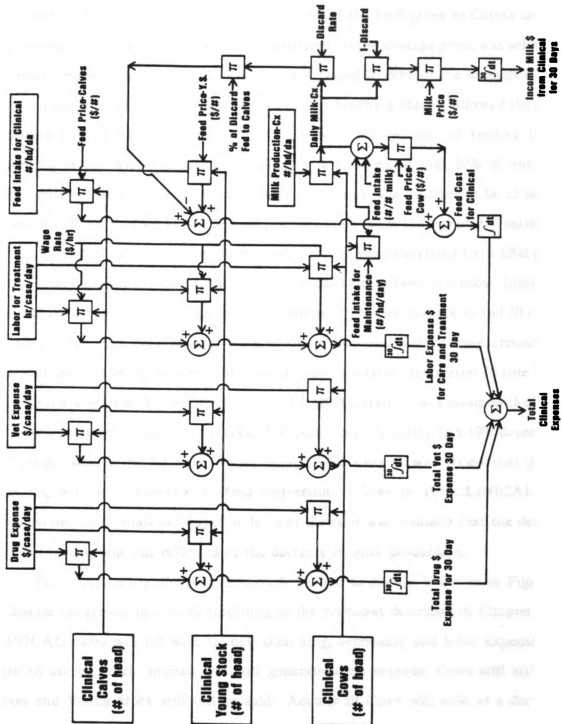


Figure 82 Computation of expenses associated with CLINICAL disease

that the average animal in the healthy calf population weighed 165 lbs (75 kg) and should be eating approximately 4 lbs. of dry matter per day. A ration of corn, soybean meal, midbloom alfalfa and trace minerals salts costs \$.04 per pound with current prices, 1987 in Michigan, from the ration balancer. Some of the feed given to Calves includes milk replacer priced at \$.07 per pound reconstituted, so the average price was set at \$.05. The total amount of daily feed for Calves was reduced by 50% of the amount of milk discarded due to antibiotic treatment of cows. This feedback feature allowed the effect of disease and antibiotic treatment in Cows to decrease the cost of feeding Calves. According to the NAHMS data (Chapter 5) it was estimated that 50% of antibiotic tainted milk is fed to Calves. The average Young Stock was assumed to be 12 months old and weigh 660 lbs (300 kg). These animals consume 16 lbs (7.3 kg) of dry matter per day at a price \$.03 per pound. For adult Cows, a ration was formulated for a 1300 pound (590 kg) body weight dry cow to determine the daily maintenance intake. Intake per pound of milk was estimated from rations developed for a cow making 60 and 20 pounds of milk per day. The average price for a ration of corn silage, alfalfa hay, ground shell corn, and soybean meal, with minerals was \$.03 per pound of dry matter (Table 81).

For Calves and Young Stock in the CLINICAL state, it was assumed that there was a 50% decrease in daily feed intake. For poor doers (Chapter 7), a 10% decrease in feed intake was estimated from Miller *et al.* (1980), since it was stated that growth decreases, without a decrease in feed conversion. Cows in the CLINICAL state produced only 10 pounds (4.5 kg) of milk. For Cows, it was assumed that the decrease in feed consumption was reflected in the decrease in milk production.

The computation of expenses directly related to disease is shown in Figure 82. As disease progresses in a herd, according to the processes described in Chapter 7, the CLINICAL states will fill with animals then drug, veterinary and labor expenses will begin to accrue. Sick animals will still generate some revenue, Cows still milk and Calves and Young Stock will still be sold. Acutely ill Cows will milk at a decreased rate. Also, feed intake, in all age groups, will be decreased during illness so that some savings will occur.

A portion of Young Stock and Calves, that have been diseased, will have chronic effects that decrease their growth rate. The animals are often called "poor doers" and the portion is the poor doer rate (Table 81). The poor doer rate only applies to animals in the IMMUNE and RECOVERED states. However, Calves that are born into the COLOSTRUM IMMUNE state are not affected. It is assumed that cows in the IMMUNE state carry no residual effects of disease. This assumption is based on the clinical experience, and the observation of no respiratory related cull in the NAHMS database (Table 81).

Income was generated by animals in all states of disease. Income was derived from the sale of milk and sale of animals. Fifty percent of the Calves born were sold as veal Calves. Heifer from the Young Stock age group were sold if the inventory of heifers exceeding the original numbers. This maintained a constant herd size and helped to account for the effects of disease on animal populations. Culling rates in cows for non-respiratory disease were estimated from the NAHMS data (Table 81).

Milk production was defined as an average 15,000 pounds (6818 kg) per lactation, at the beginning of the run, for Cows that were not in the CLINICAL state. Milk production increased annually as a function of the rate of new heifers freshening into the herd, in order to include the long term effects of genetic improvement. An equation was defined so that if 30% of the milking herd was replaced in one year, then the daily milk production parameter would increase by 2% (Radostits and Blood, 1985, pp 196-200). Milk price was set at \$12 per hundred weight.

The difference of Gross Income Dairy and total Diseased Influenced Variable Costs, was computed every 30 days. The Net Present Value (NPV) of this monthly stream of income was discounted (Barry, et.al, 1983, 206) back to the beginning of the run. This procedure served to equalize differences in the timing of disease occurrence from one scenario to another. Therefore, an epidemic that occurred in Year 1 of a run could be compared to an epidemic that occurred in Year 5, for example.

Model Application

The parameters of the simulation herd were set to define an "average" Michigan dairy herd (Table 8.1). This herd had 11 Calves in the herd, 41 Young Stock, and 81 cows. This is equivalent to the NAHMS Stratum II herd (Chapter 1). The Cows were 1300 pound (590 kg) Holsteins, milking 15,000 pounds (6818 kg) per year. The disease free herd (BASELINE) was simulated for a 5 year period by setting the initial annual Incidence density and Secondary attack rates near zero, since division by zero in the computer program produced an error. The probability of a new infection was set to zero. An initial infective was added at the beginning of the run, in order to provide disease expense comparison to disease runs that also started with one initial infective. This disease free herd served as the standard of comparison by which the Cost of Respiratory disease could be computed. The Cost of Respiratory disease was defined as the difference in 5 year NPV for the disease free herd compared to the diseased herd.

Diseased herds were computed in various manners to represent the different possibilities that might occur. Diseased herd #1 (DISEASE 1) was run with the average annual incidence densities (aID's), probability of new infection (ProbNew), and Secondary Attack Rates (SAR) set at the mean values observed in the data (Chapter 5,7). All animals were considered susceptible at the beginning of the run.

DISEASE 2 might represent the "average" DISEASE 1 herd that now adds the risk factor OHIREPOS (greater than 50% of non milking labor is hired help). According to the logistic model of Chapter 5, the addition of this factor should increase the probability of disease (odds) 28 times in Calves and 18 times in Cows. The initial aID's and SAR'S were adjusted accordingly. In DISEASE runs 3 and 4, the SAR'S were set at twice the average and 2 infectives were added to the initial population, to stimulate high disease rates. In DISEASE 4, the Case Fatality rate was set at a high level (50%) in all age groups in order to estimate the cost of an extremely pathogenic disease.

RESULTS

Model parameter settings and results are shown in Table 8.2. The high disease herds, DISEASE 3, DISEASE 4, both experienced the same distribution of case numbers. The bimodal frequency distribution is shown in Figure 8.3.

DISCUSSION

This model allows for improved estimates of the costs of respiratory disease as it includes feed savings and increased income from animal sales due to illness. The representation of the bimodal stochastic behavior of disease occurrence allows for estimation confidence intervals on the NPV. The effect of disease frequencies higher than the "average" reflected substantial costs.

The costs of respiratory disease reported in Chapter 3, would predict, \$14 per calf/year, \$195 per heifer/year, and \$1 per cow per year, for the average frequency of disease observed in the whole sample. Given the average herd size simulated, the 5 year total expected is approximately \$1,490. This should be compared to model output for DISEASE 1. However this simulation represents only one particular herd type, Stratum II. A more detailed within stratum comparison is indicated in order to make judgments. It is possible to generally conclude, as noted in Chapter 3, that the standard NAHMS procedures for cost estimation need to be adjusted for changes in the overall economic picture of the herd.

SUMMARY

The ability of the model to facilitate economic analysis of different disease scenarios and configurations has been demonstrated. Application of this model with stratum specific parameters and sample characteristics should allow for improved estimation of the cost of respiratory disease in Michigan. The application of different parameters should also allow for estimation for other diseases.

Table 8.2 Simulation results for "average" Michigan dairy herd with different levels of disease, 5 year runs.

—Model Settings—				—Simulation Results—					
Age Group	ID(0)	SAR	Initial infectives	Milk and feed costs	Purchase cost	Animal sales	Milk Sales	5 yr. NPV	Cost of disease
Baseline									
A	0	0	0	176,530	30,529	108,061	873,395	756,405	0
B	0	0	0						
C	0	0	0						
DISEASE 1									
A	.03	.106	0	154,690	28,873	91,704	726,672	634,685	121,720
B	.005	.019	0						
C	.002	.005	0						
DISEASE 2									
A	.08	.3	0	154,839	34,207	93,469	726,130	630,419	125,986
B	.005	.019	0						
C	.0034	.01	0						
DISEASE 3									
A	.03	.2	2	149,365	34,165	89,011	708,122	613,339	143,066
B	.005	.04	2						
C	.002	.01	2						
DISEASE 4									
A	.03	.2	2	125,425	54,371	92,273	706,102	595,963	160,442
B	.005	.04	2						
C	.002	.01	2						

Initial group size: calves (A) = 11, young stock (B) = 41, cows (C) = 81

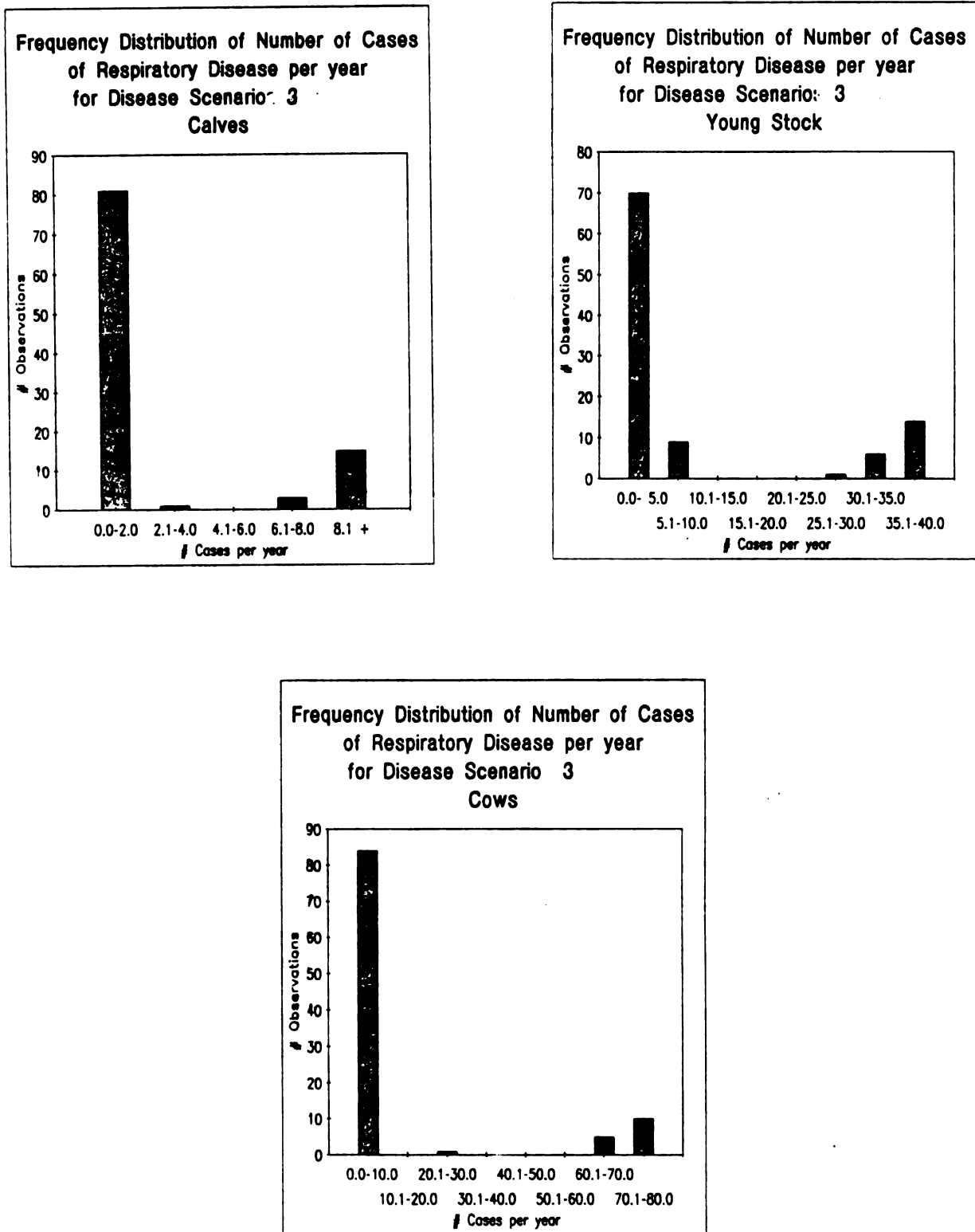


Figure 83 Bimodal distribution of number of cases from DISEASE3

SUMMARY AND CONCLUSIONS

This dissertation is directed toward the development of methodologies in analytical epidemiology and animal health economics. The system to which these methods were applied is the National Animal Health Monitoring System, and disease frequency and cost estimation in Michigan dairy cattle. Stratified random sampling of dairy herds, with prospective observation of one year was implemented. Methodological issues in the computation of disease frequencies and their variance were addressed and a standard method proposed. Issues relating to the estimation of the costs of disease were discussed, and shortcomings in the standard NAHMS methods noted.

Simulation modelling in epidemiology was reviewed for the purpose of evaluating alternative modelling strategies to be implemented in the context of NAHMS. A comprehensive classification scheme for epidemiologic simulation models was proposed.

A risk assessment analysis was performed using associative epidemiological models, and the utility of NAHMS for this purpose was discussed. Estimates of the effects of various risk factors on the occurrence of Clinical Respiratory Disease were to be incorporated into the simulation models of Chapter 7 and 8. This was accomplished only modestly, due to imprecision in the analysis due to small sample size and time frame incompatibilities between the simulation model and statistical model.

The distributed delay approach was proposed as a generic subunit to be used in a variety of infectious and non-infectious disease models. The model was applied, by way of example to Clinical Respiratory disease in dairy cattle. The model was to approximately predict the observed annual incidence density for example herds from the database. Many specifics about the herds were not available to the model, which decreased its precision. The simulation model was a useful tool for evaluating the long term economic impact of disease on the farms gross margin of Dairy Income minus Disease Influenced Variable costs. Many different scenarios could be evaluated with this model. It may also be useful as a statistical estimation tool to determine the "true" cost of disease in a population.

APPENDICES

Data collection forms for Michigan Round I, NAHMS

FORM 1 - Dairy

Initial Visit

National Animal Health Monitoring System

Producer Code No. _____:_____:20:_____

VM0 code _____

Interview date: / /
 yr mo day

1. Milking herd replacements Raised % Purchased %

No milking herd; only raises replacements

- 2. Facilities (check appropriate items)**

HOUSING	Calves	Young Stock	Lactating Cows	Dry Cows
Stanchion barn		_____	_____	_____
Loose housing		_____	_____	_____
Free stall housing		_____	_____	_____
Dry lot		_____	_____	_____
Pasture (in season)		_____	_____	_____
Individual calving stalls				
Calf hutches				
Calves in cow barn	_____			
Separate calf barn	_____			

Milking parlor used _____ Type of parlor _____

3. Farm activities: Dairy breed used _____ % _____ %

Other livestock enterprise(s) _____

Major dairy ration components (check appropriate items)

	% Raised	% Purchased
___ Hay, alfalfa or other legume	___	___
___ Hay, grass	___	___
___ Silage, corn	___	___
___ Silage, other _____	___	___
___ Other major feeds fed _____ (specify)	___	___

4. What disease problems of significance occurred in your herd during the past 2 years? _____

5. Use of veterinary or other service:

Veterinary service is used _____ times per month or _____ times per year.
Nutritional consultant is used _____ yes _____ no _____

Type of veterinary service obtained (check all that apply)

Treatment of sick livestock _____ Herd health _____ Source of vaccines _____
Disease investigation _____ General advice _____ Other (specify) _____

6. Comments? (if yes, check here ☐) Please use reverse side of page.

7. Reproductive services (check all that apply)
 _____ Pregnancy exams _____ Problem Breeders
 _____ Post-partum on all cows _____ Prebreeding on all cows

8. Type of nutritional consultation received
 Analysis of major feeds (yes or no) _____ How often (per year) _____
 Customized ration formulation based on analysis (yes or no) _____
 Milk cows _____, Dry cows _____, Young stock _____
 Adjustment of feed intake according to production level (yes or no) _____
 Grain only _____, Grain and forages _____

9. Nutritional consultant
 Commercial feed rep _____, Local feed mill _____, Extension service _____,
 Private consultant _____, Veterinarian _____

10. Record system (check all that apply):
 No systematic record system _____
 Reproductive events present lactation only _____
 Reproductive events for cows entire life _____
 Complete history for entire life (all pertinent events recorded) _____
 Milk production record for present lactation only _____
 Milk production for entire milking life _____
 DHIA _____ Permission to access, no _____ yes (please sign below)
 DHIA code # _____
 Other form of production records _____

The undersigned does hereby warrant ownership and control of a certain herd of dairy cattle, and gives permission to the Dairy Herd Improvement Association (DHIA) to allow NADDS of Michigan to examine the herd's production and somatic cell count records with the provision the records will remain confidential between DHIA, NADDS and no reference by either name or herd number will be permitted, published or otherwise released to the general public at any time. However, the material referred to may be used and otherwise utilized for scientific purposes, including publication, provided said herd's identity is protected from public disclosure. Your cooperation is completely voluntary, with no penalty for declining to participate.

Signature _____ Date _____

FORM 2 - DAIRY

Monthly Inventory and Producer Cost Report
National Animal Health Monitoring System

Print Clearly with Pen

Producer Code: 22 : : 20 : VMO: Interview Date: / / Report for the Month of

CATTLE INVENTORY:

A) Calves (birth to weaning)

Last Month + Live Born + # Bought - # Sold - # Weaned - # Died = # at End
 + + - - - =

B) Young Stock (weaned to first calving)

Last Mon + Newly Weaned + # Bought - # Sold - Disease - Non-Dis. - # - # = # at End
 + + - - - - - =

C) Cows (all cows & heifers that have calved)

Last Mon + 1st. Calf + # Bought - # Sold - Non-Dis. - C. sease - # - # = # at End
 + + - - - - - =

D) Bulls (for breeding purposes)

Last Mon + # Bought - # Sold - # Culled - # Died = # at End
 + - - - =

PRODUCER COSTS OF DOING BUSINESS:

Item	\$ Cost	Hours of Labor
Veterinary Consultation	\$ <u> </u>	<u> </u> hours
Milking Machine Maintenance	\$ <u> </u>	<u> </u> hours
Other: <u> </u> (DO NOT include test dip, etc)	\$ <u> </u>	<u> </u> hours

Milk Sold: pounds, at \$ / cwt (net price)Somatic Cell Count/Score: From: DHIA MMPA WMT Other:
(circle one, please)Bacteria Count: Hired Labor Wage Rate: \$ / hourNumber of Form 3s Submitted this month:

****Print Clearly with Pen****

Report for the Month of _____

[illegible]

VACCINES ADMINISTERED THIS MONTH:						
<u>Disease /</u> <u>Condition</u>	<u>Vaccine,</u> <u>Drug, or</u> <u>Procedure</u>	<u>Price/Dose</u>	<u># Head</u>	<u>Age Group*</u>	<u>Labor Hrs</u>	<u>Vet Cost</u>
		\$			hrs	\$
		\$			hrs	\$
		\$			hrs	\$
		\$			hrs	\$
		\$			hrs	\$
		\$			hrs	\$
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		\$			hrs	\$
		\$			hrs	\$
		\$			hrs	\$
		\$			hrs	\$

* - Age Groups = A) Calves, B) Young Stock, C) Cows, D) Bulls

FORM 3 - DAIRY

Monthly Disease Cost Report
National Animal Health Monitoring System

Print Clearly with Pen

Producer Code: 22 : : 20 : VMO: Interview Date: / /

Report for the Month of

1) Disease or Condition:

Describe signs observed and affected body parts:

2) Diagnosis affirmed by (check all that apply):

Owner/Operator VMO Private Practitioner Lab

Other (please specify):

3) Age Affected: A) Calves B) Young Stock C) Cows D) Bulls E) Calves born Dead
(circle one, please)

4) NUMBER OF CASES, AND COSTS INCURRED:

a) # Cases from Last Month:

b) # New Cases This Month: +

c) # Cases Recovered: -

d) # Cases which Died of this disease: - Loss of \$

e) # Cases Culled for this disease: - Loss of \$

f) Total Number of Cases at End of Month:

g) Weight Loss lbs. Loss of \$

h) Veterinary Service: \$

i) Vet supervised Drugs: \$ Owner Discretion Drugs: \$

j) Cost of Carcass Disposal: \$

k) Hours of Labor for Treatment: hrs

l) Number of Calves born Dead: Loss of \$ for calf(s)

m) Pounds of Milk Discarded: lbs Production Loss lbs

List Drugs Used below (please try to rank according to frequency of use)

National Animal Disease Surveillance

Producer's Daily Birth, Death and Disease Log _____, _____
Month Year

[illegible]

APPENDIX B

Table B.1 Disease groupings used in NAHMS in Michigan in round I, 1986/87.

Group	Composition
Gastrointestinal	Bloat, coccidiosis, constipation, displaced abomasum, diarrhea, enteritis, enterotoxemia, hardware, indigestion, intestinal obstruction, intestinal hemorrhage, intestinal infections, pneumoenteritis, polyphagia, ulcers, actinomycosis
Respiratory	Pneumonia, respiratory problems NOS*
Lameness	Lameness, foot rot, corns
Metabolic/nutritional	Acidosis, downer cow syndrome, ketosis, low magnesium, milk fever, nutritional deficiency, overweight, polyphagia, selenium deficiency, vitamin E deficiency, white muscle disease
Mastitis	Clinical mastitis, septic mastitis, toxic mastitis
Breeding problems	Anestrus, cystic ovaries, follicular cysts, false pregnancy, metritis, pyometra, repeat breeder, reproductive problems NOS*, vaginitis
Birth problems	Abortion, dystocia, prolapsed uterus, retained placenta, uterine torsion, vaginal tears
Multiple system	Abscesses, accidents, agalactia, allergies, encephalitis, fever, infections NOS, injuries NOS, handling injuries, tail injuries, lethargy, no milk letdown, malignant lymphoma, navel ill, neonatal death NOS, neoplasm, disease NOS, off feed, peritonitis, poisoning, poor condition, umbilical hernia, weakness, weight loss
Integumental	External parasites, fungal skin infections, hematomas, mycotic dermatitis
Urogenital system	Nephritis, urinary tract infections NOS

*NOS = not otherwise specified.

APPENDIX C

Quick Basic programs for stochastic epidemic simulation

```

DECLARE SUB EXPON (MEAN!, XVAR!)
DECLARE SUB TRIDIS (A!, B!, C!, VALCUR!)
DECLARE SUB DELLVFS (RIN!, ROUT!, ST!(), STRG!, PLR!, DEL!, DT!, K!)
*****
** PROGRAM DDDBIT - DISEASE USING DISTRIBUTED DELAY - 5/16/89
*****
** THIS PROGRAM MODELS DISEASE AND OTHER PRESSURES ON POPULATION
** (ROUTINE CULLS, GROSS MORTALITY). THE DISEASE PROCESSES
** (INFECTION AND RECOVERY) ARE MODELLED USING DISTRIBUTED DELAYS
** ADJUSTED FOR POPULATIONS AND PREVIOUS LEVELS OF INFECTION
*****
**      VARIABLE DICTIONARY (ALPHABETIZED)      **
*****      VARIABLES SET BY USER      *****
** BETAMAX : MAXIMUM VALUE THAT BETA CAN ASSUME
** BETAMIN : MINIMUM VALUE THAT BETA CAN ASSUME
** IDT%    : NUMBER OF DIVISIONS OF T FOR CALCULATIONS (1/DT)
** INF DUR% : NUMBER OF DAYS INFECTION LASTS (DURATION)
** KI      : NUMBER OF STAGES FOR INFECTED POPULATION
** KN      : NUMBER OF STAGES FOR NONINFECTED POPULATION
** MREPRO  : MEAN DISEASE REPRODUCTIVE INDEX
** NDAYS%  : NUMBER OF DAYS IN A RUN
** NRUNS%  : NUMBER OF RUNS TO PERFORM
** OPPN (2) : ORIGINAL POPULATION LEVELS:
**          1: NONINFECTED; 2: INFECTED
** PRDAY%  : PRINT DAILY DATA FLAG ( 0 = NO, 1 = YES )
** STOC%   : DON'T RUN STOCHASTICALLY FLAG ( 0 = RANDOM, 1 = NOT)
*****      VARIABLES SET DURING RUN      *****
** ATTRAT  : ATTACK RATE
** SUMATRT : SUM OF ATTACK RATES FOR AVERAGE CALCULATION
** BETA    : INFECTION CONTROL PARAMETER
** DEL     : CURRENT DELAY FOR DELAY ROUTINES
** DT      : DIVISION OF DAY 1 / IDT%
** ID (2)  : INCIDENCE DENSITY CALCULATION COMPONENTS
**          1: NEW CASES; 2: NUMBER AT RISK
** INFDEL  : DELAY FOR INFECTING PROCESS
** INFOUT  : RATE OF RECOVERY
** PLROUT (2,2) : PROPORTIONAL LOSSES BASED ON AGE AND TYPE OF LOSS
**              (A,B): A = 1: CULLING; 2: DEATH (LOSSES)
**                  B = 1: NONINFECTED; 2: INFECTED
** PLRRTE (2): PROPORTIONAL LOSS RATES:
**            1: CULLING; 2: DEATH (LOSSES)
** PPN (2)  : POPULATION LEVELS ADJUSTED THROUGH RUN (SEE OPPN)
**          1: NONINFECTED; 2: INFECTED
** SINF (KI): STORAGES FOR KI STAGES OF INFECTEDS
** RINI    : ADDITIONS TO POPULATION USED IN INFECTION DELAY
** RINN    : ADDITIONS TO POPULATION USED IN NONINFECTED DELAY
** SNON (KN): STORAGES FOR KN STAGES OF NONINFECTEDS

```

```

** RSUM (2): SUM OF TRANSFERS OF ANIMALS:
**      1: SUM OF INFECTEDS; 2: SUM OF RECOVERIES
** SHFF%   : EPIDEMIC SHUTOFF FLAG ( 0: NO, 1: YES )
** STRG (2) : STORAGE FROM DELAYS: 1: NEW DISEASED; 2: NEW RECOVERIES
** WELOUT   : RATES OF INFECTION
*****
** PREPARE FOR RUN
  CLEAR
  INPUT "Would you like hard-copy output? ( 1 = Yes, 0 = No ): "; I%
  IF I% = 1 THEN
    PS = "LPT1:"
  ELSE
    PS = "SCRN:" here----
  END IF
  OPEN PS FOR OUTPUT AS #2
  INPUT "Write Histogram to 1: Screen, 2: Printer, or 3: File - "; I%
    IF I% = 1 THEN PS = "SCRN:"
    IF I% = 2 THEN PS = "LPT1:"
    IF I% = 3 THEN INPUT "Enter File Name: "; PS
  OPEN PS FOR OUTPUT AS #3
**
*****
**      INITIALIZE ARRAYS
**
  DIM ID(2), oppn(2), PLROUT(2, 2), PLRRTE(2), ppn(2), RSUM(2)
  DIM STRG(2), BAR(3, 20)
*****
**      PROMPT USER FOR INPUT
**
  INPUT "Enter number of stages in noninfected delay: "; KN
  DIM SNON(KN)
  INPUT "Enter number of stages in infected delay: "; KI
  DIM SINF(KI)
**
**** INPUT POPULATION PARAMETERS
**
100 INPUT "Enter number of UNINFECTED cases to start with: "; oppn(1)
  INPUT "Enter number of INFECTED cases to start with: "; oppn(2)
**** INPUT DISEASE PARAMETERS
**
  INPUT "Enter number of days infection lasts per case: ", INFDUR%
  INPUT "Enter Mean Disease Reproduction Index: ", MREPRO
  INPUT "Enter mean BETA for the distribution;", BETA
**** INPUT SIMULATION PARAMETERS
**
  INPUT "Enter number of runs you wish to perform:", NRUNS%
  INPUT "Enter number of days to run simulation for:", NDAYS%
  INPUT "Enter number of divisions within each day (1/dT):", IDT%
  DT = 1! / IDT%
  INPUT "Run with random variation? ( 1 = Yes, 0 = No ):", ST%
  IF ST% = 1 THEN
    INPUT "Type of distribution: 1 = Triangular, 2 = Standard:", STOC%
    INPUT "Enter minimum value that Beta can assume: "; BETAMIN

```

```

' INPUT "Enter maximum value that Beta can assume: "; BETAMAX
  RANDOMIZE TIMER
ELSE
  STOC% = 0
END IF
SUMATRT = 0!
  SUBR% = INT((oppn(1) / 20) + .5)
  MIN = 0!
  MAX = SUBR%
  FOR I = 1 TO 20
    BAR(1, I) = MIN
    MIN = MAX + 1
    BAR(2, I) = MAX
    MAX = MAX + SUBR%
    BAR(3, I) = 0!
  NEXT I
*****
****          BEGIN RUNS          ****
**
  FOR R = 1 TO NRUNS%
**
** IF MULTIPLE RUNS, PRODUCE A HEADER
  PRINT #2,
  IF NRUNS% > 1 THEN PRINT #2, "Run # "; R
' INITIALIZE ARRAYS AND VARIABLES AT BEGINNING OF EACH RUN
  FOR B = 1 TO 2
    ppn(B) = oppn(B)
    STRG(B) = 0!
    ID(B) = 0!
    RSUM(B) = 0!
    FOR C = 1 TO 2
      PLROUT(C, B) = 0!
    NEXT C
  NEXT B
**
  ' BETA = MREPRO / (ppn(1) * INFDUR%)
  infdel = (1! / (1! - (1! - BETA) ^ ppn(2)))
** INITIALIZE STORAGES FOR DELAY ROUTINE CALLS: UNINFECTED AND
INFECTED
  FOR I = 1 TO KN
    SNON(I) = ppn(1) / KN
  NEXT I
  FOR I = 1 TO KI
    SINF(I) = ppn(2) / KI
  NEXT I
  welout = 0
  INFOUT = 0
  shff% = 0
**** SET DELAYS TO INITIAL VALUES *
  DEL = INFDUR%
  idel = infdel
**** GENERATE PLR- PROPORTIONAL LOSS RATE (CULL AND DEATH RATES)
**
  PLR = PLRRTE(1) + PLRRTE(2)

```

```

*****      LOOP FOR DAYS      *****
**
      FOR D = 1 TO NDAYS%
**** FIRST, CHECK TO SEE IF THE POPULATIONS ARE STILL THERE (SINCE THERE
ARE NO INPUTS) - IF ALL THE ANIMALS ARE GONE, END THE RUN
**
      IF ppn(1) <= 0! OR ppn(2) <= 0! GOTO 900
****      LOOP FOR DIVISIONS WITHIN DAY      *****
      FOR T = 1 TO IDT%
**
**** CALCULATE PLR LOSSES : THIS CAPTURES LOSS FOR EACH TYPE OF
PROCESS
** (THE DELAY ROUTINE DOES NOT FIGURE THESE SEPARATELY
      FOR C = 1 TO 2
        FOR I = 1 TO KN
          PLROUT(C, 1) = PLROUT(C, 1) + (ppn(1) * PLRRTE(C) / idel) * DT
        NEXT I
**
**** IF THE EPIDEMIC IS OFF, INCLUDE THE ANIMALS THAT WOULD HAVE BEEN
INFECTED
**
          IF shff% THEN
            PLROUT(C, 1) = PLROUT(C, 1) + (welout * PLRRTE(C)) * DT
          END IF
        NEXT C
**** CALCULATE PLR LOSSES FOR INFECTED POPULATION
      FOR I = 1 TO KI
        FOR C = 1 TO 2
          PLROUT(C, 2) = PLROUT(C, 2) + (ppn(2) * PLRRTE(C) / DEL) * DT
        NEXT C
      NEXT I
**
**** MODIFY PARAMETERS FOR RECOVERY DELAY
**** GENERATE RINI - ADDITIONS TO INFECTED POPULATION. IF EPIDEMIC IS
OFF, DO NOT ADD NEW CASES FROM THE INFECTING DELAY
**
          IF shff% = 0 THEN
            RINI = welout
          ELSE
            RINI = 0!
          END IF
**** STORE NEWLY RECOVERED CASES FROM PREVIOUS IDT
**
          RSUM(2) = RSUM(2) + (INFOUT * DT)
**** CALL DELAY ROUTINE
**
          CALL DELLVFS(RINI, RT, SINF(), S, PLR, DEL, DT, KI)
**** STORE VALUES
** STORE NUMBER OF ANIMALS LEFT IN INFECTED STATE
          STRG(2) = S
**** STORE RATE OF RECOVERY
          INFOUT = RT
**** PREPARE TO INFECT (DELAY WILL WORK TO ADD DISEASE
**** STORE NUMBER OF NEWLY INFECTED CASES FROM PREVIOUS IDT%

```

```

        IF shff% = 0 THEN RSUM(1) = RSUM(1) + (welout * DT)
**
**** STORE VALUES NECESSARY FOR CALCULATING INCIDENCE DENSITY
        ID(1) = ID(1) + RT * DT
        ID(2) = ID(2) + ppn(1) * DT
**** CALL DELAY ROUTINE: CREATES NEW SICK CASES
** FROM POPULATION THROUGH THE PLR
        CALL DELLVFS(RINN, RT, SNON(), S, PLR, idel, DT, KN)
**
**** STORE VALUES
** STORE NUMBER OF ANIMALS LEFT IN UNINFECTED STATE
        STRG(1) = S
**** STORE NEW RATE OF INFECTION
        welout = RT
**** STORE NEW POPULATION VALUES FOR EACH DISEASE STATE
**
        FOR B = 1 TO 2
            ppn(B) = STRG(B)
        NEXT B
**** IF EPIDEMIC IS OFF, GENERATE RINN - "UNINFECT" THE POPULATION
        IF shff% = 1 THEN
            RINN = welout
        ELSE
            RINN = 0!
        END IF
        NEXT T
**** IF REQUESTED, RANDOMIZE THE BETA TERM
**
        IF STOC% = 0 THEN BETAP = BETA
        IF STOC% = 1 THEN
            CALL EXPON(BETA, BETAP)
            CALL TRIDIS(BETAMIN, BETA, BETAMAX, BETAP)
        END IF
        IF STOC% = 2 THEN BETAP = RND
**** BREAK OUT OF LOOP IF BOTH BETA AND PPN (2) ARE TOO SMALL
**
        IF ((1! - BETAP) ^ ppn(2)) = 1! THEN
            PRINT #2, "Beta and Sick Population too small "; D, BETAP, ppn(2)
            GOTO 900
        END IF
**** GENERATE NEW INFECTION DELAY
***
        idel = (1! / (1! - (1! - BETAP) ^ ppn(2)))
**SWITCH OFF EPIDEMIC IF DISEASE REPRODUCTION INDEX FALLS OFF
        IF SHFF% = 0 AND INFOUT > (PPN(1) / IDEL) THEN
            IF shff% = 0 AND INFOUT > welout THEN
                shff% = 1
                PRINT #2, "Epidemic off on day "; D, "Sick "; RSUM(1)
                GOTO 800
            END IF
**
**** IF SELECTED, PRINT DAILY RESULTS
        IF PRDAY% THEN
            PRINT #2, "Day "; D; "Not Sick "; ppn(1), "Sick "; ppn(2);

```

```

"Total "; (ppn(1) + ppn(2))
    PRINT #2, "Recovered out: "; RSUM(2), "Dead/Culled: ";
(PLROUT(1, 1) + PLROUT(1, 2)); "/"; (PLROUT(2, 1) + PLROUT(2, 2))
    END IF
NEXT D
800 ' come here if epid. stops
**** CALCULATE AND SUM ATTACK RATE(S)
**
ATTRAT = RSUM(1) / (oppn(1) + oppn(2))
SUMATRT = SUMATRT + ATTRAT
**** CAPTURE NEW CASES IN HISTOGRAM GENERATION
    FOR I = 1 TO 20
        IF RSUM(1) >= BAR(1, I) THEN
            IF RSUM(1) <= BAR(2, I) THEN
                BAR(3, I) = BAR(3, I) + 1
            END IF
        END IF
    NEXT I
**** PRINT OUT RESULTS AT END OF RUN
**
900 IF D > NDAYS% THEN D = NDAYS%
'   PRINT #2, D; " Days Run, ", "Total at End"; ( PPN (1) + PPN (2) )
'   PRINT #2, "Total Sick"; RSUM (1), "Total Recovered"; RSUM (2)
'   PRINT #2, "Beta P: "; BETAP; " Attack Rate: "; ATTRAT
'   PRINT #2, "Culling: "; ( PLROUT (1,1) + plrout (1,2) ), "Dying:
"; ( PLROUT (2,1) + plrout (2,2) )
    PRINT #2, "Conservation Check: "; (ppn(1) + ppn(2) + RSUM(2) +
PLROUT(1, 1) + PLROUT(1, 2) + PLROUT(2, 1) + PLROUT(2, 2))
    PRINT #2, "percent error: "; (100 * ((ppn(1) + ppn(2) + RSUM(2)
+ PLROUT(1, 1) + PLROUT(1, 2) + PLROUT(2, 1) + PLROUT(2, 2)) -
(oppn(1) + oppn(2))) / (oppn(1) + oppn(2)))
NEXT R
**** PRINT OUT AVERAGE ATTACK RATE FOR RUNS
    PRINT #2,
    PRINT #2, "Average Attack Rate for "; NRUNS%; " Runs = "; (SUMATRT
/ NRUNS%)
    PRINT #2,
**** PRINT OUT HISTOGRAM
**
A$ = " ### : ### - ### : "
PRINT #3, " Runs      Cases      Number of Epidemics of
Indicated Size"
    FOR I = 1 TO 20
        PRINT #3, USING A$; BAR(3, I), BAR(1, I), BAR(2, I);
        IF BAR(3, I) > 0 THEN
            FOR J = 1 TO BAR(3, I)
                PRINT #3, "**";
            NEXT J
        END IF
        PRINT #3,
    NEXT I
INPUT "Run again? ( 1 = Yes, 0 = No ): "; YN%
IF YN% GOTO 100
END

```

```

SUB EXPON (MEAN, XVAR) STATIC
*****
*
* THIS SUBROUTINE COMPUTES AN EXPONENTIALLY DISTRIBUTED RANDOM
VARIABLE
* MEAN   : THE EXPECTED VALUE OF THE VARIABLE
* XVAR   : THE EXPONENTIALLY DISTRIBUTED RANDOM VARIABLE
*****
*
      "FOR A = 1 TO 3
      RRR = RND
      XVAR = -MEAN * LOG(RRR)
      "NEXT A
END SUB
STOP

' ** SUBROUTINE DELLVFS - DISTRIBUTED DELAY WITH TIME VARIATIONS -
5/12/89
' *****
' ***          VARIABLE DICTIONARY
' *****
' ***** FROM MAIN PROGRAM CALL:
' ** RIN   : INPUT TO POPULATION DURING DELAY
' ** ROUT  : EXIT DUE TO DELAY
' ** ST (K) : STORAGES FOR K STAGES
' ** STRG   : NUMBER OF UNITS LEFT IN POPULATION AFTER DELAY
' ** PLR    : PROPORTIONAL LOSS RATE
' ** DEL    : CURRENT DELAY
' ** DT     : DIVISION OF DAY
' ** K      : NUMBER OF STAGES IN DELAY
' ***** INTERNALLY GENERATED
' ** BDD1   : PROPORTIONAL LOSS FACTOR
' *****
' **
      SUB DELLVFS (RIN, ROUT, ST(), STRG, PLR, DEL, DT, K) STATIC
' **
' *****
' **
' ** SET PROPORTIONAL LOSS FACTOR
      BDD1 = PLR + K / DEL
REM
      K2 = K - 1
' **
' ** LOOP FOR III% SUBINTERVALS
' **
' ** LOOP TO COVER THE STAGES (LAST STAGE IS HANDLED AS SPECIAL CASE
TO
' ** COVER THE EFFECT OF ADDITIONS TO POPULATION FROM RIN)
' **
      FOR I = 1 TO K2
' **
' ** CALCULATE NEW STORAGES
' **
      ST(I) = ST(I) + DT * ((ST(I + 1) * (K / DEL)) - (ST(I) * BDD1))

```

```

' **
      NEXT I
' **
' ** CALCULATE NEW STORAGES FOR SPECIAL CASE AT LAST STAGE
' **
      ST(K) = ST(K) + DT * (RIN - (ST(I) * BDD1))
' **
' ** FILL STORAGE WITH TOTAL NUMBER OF UNITS LEFT AT END OF DELAY
' ** ( UNITS = RATE * DELAY / NUMBER OF STAGES )
' **
      STRG = 0!
' **
      FOR I = 1 TO K
        STRG = STRG + ST(I)
      NEXT I
' **
' ** SET ROUT : LOSS DUE TO DELAY
' **
      ROUT = ST(1) / (DEL / K)
' **
      END SUB

```

APPENDIX D

Quick Basic code for simulation of disease in a Dairy herd

```

DECLARE SUB EXPON (MEAN(), XVAR())
DECLARE SUB ECON (OPPN(), TAGE(), P%, R, I, IDT%, N!, DT!, NDAY%, PPN(),
PLROUT(), VRATE(), SUMBORN!, SUMBUY(), NPV, MN%, NPVVAR())
DECLARE SUB PLRSET (A!, K!, D!, POP!, SH%, DOUT!, DEL!, DT!, mort!(), CULL!(),
PLROUT(), SELL())
DECLARE SUB DELLVYS (AIN!, DIN!(), R!(), AOUT!, DOUT!(), STRG!, DEL!, MDEL!,
PLR!, DT!, KA!, kb!)
DECLARE SUB DELLVFS (RIN!, ROUT!, ST!(), STRG!, PLR!, DEL!, DT!, K!)

```

```

' *****
' ***** PROGRAM FINRUN.BAS 5/10/90 *****
' *****
  DIM OPPN(3, 3), PPN(3, 5), TPOP(3), BUY(3), WEAN(5), FRESH(5)
  DIM SUMINF(3), BETA(3), betaP(3), BETAMAX(3), ASUMBUY(3), SELL(3)
' OPPN (A,B) : ORIGINAL POPULATION - A = 1) CALVES; 2) YOUNG; 3) COWS
'           : DISEASE STATUS      - B = 1) UNINFECTED; 2) INFECTED;
'                               3) IMMUNE FROM DISEASE OR COLOSTRUM
' PPN (A,C) : POPULATION PROCESS - A = 1) CALVES; 2) YOUNG; 3) COWS
'           : DISEASE STATE      - C = 1) RECOVERED; 2) IMMUNE;
'                               3) INFECTED; 4) VACCINATED/COLOSTRUM; 5) WELL
' TPOP (A)  : TOTAL POPULATION  - A = 1) CALVES; 2) YOUNG; 3) COWS
' STOC%     : DON'T RUN STOCHASTICALLY FLAG ( 0 = RANDOM, 1 = NOT)
' BETA      : THE RANDOMLY GENERATED SECONDARY ATTACK RATE
' BETAP     : THE SECONDARY ATTACK RATE PREDICTED FROM THE
REGRESSION
'           MODEL FOR THE ANNUAL INCIDENCE DENSITY, ASSUMING
ONE
'           INFECTED IS PRESENT ON THE AVERAGE
' BETAMAX   : MAXIMUM VALUE THAT BETA CAN ASSUME
' BETAMIN   : MINIMUM VALUE THAT BETA CAN ASSUME
' BUY (A)   : PURCHASE RATE      - A = 1) CALVES; 2) YOUNG; 3) COWS
' WEAN (D)  : WEANING RATE       - D = 2) IMMUNE; 3) INFECTED;
'                               4) VACCINATED; 5) WELL
' FRESH (C) : FRESHENING RATE    - C = 1) RECOVERED; 2) IMMUNE;
'                               3) INFECTED; 4) VACCINATED; 5) WELL
' DIM CULL(3, 3), mort(3, 2), MDEL(5), DISDEL(5), Disout(3, 5)
' CULL (A,C) : CULLING RATE      - A = 1) CALVES; 2) YOUNG; 3) COWS
'           : - C = 1) RECOVERED; 2) IMMUNE;
'                               3) INFECTED; 4) VACCINATED; 5) WELL
' MORT (A,B) : MORTALITY RATE    - A = 1) CALVES; 2) YOUNG; 3) COWS
'           : - B = 1) UNINFECTED; 2) INFECTED
' DISDEL (C) : DISEASE DELAYS    - C = 1) RECOVERED; 2) IMMUNE;
'           : 3) INFECTED; 4) VACCINATED; 5) WELL
' DISOUT (A,C) DISEASE MOVEMENTS - A = 1) CALVES; 2) YOUNG; 3) COWS
'           : - C = 1) RECOVERED; 2) IMMUNE;
'           : 3) INFECTED; 4) VACCINATED; 5) WELL
' DIM AGEOUT(2, 5), PLROUT(3, 4), KK(5), VRATE(3), VOUT(3), SH%(3)
' AGEOUT (A,C) AGE GROUP MOVEMENTS - A = 1) CALVES; 2) YOUNG
'           : - C = 1) RECOVERED; 2) IMMUNE;
'           : 3) INFECTED; 4) VACCINATED; 5) WELL
' PLROUT (A,D) PLR LOSSES        - A = 1) CALVES; 2) YOUNG; 3) COWS
'                               D = 1) NON-RESPIRATORY MORTALITY
'                               = 2) NON-RESPIRATORY CULL, SALES
'                               = 3) RESPIRATORY MORTALITY
'                               = 4) RESPIRATORY CULL

```

```

' KK (C) : STAGES FOR DISEASE - C = 1) RECOVERED; 2) IMMUNE;
' : 3) INFECTED; 4) VACCINATED; 5) WELL

' VRATE (A) : VACCINATION RATES - A = 2) YOUNG; 3) COWS
VOUT (A) : NEWLY VACCINATEDS - A = 2) YOUNG; 3) COWS
' SH% (A) : SHUT OFF INFECTION - A = 1) CALVES; 2) YOUNG; 3) COWS
DIM ROUT(3), TROUT(3), IDmean(3), ID(3), TAGE(3), TTAGE(3), SUMOUT(3),
TSUMOUT(3), PROB(3)
' PROB(A) : PROBABILITY OF A NEW INFECTIVE BEING ADDED ANY
MONTH
' ROUT (A) : NUMBERS INF'D/MON - A = 1) CALVES; 2) YOUNG; 3) COWS
' TROUT (A) : NUMBERS INF'D/YR - A = 1) CALVES; 2) YOUNG; 3) COWS
' IDmean(a) : THE MEAN PREDICTED ID FOR EXPON DISTRIBUTION
' ID (A) : INCIDENCE DENSITIES - A = 1) CALVES; 2) YOUNG; 3) COWS
' TAGE (A) : NUMBERS AGING UP/MN - A = 1) CALVES; 2) YOUNG; 3) COWS
' TTAGE (A) : NUMBERS AGING UP/YR - A = 1) CALVES; 2) YOUNG; 3) COWS
' SUMOUT (A) : SUM OF PLR LOSSES/M - A = 1) CALVES; 2) YOUNG; 3) COWS
' TSUMOUT (A) : SUM OF PLR LOSSES/Y - A = 1) CALVES; 2) YOUNG; 3) COWS
DIM MID(3), MR(3), AMID(3), AMR(3), SUMBUY(3), AMON(3), tamon(3)
DIM mid2(3), AMON2(3), tamon2(3), AMID2(3), mr2(3), SAMID(3), SAMID2(3)
' MID (A) : INCIDENCE DENSITY/M - A = 1) CALVES; 2) YOUNG; 3) COWS
' MR (A) : MONTHLY RISK - A = 1) CALVES; 2) YOUNG; 3) COWS
' AMID (A) : ANNUAL IN. DENSITY - A = 1) CALVES; 2) YOUNG; 3) COWS
' AMR (A) : ANNUAL RISK - A = 1) CALVES; 2) YOUNG; 3) COWS
' SUMBUY (A) : NUMBERS PURCHASED - A = 1) CALVES; 2) YOUNG; 3) COWS
' AMON (A) : SUM ANIMAL MONTHS/M - A = 1) CALVES; 2) YOUNG; 3) COWS
' TAMON (A) : SUM ANIMAL MONTHS/Y - A = 1) CALVES; 2) YOUNG; 3) COWS
*****
' PREPARE FOR RUN
'
INPUT "Write OUTPUT to 1: Screen, 2: Printer, or 3: File - "; I%
IF I% = 1 THEN P$ = "SCRN:"
IF I% = 2 THEN P$ = "LPT1:"
IF I% = 3 THEN INPUT "Enter File Name: "; P$
" OPEN P$ FOR OUTPUT AS #2
'
*****
' INPUT USER VARIABLES
'
KK(1) = 6: KK(2) = 6: KK(3) = 6: KK(4) = 6: KK(5) = 6
KA = 6
DIM DOUTYS(KA, 5), PPNYS(KA, 5)
DIM DYS(KA), YOLDR(KA), YOLDV(KA), DIN(KA)
'
KMAX = 0
FOR D = 2 TO 5
IF KK(D) > KMAX THEN KMAX = KK(D)
NEXT D
DIM CALF(5, KMAX), COW(5, KMAX), P(KMAX)
IF KK(1) > KMAX THEN KMAX = KK(1)
DIM YNG(5, KA, KMAX), PY(KA, KMAX)
' **
100 INPUT "Do you want MONTHLY PRINT OUT also (1/0)?:"; MN%
INPUT "Would you like to run $ FINANCES? (Y/N)?:"; E$
INPUT "Run with random variation? ( 1= Yes, 0 = No )?"; STOC%
IF STOC% = 1 THEN
PRINT #2, "RANDOMIZE ON 3, MONTHLY"

```

```

' VRATE (A) : VACCINATION RATES - A = 2) YOUNG; 3) COWS'
VOUT (A) : NEWLY VACCINATEDS - A = 2) YOUNG; 3) COWS
' SH% (A) : SHUT OFF INFECTION - A = 1) CALVES; 2) YOUNG; 3) COWS
  DIM ROUT(3), TROUT(3), IDmean(3), ID(3), TAGE(3), TTAGE(3),
SUMOUT(3), TSUMOUT(3), PROB(3)
' PROB(A) : PROBABILITY OF A NEW INFECTIVE BEING ADDED ANY
MONTH
' ROUT (A) : NUMBERS INF'D/MON - A = 1) CALVES; 2) YOUNG; 3) COWS
' TROUT (A) : NUMBERS INF'D/YR - A = 1) CALVES; 2) YOUNG; 3) COWS
' IDmean(a) : THE MEAN PREDICTED ID FOR EXPON DISTRIBUTION
' ID (A) : INCIDENCE DENSITIES - A = 1) CALVES; 2) YOUNG; 3) COWS
' TAGE (A) : NUMBERS AGING UP/MN - A = 1) CALVES; 2) YOUNG; 3)
COWS
' TTAGE (A) : NUMBERS AGING UP/YR - A = 1) CALVES; 2) YOUNG; 3)
COWS
' SUMOUT (A) : SUM OF PLR LOSSES/M - A = 1) CALVES; 2) YOUNG; 3)
COWS
' TSUMOUT (A) : SUM OF PLR LOSSES/Y - A = 1) CALVES; 2) YOUNG; 3)
COWS
  DIM MID(3), MR(3), AMID(3), AMR(3), SUMBUY(3), AMON(3), tamon(3)
  DIM mid2(3), AMON2(3), tamon2(3), AMID2(3), mr2(3), SAMID(3), SAMID2(3)
' MID (A) : INCIDENCE DENSITY/M - A = 1) CALVES; 2) YOUNG; 3)
COWS
' MR (A) : MONTHLY RISK - A = 1) CALVES; 2) YOUNG; 3) COWS
' AMID (A) : ANNUAL IN. DENSITY - A = 1) CALVES; 2) YOUNG; 3) COWS
' AMR (A) : ANNUAL RISK - A = 1) CALVES; 2) YOUNG; 3) COWS
' SUMBUY (A) : NUMBERS PURCHASED - A = 1) CALVES; 2) YOUNG; 3)
COWS
' AMON (A) : SUM ANIMAL MONTHS/M - A = 1) CALVES; 2) YOUNG; 3)
COWS
' TAMON (A) : SUM ANIMAL MONTHS/Y - A = 1) CALVES; 2) YOUNG; 3)
COWS
' *****
'
' PREPARE FOR RUN
'
  INPUT "Write OUTPUT to 1: Screen, 2: Printer, or 3: File - "; I%
  IF I% = 1 THEN P$ = "SCRN:"
  IF I% = 2 THEN P$ = "LPT1:"
  IF I% = 3 THEN INPUT "Enter File Name: "; P$
  OPEN P$ FOR OUTPUT AS #2
' *****
'
' INPUT USER VARIABLES
'
KK(1) = 6: KK(2) = 6: KK(3) = 6: KK(4) = 6: KK(5) = 6
KA = 6
  DIM DOUTYS(KA, 5), PPNYS(KA, 5)
  DIM DYS(KA), YOLDR(KA), YOLDV(KA), DIN(KA)
'
  KMAX = 0
  FOR D = 2 TO 5
    IF KK(D) > KMAX THEN KMAX = KK(D)
  NEXT D
  DIM CALF(5, KMAX), COW(5, KMAX), P(KMAX)
  IF KK(1) > KMAX THEN KMAX = KK(1)
  DIM YNG(5, KA, KMAX), PY(KA, KMAX)
' **

```

```

100  INPUT "Do you want MONTHLY PRINT OUT also (1/0)"; MN%
      INPUT "Would you like to run $ FINANCES? (Y/N)"; E$
      INPUT "Run with random variation? ( 1= Yes, 0 = No )"; STOC%
      IF STOC% = 1 THEN
        PRINT #2, "RANDOMIZE ON ", MONTHLY"
        RANDOMIZE TIMER
      END IF

      INPUT "Enter number of runs you wish to perform: "; NRUNS%
      INPUT "Enter number of days each run lasts: "; NDAYS%
      INPUT "Enter number of divisions per day (1/dt): "; IDT%
      DT = 1 / IDT%
      NID = NRUNS% * (NDAYS% / 360) 'number of aID's run if >360 days
      DIM IDVAR(3, NID), SUMSQU(3), SUMVAL(3), VARIAN(3),
      NPVVAR(NRUNS%)
      ' **
      ' SET STARTING SECONDARY ATTACK RATES AS A FUNCTION OF
      ANNUAL ID'S
      PROB(1) = .15: PROB(2) = .07: PROB(3) = .06
      ,
      INPUT "COMMENT"; CM$
      "END IF
FOR P% = 1 TO 1
  IF P% = 1 THEN
    P$ = "basereal"
    IF I% = 3 THEN OPEN P$ FOR OUTPUT AS #2
    PRINT #2, "*****FINRUN*****"; P%
    OPPN(1, 1) = 11: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    OPPN(2, 1) = 41: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    OPPN(3, 1) = 81: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    PROB(1) = 0: PROB(2) = 0: PROB(3) = 0
    betaP(1) = .0000001: betaP(2) = .000000001#: betaP(3) = .000000001#
    IDmean(1) = .00000001#: IDmean(2) = .000000001#: IDmean(3) = .000000001#
    CM$ = "BASELINE_REAL "
  END IF
  IF P% = 2 THEN
    P$ = "D1REAL"
    CM$ = "DISEASE1_REAL"
    IF I% = 3 THEN OPEN P$ FOR OUTPUT AS #2
    PRINT #2, "*****FINRUN*****"; P%
    OPPN(1, 1) = 11: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    OPPN(2, 1) = 41: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    OPPN(3, 1) = 81: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    PROB(1) = .15: PROB(2) = .07: PROB(3) = .06
    betaP(1) = .106#: betaP(2) = .019: betaP(3) = .005
    IDmean(1) = .03#: IDmean(2) = .005: IDmean(3) = .002
  END IF
  IF P% = 3 THEN
    P$ = "D2REAL"
    CM$ = "DISEASE2_REAL"
    IF I% = 3 THEN OPEN P$ FOR OUTPUT AS #2
    PRINT #2, "*****FINRUN*****"; P%

    OPPN(1, 1) = 11: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    OPPN(2, 1) = 41: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    OPPN(3, 1) = 81: OPPN(1, 2) = 0: OPPN(1, 3) = 0
    PROB(1) = .15: PROB(2) = .07: PROB(3) = .06

```

```

betaP(1) = 3#: betaP(2) = .019: betaP(3) = .01
IDmean(1) = .08#: IDmean(2) = .005: IDmean(3) = .0034
END IF
IF P% = 4 THEN
  P$ = "d3realTST"
  IF I% = 3 THEN OPEN P$ FOR OUTPUT AS #2
  PRINT #2, "*****FINRUN*****"; P%
  OPPN(1, 1) = 9: OPPN(1, 2) = 2: OPPN(1, 3) = 0
  OPPN(2, 1) = 39: OPPN(1, 2) = 2: OPPN(1, 3) = 0
  OPPN(3, 1) = 79: OPPN(1, 2) = 2: OPPN(1, 3) = 0
  PROB(1) = .15: PROB(2) = .07: PROB(3) = .06
  betaP(1) = .2: betaP(2) = .04: betaP(3) = .01#
  IDmean(1) = .03: IDmean(2) = .005: IDmean(3) = .002
  CM$ = "DISEASE3_REAL "
END IF
IF P% = 5 THEN
  P$ = "D4REALTST"
  IF I% = 3 THEN OPEN P$ FOR OUTPUT AS #2
  PRINT #2, "*****FINRUN*****"; P%
  OPPN(1, 1) = 9: OPPN(1, 2) = 2: OPPN(1, 3) = 0
  OPPN(2, 1) = 39: OPPN(1, 2) = 2: OPPN(1, 3) = 0
  OPPN(3, 1) = 79: OPPN(1, 2) = 2: OPPN(1, 3) = 0
  PROB(1) = .15: PROB(2) = .07: PROB(3) = .06
  betaP(1) = .2: betaP(2) = .04: betaP(3) = .01#
  IDmean(1) = .03: IDmean(2) = .005: IDmean(3) = .002
  CM$ = "DISEASE4.REAL "
END IF
' ** CULL AND MORTALITY RATES - AVERAGES
  WEANAGE = 120: WEANAGE2 = 140
  FRESHAGE = 27: FRESH2 = 29 ' IN MONTHS
  " VRATE(1) = .0000: FOR A = 2 TO 3: VRATE(A) = .0018: NEXT A
  BUY(1) = 0: BUY(2) = 0: BUY(3) = 0
  mort(1, 1) = .001: mort(1, 2) = .02 '=CASE FATALITY RATE
  CULL(1, 1) = 0: CULL(1, 2) = .000006: SELL(1) = 0
  ,
  mort(2, 1) = .000024: mort(2, 2) = .013 '=CASE FATALITY RATE
  CULL(2, 1) = 0: CULL(2, 2) = 83: SELL(2) = 0
  ,
  mort(3, 1) = .000106: mort(3, 2) = .000028 '= CASE FATALITY RATE
  CULL(3, 1) = .0008: CULL(3, 2) = 0
  CULLBASE = CULL(3, 1)
  IF P% = 5 THEN
    mort(1, 2) = .07: mort(2, 2) = .07: mort(3, 2) = .07
    PRINT #2, "HI CASE FATALITY IN all ages "
  END IF
  BIRTH = (1 / 360) * .43
  FOR R = 1 TO NRUNS%
  ,
    IF NRUNS% > 1 THEN
      PRINT #2, "Run "; R: PRINT #2,
    END IF
  , **
  IMDUR = 360: INFDUR = 7: VDUR = 270
  DISDEL(1) = 0
  DISDEL(2) = IMDUR
  DISDEL(3) = INFDUR
  DISDEL(4) = VDUR
  DISDEL(5) = 0

```

```

' DISDEL (1) AND DISDEL (5) WILL CHANGE AT EACH DT
' CONVERT WEANING AGE IN DAYS TO DAILY WEANING RATES
FOR I = 1 TO 5: WEAN(I) = 1 / WEANAGE: NEXT I
    WEAN(2) = 1 / WEANAGE2
' CONVERT FRESHENING AGE AND WEANING AGE INTO DAILY RATES
    FRESHR = 1 / ((FRESHAGE * 30) - WEANAGE)
FOR I = 3 TO 5: FRESH(I) = FRESHR: NEXT I
    FRESHRL = 1 / (FRESH2 * 30 - WEANAGE)
FOR I = 1 TO 2: FRESH(I) = FRESHRL: NEXT I

VAGE = 10
,
' CONVERT VACCINATION AGE FROM MONTHS FROM BIRTH TO DAYS
FROM WEANING
,
    VAGE = (VAGE * 30) - (1 / WEAN(5))
,
' ALEV ( # DAYS PER AGE LEVEL IN YOUNG STOCK )
,
    ALEV = ((1 / FRESH(5)) - (1 / WEAN(5))) / KA
,
' CREATE VLEV - AGE LEVEL WHEN YOUNG STOCK WILL BE
VACCINATED
,
    VLEV = INT(VAGE / ALEV)
    IF VLEV < (VAGE / ALEV) THEN VLEV = VLEV + 1
    VYOUT = 0
, **
' INITIALIZE POPULATIONS : BOTH COUNTS AND VALUES FOR DELAY
USE
,
    FOR A = 1 TO 3
        SUMBUY(A) = 0
        ROUT(A) = 0
        TAGE(A) = 0
        SUMOUT(A) = 0
        TPOP(A) = 0
    NEXT A
    A = 1
        PPN(A, 2) = OPPN(A, 3)
        PPN(A, 3) = OPPN(A, 2)
        PPN(A, 5) = OPPN(A, 1)
    A = 3
        PPN(A, 2) = OPPN(A, 3)
        PPN(A, 3) = OPPN(A, 2)
        PPN(A, 5) = OPPN(A, 1)
,
    FOR K2 = 1 TO KA
        PPNYS(K2, 2) = OPPN(2, 3) / KA
        PPNYS(K2, 3) = OPPN(2, 2) / KA
        PPNYS(K2, 5) = OPPN(2, 1) / KA
    NEXT K2
REM ****
    FOR K = 1 TO KMAX
        CALF(3, K) = OPPN(1, 2) / (KK(3))
        CALF(2, K) = OPPN(1, 3) / KK(2)
        COW(3, K) = OPPN(3, 2) / (KK(3))
        COW(2, K) = OPPN(3, 3) / KK(2)

```

```

CALF(5, K) = OPPN(1, 1) / (KK(5))
COW(5, K) = OPPN(3, 1) / (KK(5))
FOR K2 = 1 TO KA
  YNG(2, K2, K) = PPNYS(K2, 2) / KK(2)
  YNG(3, K2, K) = PPNYS(K2, 3) / (KK(3))
  YNG(5, K2, K) = PPNYS(K2, 5) / (KK(5))
NEXT K2
NEXT K
FOR D = 1 TO 5
  TPOP(A) = TPOP(A) + PPN(A, D)
NEXT D

, *****
,
  FOR N = 1 TO NDAYS%
, *****
,
  RANDOMIZE STARTING NUMBER OF INFECTEDS AND SAR'S
, **
,
  FOR A = 1 TO 3
    IF STOC% = 0 THEN BETA(A) = betaP(A)
    ID(A) = IDmean(A)
  NEXT A
  IF STOC% = 1 THEN
    IF N = 1 OR (N MOD 30) = 0 THEN
      CALL EXPON(betaP(), BETA())          'RAM
      FOR A = 1 TO 3
        IF RND < PROB(A) THEN
          PPN(A, 3) = PPN(A, 3) + 1
        ELSE PPN(A, 3) = PPN(A, 3)
        END IF
      NEXT A
    END IF
  END IF
,
,
  COW INVENTORY CONTROL **DAILY *****
  DIFF = TPOP(3) - (OPPN(3, 1) + OPPN(3, 2) + OPPN(3, 3))
  DIFFPER = DIFF / (OPPN(3, 1) + OPPN(3, 2) + OPPN(3, 3))
  IF INT(DIFF) > 0 THEN
    CULL(3, 1) = DIFF * (1 / 30) 'Increase cull to DIFF per month
    BUY(3) = 0
  ELSEIF INT(DIFF) = 0 THEN
    CULL(3, 1) = CULLBASE
    BUY(3) = 0
  ELSE
    BUY(3) = -DIFF * (1 / 30) 'buy at DIFF per month
    CULL(3, 1) = CULLBASE
  END IF
,
  YOUNG STOCK INVENTORY CONTROL - SELL DAIRY HEIFERS IF >
  ORIGINAL SIZE
  DIFFYS = TPOP(2) - (OPPN(2, 1) + OPPN(2, 2) + OPPN(2, 3))
  IF INT(DIFFYS) > 0 THEN
    SELL(2) = DIFFYS * (1 / 30)
  ELSE
    SELL(2) = 0
  END IF
, *****
,
  FOR I = 1 TO IDT%

```

```

,
, *****
,
,           COW PROCESSING
,
,   SET VARIABLE FOR ANIMAL AGE GROUP (A)
,
,       A = 3
,
,   SET DISEASE DELAYS FOR COWS
REM** IF ALL 3 GROUPS MIX THEN INCREASE THE NUMBER OF
INFECTIVE CONTACTS
    CONTACT$ = "N"  "applies to all ages
    IF CONTACT$ = "Y" OR CONTACT$ = "y" THEN
        SUMINF(A) = PPN(1, 3) + PPN(2, 3) + PPN(3, 3)
    ELSE
        SUMINF(A) = PPN(A, 3)
    END IF
,
    IF SUMINF(A) >= 1! THEN
        IF BETA(A) < 1! THEN DISDEL(5) = (1! / (1! - (1! - BETA(A)) ^
SUMINF(A)))
        ELSE
            DISDEL(5) = 365 / ID(A)
        END IF
,
,   Compute more accurate # at risk
    AMON2(A) = AMON2(A) + DT * (PPN(A, 5)) / 30!
,
,   HOLD RECOVERING (DISOUT (A,2)) AND UNVACCINATING
(DISOUT(A,4)) COWS
,
    OLDM = Disout(A, 2)
    OLDV = Disout(A, 4)
,
,   LOOP FOR 4 DISEASE STATES ( NO RECOVERED STATE - ASSUME NO
LOSS)
,
    FOR D = 2 TO 5
,
,   SELECT DISEASE DELAY AND NUMBER OF STAGES, AND PUT
WORKING VS OF
,   POPULATION IN P
,
        DEL = DISDEL(D)
        K = KK(D)
        FOR K2 = 1 TO K
            P(K2) = COW(D, K2)
        NEXT K2
,
,   CALCULATE RIN (ADDITIONS): INCLUDES AGING HEIFERS, AND
CHANGES IN
,   DISEASE STATES
,
        RIN = AGEOUT(2, D)
        IF D = 2 THEN RIN = RIN + Disout(A, 3)
        IF D = 3 THEN RIN = RIN + Disout(A, 5)
        IF D = 4 THEN RIN = RIN + VOUT(A)
        IF D = 5 THEN

```

```

      RIN = RIN + OLDM + OLDV + BUY(A) + AGEOUT(2, 1)
      SUMBUY(A) = SUMBUY(A) + (BUY(A) * DT)
    END IF
  ,
  ' IF EPIDEMIC IS OFF (SH%=1), DIVERT 'SICK' ANIMALS BACK TO WELL
  GROUP
  ,
      IF SH%(A) = 1 THEN
        IF D = 3 THEN RIN = AGEOUT(2, D)
        IF D = 5 THEN RIN = RIN + Disout(A, 5)
      END IF
  ,
  ' CALCULATE PLR (PROPORTIONAL LOSS RATE) INCLUDES CULLS
  AND MORTALITY
  ' AND CALL PLRSET TO COUNT UP LOSSES BASED ON TYPE AND
  DISEASE STATE
  ,
      PLR = mort(A, 1) + CULL(A, 1) + SELL(A)
      IF D = 2 THEN PLR = PLR + CULL(A, 2)
      IF D = 3 THEN PLR = PLR + mort(A, 2)
      IF D = 5 THEN PLR = PLR + VRATE(A)
      CALL PLRSET(A, K, D, PPN(A, D), SH%(A), Disout(A, 5), DEL, DT,
mort(), CULL(), PLROUT(), SELL())
  ,
  ' CALCULATE VACCINATIONS
  ,
      IF D = 5 THEN VOUT(A) = PPN(A, D) * VRATE(A)
  ,
  ' CALL DELAY ROUTINE TO ADD NEWS, MOVE ANIMALS THROUGH
  DISEASE STATE,
  ' AND REMOVE LOSSES FROM PLR
  ,
      CALL DELLVFS(RIN, RT, P(), STRG, PLR, DEL, DT, K)
  ,
  ' STORE MOVEMENT (DISOUT) AND NEW POPULATION (PPN). IF ANY
  POPULATION
  ' FIGURES GO < 0, ZERO ALL POPULATIONS
  ,
      Disout(A, D) = RT
      IF STRG > 0 THEN
        PPN(A, D) = STRG
        FOR K2 = 1 TO K
          COW(D, K2) = P(K2)
        NEXT K2
      ELSE
        PPN(A, D) = 0
        FOR K2 = 1 TO K
          COW(D, K2) = 0
        NEXT K2
      END IF
  ,
      NEXT D
  ,
      TPOP(A) = 0
      FOR D = 1 TO 5
        TPOP(A) = TPOP(A) + PPN(A, D)
      NEXT D

```

```

,
' EPIDEMIC CHECK FOR COWS
,
    IF PPN(A, 5) / DISDEL(5) < Disout(A, 3) THEN
        " IF DISOUT(A, 5) < DISOUT(A, 3) THEN
        " IF DISOUT(A, 5) < 1 / DISDEL(3) THEN
        IF SH%(A) = 0 THEN SH%(A) = 1 ' PRINT "Epidemic OFF for Cows,
Day "; n
    ELSE
        IF SH%(A) = 1 THEN SH%(A) = 0 ' PRINT "Epidemic ON for Cows,
Day "; n
    END IF
,
"PRINT #2, "del="; DISDEL(5); "A"; A
"PRINT #2, "DISOUT"; DISOUT(A, 5); "1/INFDEL"; 1 / DISDEL(3); "INFOUT";
DISOUT(A, 3)
' ** UPDATE ROUT
,
    IF SH%(A) = 0! THEN ROUT(A) = ROUT(A) + Disout(A, 5) * DT
    IF ROUT(A) < 0! THEN ROUT(A) = 0!
,
=====
,
    YOUNG STOCK PROCESSING
,
' SET VARIABLE FOR ANIMAL AGE GROUP (A)
,
    A = 2
,
' SET DISEASE DELAYS FOR YOUNG STOCK
,
REM** IF ALL 3 GROUPS MIX THEN INCREASE THE NUMBER OF
INFECTIVE CONTACTS
    IF CONTACT$ = "Y" OR CONTACT$ = "y" THEN
        SUMINF(A) = PPN(1, 3) + PPN(2, 3) + PPN(3, 3)
    ELSE
        SUMINF(A) = PPN(A, 3)
    END IF
,
    IF SUMINF(A) >= 1! THEN
        IF BETA(A) < 1! THEN DISDEL(5) = (1! / (1! - (1! - BETA(A)) ^
SUMINF(A)))
    ELSE
        DISDEL(5) = 365 / ID(A)
    END IF
    DISDEL(1) = DISDEL(5)
,
' Compute more accurate # at risk
    AMON2(A) = AMON2(A) + DT * (PPN(A, 5) + PPN(A, 1)) / 30!
,
' LOOP FOR 5 DISEASE STATES
,
    FOR D = 1 TO 5
,
' SET DISEASE DELAY (DEL), MATURATION DELAY (MDEL) AND
NUMBER OF STAGES,
' AND PUT WORKING VERSION OF POPULATION IN PY

```

```

,
    K = KK(D)
    DEL = DISDEL(D)
    MDEL = KA / ((1 / FRESH(D)) - (1 / WEAN(D)))
    FOR K2 = 1 TO K
        FOR K1 = 1 TO KA
            PY(K1, K2) = YNG(D, K1, K2)
        NEXT K1
    NEXT K2
,
, CALCULATE PLR (PROPORTIONAL LOSS RATE); INCLUDES CULLS AND
MORTALITY
,
    PLR = mort(A, 1) + CULL(A, 1) + SELL(A)
    IF (D = 1) OR (D = 2) THEN PLR = PLR + CULL(A, 2)
    IF D = 3 THEN PLR = PLR + mort(A, 2)
    IF D = 5 THEN PLR = PLR + (VRATE(A) / KA)
,
, CALCULATE AGE INPUTS (AIN) FOR YOUNG STOCK
,
    AIN = 0
    IF D > 1 THEN AIN = AGEOUT(1, D)
    IF D = 5 THEN
        AIN = AIN + BUY(A)
        SUMBUY(A) = SUMBUY(A) + (BUY(A) * DT)
    END IF
,
, CALCULATE DISEASE INPUTS (DIN), AND CALL PLRSET TO COUNT UP
LOSSES BASED ON TYPE AND DISEASE STATE
,
    CALL PLRSET(A, K, D, PPNYS(A, D), SH%(A), Disout(A, 5), DEL,
DT, mort(), CULL(), PLROUT(), SELL())
,
    FOR A2 = 1 TO KA
        IF D = 1 THEN
            YOLDR(A2) = DOUTYS(A2, D)
            DIN(A2) = DOUTYS(A2, 2)
        END IF
        IF D = 2 THEN DIN(A2) = DOUTYS(A2, 3)
        IF D = 3 THEN DIN(A2) = DOUTYS(A2, 5)
        IF D = 4 THEN
            YOLDV(A2) = DOUTYS(A2, D)
            IF A2 = VLEV THEN DIN(A2) = VYOUT
        END IF
        IF D = 5 THEN DIN(A2) = YOLDV(A2) + YOLDR(A2)
,
, IF EPIDEMIC IS OFF, DIVERT 'SICK' ANIMALS BACK TO WELL GROUP
,
    IF SH%(A) = 1 THEN
        IF D = 3 THEN DIN(A2) = 0
        IF D = 5 THEN DIN(A2) = DIN(A2) + DOUTYS(A2, 5) +
YOLDR(A2)
    END IF
,
    NEXT A2
,
    IF D = 5 THEN VYOUT = PPNYS(VLEV, 5) * VRATE(A)

```

```

      TAGE(A) = TAGE(A) + (AGEOUT(A, D) * DT)
' CALL DELAY ROUTINE TO ADD NEW CASES, MOVE ANIMALS
THROUGH BOTH AGE
' AND DISEASE STATES, AND REMOVE LOSSES DUE TO PLR
,
      DEL = K / DEL
      CALL DELLVYS(AIN, DIN(), PY(), AOUT, DYS(), STRG, DEL,
MDEL, PLR, DT, KA, K)
,
' STORE MOVEMENT (DISOUT AND AOUT) AND UPDATE NEW
POPULATIONS (PPNYS)
,
      Disout(A, D) = 0!
,
      FOR A2 = 1 TO KA
        DOUTYS(A2, D) = DYS(A2)
        Disout(A, D) = Disout(A, D) + DYS(A2)
        PPNYS(A2, D) = 0!
      NEXT A2
      AGEOUT(A, D) = AOUT
      IF STRG > 0! THEN
        S% = 1
      ELSE
        S% = 0
      END IF
      PPN(2, D) = STRG * S%
,
      FOR K2 = 1 TO K
        FOR K1 = 1 TO KA
          YNG(D, K1, K2) = PY(K1, K2) * S%
          PPNYS(K1, D) = PPNYS(K1, D) + PY(K1, K2) * S%
        NEXT K1
      NEXT K2
,
      NEXT D
,
      TPOP(A) = 0!
      FOR D = 1 TO 5
        TPOP(A) = TPOP(A) + PPN(A, D)
      NEXT D

' EPIDEMIC CHECK FOR YOUNG STOCK
      IF (PPN(A, 5) + PPN(A, 1)) / DISDEL(5) < Disout(A, 3) THEN
,
        " IF DISOUT(A, 5) < DISOUT(A, 3) THEN
        " IF DISOUT(A, 5) < 1 / DISDEL(3) THEN
          IF SH%(A) = 0 THEN SH%(A) = 1 ' PRINT "Epidemic OFF for
Young Stock, Day "; n
        ELSE
          IF SH%(A) = 1 THEN SH%(A) = 0 ' PRINT "Epidemic ON for
Young Stock, Day "; n
        END IF
      "PRINT #2, "DISOUT"; DISOUT(A, 5); "INFOUT"; DISOUT(A, 3)
      "PRINT #2, "del="; DISDEL(5); "A"; A
      "PRINT #2, "DISOUT"; DISOUT(A, 5); "1/INFDEL"; 1 / DISDEL(3); "INFOUT";
DISOUT(A, 3)

```

```

,
' ** UPDATE ROUT
,
      IF SH%(A) = 0 THEN ROUT(A) = ROUT(A) + (Disout(A, 5) +
Disout(A, 1)) * DT
      IF ROUT(A) < 0 THEN ROUT(A) = 0
,
-----
,
      CALF PROCESSING
,
' SET VARIABLE FOR ANIMAL AGE GROUP (A)
,
      A = 1
,
' SET DISEASE DELAYS FOR CALVES
,
REM** IF ALL 3 GROUPS MIX THEN INCREASE THE NUMBER OF
INFECTIVE CONTACTS
      IF CONTACT$ = "Y" OR CONTACT$ = "y" THEN
        SUMINF(A) = PPN(1, 3) + PPN(2, 3) + PPN(3, 3)
      ELSE
        SUMINF(A) = PPN(A, 3)
      END IF
,
      IF SUMINF(A) >= 1 THEN
        IF BETA(A) < 1 THEN DISDEL(5) = (1 / (1 - (1 - BETA(A)) *
SUMINF(A)))
        ELSE
          DISDEL(5) = 365 / ID(A)
        END IF
      PRINT #2, "del="; DISDEL(5); "A"; A; "SUMI"; SUMINF(A)
,
' Compute more accurate # at risk
      AMON2(A) = AMON2(A) + DT * (PPN(A, 5)) / 30#
,
' LOOP FOR 4 DISEASE STATES (NO RECOVERED STATE - CALVES AGE
TOO SOON)
,
      FOR D = 2 TO 5
,
' CALCULATE AGEOUT (AGING INTO YOUNG STOCK); CALCULATE
LIKE A PLR
,
      AGEOUT(A, D) = PPN(A, D) * WEAN(D)
      TAGE(A) = TAGE(A) + (AGEOUT(A, D) * DT)
,
' SELECT DISEASE DELAY AND NUMBER OF STAGES, AND PUT
WORKING VS OF
' POPULATION IN P
,
      DEL = DISDEL(D)
      K = KK(D)
      FOR K2 = 1 TO K
        P(K2) = CALF(D, K2) - (AGEOUT(A, D) * DT / K)
      NEXT K2
,
' CALCULATE PLR (PROPORTIONAL LOSS RATE); INCLUDES CULLS

```

AND MORTALITY

' STORE OLD PLR VALUES (USED FOR IMMUNE, VACCINATED) FOR
NON-DELAYS

' THEN, CALL PLRSET TO COUNT UP LOSSES BASED ON TYPE AND
DISEASE STATE

```

      PLR = mort(A, 1) + CULL(A, 1) + SELL(A)
      IF D = 2 THEN PLR = PLR + CULL(A, 2)
      IF D = 3 THEN PLR = PLR + mort(A, 2)
      IF D = 2 OR D = 4 THEN OLDPLR = PLROUT(A, D)
      CALL PLRSET(A, K, D, PPN(A, D), SH%(A), Disout(A, 5), DEL, DT,
mort(), CULL(), PLROUT(), SELL())

```

' MODIFY POPULATIONS, ETC. USING DELAYS (INFECTED OR WELL),
OR

' MAKING CHANGES MANUALLY (IMMUNE OR VACCINATED)

```

      IF D = 3 OR D = 5 THEN
      IF D = 3 THEN
      RIN = Disout(A, 5)
      IF SH%(A) = 1 THEN RIN = 0!
      ELSE
      RIN = (((PPN(3, 5) + PPN(3, 3)) * BIRTH)) + BUY(A)
      SUMBORN = SUMBORN + DT * (TPOP(3) * BIRTH)
      SUMBUY(A) = SUMBUY(A) + (BUY(A) * DT)
      PLR = PLR + VRATE(A)
      IF SH%(A) = 1 THEN RIN = RIN + Disout(A, 5)
      END IF
      CALL DELLVFS(RIN, RT, P(), STRG, PLR, DEL, DT, K)
      Disout(A, D) = RT
      ELSE

```

' CALCULATE RIN2 - NUMBER OF ANIMALS TO ADD TO NON-DELAY
STATE

' CALVES (A STATE, NOT A RATE)

```

      IF D = 2 THEN
      RIN2 = Disout(A, 3) - AGEOUT(A, D)
      ELSE
      RIN2 = ((PPN(3, 4) + PPN(3, 2)) * BIRTH) - AGEOUT(A, D)
      END IF
      PPN(A, D) = PPN(A, D) + (RIN2 * DT) - (PLROUT(A, D) -
OLDPLR)
      END IF

```

' RESTORE DELAY ARRAY

```

      IF D = 3 OR D = 5 THEN
      PPN(A, D) = 0!
      FOR K2 = 1 TO K
      CALF(D, K2) = P(K2)
      PPN(A, D) = PPN(A, D) + P(K2)
      NEXT K2
      END IF

```

' ZERO OUT IF POPULATION GOES NEGATIVE

```

      IF PPN(A, D) <= 0! THEN

```

```

        PPN(A, D) = 0
        FOR K2 = 1 TO K
            CALF(D, K2) = 0
        NEXT K2
    END IF
,
    NEXT D
,
    TPOP(A) = 0
    FOR D = 1 TO 5
        TPOP(A) = TPOP(A) + PPN(A, D)
    NEXT D
, EPIDEMIC CHECK FOR CALVES
,
    IF PPN(A, 5) / DISDEL(5) < Disout(A, 3) THEN
        "IF DISOUT(A, 5) < DISOUT(A, 3) THEN
        "IF DISOUT(A, 5) < 1 / DISDEL(3) THEN
            IF SH%(A) = 0 THEN SH%(A) = 1 'PRINT "Epidemic OFF for
Calves, Day "; n
            ELSE
                IF SH%(A) = 1 THEN SH%(A) = 0 ' PRINT "Epidemic ON for
Calves, Day "; n
            END IF
        "PRINT #2, "DISOUT"; DISOUT(A, 5); "INFOUT"; DISOUT(A, 3)
        "PRINT #2, "del="; DISDEL(5); "A"; A
        "PRINT #2, "DISOUT"; DISOUT(A, 5); "1/INFODEL"; 1 / DISDEL(3); "INFOUT";
DISOUT(A, 3)
,
    ** UPDATE ROUT
        IF SH%(A) = 0 THEN ROUT(A) = ROUT(A) + Disout(A, 5) * DT
        IF ROUT(A) < 0 THEN ROUT(A) = 0
,
    ***** CALCULATE FINANCIAL STATISTICS*****
        IF ES = "Y" OR ES = "y" THEN CALL ECON(OPPN(), TTAGE(), P%, R, I,
IDT%, N, DT, NDAYS%, PPN(), PLROUT(), VRATE(), SUMBORN, SUMBUY(),
NPV, MN%, NPVVAR())
    NEXT I
, PRINT DAILIES
    TSUM = 0
    TSUMOT = 0
    OSUM = 0
    TSUMBUY = 0
,
    FOR A = 1 TO 3
        "
        TPOP(A) = 0
        "
        PRINT #2, "Day "; N; ", Age Group "; A
        FOR D = 1 TO 5
            IF D < 3 THEN OSUM = OSUM + OPPN(A, D)
            "
            PRINT #2, USING " #) #####.#### "; D, PPN (A,D);
            "
            TPOP(A) = TPOP(A) + PPN(A, D)
        NEXT D
        "
        PRINT #2, TPOP (A)
        "
        PRINT #2, "Losses: ";
        SUMOUT(A) = 0
        FOR J = 1 TO 4
            SUMOUT(A) = SUMOUT(A) + PLROUT(A, J)
            "
            PRINT #2, USING " #####.#### "; PLROUT (A,J);
            "
        NEXT J

```

```

PRINT #2, SUMOUT (A)
IF A < 3 THEN PRINT #2, "Aging Out"; TAGE (A);
"IF A = 1 THEN PRINT #2, "Diseased: "; ROUT(A); " Check: "; (100! *
((TPOP(A) + SUMOUT(A) + TAGE(A)) - (OPPN(A, 1) + OPPN(A, 2))) / (OPPN(A, 1)
+ OPPN(A, 2)))
"IF A > 1 THEN PRINT #2, "Diseased: "; ROUT(A); " Check: "; (100! *
((TPOP(A) + SUMOUT(A) + TAGE(A) - TAGE(A - 1)) - (OPPN(A, 1) + OPPN(A,
2))) / (OPPN(A, 1) + OPPN(A, 2)))
TSUM = TSUM + TPOP(A)
TSUMOT = TSUMOT + SUMOUT(A)
TSUMBUY = TSUMBUY + SUMBUY(A)
NEXT A
PRINT OUT MONTHLY STATISTICS

IF (N MOD 30) = 0 OR N = NDAYS% THEN

IF MN% = 1 THEN PRINT #2, " "
IF MN% = 1 THEN PRINT #2, "##### MONTHLY DISEASE
REPORT #####"; "M ="; N / 30
FOR A = 1 TO 3
IF MN% = 1 THEN PRINT #2, "— A="; A, "Current Beta="; BETA(A)
IF MN% = 1 THEN PRINT #2, "Losses";
FOR J = 1 TO 4
IF MN% = 1 THEN PRINT #2, USING "###.#### "; PLROUT(A, J);
PLROUT(A, J) = 0
NEXT J
IF MN% = 1 THEN PRINT #2, "Sumout"; SUMOUT(A)
IF A = 1 THEN
tagein = SUMBORN
ELSE
tagein = TAGE(A - 1)
END IF
IF MN% = 1 THEN PRINT #2, "TPop."; TPOP(A); "Tagein"; tagein; "Tageout";
TAGE(A); "BUY"; SUMBUY(A); "CASES"; ROUT(A)
NEXT A
END IF
IF (N MOD 30) = 0 OR N = NDAYS% THEN
FOR A = 1 TO 3
AGE = -TAGE(A)
IF A > 1 THEN AGE = AGE + TAGE(A - 1)
AMON = TPOP(A) + 5 * (AGE + SUMBUY(A) - SUMOUT(A))
tamon(A) = tamon(A) + AMON
MID(A) = 100! * ROUT(A) / AMON
MR(A) = 1! - EXP(-MID(A))
mid2(A) = 100! * ROUT(A) / AMON2(A)
tamon2(A) = tamon2(A) + AMON2(A)
AMON2(A) = 0
mr2(A) = 1! - EXP(-mid2(A))
TROUT(A) = TROUT(A) + ROUT(A)
ROUT(A) = 0
TTAGE(A) = TTAGE(A) + TAGE(A)
TSUMOUT(A) = TSUMOUT(A) + SUMOUT(A)
ASUMBUY(A) = ASUMBUY(A) + SUMBUY(A)
SUMOUT(A) = 0
SUMBUY(A) = 0
ASBORN = ASBORN + SUMBORN
SUMBORN = 0
IF MN% = 1 THEN PRINT #2, "Incidence density, mID(appx/exact): ";

```

```

MID(A, "/", mid2(A)
      IF MN% = 1 THEN PRINT #2, "One month Risk (appx/exact) ";
MR(A, "/", mr2(A)
REM " IF (N MOD 360) = 0 OR N = NDAYS% THEN PRINT #2, " Check: "; (100!
* ((TPOP(A) + SUMOUT(A) + TAGE(A) - TAGE(A - 1)) - (OPPN(A, 1) + OPPN(A,
2) + OPPN(A, 3))) / (OPPN(A, 1) + OPPN(A, 2) + OPPN(A, 3)))
NEXT A
      IF MN% = 1 THEN PRINT #2, " Big Check % : "; 100! * ((TSUM - OSUM +
TSUMOUT - TSUMBUY) / OSUM)
      " END IF
,
      FOR A = 1 TO 3
      TAGE(A) = 0!
      NEXT A
      END IF
,
PRINT OUT ANNUAL STATISTICS
      IF (N MOD 360) = 0 OR N = NDAYS% THEN
,
PRINT #2, "***** ANNUAL DISEASE STATISTICS ***** Year #"; N / 360
PRINT #2, CM$
IF STOC% = 1 THEN PRINT #2, "RANDOM ON *****"
      FOR A = 1 TO 3
      IF A = 1 THEN ASUMBUY(A) = ASBORN + ASUMBUY(A)
      PRINT #2, "A="; A
      PRINT #2, "Current TPOP="; USING "####.#"; TPOP(A);
      PRINT #2, " Infecteds="; USING "####.#"; PPN(A, 3);
      PRINT #2, " Susep's="; USING "####.#"; PPN(A, 5) + PPN(A, 1);
      PRINT #2, " Immune="; USING "####.#"; PPN(A, 2) + PPN(A, 4);
      PRINT #2, "Agedout="; USING "####.#"; TTAGE(A);
      PRINT #2, " B/purc="; USING "####.#"; ASUMBUY(A);
      PRINT #2, " Tot. Losses ="; USING "####.#"; TSUMOUT(A);
      PRINT #2, " Tot. CASES="; USING "####.#"; TROUT(A)
      AMID(A) = 100! * TROUT(A) / tamon(A)
      AMID2(A) = 100! * TROUT(A) / tamon2(A)
      tamon2(A) = 0!
      TROUT(A) = 0!
      tamon(A) = 0!
      TTAGE(A) = 0!
      TSUMOUT(A) = 0!
      ASUMBUY(A) = 0! ASBORN = 0!
      PRINT #2, "aID (apprx)="; USING "####.#"; AMID(A);
      PRINT #2, " aID (exact) ="; USING "####.#"; AMID2(A)
      NEXT A
,
      TOTAL ANNUAL RATES FOR MULTIPLE RUNS
      FOR A = 1 TO 3
      SAMID(A) = SAMID(A) + AMID(A)
      SAMID2(A) = SAMID2(A) + AMID2(A)
      NEXT A
      END IF
,
      NEXT N
,
*** STORE VALUES FOR VARIANCE FOR APPROX aID *****
      FOR A = 1 TO 3
      IDVAR(A, R) = AMID(A)
      NEXT A
,
,
RESET ARRAYS FOR NEW RUNS

```

```

FOR D = 1 TO 5
  FOR A = 1 TO 3
    VOUT(A) = 0!
    PPN(A, D) = 0!
    Disout(A, D) = 0!
    IF A < 3 THEN AGEOUT(A, D) = 0!
    IF D < 5 THEN PLROUT(A, D) = 0!
    IF D = 1 THEN
      ROUT(A) = 0!
      SH%(A) = 0!
      TAGE(A) = 0!
    END IF
  NEXT A
  FOR A = 1 TO KA
    IF D = 1 THEN
      YOLDV(A) = 0!
      YOLDR(A) = 0!
    END IF
    PPNYS(A, D) = 0!
    DOUTYS(A, D) = 0!
    FOR C = 1 TO KK(D)
      YNG(D, A, C) = 0!
    NEXT C
  NEXT A
  FOR C = 1 TO KK(D)
    CALF(D, C) = 0!
    COW(D, C) = 0!
  NEXT C
NEXT D
, *****
  IF R = NRUNS% AND NRUNS% > 1 THEN
    IF STOC% = 1 THEN PRINT #2, "MONTHLY RANDZ. W
EXPONENTIAL DISTRIB."
    FOR A = 1 TO 3
      PRINT #2, "Starting BETA0 mean"; USING "###.##"; betaP(A)
      PRINT #2, "Average aID's (appx.) for "; NRUNS%; "Runs"; SAMID(A) /
NRUNS%; "A="; A; ""
      PRINT #2, "Average aID's (exact) for "; NRUNS%; "Runs"; SAMID2(A) /
NRUNS%; "A="; A
    NEXT A
  END IF
NEXT R
,
' * CALCULATE VARIANCE FOR APPX aID ****
  IF NRUNS% > 1 THEN
    FOR A = 1 TO 3
      FOR R = 1 TO NID
        SUMSQU(A) = SUMSQU(A) + IDVAR(A, R) ^ 2
        SUMVAL(A) = SUMVAL(A) + IDVAR(A, R)
      NEXT R
      VARIAN(A) = (SUMSQU(A) - (SUMVAL(A) ^ 2 / NID)) / (NID - 1)
      PRINT #2, "A"; A; "Variance"; USING "###.###"; VARIAN(A); NRUNS%;
"Runs"; "SSQU"; SUMSQU(A); "SUMVAL"; SUMVAL(A)
    NEXT A
  ' COMPUTE MEAN AND VARIANCE OF NPV
  FOR R = 1 TO NRUNS%
    NPVSUM! = NPVSUM + NPVVAR(R)

```

```

      NPVSQU! = NPVSQU + NPVVAR(R) ^ 2
    NEXT R
    NPVMEAN = NPVSUM! / NRUNS%
    VARNPV = (NPVSQU! - (NPVSUM! ^ 2 / NRUNS%)) / (NRUNS% - 1)
    PRINT #2, "Mean of NPV's at end of Run $"; NPVMEAN; "Variance ";
VARNPV
  END IF
  FOR A = 1 TO 3
    SUMSQU(A) = 0!
    SUMVAL(A) = 0! VARIAN(A) = 0!
    NPVSUM! = 0! NPVSQU! = 0!
    FOR R = 1 TO NID: IDVAR(A, R) = 0! NEXT R
  NEXT A

  BEEP
  INPUT "Would you like to run again? ( Y/N ): "; YN$
  IF YN$ = "Y" OR YN$ = "y" THEN 100
,
,
, *****
,
  STOP
  CLOSE #2
999 NEXT P%
  END
, *****
SUB EXPON (MEAN(), XVAR()) STATIC
, *****
, THIS SUBROUTINE COMPUTES AN EXPONENTIALLY DISTRIBUTED
RANDOM VARIABLE
, MEAN   : THE EXPECTED VALUE OF THE VARIABLE
, XVAR   : THE EXPONENTIALLY DISTRIBUTED RANDOM VARIABLE
, *****
,
  FOR A = 1 TO 3
    RRR = RND
    XVAR(A) = -MEAN(A) * LOG(RRR)
  NEXT A
,
END SUB
, *****
DECLARE SUB PRODN (N!, PPN!), PRODRTE(), disrte(), DISMILK(), dismilkt!,
TOTMILK!, SOLDMILK!, DT!)
DECLARE SUB COST (N!, PPN!, DAYDRUG(), DRUGCOST!, DAYVET(),
VETCOST!, WAGERTE!, LABRTX(), LABRCOST!, VRATE(), VACPRICE!,
VACCOST!, DAYINTK(), FEEDCOST!, FEEDTOT(), DISMILK(), POORATE(),
pricFEED(), DT!)

  SUB COST (N, PPN(), DAYDRUG(), DRUGCOST, DAYVET(), VETCOST,
WAGERTE, LABRTX(), LABRCOST, VRATE(), VACPRICE, VACCOST,
DAYINTK(), FEEDCOST, FEEDTOT(), DISMILK(), POORATE(), pricFEED(), DT)
  STATIC
, *****
, ** THIS PROGRAM CALCULATES THE COSTS OF ANIMAL PRODUCTION
THAT ARE VARIABLE
, ** ON THE NUMBER AND LEVEL OF DISEASED ANIMALS IN A DAIRY
HERD. COSTS
, ** THAT ARE THE SAME FOR A DISEASED AND WELL ANIMAL ARE
IGNORED.

```

```

' ** MILK PRODUCTION COSTS ARE NOT COMPUTED HERE SINCE THEY
ARE DONE AT THE
' ** END OF THE MONTH AS A FUNCTION OF TOTMILK PRODUCED.
' ** THE SUBROUTINE COMPUTES COSTS ON A DAILY (EVERY DT) BASIS.
THE TOTALS
' ** AT THE END OF A MONTH/YEAR ARE COMPUTED IN THE MAIN
PROGRAM AND RESET TO 0.
' ** DISCARDED MILK THAT IS FED TO CALVES IS USED TO DECREASE
THE DAILY FEED
' ** OF CALVES IN THIS SUBROUTINE.
' *****
' ***** VARIABLE LIST - VARIABLES ORIGINATING IN DISEASE
PROGRAM *****
' ** PPN (A,C) : POPULATIONS - A = 1) CALVES; 2) YOUNG STOCK; 3) COWS
' ** C = 1) RECOVERED; 2) IMMUNE; 3) SICK;
' ** 4) VACCINATED; 5) WELL
' ** VACCANTE FLOW (A) ?//
' ** DISMILK (D) : DISCARD MILK #/DAY - D = 1) DISCARDED ONLY; 2)
FED TO CALVES

' ***** VARIABLE LIST - VARIABLES ORIGINATING IN THIS PROGRAM
*****
' ** DRUG (A) : DAILY DRUG TREATMENT COSTS
' ** DRUGCOST : TOTAL MONTHLY DRUG TREATMENT COSTS FOR 3
AGES
' ** VET (A) : DAILY COSTS FOR VETERINARY SERVICES FOR
TREATMENT OF CASES
' ** VETCOST : TOTAL MONTHLY VET COSTS FOR ALL 3 AGES
' ** LABOR(A) : DAILY HOURS FOR CARE AND TREATMENT
' ** LABRCOST : TOTAL MONTHLY COST OF LABOR FOR CARE AND
TREATMENT
' ** VACC (A) : DAILY COSTS TO VACCINATE AGE GROUP (A)
' ** VACCOST : TOTAL MONTHLY VACCINATIONS COSTS
' ** FEEDSICK (A) : RATE OF FEEDING TO SICK CALVES AND YOUNG
STOCK
' ** FEEDPOOR (A) : RATE OF FEEDING TO POOR DOING CALVES AND
YOUNG STOCK
' ** FEEDWELL (A) : RATE OF FEEDING TO NON CLINICAL (WELL)
CALVES AND YOUNG
' ** FEEDTOT (A) : MONTHLY TOTAL OF FEED FED IN #'S
' ** FEEDCOST : TOTAL MONTHLY COST TO FEED CALVES AND
YOUNG ALL DISEASE
' ** POORATE (A) : % OF RECOVERED AND IMMUNE THAT ARE POOR
DOERS
' *****
' **
DIM DRUG(3), VET(3), VACC(3), FEEDSICK(3), FEEDPOOR(3),
FEEDWELL(3), LABOR(3), NONPOOR(3)
' ** INITIALIZE VAR'S THAT ARE SUM OF INTEGRANDS, ACROSS AGE
GROUPS
' **
' ** CALCULATE FEEDING RATES AND COSTS FOR CALVES AND YOUNG
STOCK
' **
A = 1
NONPOOR(A) = 1 - POORATE(A)
FEEDSICK(A) = (PPN(A, 3) * DAYINTK(A, 3))
FEEDPOOR(A) = (PPN(A, 2) * POORATE(A) * DAYINTK(A, 2))

```

```

      FEEDWELL(A) = (((PPN(A, 5) + PPN(A, 4) + NONPOOR(A) * PPN(A, 2)) *
DAYINTK(A, 1)) - DISMILK(2))
, **

```

```

      A = 2
      FEEDSICK(A) = (PPN(A, 3) * DAYINTK(A, 3))
      FEEDPOOR(A) = ((PPN(A, 2) + PPN(A, 1)) * POORATE(A) * DAYINTK(A,
2))

```

```

      FEEDWELL(A) = ((PPN(A, 5) + PPN(A, 4) + NONPOOR(A) * (PPN(A, 2) +
PPN(A, 1))) * DAYINTK(A, 1))

```

```

      FOR A = 1 TO 2
      FEEDTOT(A) = (FEEDTOT(A) + DT * (FEEDSICK(A) + FEEDPOOR(A)
+ FEEDWELL(A)))

```

```

      " NEED TO ADD COW FEEDCOST FOR TOTAL "

```

```

      NEXT A

```

```

      FEEDCOST = FEEDTOT(1) * pricFEED(1) + FEEDTOT(2) * pricFEED(2)
"PRINT #2, a; "FEEDTOT(2)"; FEEDTOT(2); "FEEDCOST"; FEEDCOST; "price";
pricFEED(a)

```

```

      A = 3

```

```

      FEEDCOW = FEEDCOW + ((PPN(A, 5) + PPN(A, 2) + PPN(A, 3) +
PPN(A, 4)) * DAYINTK(A, 1))

```

```

, **

```

```

, ** CALCULATE COST ASSOCIATED WITH TREATMENT

```

```

, **

```

```

      FOR A = 1 TO 3

```

```

      DRUG(A) = PPN(A, 3) * DAYDRUG(A)

```

```

      DRUGCOST = DRUGCOST + DT * DRUG(A)

```

```

      VET(A) = PPN(A, 3) * DAYVET(A)

```

```

      VETCOST = VETCOST + DT * VET(A)

```

```

      LABOR(A) = PPN(A, 3) * LABRTX(A) * WAGERTE

```

```

      LABRCOST = LABRCOST + DT * LABOR(A)

```

```

, **

```

```

, ** CALCULATE VACCINATION COSTS BASED ON FLOW INTO
VACCINATED STATE

```

```

, **

```

```

      VACC(A) = PPN(A, 5) * VRATE(A) * VACPRICE

```

```

      VACCOST = VACCOST + DT * VACC(A)

```

```

      NEXT A

```

```

, *****

```

```

      END SUB

```

```

SUB ECON (OPPN(), TTAGE(), P%, R, I, IDT%, N, DT, NDAY%, PPN(),
PLROUT(), VRATE(), SUMBORN, SUMBUY(), NPV, MN%, NPVVAR()) STATIC
, *****

```

```

, ** SUBROUTINE IS CALLED ONLY IF THE ECONOMIC ANALYSIS OPTION
IS ON FROM

```

```

, ** "EPIMOD" (BIGD). IT CALCULATES ALL THE IMPORTANT FINANCIAL
INFO.

```

```

, ** SOME SUBROUTINES ARE CALLED EVERY DT, AS THEY USE DAILY
STATE VALUES

```

```

, ** EPIMOD. TOTAL RESULTS ARE COMPUTED EVERY 30, AND 360! DAYS.

```

```

, ** THE NET PRESENT VALUE OF THE SERIES OF MONTHLY NET
INCOMES OVER VARIABLE

```

```

, ** COSTS ARE COMPUTED AS WELL AS TOTAL FOR THE ENTIRE RUN.

```

```

, *****

```

```

, ***** VARIABLE LIST - VARIABLES ORIGINATING IN DISEASE
PROGRAM *****

```

```

' ** PPN (A,C) : POPULATIONS - A = 1) CALVES; 2) YOUNG STOCK; 3) COWS
' **               C = 1) RECOVERED; 2) IMMUNE; 3) SICK;
' **               4) VACCINATED; 5) WELL
' ** PLROUT (A,E) TOT. POP. LOSSES - A = 1) CALVES; 2) YOUNG STOCK; 3)
COWS
' **               - E = 1) MORT, 2) CULL, 3) RESP MORT, 4) RESP CULL
' ** VRATE (A) : PARAMETER FOR PORTION OF A THAT IS
VACCINATED EACH DAY
' ** SUMBUY(A) : THE TOTAL NUMBER OF ANIMALS PURCHASED
SINCE BEGINNING

```

```

' ***** VARIABLES ORIGINATING IN ECON *****
' ** SOLDVAL (A,B) : VALUE OF ANIMALS SOLD
' ** CULLVAL (A,B) : CULL VALUES - A = 1) CALVES; 2) YOUNG STOCK; 3)
COWS
' **               - B = 1) RESP. POOR DOERS; 2) WELL (NOT RESP)
' ** VALMILK : VALUE OF MILK SOLD THIS MONTH
' ** PLRBIT (B) : SELECTED FROM PLROUT - B = 1) RESPIRATORY, 2) NOT
RESP

```

```

' ***** PRICE AND COST PARAMETERS USED IN ECON *****
' ** DAYDRUG (A) : DAILY COST OF DRUG TREATMENT PER CASE
' ** DAYVET (A) : DAILY COST OF VETERINARY SERVICES PER CASE
' ** LABRTX (A) : DAILY HOURS OF LABOR PER CASE
' ** WAGERTE : HOURLY WAGE RATE FOR SKILLED HIRED HELP
' ** VACPRICE : PER DOSE PRICE OF GENERIC DISEASE VACCINE
' ** DAYINTK (A,F) DAILY INTAKE OF FEED PER POUND OF BODY
WEIGHT OR MILK
' **               A = 1) CALVES; 2) YOUNG STOCK; 3) COWS
' **               F = 1) WELL; 2) POOR DOERS; 3) SICK
' ** PRICFEED (A) : AVERAGE PRICE OF FEED PER POUND FOR EACH
AGE GROUP
' **

```

```

' ***** PRODUCTION AND GROWTH PARAMETERS *****
' ** POORATE (A) : % OF RECOVERED AND IMMUNE THAT ARE POOR
DOERS
' ** PRODRTE (B) : DAILY RATES OF MILK PRODUCTION - 1) NOT WELL; 2)
WELL
' ** DISRTE (D) : DISC. RATES - D = 1) DISCARDED ONLY; 2) FED TO
CALVES

```

```

' *****
' DIMENSION NEW ARRAYS
      DIM PLRBIT(2), OLDPLRT(3, 2), CULLVAL(3, 2), PRODRTE(2), disrte(2),
POORATE(3)
      DIM MILK(2), DISCARD(2), DISMILK(2), SOLDVAL(3, 2), OLDBUY(3),
PURPRICE(3)
      DIM DAYDRUG(3), DAYVET(3), LABRTX(3), pricFEED(3), DAYINTK(3, 3),
FEEDTOT(3)
' **
' **
' ** INITIALIZE FOR BEGINNIG OF RUN
      IF N = 1 THEN
' ** INITIALIZE PRICE VARIABLES
          MILKPRIC = .12
          DEACPRIC = 120
          DISCOUNT = .1

```

```

PURPRICE(1) = 200: PURPRICE(2) = 400: PURPRICE(3) = 1500
CULLVAL(1, 1) = 100: CULLVAL(1, 2) = 120!
CULLVAL(2, 1) = 150: CULLVAL(2, 2) = 1000! "sale for dairy (2,2)
CULLVAL(3, 1) = 0: CULLVAL(3, 2) = 546
' ** INITIALIZE COST VARIABLES
A = 1
DAYDRUG(A) = .5
DAYVET(A) = .05
LABRTX(A) = 33 'HRS ??????????
pricFEED(A) = .05 $ PER POUND
DAYINTK(A, 1) = 4: DAYINTK(A, 2) = 3.5: DAYINTK(A, 3) = 2!

A = 2
DAYDRUG(A) = .47
DAYVET(A) = .03
LABRTX(A) = .034 'HRS
pricFEED(A) = .03 $ PER POUND
DAYINTK(A, 1) = 16: DAYINTK(A, 2) = 14: DAYINTK(A, 3) = 8!

A = 3
DAYDRUG(A) = 1.8
DAYVET(A) = .75
LABRTX(A) = .08 'HRS
pricFEED(A) = .03 $ PER POUND
WAGERTE = 5.5 ' $/HR
DAYINTK(A, 1) = 24!
VACPRICE = 1!
INTKMILK = 3 '# of feed/pound of milk
VCOSTMLK = .01 ' VARIABLE COST/ # MILK , EG. ADVERTISING,
SHIPPING
' ** INITIALIZE OTHER FINANCIAL AND PRODUCTION PARAMETERS
POORATE(3) = 0: POORATE(2) = .01: POORATE(1) = .1
PRODRTE(1) = 10: PRODRTE(2) = 41.7: disrte(1) = .5: disrte(2) = .5

END IF
IF N = 1 THEN NPVLONG = 0!
' ***** CALL IMPORTANT SUBROUTINES EACH DT *****
CALL COST(N, PPN(), DAYDRUG(), DRUGCOST, DAYVET(), VETCOST,
WAGERTE, LABRTX(), LABRCOST, VRATE(), VACPRICE, VACCOST,
DAYINTK(), FEEDCOST, FEEDTOT(), DISMILK(), POORATE(), pricFEED(), DT)
CALL PRODN(N, PPN(), PRODRTE(), disrte(), DISMILK(), dismilk,
TOTMILK, SOLDMILK, DT)

' *****
IF ((N MOD 30) = 0 OR N = NDAY%) AND I = IDT% THEN
' ***** COMPUTE MONTHLY TOTALS *****
' ** CALUCULATE VALUE OF ANIMALS BEING SOLD
' **
FOR A = 1 TO 3
PLRBIT(1) = PLROUT(A, 4)
PLRBIT(2) = PLROUT(A, 2)
FOR B = 1 TO 2
SOLDVAL(A, B) = CULLVAL(A, B) * PLRBIT(B)
NEXT B
NEXT A
DEACVAL = DEACPRIC * (SUMBORN) 'SUMBORN IS 50% OF YTD
BIRTHS
CALFVAL = (SOLDVAL(1, 1) + SOLDVAL(1, 2) + DEACVAL)
YNGVAL = (SOLDVAL(2, 1) + SOLDVAL(2, 2))

```

```

COWVAL = (SOLDVAL(3, 1) + SOLDVAL(3, 2))
IF MN% = 1 THEN PRINT #2, "***** MONTHLY FINANCIAL REPORT
***** Month #"; N / 30
IF MN% = 1 THEN PRINT #2, "INCOME:"
IF MN% = 1 THEN PRINT #2, "Animal sales:"; " Calves= $"; CALFVAL; " Young=
$"; YNGVAL; "Cows= $"; COWVAL
  FOR A = 1 TO 3
    FOR B = 1 TO 2
      INCMCULL = INCMCULL + SOLDVAL(A, B)
      SOLDVAL(A, B) = 0
    NEXT B
  NEXT A
  INCMCULL = INCMCULL + DEACVAL
IF MN% = 1 THEN PRINT #2, "Total Cull income = $"; INCMCULL
' ** MONTHLY GROSS MILK INCOME
  VALMILK = SOLDMILK * MILKPRIC
IF MN% = 1 THEN PRINT #2, " Milk: "; TOTMILK; "# produced, "; SOLDMILK; "#
sold for $"; VALMILK
IF MN% = 1 THEN PRINT #2, "      Gross value of discarded Milk $"; dismilkt *
MILKPRIC
' ** GROSS MONTHLY INCOME
  GMONINC = VALMILK + INCMCULL
IF MN% = 1 THEN PRINT #2, "----- Gross monthly income$";
GMONINC
' ** TOTAL MONTHLY VARIABLE COSTS
  FOR A = 1 TO 3      ' Watch the buy rates and inventory control
    PURCOST = PURCOST + (SUMBUY(A)) * PURPRICE(A)
    '4/17/90 problem   SUMBUY(A) = 0
  NEXT A
  FEEDMILK = TOTMILK * INTKMILK * pricFEED(3) + FEEDCOW
  MLKCONST = FEEDMILK + TOTMILK * VCOSTMLK
  DISCOST = DRUGCOST + VETCOST + LABRCOST
' **
  MVCOST = MLKCONST + PURCOST + DRUGCOST + VETCOST +
LABRCOST + VACCOST + FEEDCOST
IF MN% = 1 THEN PRINT #2, "VARIABLE COSTS."
IF MN% = 1 THEN PRINT #2, "Milk Production, includes variable and feed costs $";
MLKCONST
IF MN% = 1 THEN PRINT #2, "Feeding Calves & Young $"; FEEDCOST
IF MN% = 1 THEN PRINT #2, "Cow Purchases. $"; PURCOST
IF MN% = 1 THEN PRINT #2, "Disease Expenses:"; DISCOST
IF MN% = 1 THEN PRINT #2, "Drugs $"; DRUGCOST; "Vet Exp $"; VETCOST;
"Labor $"; LABRCOST; "Vacc"; VACCOST
IF MN% = 1 THEN PRINT #2, "----- Tot. Mon. Variable Cost $";
MVCOST
' ** GROSS MARGIN DAIRY OVER DISEASE COSTS ***
  MNETINC = GMONINC - MVCOST
IF MN% = 1 THEN PRINT #2, "***** DAIRY MARGIN Over Variable
Costs for Month #"; N / 30; "$"; MNETINC
IF MN% = 1 THEN PRINT #2, ""
' **
' *** COMPUTE NET PRESENT VALUE OF SERIES OF MONTHLY
PAYMENTS
' **
  DISCOUNT = DISCOUNT / 12
  NINT% = (N / 30)      'total months of run
  nMON% = NINT%
  "IF N >= 360 THEN nMON% = (N MOD 360) : PRINT nMON%

```

```

      NPV = NPV + MNETINC / ((1 + DISCOUNT) ^ nMON%) ' for the year
      NPVLONG = NPVLONG + MNETINC / ((1 + DISCOUNT) ^ NINT%) 'for
whole run
' ** COMPUTE ANNUAL TOTALS
      TGINC = TGINC + GMONINC
      TMVCOST = TMVCOST + MVCOST
      TMARGIN = TGINC - TMVCOST
      TMLKCOST = TMLKCOST + MLKCOST
      TINCMCUL = TINCMCUL + INCMCULL
      TVALMILK = TVALMILK + VALMILK
      TDISCOST = TDISCOST + DISCOST
      TVACCOST = TVACCOST + VACCOST
      TFEEDCOS = TFEEDCOS + FEEDCOST
      TDRUGCOS = TDRUGCOS + DRUGCOST: TVETCOST = TVETCOST +
VETCOST
      TLABRCOS = TLABRCOS + LABRCOST
      TPURCOST = TPURCOST + PURCOST
' ** ZERO MONTHLY TOTALS
      GMONINC = 0: MVCOST = 0: PURCOST = 0
      INCMCULL = 0: MLKCOST = 0
      VALMILK = 0: SOLDMILK = 0: TOTMILK = 0: dismilk = 0
DISMILK(1) = 0
      DISMILK(2) = 0: DISCOST = 0: DRUGCOST = 0: VETCOST = 0
LABRCOST = 0
      VACCOST = 0: FEEDCOST = 0: FEEDTOT(1) = 0: FEEDTOT(2) = 0
FEEDCOW = 0
      END IF
' *** PRINT ANNUAL TOTALS
IF (N MOD 360) = 0 OR N = NDAY% THEN
      IF I = IDT% THEN
' ** ADJUST MILK PRODUCTION ACCORDING TO NEW HEIFERS
FRESHENING
      IF (TTAGE(2) / (OPPN(3, 1) + OPPN(3, 2) + OPPN(3, 3))) > 3 THEN
          PRODRTE(2) = PRODRTE(2) * (102)
      END IF

PRINT #2, ""
PRINT #2, " ***** ANNUAL FINANCIAL REPORT ***** Year
#", N / 360
PRINT #2, " — ANNUAL DAIRY INCOME—"
PRINT #2, " Total Animal Sales $"; USING "#####.##"; TINCMCUL
PRINT #2, " Milk Sales          $"; USING "#####.##"; TVALMILK
PRINT #2, " _____ ANNUAL Gross Dairy income$"; USING
"#####.##"; TGINC
PRINT #2, " — ANNUAL VARIABLE COSTS—"
PRINT #2, "Milk Production, includes variable and feed costs $"; USING
"#####.##"; TMLKCOST
PRINT #2, "Feeding Calves & Young $"; USING "#####.##"; TFEEDCOS
PRINT #2, "Cow Purchases $"; USING "#####.##"; TPURCOST
PRINT #2, "Disease Expenses $"; USING "#####.##"; TDISCOST
PRINT #2, "   Drugs $"; USING "#####.##"; TDRUGCOS;
PRINT #2, " Vet Exp $"; USING "#####.##"; TVETCOST
PRINT #2, "   Labor $"; USING "#####.##"; TLABRCOS;
PRINT #2, " Vacc"; USING "#####.##"; TVACCOST
PRINT #2, " _____ Tot. ANNUAL. Variable Cost: $"; USING
"#####.##"; TMVCOST
PRINT #2, " _____"
PRINT #2, " — GROSS MARGIN DAIRY OVER DISEASE COSTS—$";

```

```

USING "#####.##"; TMARGIN
PRINT #2, "NET PRESENT VALUE of Dairy Income/Variable DISEASE
costs,RunTD $"; USING "#####.##"; NPVLONG
PRINT #2, ""
' **
PRINT #2, "NEW daily prod"; PRODRTE(2)
' ** ZERO END OF YEAR VARIABLES
      TGINC = 0; TMVCOST = 0; TMARGIN = 0; TMLKCOST = 0;
      TINCMCUL = 0; TVALMILK = 0; TDISCOST = 0; TVACCCOST = 0;
      TFEEDCOS = 0; TDRUGCOS = 0; TVETCOST = 0;
      TLABRCOS = 0; TPURCOST = 0;

      END IF
      END IF
      IF N = NDAY% AND I = IDT% THEN NPVVAR(R) = NPVLONG

' **
' *****
' **
      END SUB   'ECON

SUB PRODN (N, PPN(), PRODRTE(), disrte(), DISMILK(), dismilkt, TOTMILK,
SOLDMILK, DT) STATIC
' *****
' ** THIS PROGRAM TRACKS HERD PRODUCTION: MILK AND ANIMAL
SALES. IN MILK
' ** PRODUCTION, IT IS ASSUMED THAT SICK ANIMALS WILL PRODUCE
LESS THAN
' ** HEALTHY ANIMALS, THAT SOME PRODUCTION IS DISCARDED WHEN
THE ANIMAL IS
' ** SICK AND ASSUMED TO BE UNDER TREATMENT, AND THAT SOME
DISCARDED MILK
' ** WILL BE FED BACK TO CALVES, WHICH WILL HELP OFFSET THE
LOSS IN MILK
' ** INCOME BY REDUCING THE QUANTITY OF MILK REPLACER
NEEDED TO FEED
' ** CALVES. IN ANIMAL SALES, IT IS ASSUMED, FOR COWS, THAT
NON-RESPIRATORY CULLS
' ** WILL INCLUDE ROUTINE SALES, PRODUCTION CULLS, AND CULLS
TO OTHER
' ** CAUSES. IN ADDITION, IT IS ASSUMED THAT THE VALUE RECEIVED
FOR
' ** DIFFERENT AGE GROUPS AND CULL REASONS WILL AFFECT THE
SELLING PRICE
' ** OF THE ANIMAL. THESE VALUES DO NOT CONSIDER THE COST OF
REPLACEMENT.
' *****
' ***** VARIABLE LIST - VARIABLES ORIGINATING IN DISEASE
PROGRAM *****
' ** PPN (A,C) : POPULATIONS - A = 1) CALVES; 2) YOUNG STOCK; 3) COWS
' **                      C = 1) RECOVERED; 2) IMMUNE; 3) SICK;
' **                      4) VACCINATED; 5) WELL
' ***** VARIABLE LIST - VARIABLES ORIGINATING IN THIS PROGRAM
*****
' **** SOME VARIABLES WILL NOT BE USED IN THIS SUB. BUT
ORIGINATED HERE
' ** MILKPRIC : PRICE OF MILK PER POUND
' ** PRODRTE (B) : DAILY RATES OF MILK PRODUCTION - 1) NOT WELL;

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```

2) WELL
' ** DISRTE (D) : DISC. RATES - D = 1) DISCARDED ONLY; 2) FED TO
CALVES
' ** MCOW (B) : MILKING POPULATIONS - 1) NOT WELL; 2) WELL
' ** MILK (B) : POUNDS OF MILK PRODUCTION - B = 1) NOT WELL; 2)
WELL
' ** DISMILK (D) : DISCARD #S - D = 1) DISCARDED ONLY; 2) FED TO
CALVES
' ** TOTMILK : TOTAL POUNDS OF MILK PRODUCED month
' ** SOLDMILK : TOTAL POUNDS OF MILK SOLD THIS month
' *****
' **
      DIM mcow(2), MILK(2)
' **
' ** CALCULATE NUMBER OF COWS MILKING
' **
      mcow(1) = PPN(3, 3)
      mcow(2) = PPN(3, 2) + PPN(3, 4) + PPN(3, 5)
' **
' **
' ** CALCULATE POUNDS OF MILK PRODUCED
' **
      FOR B = 1 TO 2
        MILK(B) = mcow(B) * PRODRTE(B) ' a flow
        TOTMILK = TOTMILK + DT * MILK(B)
      NEXT B
' **
' ** CALCULATE DISCARDS
' **
      FOR D = 1 TO 2
        DISMILK(D) = mcow(1) * PRODRTE(1) * disrte(D)
        dismilkt = dismilkt + DISMILK(D) * DT
      NEXT D
' **
' ** CALCULATE VALUE OF PRODUCTION
' **
      SOLDMILK = TOTMILK - dismilkt
' **
' **
' *****
' **
      END SUB
      STOP

' ** SUBROUTINE DELLVFS - DISTRIBUTED DELAY WITH TIME
VARIATIONS - 5/12/89
' *****
' ***
          VARIABLE DICTIONARY
' *****
' ***** FROM MAIN PROGRAM CALL:
' ** RIN : INPUT TO POPULATION DURING DELAY
' ** ROUT : EXIT DUE TO DELAY
' ** ST (K) : STORAGES FOR K STAGES
' ** STRG : NUMBER OF UNITS LEFT IN POPULATION AFTER DELAY
' ** PLR : PROPORTIONAL LOSS RATE
' ** DEL : CURRENT DELAY
' ** DT : DIVISION OF DAY
' ** K : NUMBER OF STAGES IN DELAY

```

```

' ***** INTERNALLY GENERATED
' ** BDD1 : PROPORTIONAL LOSS FACTOR
' *****
' **
' SUB DELLVFS (RIN, ROUT, ST(), STRG, PLR, DEL, DT, K) STATIC
' **
' *****
' **
' ** SET PROPORTIONAL LOSS FACTOR
' BDD1 = PLR + K / DEL
REM
' K2 = K - 1
' **
' ** LOOP FOR III% SUBINTERVALS
' **
' ** LOOP TO COVER THE STAGES (LAST STAGE IS HANDLED AS SPECIAL
' CASE TO
' ** COVER THE EFFECT OF ADDITIONS TO POPULATION FROM RIN)
' **
' FOR I = 1 TO K2
' **
' ** CALCULATE NEW STORAGES
' **
' ST(I) = ST(I) + DT * ((ST(I + 1) * (K / DEL)) - (ST(I) * BDD1))
' **
' NEXT I
' **
' ** CALCULATE NEW STORAGES FOR SPECIAL CASE AT LAST STAGE
' **
' ST(K) = ST(K) + DT * (RIN - (ST(I) * BDD1))
' **
' ** FILL STORAGE WITH TOTAL NUMBER OF UNITS LEFT AT END OF
' DELAY
' ** ( UNITS = RATE * DELAY / NUMBER OF STAGES
' STRG = 0
' **
' FOR I = 1 TO K
' STRG = STRG + ST(I)
' NEXT I
' **
' ** SET ROUT : LOSS DUE TO DELAY
' **
' ROUT = ST(1) / (DEL / K)
' **
' END SUB

' SUB DELLVYS (AIN, DIN(), R(), AOUT, DOUT(), STRG, DEL, MDEL,
' PLR, DT, KA, kb) STATIC
' *****
' ** THIS SUBROUTINE PERFORMS A SORT OF TWO-DIMENSIONAL
' DISTRIBUTED DELAY
' ** FOR YOUNG STOCK - FOR BOTH THE DISEASE PROCESSES AND THE
' AGING PROCESS
' *****
' ** AIN - AGING INPUT - CALVES WEANING
' ** DIN (KA) - DISEASE INPUTS - ANIMALS PROGRESSING THRU
' DISEASE STATES
' ** R (KA,KB) - ARRAY WITH STAGES

```

```

' ** AOUT    - AGING OUTPUT - ANIMALS WHICH WILL MOVE TO THE
NEXT AGE
' ** DOUT (KA) - DISEASE OUTPUT - ANIMALS PROGRESSING TO NEXT
DISEASE ST.
' ** STRG    - TOTAL STORAGE = NUMBER OF ANIMALS IN THIS DELAY
' ** DEL     - DELAY FOR THE DISEASE PROCESS
' ** MDEL    - DELAY FOR THE AGING (MATURATION) PROCESS
' ** PLR     - PROPORTIONAL LOSS RATE
' ** DT      - DT
' ** KA      - NUMBER OF STAGES IN AGING DELAY
' ** KB      - NUMBER OF STAGES IN DISEASE DELAY
' =====
' **
' **** SET Ks FOR LOOPING
' **
      A2 = KA - 1
      B2 = kb - 1
' **
' **** LOOP FOR AGE AND DISEASE STAGES *****
' **
      FOR A = 1 TO A2
' **
        FOR B = 1 TO B2
' **
          ' ** FIRST, CALCULATE ADJUSTMENTS DUE TO AGING AND PLR
          AAA = (R(A + 1, B) * MDEL) - (R(A, B) * (MDEL + PLR))
' **
          ' ** CALCULATE ADJUSTMENTS DUE TO CHANGES THROUGH DISEASE
          STATE
          DDD = (R(A, B + 1) * DEL) - (R(A, B) * DEL)
' **
          ' **** CHANGE STATE
          R(A, B) = R(A, B) + (DT * (AAA + DDD))
' **
          NEXT B
' **
' **** SPECIAL CASE HANDLING OF LAST DISEASE STAGE : ADD IN DINs
*****
' **
          AAA = (R(A + 1, kb) * MDEL) - (R(A, kb) * (MDEL + PLR))
          DDD = DIN(A) - (R(A, kb) * DEL)
          R(A, kb) = R(A, kb) + (DT * (AAA + DDD))
' **
          NEXT A
' **
' **** SPECIAL CASE HANDLING OF LAST AGE STAGE : ADD IN AIN
*****
' **
          FOR B = 1 TO kb
            AAA = AIN / kb - (R(KA, B) * (MDEL + PLR))
            ' AAA = AIN - (R(KA, B) * (MDEL + PLR))

            IF B < kb THEN
              DDD = (R(KA, B + 1) * DEL) - (R(KA, B) * DEL)
            ELSE
              DDD = DIN(KA) - (R(KA, B) * DEL)
            END IF
            R(KA, B) = R(KA, B) + (DT * (AAA + DDD))
          
```

```

      NEXT B
' **
' **** SUM AGEOUTS FOR AOUT - MOVEMENT TO COWS
*****
' **
      AOUT = 0
' **
      FOR B = 1 TO kb
        AOUT = AOUT + (R(1, B) * MDEL)
      NEXT B
' **
' **** CALCULATE STORAGE AND PREPARE DISEASE OUTS (DOUT)
*****
' **
      STRG = 0
' **
      FOR A = 1 TO KA
' **
        FOR B = 1 TO kb
          STRG = STRG + R(A, B)
        NEXT B
' **
        DOUT(A) = R(A, 1) * DEL
' **
      NEXT A
' **
*****
' **
      END SUB

      SUB PLRSET (A, K, D, POP, SH%, DOUT, DEL, DT, MORT(), CULL(),
PLROUT(), SELL()) STATIC
' ****
' ** THIS SUBROUTINE CALCULATES PLR LOSSES FROM CULLING AND
MORTALITY FOR
' ** BOTH RESPIRATORY AND NON-RESPIRATORY CAUSES
*****
' ** A      - AGE GROUP : 1 - CALVES, 2 - YOUNG STOCK, 3 - COWS
' ** K      - NUMBER OF STAGES FOR CURRENT DISEASE STATE
' ** D      - DISEASE STATE
' ** POP    - POPULATION TO APPLY PLR TO
' ** DOUT   - DISOUT (A,5) - ADD WELL ANIMALS BACK IN IF EPIDEMIC
OFF
' ** DEL    - DELAY FOR DISEASE STATE
' ** MORT (A,B) MORT RATE FOR A AGE GROUP, 1 = NON-RESPIRATORY,
2 = RESP.
' ** CULL (A,D) CULL RATE FOR A AGE GROUP, D DISEASE STATE
' ** PLROUT (A,B) - PROPORTIONAL LOSSES : 3 AGE GROUPS (INDEX A)
' ** B: 1) NON-RESP MORT, 2) NON-RESP CULL, 3) RESP MORT, 4) RESP
CULL
*****
' **
' **
'      FOR I = 1 TO K
' **
' **** CALCULATE LOSSES FOR NON-RESPIRATORY LOSSES
' **
      PLROUT(A, 1) = PLROUT(A, 1) + DT * (MORT(A, 1) * POP)

```

```

      PLROUT(A, 2) = PLROUT(A, 2) + DT * ((SELL(A) + CULL(A, 1)) * POP)
'F D = 5 AND A = 3 THEN PRINT #2, "PLROUT,CULL"; PLROUT(A, 2); "A"; A
' **
' ** CALCULATE RESPIRATORY LOSSES FOR THE IMMUNE AND
INFECTED STATES
' **
      IF D = 2 THEN PLROUT(A, 4) = PLROUT(A, 4) + DT * (CULL(A, 2) * POP)
      IF D = 3 THEN PLROUT(A, 3) = PLROUT(A, 3) + DT * (MORT(A, 2) *
POP)
' **
' ** CALCULATE IN RECYCLES IF DISEASE STATE IS WELL AND
EPIDEMIC IS OFF
' **
      IF D = 5 THEN
        PLROUT(A, 1) = PLROUT(A, 1) + DT * (MORT(A, 1) * SH% * (DOUT))
        PLROUT(A, 2) = PLROUT(A, 2) + DT * (CULL(A, 1) * SH% * DOUT)

      END IF
' **
'   NEXT I
' **
' *****
' **
      END SUB

```

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