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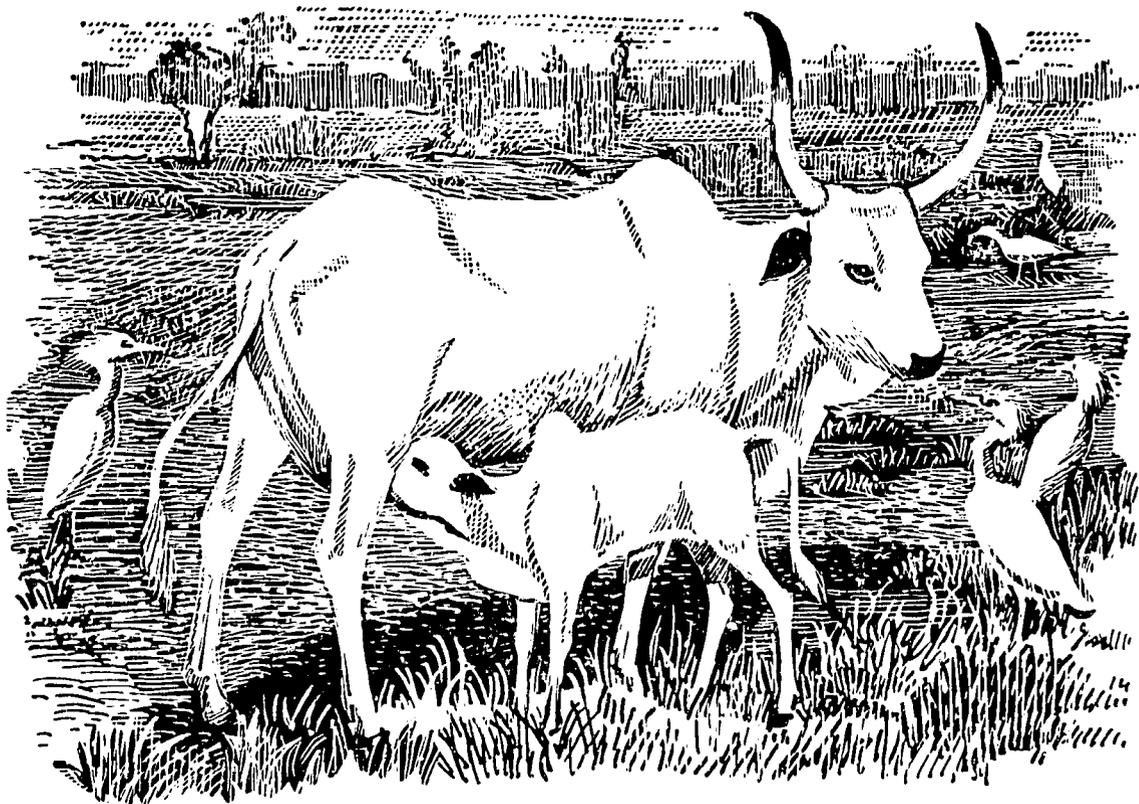
Veterinary epidemiology and economics in Africa

A manual for use in the design and
appraisal of livestock health policy

S.N.H. Putt, A.P.M. Shaw, A.J. Woods,
L. Tyler and A.D. James



International Livestock Centre for Africa



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This manual was prepared largely from notes on lectures given by the authors. Many of the concepts introduced in the manual are not new and can be found in most standard textbooks on epidemiology, economics and statistics. The authors wish to acknowledge in particular the contribution of Schwabe, Riemann and Franti's "*Epidemiology in Veterinary Practice*", Leech and Sellers' "*Statistical Epidemiology in Veterinary Science*" and Gittinger's "*Economic Analysis of Agricultural Projects*", which provided inspiration for certain parts of this manual.

FOREWORD

The value of epidemiological investigation as a basis for the treatment and control of animal disease has been recognised for many decades, but the need to apply economic techniques to the formulation and assessment of disease control activities only became apparent about 15 years ago. This arose in part from burgeoning veterinary expenditure demands associated with new, but costly, technology and in part from growing awareness of the significant influence of economic and social factors on patterns of ill-health and disease. FAO published a collation of disease losses in 1963, but it was concern in WHO over the zoonoses which led to the first international initiative, at Reading University in 1972, to develop new methods for the economic, as well as epidemiological, evaluation of animal health programmes.

Since then many national and international agencies have become involved and research and training units have sprung up at several universities around the world. An international society and various national societies have also been formed to provide forums for discussion of the more profound understanding that is emerging of how to improve the health, welfare and productivity of animals. The team which has prepared this manual has demonstrated how representatives of a wide variety of disciplines can, and should, work together not only to control and avoid the major disease hazards which can still decimate animal populations, but also to define how genetics, management, nutrition and environmental adjustment can complement specific veterinary measures. Each member has contributed to a wide variety of research projects and field investigations over the past decade and in so doing, has crystallised a contribution to the training of disease control planners and animal health advisers in Britain and overseas.

Recognising the need to provide such material for reference purposes and a wider range of training activities in Africa, ILCA and VEERU decided to join forces in publishing this manual. While Africa is the main focus, we feel sure that this manual will prove useful in other continents of the world and will further the long-term wellbeing of animals, in their many roles, as well as of people.

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1. AN INTRODUCTION TO THE PLANNING AND EVALUATION OF DISEASE CONTROL POLICY

1.1 INTRODUCTION

The purpose of this manual is to set out some of the basic techniques involved in the planning, monitoring and evaluation of livestock disease control programmes in Africa. This involves the use of a range of scientific disciplines and approaches which have to be coordinated if satisfactory strategies for the control of animal diseases are to be conceived, developed and implemented.

While an understanding of the epidemiology of a particular disease is vital in the planning and execution of disease control programmes, the process does not stop there. Disease control activities normally involve the expenditure of considerable resources in terms of finance, facilities and trained manpower. Such resources are in limited supply in Africa, particularly in these days of worldwide economic recession. Because of this, both African governments and donor agencies face extremely difficult resource allocation problems. How much of these scarce resources, for example, should be allocated to promoting agricultural development and how much to industrial development? How much should go to education or public health services or security?

Within the field of disease control itself, choices have to be made as to which diseases merit priority in their control. Developments in the animal health sciences have

meant that a range of different techniques or strategies may be available for the control of a particular disease, but which one is likely to give the best return for the effort spent? It is against this background of extremely complex choices and considerations that animal health activities have to be planned, evaluated and executed.

A set of tools and a series of concepts are therefore needed, which enable disease problems to be identified and tackled in ways that make the most efficient use of the resources available. The purpose of this manual is to acquaint the reader with some of these tools and concepts. Obviously, it will not be possible to cover in one manual all of the many complex issues involved in the planning and evaluation of animal health programmes. If, however, the manual serves to alert the reader to the various potentials and limitations of some of the techniques available, so that he or she is encouraged to explore them further and bring them to bear on the many problems faced in the course of his or her professional duties, then it will have fulfilled its purpose.

1.2 THE PLANNING PROCESS

1.2.1 The systems approach to livestock development

The veterinarian in Africa has two rather different functions with regard to livestock health and development. The first is to provide health services to existing livestock populations in existing production systems. The second centres on the premise that a major need in Africa is the develop-

ment of livestock production; this implies changing existing production systems, and it is a function of the veterinarian to help bring about such changes.

Introducing changes in any livestock production system involves interfering in a very complex process. Livestock production systems, like all other systems, consist of an assembly of related components which combine for some common purpose. It is simply not possible to change one component in isolation without affecting the other components of the system.

For example, when building a dip the aspects that need to be taken into consideration are inputs, dipping and outputs. These aspects are closely interrelated and must be considered from a holistic point of view.

Inputs. What inputs do we need to consider? The animals are the most obvious. Will owners really dip their cattle? How frequently will the cattle need to be dipped? How far will they need to walk to the dip? Will they have easy access and is there a danger of them damaging crops on their way to the dip? Will the coming together of animals at the dip provide a means of spreading other diseases? Acaricide is another input. What acaricide will be used? Can it be delivered regularly and stored securely? The need for water must also be examined. Are water supplies adequate and can they be made available on a year-round basis?

Dipping. The dipping activity itself can then be considered. Is skilled supervision available and where will the staff live? What measures will be necessary to ensure that the dip is properly obtained and the dip wash kept at the right concentration? Are problems of acaricide resistance likely to arise and how can these be prevented or controlled?

Output. What is important on the output side? We will create a population of dipped cattle and we hope that they will be healthier. Will this result in an increase in the cattle population? How will this larger population be fed and watered? How will farmers sell the surplus? Do the marketing facilities have to be improved? Do the prices of cattle and their products need to be manipulated in order to encourage their sale? And lastly, what is the cost of all this? Who is going to pay for it and how is this payment to be arranged?

We can see, therefore, that what started off as a relatively simple idea, "build a dip" may in fact have many as-

pects. These can be multiplied even further if we consider another component of the system, the host-parasite-vector relationship in the tick-transmitted disease present. Suppose that prior to the installation of the dip, the climate is such that the tick population is at a high enough level throughout the year to ensure that the challenge to young stock will convert an age immunity into a state of active immunity. This may have resulted in a generally low level of mortality. What is the effect of dipping? We reduce the tick challenge to a level at which adult cattle do not acquire an active immunity. All goes well until, at a time favourable to tick multiplication, the dip breaks down and dipping ceases. We have created a population of susceptible adult cattle and an epidemic ensues causing a high level of mortality in these susceptible animals.

Many attempts at livestock improvement have failed because the total impact of the change envisaged has not been identified. Since livestock projects frequently cover large areas, affect many people and absorb large amounts of money, the systems approach is invaluable in the planning process.

1.2.2 Stages in the planning process

For convenience, the planning process can be divided into three main stages:

Stage 1 – Establishing goals and targets for the animal health programme

This is an initial stage during which the information available on the livestock sector as a whole, and on the potential demand for livestock products, is examined to assess:

- The present situation in livestock production and future trends.
- The effect disease is having on the present situation as well as the effects it is likely to have in the future.
- The potential for intervention in animal health, the resources available, and the types of intervention that are technically possible.

Stage 2 – Project identification, design and appraisal

Several steps are involved in this stage. Given the goals and targets, and the resources and approaches available to deal with disease, a set of possible projects can be

identified. These should cover both the different disease problems and the different ways in which the problems could be tackled. A rough design for the projects is made and their technical, social, organisational/institutional, financial and economic feasibility is evaluated. After this a more detailed designing and planning exercise is undertaken for those projects that appear promising.

Stage 3 – Project implementation, monitoring, control and evaluation

Here again several steps can be distinguished, starting from the time when the project actually takes off. The monitoring and control activities carried out during this stage enable the necessary adjustments to be made in the project design as the project progresses. The information generated from these activities will provide feedback to all levels of the planning process, and will also be used in the final evaluation of the project once it has ended or a particular phase has been completed.

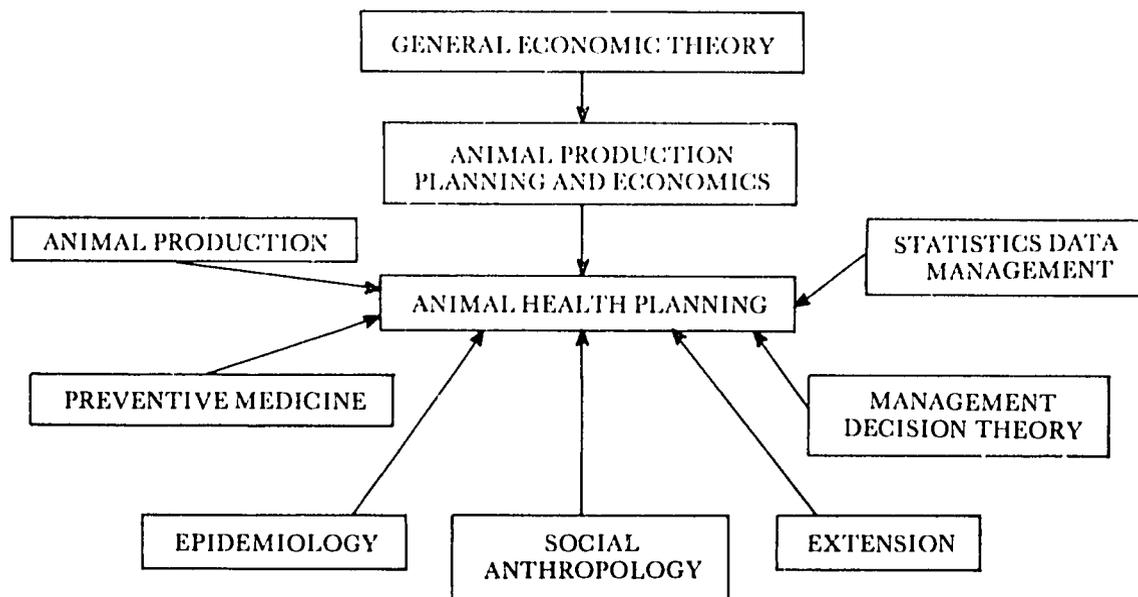
1.2.3 The role of various disciplines in the planning process

The planning and evaluation of animal health programmes involves a series of relationships, many of them very close, with a variety of scientific disciplines. These relationships are illustrated in Figure 1.

The disciplines and techniques involved may be grouped under two heads: the specific disciplines that are essential to the understanding of animal health problems (epidemiology and livestock production), and the general ones (statistics, information systems and economics) that have a role to play in any planning exercise, and whose specific application in the area of disease control is described in this manual.

The figure indicates the need for an inter-disciplinary approach involving the close and continuous cooperation of the various disciplines concerned. This is easily said

Figure 1. *The major disciplines involved in the planning and evaluation of animal health programmes.*



but presents practical problems with regard to real and imaginary conflicts of interest, the general human tendency towards demarcation and the creation, and indeed physical separation, of departments.

Before concluding this chapter, two major points need to be emphasised:

- Planning and evaluation of animal health programmes require a clear understanding of *both* the

epidemiology of the diseases in question *and* the livestock production systems involved.

- Such an understanding can only be achieved through the availability of reliable and up-to-date information at all stages of the planning and evaluation process.

2. EPIDEMIOLOGY: SOME BASIC CONCEPTS AND DEFINITIONS

2.1 INTRODUCTION

A question frequently asked is, "What is epidemiology"? There are many different definitions of the term. In the main, people attempting to define epidemiology have normally done so in the context of their own particular interests or needs. A useful general definition is that given by Schwabe et al (1977), which defines epidemiology as the study of disease in populations. It thus differs from the more conventional medical approaches to the study of disease that are normally concerned with the study of disease processes in affected individuals. While the objective of the latter is to find cures for diseases in individuals already affected, epidemiology is basically concerned with the reasons why those individuals became diseased in the first place.

Inherent in the epidemiological approach is the belief that the frequency of occurrence of a disease in a population is governed by the interaction of a large number of different factors or determinants. The epidemiologist believes that by studying these interactions it may become possible to manipulate some of the determinants involved, and so reduce the frequency with which the disease in question occurs in a population.

At this stage it is necessary to ascertain what is meant by the terms population and determinant.

A *population* can be defined as the complete collection of individuals that have some particular characteristic(s) in common. Depending on the characteristic(s) being considered, a population can be very large or very small. For example, one may wish to study a particular disease in a particular cattle population in a particular country. That cattle population could consist of:

All the cattle in the country

or

All the dairy cattle in the country

or

All the dairy cattle of a certain breed in the country etc.

Another term often used in epidemiological studies is *population at risk*. This is usually a subset of the original, defined population and comprises the total number of individuals in that original population that are considered capable of acquiring the particular disease or disease characteristic being studied.

For instance, we might be interested in studying the frequency with which abortion occurs in a population of dairy cattle of a certain breed in a certain country. The population at risk would not be all the individual animals of that particular dairy breed in that country, since this would include males, steers and immature females, all of which would not or could not be pregnant and therefore could not abort! It would consist of female cattle of that breed which were of breeding age. However, if the characteristic being studied was infection by one of the infectious agents that can cause abortion, such as *Brucella abortus*, the population at risk would have to include all calves, adult males, steers and immature females of the particular breed

in question, since all these individuals could potentially become infected with this organism.

A *determinant* is any factor or variable that can affect the frequency with which a disease occurs in a population. Determinants can be broadly classified as being either intrinsic or extrinsic in nature. Intrinsic determinants are physical or physiological characteristics of the host or disease agent (or intermediate host or vector, if present) which are generally determined genetically. Extrinsic determinants are normally associated with some form of environmental influence on the host or disease agent (or intermediate host or vector, if present). They may also include interventions made by man into the disease process by the use of drugs, vaccines, dips, movement controls and quarantines. The role of determinants in the disease process is discussed in more detail later on in this chapter.

Since the determinants of disease are often varied, the epidemiologist may have to draw on a number of different scientific disciplines and techniques if he is to study them. The epidemiological approach is, therefore, a holistic one and the "art" of epidemiology lies in the ability of the epidemiologist to coordinate the use of such disciplines and techniques in a disease investigation, and to produce from the results generated a composite and comprehensive picture of how a particular disease maintains itself in nature.

If we accept the premise that the frequency with which a disease occurs in a population is governed by a large number of determinants, it would be expected that some of these, particularly the extrinsic ones, would vary in space and time. It follows, therefore, that disease is a dynamic process. The type and pattern of diseases in livestock differ from country to country, area to area, species to species and production system to production system. Furthermore, the range and importance of the disease problems encountered may change dramatically over time within the criteria mentioned. The effective control of disease depends as much on a thorough understanding of the many complex factors that govern the changes taking place in a disease process as it does on the provision of veterinary inputs such as drugs, vaccines and dips.

2.2 INTRINSIC DETERMINANTS OF DISEASE

2.2.1 Disease agents as determinants of disease

Agents associated with disease can be categorised into two broad groups:

- "Living" agents, such as viruses, bacteria, rickettsia, protozoa, helminths, arthropods etc.
- "Non-living" agents, such as heat and cold, water, nutrients, toxic substances etc.

Since infectious diseases of livestock are generally regarded as being of prime importance in Africa, the following discussion is concerned principally with the determinants associated with the so-called living disease agents.

In instances of infectious disease, the presence or absence of the aetiological agent is the main determining factor in the epidemiology of the disease. Obviously, disease cannot occur in the absence of the agent, but, conversely, disease need not always result from the presence of the agent. This leads us to the important epidemiological distinction between infection and disease.

- *Infection* can be defined as the invasion of a living organism, the host, by another living organism, the agent.
- *Disease* can be defined as a derangement in the function of the whole body of the host or any of its parts.

Infectivity, virulence and pathogenicity

Whether infection takes place or not may depend on a whole range of determinants, both intrinsic and extrinsic, which affect the host and the agent (and the intermediate host or the vector, if present).

Infectivity is a measure of the ability of a disease agent to establish itself in the host. This term can be used qualitatively, when an agent is referred to as being of low, medium or high infectivity, or quantitatively. Attempts to quantify infectivity normally involve the use of a statistic known as ID_{50} . This refers to the individual dose or numbers of the agent required to infect 50% of a specified population of susceptible animals under controlled environmental conditions.

Having become infected, the host may or may not become diseased, and this is again determined by a range of intrinsic and extrinsic determinants affecting the agent and the host. Two terms – virulence and pathogenicity – are often used to describe the ability of the agent to cause disease.

Virulence can be defined as a measure of the severity of a disease caused by a specified agent. In its strict sense, virulence is a laboratory term and is used to measure the varying ability of disease agents to produce disease under controlled conditions. It is often quantified by a statistic known as LD₅₀ which refers to the individual dose or numbers of the agent which will kill 50% of a specified population of susceptible animals under controlled environmental conditions.

Pathogenicity is an epidemiological term used to describe the ability of a particular disease agent of known virulence to produce disease in a range of hosts under a range of environmental conditions.

Host/agent relationships

The relationships between infection and disease are frequently dynamic in nature. They centre on the “balance” that can be achieved between the resistance mechanism of the host and the infectivity and virulence of the agent. Disease outbreaks caused by the introduction of an agent into a susceptible host population which has not been previously exposed to that agent normally result in a disease of high pathogenicity with commensurate severe losses in the host population. Such a process is actually detrimental to the agent’s survival, since by killing off the host population it adversely affects both its ability to reproduce and its chances of gaining access to new susceptible hosts. An agent can therefore improve its chances of survival by increasing its infectivity and decreasing its pathogenicity, and some agents have a natural tendency to do this under certain circumstances.

Since a commensal or parasitic relationship confers no benefits to the hosts, they tend to develop means of resisting infection by disease agents. While the agents, in order to survive, develop methods of circumventing the hosts’ defences. Disease agents normally have much shorter generation intervals and can multiply much more rapidly than

their hosts, and therefore tend to evolve much quicker. This rapid evolution usually enables the agents to keep comfortably ahead of the hosts’ defence mechanisms. There are many mechanisms by which infectious agents can avoid or overcome the defences of the host. The two mechanisms whose consequences are of particular importance in the field of livestock disease control are the carrier state and antigenic variation.

Creation of the carrier state. The term “carrier” is used to describe an individual that is infected by a disease agent and is capable of disseminating that disease agent but shows no sign of clinical disease. Three types of carrier state are recognised:

- The *true carrier*, which is an infected individual capable of disseminating the infectious agent but which never exhibits clinical signs of disease. True carriers occur in various diseases, including salmonellosis.

- The *incubatory carrier*, which is an infected individual capable of disseminating the infectious agent while the disease is still in the incubatory stage. In foot-and-mouth disease, for instance, infected animals are most infectious 12 to 24 hours before the clinical signs of the disease appear.

- The *convalescent carrier*, which is an individual that continues to disseminate the infectious agent after the clinical signs of the disease have disappeared. Convalescent carriers occur in such diseases as contagious bovine pleuropneumonia.

Antigenic variation. Some species of disease agent seek to evade the hosts’ defence mechanisms by altering their antigenic characteristics. The most extreme case of antigenic variation occurs in trypanosomiasis, where infection in the host usually takes the form of a series of parasitaemias each one of which involves a form of trypanosome antigenically different from the preceding one. This type of antigenic variation occurs during the course of a single infection.

Another type of antigenic variation occurs in certain agents, such as the foot-and-mouth disease virus, that are highly infectious in nature and that depend for their survival on a continuous cycling through host populations of relatively long-lived animals. The ability to reinfect the same host at a later date is obviously desirable for the agent’s survival, and this is dependent on the generation of a relatively

short-lived immunity combined with the ability of the agent to undergo antigenic variation during its passage through the host population. In such circumstances there is a strong selection pressure for antigenic variants. The two main types of variation are:

- *Antigenic drift*, which involves only minor changes in antigenicity, so that hosts previously infected with the agent retain a certain degree of immunity to the drifted strain.
- *Antigenic shift*, which involves a major change in antigenicity, so that previously infected individuals possess little or no immunity to the shifted agent.

Antigenic shifts are of particular significance when the control of a disease is being attempted by vaccination, since in effect they represent the introduction of a new agent against which the existing vaccine is likely to confer little or no immunity.

The capacity of parasites to evolve rapidly has important implications in other areas of disease control. The very act of introducing a control measure or disease treatment may, in itself, create conditions whereby a strong pressure is exerted on the agent population to select strains which are resistant to the measure or treatments imposed. The evolution of such resistant strains will, in turn, jeopardise the effectiveness of the control measure or treatment. Resistant strains of agents are most likely to develop when the measures or treatments are carried out on a wide scale but improperly – as, for example, in the case of antibiotic resistance arising through the widespread, unsupervised use of antibiotics by livestock producers.

Other terms used to further define host/agent relationships include:

- *Incubation period*, which is the period of time that elapses from the infection of the host by the agent to the appearance of clinical symptoms.
- *Prepatent period*, which is the period between the infection of the host by the agent and the detection of the agent in the tissues or secretions of the host.
- *Period of communicability*, which is the period of time during which an infected host remains capable of transmitting the infective agent.

Methods of transmitting infectious agents

Ascertaining the means by which disease agents are transmitted is a major objective in epidemiological studies, since once the mechanisms by which a particular disease is transmitted are understood, it may become possible to introduce measures to prevent transmission from taking place.

There are three main ways by which disease agents are transmitted from infected to susceptible hosts. An agent may be transmitted through contact between infected and susceptible individuals, or it may be conveyed between these individuals by means of an inanimate object or via another animal serving as a vector or intermediate host. These methods of transmission are not mutually exclusive; the same disease agent may be transmitted by more than one of the following ways.

Contact transmission. In contact transmissions the agent is conveyed between hosts through direct physical contact, as in the case of venereally transmitted diseases such as vibriosis or trichomoniasis, or through indirect contact.

In cases of indirect contact the agent is normally contained in the excretions, secretions or exhalations of the infected host i.e. in the faeces, urine, milk, saliva, placenta and placental fluids, or as aerosols or droplets in the breath. Susceptible hosts contract the infection either by direct exposure to these or through exposure to substances contaminated by them. Diseases spread in this fashion include rinderpest, foot-and-mouth disease, Newcastle disease, and contagious bovine pleuropneumonia.

Contact transmissions can be further distinguished according to whether they occur horizontally between individuals of the same generation or vertically between individuals of different generations. In vertical transmissions the infectious agent is usually passed from dam to offspring either in the uterus or through the colostrum.

The main factors determining whether or not transmission takes place in contact-transmitted diseases are:

- The ability of the agent to survive in the environment. Rinderpest virus, for example, is easily destroyed in the environment, so contact between infected and susceptible individuals must be close and immediate for transmission to take place, whereas, under certain circumstances, foot-and-mouth disease can spread between widely separated stock.

- The extent of the contact that occurs between infected and susceptible individuals of the host populations and their mobility within these populations. The control of livestock movements is, therefore, a vital factor in the control of contact-transmitted diseases which, in Africa, normally occur more frequently during the dry season when livestock movements are at their highest.

Vehicular transmission. In vehicular transmission the agent is transferred between infected and susceptible hosts by means of an inanimate substance or object (sometimes called *fomite*), such as water, foodstuffs, bedding materials, veterinary equipment and pharmaceuticals, or on the skin, hair or mouthparts of animals. In contrast to indirect transmission, the survival time of the agent in or on the vehicle is usually prolonged. This means, in effect, that vehicular transmission can take place over greater distances and over longer time periods. Hygiene, disinfection and control over the distribution of likely vehicles of transmission are important factors in the control of vehicularly transmitted diseases.

Certain agents may take the opportunity to reproduce themselves during vehicular transmission. This occurs in the transmission of food-borne bacteria, such as salmonella and coliforms, and underlines the importance of strict hygiene in the handling of foodstuffs and livestock feeds, since a small initial contamination may eventually result in the gross contamination of a whole batch of food or feed.

Vectors and intermediate hosts. Confusion frequently arises between the terms "vector", "intermediate host" and "definitive host". The latter two terms are essentially parasitological terms and describe the different types of hosts that are biologically necessary in the lives of agents with relatively complicated life cycles.

- A *definitive host* is a host in which the agent undergoes a sexual phase of its development.
- An *intermediate host* is a host in which the agent undergoes an asexual phase of its development.

The definitive host is usually a vertebrate, while intermediate hosts can be either vertebrates or invertebrates.

- A *vector* is an invertebrate animal that actively transmits an infectious agent between infected and susceptible vertebrates.

Essentially, vectors can transmit infectious agents in two ways. They can serve as a vehicle whereby the infectious agent is conveyed from one host to another without undergoing a stage of development or multiplication. This is known as *mechanical* transmission. Alternatively, the infectious agent can undergo some stage of development or multiplication in the vector – this is known as *biological* transmission – and in this case the vector is serving either as an intermediate or definitive host, depending on which stage of the development cycle of the agent takes place within it. Vertebrate intermediate hosts play the same role in the transmission of their disease agents as biological vectors.

In mechanical transmission the agent is carried on the skin or mouthparts of the vector from an infected to a susceptible host. The survival time of the agent in or on the vector is usually short, and as a result the transmission of the agent has to be accomplished rapidly. The carriers are normally winged haematophagous insects, and transmission usually takes place when susceptible and infected hosts are in close proximity and when large numbers of vectors are present.

In biological transmission, since the agent develops in the vector, a period of time elapses between the acquisition of the infectious agent by the vector and its becoming infective. Once it has become infective, the vector may remain so, normally for a considerable period if not the rest of its life. This provides more than a single opportunity for disease transmission.

In addition, vectors may be able to pass the agent on to their own offspring transovarially. *Transovarial* transmission enables an infectious agent to be maintained in a vector population through many generations without that population having to be reinfected, and, as such, the vector population remains a continuous source of risk. If transovarial transmission does not occur, at least one stage in each generation of the vector must become infected before transmission of the agent can take place.

Arthropod vectors that undergo metamorphosis have the capacity to pass an agent from one developmental stage to the next. This is known as *transtadial* transmission. Usually in transtadial transmission, one developmental stage becomes infected with the disease agent and the following stage transmits it. If different developmental stages feed on

different host species, transtadial transmission can provide a mechanism for an inter-species transmission of disease agents.

2.2.2 Host determinants

The main intrinsic determinants in the host which can influence the frequency of occurrence of infection and disease are species, breed, age and sex.

Species susceptibilities and natural reservoirs

Most disease agents are capable of infecting a range of animal species, both vertebrate and invertebrate. The severity of the disease resulting from such infections may, however, vary between the species concerned. While certain host species may be refractory to infection with certain disease agents, e.g. equines to the foot-and-mouth disease virus, very few disease agents are in fact restricted to one host species.

The multi-species susceptibility to disease agents is particularly important if the species concerned are able to maintain the disease agent within their populations i.e. to function as *natural reservoirs* of infection. The failure of programmes aimed at controlling a certain disease in one species has often been blamed on the presence of natural reservoir species, because they can reintroduce the infectious agent.

When investigating the potential of a certain species to act as a natural reservoir of a particular disease agent, and the implications this would have on disease control policy, the following considerations need to be borne in mind:

Infection with the disease agent. Although it may be possible to infect a certain host species with a disease agent under laboratory conditions, this may only be achievable by using a method of transmission that does not occur naturally (e.g. intracerebral inoculation). If this is the case, that particular host species is unlikely to play a significant role in the epidemiology of the disease.

Ability of a host species to maintain a disease agent. It may prove possible to demonstrate that a particular host species can be infected by a certain disease agent and that that infection can be accomplished by a natural means of transmis-

sion. A further question then needs to be asked, namely, is that species capable of maintaining the agent within its populations for significant periods of time? If this is not the case, then although that particular species may be involved in the localised spread of the disease agent during an outbreak, it will not serve as a continuous source of infection. As such, the importance of that species in the overall epidemiology of the disease may be reduced, and it may become possible to contemplate a disease control programme in which control measures do not have to be applied to that particular host species. In rinderpest control, for example, it has proved possible to control and perhaps even eradicate the disease by concentrating control measures solely on cattle populations, in spite of the presence of species of wild game which are also susceptible to the disease.

Transmission from the natural reservoir. Even if a species can function as a natural reservoir for a particular disease agent, transmission from that reservoir to domestic livestock may only occur rarely and in certain, clearly defined circumstances. If this is the case, the reservoir species is unlikely to cause a major problem in the initial control of the disease in question. However, when the frequency of occurrence of the disease has been reduced to a low level, and eradication of the disease becomes a possibility, the implications of the presence of reservoir host species for the success of the proposed eradication programme may have to be re-assessed.

Breed susceptibilities

Within a host species, wide ranges of susceptibility to a particular disease are often observed between different breeds. In Africa, for example, certain breeds of cattle, horses, sheep and goats are more tolerant of trypanosomiasis than others. *Bos taurus* breeds of cattle are generally more susceptible to ticks and tick-borne diseases than *Bos indicus*. It is important, however, to distinguish between the differences in susceptibility that are genuinely related to breed or species and the differences that may arise as a result of previous exposure to infection.

Within breeds too, differences in susceptibility to the same disease agent have been noted between strains or families. This has led, in recent years, to the development

of breeding programmes designed to select for disease resistance. Selective breeding has been pioneered in the poultry industry where a large number of different "lines" of poultry have been developed that are resistant to such diseases as Marek's disease, salmonellosis, and even vitamin D and manganese deficiencies. Pigs, too, can be selected for their resistance to atrophic rhinitis and some forms of colibacillosis. There are breeding programmes in Australia selecting for tick resistance in cattle, and in Great Britain there is increasing evidence that a similar approach could be adopted for the control of certain forms of mastitis and metabolic disorders in high-yielding dairy cattle. In Africa, trypanotolerant breeds of livestock are receiving increasing attention as a possible solution to the trypanosomiasis problem in certain areas.

Breeding for disease resistance is probably most applicable as a disease control option in instances where particular disease agents are ubiquitous in the environment, or of non-infectious diseases caused by multi-causal determinants, or where other methods of control have proved unsatisfactory.

Differences in species or breed susceptibility to disease must be taken into account when introducing new breeds or species into new environments. The new breed or species may be exposed to disease agents to which the local breeds or species are resistant but to which the new breed or species is highly susceptible. Conversely, the imported breed or species may itself introduce a new disease agent to which it is resistant but to which local breeds or species are susceptible. This factor has become the cause for much concern in recent years given the rapid development of international transport facilities whereby livestock and their products can easily be conveyed from one part of the world to another. Furthermore, because of improvements in the disease investigation and diagnostic facilities of many veterinary services, disease agents are being identified that cause little or no disease in indigenous livestock populations but which have the potential to cause a severe problem in the more susceptible livestock populations of other countries should these agents be imported. Bluetongue is an example of a disease which has attained prominence in this way.

Age susceptibilities

Differences in susceptibility to disease are often seen between different age groups. For example, young animals are generally less susceptible to tick-borne diseases than older animals. There is, however, often a problem in distinguishing between true age resistance in young animals and passive resistance occasioned by the transfer of maternal antibodies via the placenta or in the colostrum. A false impression of age susceptibility may also be created when a highly infectious disease occurs frequently in a population. It may, for instance, appear that only young individuals are affected by the disease in question. This may not be due to a difference in age susceptibility but simply because the older individuals, who had been infected previously, represent a surviving and immune population.

Sex associations in disease

In these associations the clinical signs of disease are associated with sexual attributes, as in the case of diseases of the reproductive tract, rather than with the fact that males may be more susceptible than females or vice versa. Sometimes, too, one particular sex may be regarded by farmers as being of greater value than the other and will therefore receive a correspondingly greater amount of care and attention when sick.

2.3 EXTRINSIC DETERMINANTS OF DISEASE

Extrinsic determinants of disease are important in epidemiology in that they can have effects on the host, on the agent, and on the interactions between the host and the agent. They can also affect any intermediate hosts or vectors involved in the transmission of a disease, and thus determine the type and extent of the disease transmission taking place.

There are three major extrinsic determinants. The first two are climate and soils, which, by interacting in a variety of ways, affect the environment of the host, the agent, and the intermediate host or vector, if they are present. The third major factor is man, who, uniquely among animals,

has the ability to modify both the environment in which he lives and the environment in which he keeps his livestock.

2.3.1 Climate

When considering climate as a determinant of disease, a distinction is normally made between the macroclimate or weather, and the microclimate. The term microclimate refers to the actual climatic conditions prevailing in the specific, restricted environment where the host, agent, vector or intermediate host actually live. While man is as yet largely incapable of deliberately manipulating macroclimates, he can control and manipulate microclimates to some extent.

Macroclimates. A large number of different factors combine to make up the macroclimate. Some of these factors (heat, cold, rainfall, wind, humidity etc) can act as disease agents in their own right, either individually or in combinations. As such they can cause disease in young and newborn animals which are particularly sensitive to heat, cold and dehydration. In older animals they tend to act more as indirect determinants of disease in that they can produce – either alone or in combinations with other managerial and nutritional determinants – “stress” conditions in the host, which may lower its resistance both to infection and, if infection takes place, to disease.

Macroclimates can also affect the ability of a disease agent, or its intermediate host or vector, to survive in the environment. If the effects of weather on disease agents and their intermediate hosts or vectors are known, it may be possible to predict when host populations are at a particular risk of contracting disease and thereby to implement appropriate control measures at strategic times. This approach has been used with success in the control of such diseases as helminthiasis, ticks and tick-borne diseases, trypanosomiasis, foot-and-mouth disease, and in mineral and other nutritional deficiencies.

Microclimates. While macroclimates can have a direct effect on microclimates, the study of macroclimates alone can frequently be misleading in achieving an understanding of the epidemiology of a disease. Regions where existing macroclimatic conditions might be thought unsuitable for the transmission of a disease may, in fact, contain limited areas

where the microclimatic conditions are suitable for the survival of the disease agent and its vector or intermediate host. (An example may be a water hole or an irrigated pasture in an arid environment). Such areas often provide enhanced conditions for disease transmission, since they may prove attractive to livestock, particularly at those times of the year when the macroclimate is at its most severe. If the host and the agent (and the vector or intermediate host, if they exist) are in close contact, the transmission of disease can be effected rapidly and easily. Thus, in arid areas, the transmission of such diseases as helminthiasis and trypanosomiasis may in fact take place during the dry season when the hosts, the agent and the vector are all concentrated around permanent water sources. High contact rates in these areas also favour the introduction and transmission of rinderpest, foot-and-mouth disease and contagious bovine pleuropneumonia.

2.3.2 Soils

By interacting with climate, soils determine vegetation and the environment in which the livestock are kept. The main effect of vegetation is on nutrition. Soils therefore act indirectly as determinants of disease by causing starvation, if there is little or no vegetation, or nutritional imbalances such as protein, energy, vitamin or mineral deficiencies. Malnutrition can be the direct cause of disease, or it can stress the host and thus increase its susceptibility to infection and disease from other sources. Soils can also have an effect on the ability of the agent to survive in the environment, through such factors as waterlogging, pH etc.

2.3.3 Man

Man is often able to create favourable, artificial microclimates for livestock rearing by providing such inputs as housing, water supplies, irrigation etc. Unfortunately, this often results in the creation of conditions favourable for the survival of disease agents and their intermediate hosts or vectors. This means that, by altering the environment, man can alter the determinants of the diseases present in that environment. The changes in determinants will favour some diseases and be detrimental to others. Thus changes in systems and methods of production will result in changes

in the relative importance of the diseases present, with perhaps some new diseases being introduced and others disappearing. The epidemiologist should be alert to such changes and should attempt to predict the likely effect that these will have on the overall disease picture, so that potentially dangerous situations can be averted or controlled.

Man is also able to interfere directly in the disease process through the use of drugs, vaccines, movement controls, quarantines etc. Among the main tasks of the epidemiologist is the investigation of the efficacy of such measures, as well as to design ways in which they can be used most efficiently and to monitor the effects of their introduction on disease incidence.

2.4 DESCRIBING DISEASE EVENTS IN POPULATIONS

The first priority in investigating the epidemiology of a disease is to describe accurately the nature of the problem being investigated. Comprehensive and accurate description of disease problems often provides valuable insights into the epidemiology of the disease being investigated and allows hypotheses about likely determinants to be formulated.

A description of a disease problem should specify the disease and the population at risk, give information on the distribution of events in time and space, and include an attempt to quantify disease events.

Disease diagnosis. If the disease is infectious in nature, the disease agent involved should also be identified. For the disease agent to be infectious it must fulfil Koch's postulates that:

- The agent should be present in all cases of the disease;
- It can be isolated and grown in pure culture; and
- It should be capable of producing the disease when inoculated into healthy animals.

One of the problems associated with these postulates is that they do not take into account the differences between different strains of agents, particularly in their virulence, pathogenicity, and infectivity, which may be important in the epidemiology of the disease. We shall have more to say on the problems of disease diagnosis in Chapter 4.

Populations at risk. These can be identified by studying the distribution of the disease within host populations by species, breed, age and sex. Descriptions of population densities and movements are also of great value, particularly when the disease is transmitted by contact.

Distribution of disease events in time and space. This generally involves looking for the "clustering" of disease events in time, space or both.

The clustering of disease events in space can often be demonstrated by the use of conventional mapping techniques. This type of clustering may indicate the presence of a particular determinant or determinants (e.g. a vector, a mineral deficiency etc) in an area. It should be remembered, however, that clustering in space occurs naturally in the case of contact – transmitted diseases, and that it may also be a function of host-population density.

The clustering of disease events in time may indicate that the host population was exposed to a common source of the disease or its determinant. Outbreaks of diseases transmitted by such vehicles as water or foodstuffs frequently exhibit clustering in time, as in the case of food poisonings. Seasonal clustering of disease events often indicates the influence of climatic determinants in some form or other.

The distribution of disease events in populations in time and space can be described by three basic descriptive terms. These are: endemic, epidemic and sporadic.

An *endemic* disease is a disease that occurs in a population with predictable regularity and with only minor deviations from its expected frequency of occurrence. In endemic diseases, disease events are clustered in space but not in time. Note that a disease may be endemic in a population at any frequency level, provided that it occurs with predictable regularity. Additional terms can be used to describe endemic diseases according to their frequency of occurrence. Thus:

- *Hyperendemic* is an endemic disease that affects a high proportion of the population at risk.
- *Mesoendemic* is an endemic disease that affects a moderate proportion of the population at risk.
- *Hypoendemic* is an endemic disease that affects a small proportion of the population at risk.

An *epidemic* disease is a disease that occurs in a population in excess of its normally expected frequency of occurrence. In an epidemic disease, disease events are clustered in time and space. Note that a disease may be epidemic even at a low frequency of occurrence, provided that it occurs in excess of its expected frequency.

A *pandemic* is a large epidemic affecting several countries or even one or more continents.

A *sporadic* disease is a disease that is normally absent from a population but which can occur in that population, although rarely and without predictable regularity.

Many epidemics of infectious disease occur in a regular, cyclical fashion over a prolonged period of time. This is because with an increasing frequency of occurrence of the disease in a host population, the number of susceptible hosts decreases as individuals within that population become infected, and then either die or recover and become immune to reinfection. As the number of susceptible hosts decreases, so does the opportunity for disease transmission. This, in turn, means that the frequency of occurrence of new cases of the disease declines. A period of time then

elapses during which new susceptible individuals are born into the host population. The number of susceptible hosts in the population thus increases, and the opportunities for the disease agent to find a susceptible host are enhanced. As a result the frequency of occurrence of the disease may increase and a new epidemic may take place.

When assessing the efficacy of measures introduced to control epidemics, an attempt should be made to distinguish between a decline in the frequency of occurrence of the disease due to a control measure, and a natural decline in the epidemic cycle. Epidemics can be prevented if the level of immunity in the host population can be sustained. It is important, therefore, in instances where the control of an infectious disease is being attempted by vaccination, that coverage be maintained in the host population even when the disease is occurring rarely.

Quantification of disease events. Any description of a disease problem should include an attempt at quantification. The methods by which disease events in populations are quantified are described in Chapter 3.

3. THE USE OF DESCRIPTIVE STATISTICS IN THE PRESENTATION OF EPIDEMIOLOGICAL DATA

3.1 INTRODUCTION

Evidence of the presence, nature and severity of a disease will usually be contained in statistical data of some kind. These may take the form of counts of the numbers of diseased animals, physical measurements of a sample of animals, the measurement of one or more biological variables that are likely to be affected by the presence of the disease, and so on. Any report on the disease will have to include at least a descriptive presentation of the statistical evidence.

There are several basic methods and measures which are commonly used to display and summarise sets of data. The choice of technique used depends mainly on the kind of data involved. Data come in two main categories – *categorical (discrete)* and *continuous (numerical)* data. Categorical data are data that can be allocated to distinct categories, and normally take the form of counts. Categorical data found in epidemiology may take the form of *dichotomous* data i.e. data that can have only two values (e.g. diseased or non-diseased, infected or non-infected). Continuous data consist primarily of measurements, which, although they can be classified into defined categories, have the theoretical possibility of being infinitely subdividable. For example, the weight of a chicken could be 1.45 kg, 1.453 kg, 1.45327856 kg etc.

In this chapter we will be looking at some of the more common and useful methods for summarising both categorical and continuous data.

3.2 TABLES AND GRAPHS

Table 1 consists of the liveweights of 150 chickens selected randomly in a large market during a day on which approximately 4000 chickens were sold.

Table 1. *Weights (kg) of a sample of 150 chickens sold in a market.*

1.40	1.09	1.74	1.48	1.82	1.09	1.52	1.41	1.83	1.22
1.34	1.68	1.25	1.65	1.14	1.33	1.06	1.71	1.17	1.51
1.36	1.34	1.03	1.24	1.06	1.12	1.15	1.57	1.38	1.40
1.39	1.31	1.50	1.10	1.45	1.34	1.38	1.35	1.49	1.58
1.25	1.42	1.64	1.57	1.53	1.18	1.39	1.34	1.13	1.23
1.17	1.88	1.30	1.27	1.01	1.63	1.47	1.23	1.48	1.48
1.37	1.42	1.22	1.47	1.31	1.05	1.61	1.41	1.17	1.45
1.43	1.22	1.40	1.14	1.53	1.25	1.02	1.30	1.35	1.37
1.69	1.37	1.11	1.30	1.05	1.19	1.36	1.63	1.44	1.29
1.35	1.59	1.94	1.51	1.78	1.37	1.11	1.38	1.53	1.44
1.47	1.39	1.55	1.76	1.43	1.37	1.67	1.36	1.31	1.41
1.36	1.26	1.17	1.15	1.79	1.46	1.35	1.29	1.50	1.26
1.36	1.41	1.36	1.32	1.08	1.28	1.33	1.29	1.42	1.50
1.32	1.39	1.20	1.68	1.20	1.35	1.56	1.57	1.37	1.27
1.25	1.38	1.56	1.60	1.74	1.40	1.11	1.60	1.21	1.44

It is not easy to make sense of these figures displayed in this form. What can we do to make them more intelligi-

ble? Perhaps the first thing which will occur to most of us is to calculate the *mean* (i.e. sample average) by adding all these values and dividing by 150. Doing this, we find that the mean weight of chickens in the sample is 1.3824 kg. How useful is this number? By itself, not very useful. For example, it does not allow us to draw the conclusion that "most of the chickens weighed about 1.38 kg".

Adding the information that the lightest chicken weighed 1.01 kg and the heaviest 1.94 kg, we might say that the range of the sample was 0.93 kg (1.94 - 1.01), with a mean weight of 1.3824 kg. However, this does not rule out the possibility that the weights were evenly spread throughout the range, or indeed that about half were at the low end and the remainder at the upper end of the range. In other words, we would like to know precisely how the values were distributed throughout the range. The simplest way to do this is to draw up a frequency table (see Table 2).

Table 2. Frequency table of the individual weights of 150 chickens.

Grouped interval of chicken weights (kg)	Frequency ^a	Relative frequency (%)	Cumulative frequency ^b	Relative cumulative frequency (%)
1.00-1.09	10	(6.7)	10	(6.7)
1.10-1.19	16	(10.7)	26	(17.3)
1.20-1.29	21	(14.0)	47	(31.3)
1.30-1.39	39	(26.0)	86	(57.3)
1.40-1.49	26	(17.3)	112	(74.7)
1.50-1.59	17	(11.3)	129	(86.0)
1.60-1.69	11	(7.3)	140	(93.3)
1.70-1.79	6	(4.0)	146	(97.3)
1.80-1.89	3	(2.0)	149	(99.3)
1.90-1.99	1	(0.7)	150	(100.0)

^a Number of values in each interval.

^b Cumulative number of values up to the end of a particular interval.

The relative frequencies (column 3) were obtained by dividing the number of values in each interval by the total number of chickens in the sample and converting the result

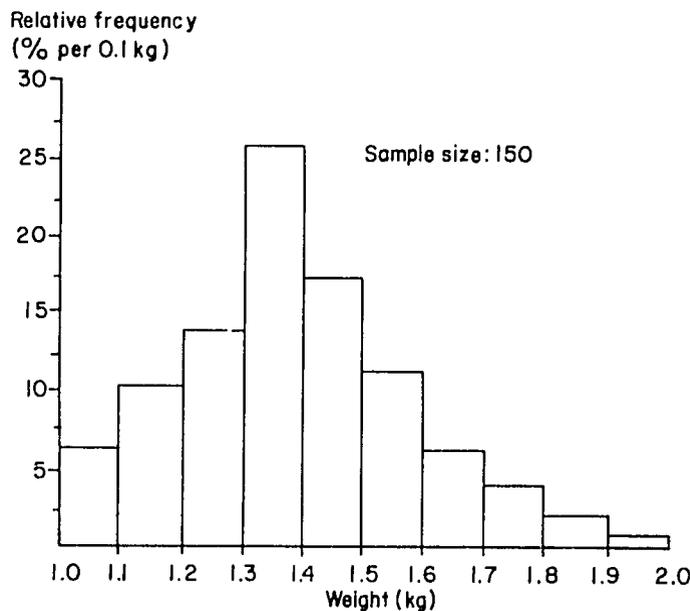
to a percentage. For example, the relative frequency of the first interval is:

$$(10/150) \times 100 = 6.7\%$$

Looking down the column of relative frequencies we see that 17.3% of the sampled chickens weighed between 1.40 and 1.49 kg, and over half (57.3%) weighed between 1.20 and 1.49 kg. The *cumulative* and *relative cumulative frequencies* also given in the table are useful in answering questions about the extremes or *tails of the distribution*. For example, 17.3% of chickens in the sample weighed less than 1.20 kg and 14% (100 - 86) weighed at least 1.60 kg.

The information in Table 2 can also be presented as a graph (Figure 2). Frequency tables are often presented as special types of graphs called *histograms*.

Figure 2. Histogram of the frequency distribution of chicken weights from Table 1.



The area of each block in the histogram should be proportional to the relative frequency of the corresponding interval. Only when the class intervals are all of equal size,

as in this case, will the height of each block be proportional to the frequency.

Measured to the nearest hundredth of a kilogram, the chicken weights ranged from 1.01 to 1.94 kg i.e. there were 94 possible values in the range. If we had measured the weights to the nearest gram, there would have been 940 possible values in the range. In order to draw up a frequency table like Table 2, it is necessary to collapse the data into classes defined by intervals on the scale of measurement. Sometimes data can take only a limited range of values, and then it may be neither necessary nor desirable to group different values into the same classes. An example is Table 3 which gives the frequency of different parturitions in a herd of 153 cows.

Table 3. Frequency of different parturitions in a herd of 153 cows.

	Parturition number				
	0	1	2	3	4
Number of cows	26	38	47	24	18
Relative frequency (%)	0.17	0.25	0.31	0.16	0.12
Cumulative relative frequency (%)	0.17	0.42	0.73	0.89	1.01

It does not make sense to try to draw a histogram of this data set. Other possible methods of graphical presentation will be suggested below, though, in this case, the table is by itself a clear method of presenting the data.

We could use the data to calculate the mean number of parturitions –
 $[(26 \times 0) + (38 \times 1) + (47 \times 2) + (24 \times 3) + (18 \times 4)] / 153 = 1.80$
 – but this is unlikely to be a useful piece of information unless we wanted to compare two different herds. Even then, it would be better to give the complete sets of parturition data for both herds.

3.3 BAR AND PIE CHARTS

Categorical data that take only two possible values are often referred to as *dichotomous*, and we will be interested mainly in the proportions belonging to each category. Note

that the use of numerical labels for categorical variables may sometimes be confusing, but it does not deprive the latter of their categorical status. The important question is whether the numerical labels still behave as numbers in the usual sense.

This may be demonstrated on the following example. Three common causes of death in chickens are salmonellosis, coccidiosis and Newcastle disease, and their frequencies in a sample of 59 dead birds are shown in Table 4. For convenience of data storage, the variables were given code numbers 1, 2, 3 and 4, as shown in the table. However, these are not numbers in the usual sense. For example, we cannot say that 2 (coccidiosis) is greater than 1 (salmonellosis), and so on. They are just simpler versions of the original labels. It would therefore be silly to try to work out the mean of these coded data; the most we can do is to give tables of frequencies or percentages.

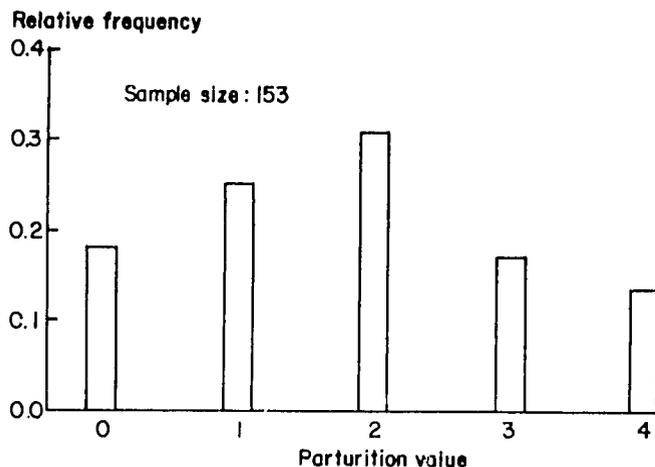
Table 4. Frequencies of causes of death in a sample of 59 chickens.

Cause	Code	No. of deaths	Relative frequency (%)
Salmonellosis	(1)	12	0.20
Coccidiosis	(2)	7	0.12
Newcastle disease	(3)	30	0.51
Other	(4)	10	0.17

As was pointed out a histogram would not be a suitable means of presenting the data in Table 3, and this applies also for Table 4. The data in these tables can be presented graphically either in a *bar chart* or a *pie chart*. Figure 3 is a bar chart showing the relative frequencies of the different parturition values given in Table 3.

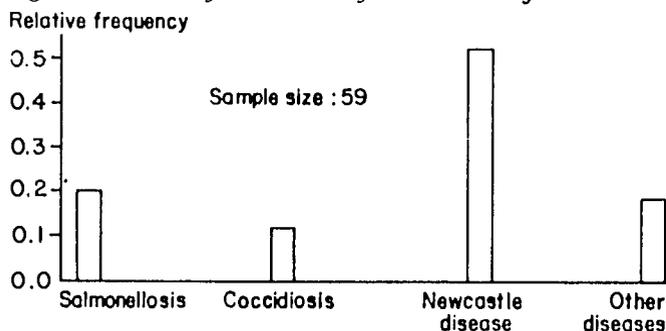
Notice the differences between a bar chart and a histogram: there should be a gap between adjacent bars in the bar chart to emphasise that the data can take only the discrete values actually marked on the horizontal axis, and each bar should have exactly the same width, with the height proportional to the relative frequency of the value over which it is centred.

Figure 3. Bar chart of parturition data from Table 3.



The data on chicken pathology (Table 4) can also be displayed in a bar chart (Figure 4). However, unlike in Figure 3 where the different parity values have the usual, natural ordering, in Figure 4 the order of the different "values", i.e. diseases, on the horizontal axis is arbitrary. Remember, when there is a natural order, it must be adhered to; when the data are categorical, any ordering may be chosen.

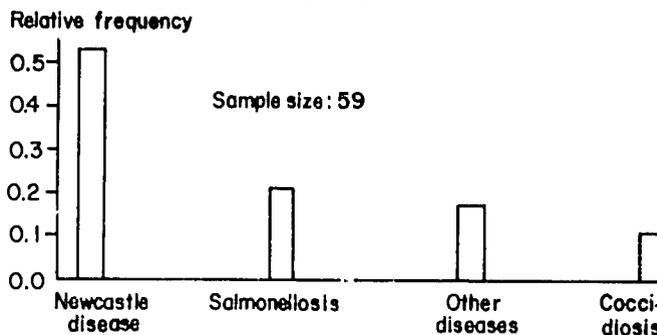
Figure 4. Bar chart of data on causes of death in chickens from Table 4.



Frequently, it may be helpful to present categorical data in a decreasing order of frequency, as was done in Figure 5.

For purely categorical data, the pie chart is a common alternative to the bar chart. The pie chart is a circle divided

Figure 5. Alternative bar chart of data from Table 4.



into as many sectors as there are categories. The area of each sector is made proportional to the relative frequency of the corresponding category by calculating the angle which the sector makes at the centre of the circle. As the total of all the angles is 360° , we need only to divide the 360° in the correct proportions among the various categories to obtain the corresponding areas.

From Table 4 we know, for example, that the relative frequency of salmonellosis is 0.20. The corresponding angle is $360 \times 0.20 = 72^\circ$. Similarly, the angles corresponding to coccidiosis and Newcastle disease are 43° and 187° , respectively, rounded to the nearest degree. The resulting pie chart is shown in Figure 6.

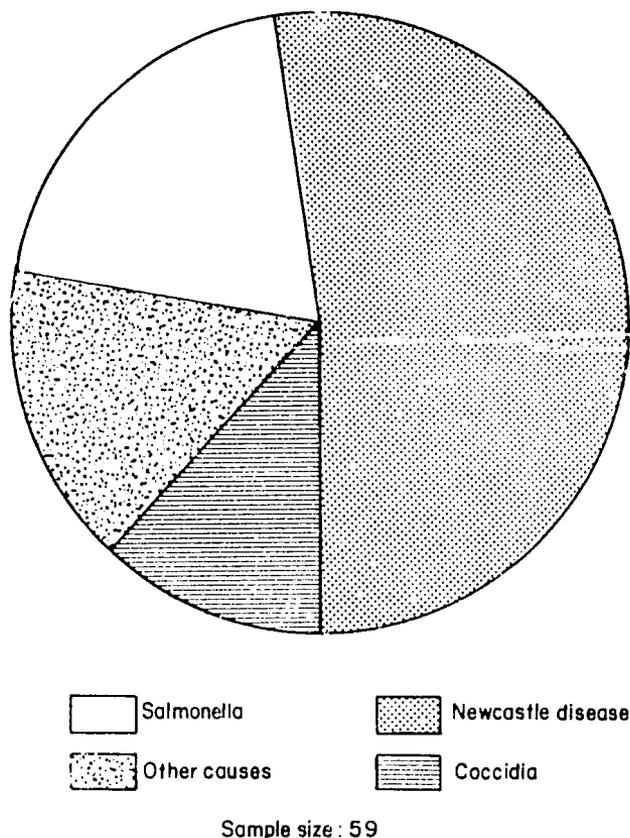
Note that in histograms, pie charts and bar charts the sample size should always be quoted.

3.4 CLASSIFICATION BY VARIABLE

All the examples discussed so far have involved observations of a single variable in a single population of animals. However, we may wish to subdivide a population into several subgroups in order to investigate possible differences between them. For example, cattle may be classified by sex, breed, geographic location, disease status etc. In epidemiological investigations, the classificatory variables will usually be categorical and will frequently be referred to as factors or determinants.

True numerical variables can also be used as classifying factors, either in the form of the values of the variable, if it takes only a small number of values, or class intervals.

Figure 6. Pie chart of relative frequencies of causes of death in 59 chickens, based on Table 4.



For example, each animal that provided data for Table 3 could be classified by its number of parturitions, thus dividing the sample into five groups, while the chickens whose weights are given in Table 1 could be divided into 10 distinct weight groups, using the class intervals of Table 2 to define the different levels of the factor "liveweight".

The choice of factors and the number of levels of each factor will depend on the degree of prior knowledge of the population to be studied, the expected scientific significance of the factors, and the measures available to the investigator. Table 5 is a contrived table displaying counts of

ascaris infections in pigs according to three factors: the management system (two levels; raised indoors or outdoors), the occurrence of ascaris eggs in a sample of faeces from each pig (two levels; present or absent), and the degree of whitespot observed in the liver of each pig after slaughter (three levels; absent, slight or severe).

Table 5. Contrived table based on evidence of ascaris infection in pigs: An example of a three-factor table with marginal totals.

Whitespot	Ascaris eggs	Management system		Any system
		Indoors	Outdoors	
Absent	Absent	503*	112*	615
	Present	141*	38*	179
	Total	644	150	794
Slight	Absent	231*	75*	306
	Present	87*	30*	117
	Total	318	105	423
Severe	Absent	79*	32*	111
	Present	71*	17*	88
	Total	150	49	199
Any whitespot condition	Absent	813	219	1032
	Present	299	85	384
	Total	1112	304	1416

* Recorded data.

In any table, it is often useful to give the marginal totals i.e. to sum the counts over all the levels of the different factors. This makes it easier to extract any subtables that may be of interest, and the marginal tables are needed anyway for the analysis of the data (see Chapter 5). On the other hand, marginal totals can greatly increase the size of a table. In Table 5, for instance, only the values marked with an asterisk are strictly necessary, while the remaining entries (24 out of 36) give supplementary information. The use of marginal totals is a matter of personal judgement: in general, if it is thought that the complete table might confuse rather than clarify the issues, then the totals are better left out.

Table 6 shows one of the two-factor tables that can be derived from Table 5.

Table 6. *Two-factor table derived from Table 5.*

Whitespot	Ascaris eggs		Total
	Absent	Present	
Absent	615 (59) ^a	179 (47)	794 (56)
Slight	306 (30)	117 (30)	423 (30)
Severe	111 (11)	88 (23)	199 (14)
Total	1032 (100)	384 (100)	1416 (100)

^a Figures in parentheses give the relative frequencies (%) of whitespot conditions.

With multi-factor tables there are always several options for presenting relative frequencies. In Table 6, for example, the relative frequency of the different whitespot conditions is given for each level of the ascaris egg factor. Alternatively, the frequency of each level of ascaris eggs could be given relative to the totals within each level of whitespot severity, or the frequency of each of the six possible whitespot-ascaris egg combinations could be calculated relative to the total number of pigs in the sample. The option chosen will depend on the point that one wants to make, but the table should make it clear which relative frequencies are given. In interpreting tables presented by other investigators care should be taken to clarify which relative frequencies are being presented or discussed.

3.5 QUANTIFICATION OF DISEASE EVENTS IN POPULATIONS

Data used to quantify disease events in populations are often dichotomous in nature i.e. an animal can either be infected with a disease agent or not infected. Such data are frequently presented in the form of an epidemiological *rate*.

In epidemiology, a rate can be defined as the number of individuals having or acquiring a particular characteristic (normally an infection, a disease or a characteristic associated with a disease) during a period of observation, divided by the total number of individuals at risk of having or acquiring that characteristic during the observation peri-

od. The expression is then multiplied by a factor, normally a multiple of 10, to relate it to a specified unit of population.

Rates are commonly expressed as decimals, percentages, or events per standard units of population e.g. per 1000, 10 000 animals etc. This produces a standardised measure of disease occurrence and therefore allows comparisons of disease frequencies over time to be made between or within populations. Note that in a rate, the numerator is always included in the denominator, while in a ratio it is not included. In an epidemiological rate, the period of observation should always be defined.

It is difficult to make valid comparisons of disease events between or within populations unless a denominator can be calculated. The use of "dangling numerators" to make comparisons is one of the biggest "crimes" that the epidemiologist can commit, and it should be avoided whenever possible.

For example, suppose we were interested in comparing the numbers of cases of infection with a particular disease agent over a particular time period in two herds of cattle of the same breed but under different management systems. We are told that in herd A the number of animals infected with the disease agent in question in the month of June 1983 was 25, while in herd B the number of animals infected with the same disease agent in the same month was 50. We might therefore conclude, erroneously, that the disease was a greater problem in herd B than in herd A. Note that we did not know the denominator i.e. the population of animals at risk of being infected with the disease agent in each herd. Suppose we investigated further and found that the population at risk in herd A during the month of June was 100 while in herd B it was 500. Then, calculating a rate for each herd, we find that the rate of infection in herd A was 25/100 or 0.25 or 25% or 250 in 1000, while in herd B it was 50/500 or 0.10 or 10% or 100 in 1000. The true position, therefore, is that the disease was a greater problem in herd A!

The two main types of rates used in veterinary epidemiology are:

- *Morbidity rates*, which are used to measure the proportion of affected individuals in a population or the risk of an individual in a population of becoming affected.

- *Mortality rates*, which measure the proportion of animals dying in a population.

Morbidity rates

Morbidity rates include incidence, attack, prevalence and proportional morbidity rates.

Incidence rate is the number of new cases of a disease occurring in a specified population during a specified time period, divided by the average number of individuals in that population during the specified time period.

For example, suppose that out of an average population of 4000 cattle in a quarantine camp, 600 animals developed symptoms of rinderpest during the month of June. The incidence of rinderpest in that quarantine camp for the month of June was $600/4000 = 0.15$ or 15% or 150 new cases per 1000 animals.

The incidence rate is a way of measuring the risk that a susceptible individual in a population has of contracting a disease during a specified time period. Therefore, if a susceptible animal had been introduced into the quarantine camp on 1 June, it would have had a 15% chance of contracting rinderpest by the end of the month.

When calculating incidence rates, problems frequently arise in estimating the denominator. Because of births, deaths, sales, movements etc, livestock populations rarely remain stable over periods of time, and such fluctuations in the denominator will obviously affect the calculation of the incidence rate. There are various ways of estimating the denominator in incidence rate calculations. These normally involve measuring the population at various intervals during the study period and averaging the results.

For instance, suppose that in our previous example there were 4000 animals present at the beginning of June but that 100 animals died of the disease by the end of the second week and a further 300 by the end of the month. Assuming that no new animals were introduced or born, the animal population in the quarantine camp at the start of the observation period was therefore 4000, at the mid-period 3900 and at the end 3600. We might decide to calculate the denominator by taking the populations present at the beginning and end of the observation period and averaging them:

$$(4000 + 3600)/2 = 3800$$

The corresponding incidence rate would be $600/3800 = 0.158$ or 15.8%.

Alternatively, we might take the populations present at the beginning, middle and end of the observation period and average them –

$$(4000 + 3900 + 3600)/3 = 3833$$

– and the incidence rate in this case would be $600/3833 = 0.156$ or 15.6%.

Note that the different methods of calculating the denominator have resulted in slightly differing estimates of incidence. Because of this, the method used in calculating the denominator should always be specified when comparisons of incidence are being made, and the same method should be used throughout. Due to difficulties in the calculation of the denominator in incidence rates, another form of morbidity rate, the attack rate, is sometimes used.

The *attack rate* is the total number of cases of a disease occurring in a specified population during a specified time period, divided by the total number of individuals in that population at the start of the specified time period. The denominator, therefore, remains constant throughout the period of observation. Thus, in our previous example, the attack rate would be $600/4000 = 15\%$.

Strictly speaking, the definition of the attack rate requires that all cases of disease, not just new cases, are included in the numerator. Attack rates are normally used, however, to quantify the progress of a disease during an outbreak. In most instances there would have been no cases of the disease in question prior to the onset of the outbreak, so that all the cases are, in fact, new cases, and the attack rate becomes a modified form of incidence rate.

Prevalence rate is the total number of cases of a disease occurring in a specified population at a particular point in time, divided by the total number of individuals in that population present at that point in time.

For example, suppose that in a population of 4000 cattle held at a quarantine camp there were 60 cases of rinderpest when the population was examined on June 18. The prevalence of rinderpest at that camp on 18 June would then be $60/4000 = 0.015$ or 1.5% or 15 cases per 1000 animals.

Note that prevalence is a cross-sectional measure referring to the amount of disease present in a population at a particular point in time, hence the term *point prevalence*. However, when dealing with large populations, point pre-

valence becomes almost impossible to obtain, since it is not possible to examine all the individuals in that population at a particular point in time. In general, therefore, measurements of prevalence have to take place over a period of time, and this is known as *period prevalence*. Provided that the time taken to measure the prevalence remains reasonably short, this parameter retains a fair degree of precision. If, however, the time interval becomes too long, a significant number of new cases of the disease will have occurred since the start of the measurement period. The parameter then becomes a mixture of point prevalence and incidence and, as such, loses precision.

The terms incidence and prevalence are frequently confused and misused. Confusion normally arises due to a failure to define accurately the denominator i.e. the actual population being considered. This can result in the population at risk being either ignored or not considered in its entirety.

Examples of this can be found in reports from veterinary offices or laboratories, in which the term "incidence" is often used to express the number of diagnoses or isolations of a particular disease agent as a percentage of the total number of diagnoses or isolations performed. In this case the denominator is not the population of individuals at risk from the disease, and the rate calculated resembles a form of a proportional morbidity rate.

A *proportional morbidity rate* is the number of cases of a specific disease in a specified population during a specified time period, divided by the total number of cases of all diseases in that population during that time period.

For example, suppose that an outbreak of contagious bovine pleuropneumonia (CBPP) occurs in a herd of cattle. During a 6-month period there are 45 cases of different diseases, including 18 cases of contagious bovine pleuropneumonia. The proportional morbidity rate for contagious pleuropneumonia in that herd for the 6 months would then be $18/45 = 0.4$ or 40% or 400 cases of CBPP in 1000 cases of all diseases.

Mortality rates

The most commonly used mortality rates are crude death rate and cause-specific death rate.

Crude death rate is the total number of deaths occurring in a specified population during a specified time period, divided by the average number of individuals in that population during the specified time period.

The denominator for this rate can be estimated in the same ways as that for an incidence rate. Note, the method of calculating the denominator should always be defined and the same method used throughout to enable meaningful comparisons to be made.

Example: Suppose that in a herd of cattle there were 40 deaths in a year. The number of animals in the herd at the start of the year was 400, at mid-year 420, and at the end of the year 390. The average herd size could therefore be either

$$(400 + 390)/2 = 395$$

or

$$(400 + 420 + 390)/3 = 403$$

Depending on which method we used to calculate the denominator, the crude death rate would be either $40/395 = 0.101$ (10.1%) or $40/403 = 0.099$ (9.9%).

Cause-specific death rate is a useful mortality rate and can be defined as the total number of deaths occurring from a specified cause in a specified population during a specified time period, divided by the average number of individuals in that population during that time period. The denominator is calculated in the same way as for an incidence or crude death rate, and the same caveats apply in its calculation.

Example: Suppose that there were 20 deaths from babesiosis in the herd mentioned above, then the death rate due to babesiosis in that herd would be either $20/395 = 0.051$ (5.1%) or $20/403 = 0.050$ (5.0%).

Other useful mortality rates

Proportional mortality rate is the total number of deaths occurring from a specified disease in a specified population during a specified time period, divided by the total number of deaths in that population during that time period.

Example: Suppose that out of 40 deaths in a herd 20 were from babesiosis, then the proportional mortality rate due to that disease would be $20/40 = 0.5$ or 50%.

Case fatality rate is the number of deaths from a specified disease in a specified population during a

specified time period, divided by the number of cases of that disease in that population during the time period.

Example: Suppose there were 50 cases of babesiosis in the herd, then the case fatality rate due to babesiosis would be $20/50 = 0.4$ or 40%.

The rates described above are those that are most likely to be used in epidemiological studies in Africa. Details of other rates, how to calculate them, and their potential uses can be found in Schwabe et al (1977).

The use of specific rates

In epidemiology, we are nearly always involved in studying the effects of determinants on the frequency of occurrence of disease. This often involves the comparison of some of the rates mentioned previously, either in the same population over time – normally before and after a determinant is added or removed – or between populations – either with or without an added determinant, or with different frequencies of occurrence of the determinant, either at the same point in time or over a period of time.

For such comparisons to be valid, the comparison groups should differ from one another only in the presence, absence, or frequency of occurrence of the particular determinant being studied. Since epidemiology usually involves the study of determinants under uncontrolled field conditions, these criteria are extremely difficult to fulfil. Nevertheless, if rates are expressed in such a form as to ignore the different characteristics which may be present within the disease agents or host populations being compared, there is a danger that such rates may give an oversimplified and even false impression of the actual situation.

Rates can be made more specific, and the comparisons between them more valid, by taking into account various different characteristics. Differences in subspecies and strains of disease agents can be accounted for by clearly defining the subspecies or strain being studied and by making sure that only those individuals affected by that particular subspecies or strain are included in the numerator. Differences in the characteristics of host populations due to age, breed and sex can be expressed by calculating rates which take these specific characteristics into consideration.

Thus, for example, one could calculate an *age-specific incidence rate* which is defined as the number of new cases of

a disease occurring among individuals of a specified age group in a specified population during a specified time period, divided by the average number of individuals in that specified age group in that population during that time period. Alternatively, one could calculate a *breed-specific incidence rate* which is defined as the total number of new cases of a disease occurring among individuals of a specific breed in a specified population during a specified time period, divided by the average number of individuals of that breed in that population during that time period. One could go even further and calculate an *age-breed specific incidence rate* which is defined as the total number of new cases of a disease occurring among individuals in a specified age group of a specified breed in a specified population, divided by the average number of individuals of that specific age and breed in that population during that time period.

The same procedures can be applied to other morbidity and mortality rates. A large variety of specific rates can thus be calculated by using appropriate definitions of the numerator and the denominator. As a general principle, rates should be made as specific as the data allow, but not so specific as to make the numbers involved too small for statistical analysis. For analytical purposes there is little or no advantage in calculating and comparing age- or breed-specific rates if an age-breed specific rate can be calculated.

The following is an example illustrating the advantages of using specific rates in making comparisons. Suppose we wished to assess the efficiency of a tick control programme in two East Coast fever (ECF) endemic areas, where the level of disease challenge, the environmental conditions and the systems of management were approximately the same. In area A there was an average population of 10 000 head of cattle present during a 1-month study period, and 500 animals from that population developed symptoms of ECF during that period. In area B there was an average population of 15 000 head of which 1500 developed symptoms of the disease during the study period. The crude incidence rate of the disease in area A was $500/10\ 000 = 5\%$ and in area B $1500/15\ 000 = 10\%$. We might conclude, therefore, that the tick control programme in area A was more efficient than in area B.

Suppose we also found that the cattle population in area A was made up of 400 crossbred Holsteins and 9600 East African Shorthorned Zebus, while that in area B con-

sisted of 4500 crossbred Holsteins and 10 500 East African Shorthorned Zebus. We are now able to calculate breed-specific incidence rates as indicated in Table 7.

Table 7. *Breed-specific incidence rates of East Coast fever in two cattle populations.*

Area	Breed	Number of cattle	Number of new cases of ECF	Incidence (%)
A	Crossbred Holstein	400	97	24.5
	East African Shorthorned Zebu	9 600	403	4.2
	Total	10 000	500	5.0
B	Crossbred Holstein	4 500	1 059	23.5
	East African Shorthorned Zebu	10 500	441	4.2
	Total	15 000	1 500	10.0

Note that whereas the crude incidence rates remain 5% and 10% respectively, there is no difference in the breed-specific incidence rates for East African Shorthorned Zebus between the two areas and the rate for crossbred Holsteins is, if anything, less in area B than it is in area A. The difference in the crude incidence rates between the two areas is due to the fact that the much more susceptible crossbreds make up only 4% of the cattle population in area A whereas in area B they represent 30% of the cattle population.

3.6 METHODS OF SUMMARISING NUMERICAL DATA

We have already discussed the (arithmetic) mean and noted that, by itself, the mean gives no indication of how

the data are dispersed about the mean value. We resolved this problem by drawing a histogram, but graphical presentation may not be always convenient and we might like to be able to reduce a data set to a few meaningful values.

At this stage, it is necessary to introduce some simple algebraic notations to express a set of data values. For example, we could refer to the data in Table 1 as X_1, X_2, \dots, X_{150} , where $X_1 = 1.40$ and $X_{150} = 1.44$. If we wanted to refer to a more general data set without fixing the total number of values it contains, we could write X_1, X_2, \dots, X_n , and say that the data contain n different values or observations. We will not always use the letter X ; when we want to refer to different data set in the same context, we will use a different letter for each set. The arithmetic mean for a given data set will be expressed by the appropriate letter with a bar over it. For example:

$$\bar{X} = (X_1 + X_2 + \dots + X_n)/n$$

In statistics it is common to add sets of numbers together, and we shall use a special symbol to denote that operation, namely:

$$\sum_{i=1}^n X_i$$

which means the sum of all X 's from $i = 1$ to $i = n$ i.e.:

$$\sum_{i=1}^n X_i = X_1 + X_2 + \dots + X_n$$

or often we just write ΣX or ΣX_i .

For example, we can write $\bar{X} = 1/n \Sigma X$.

We now return to our problem of looking for a way to describe the "scatter" of values about the mean value \bar{X} . It turns out, for a variety of reasons, that a convenient value is the standard deviation (S), calculated as follows:

$$S = \sqrt{\frac{\sum (X_i - \bar{X})^2}{n - 1}}$$

This formula says: "Find the distance of each individual value X from the mean, square that distance, and then find the average squared distance; finish by taking the square root of the average". Many different formulae can be found in elementary books on statistics for calculating the standard deviation. The best solution is probably to

buy a cheap calculator with this calculation built in. Alternatively, the following formula can be used:

$$S = \sqrt{\frac{\sum X_i^2 - (\sum X_i)^2/n}{n-1}}$$

This formula gives the same answer as the previous one but is easier to manipulate on a calculator. Using this formula, the standard deviation for the data in Table 1 was calculated as 0.1931.

There is a point to be made here about suitable levels of accuracy. A calculator may give $S = 0.1930736$, but this number has too many decimal places to be intelligible. About four significant figures is the maximum that will be absorbed by most readers of a paper or report, and many will notice only the first two.

How to make use of the pair of numbers \bar{X} and S to grasp the main features of a data set will be explained later. One problem with the mean as an indicator of the "centre" of the data is that its value can be markedly affected by the presence of a few extreme values. Suppose, to take an

exaggerated case, there are 20 farmers living in a village of whom 19 earn US\$ 1000 per annum and the twentieth earns US\$ 1 000 000 per annum. The average (i.e. per caput) earnings of the 20 individuals is almost US\$ 51 000 per annum, which is very misleading. Data with a few very large or very small values as compared to the remainder of the set, are said to be *skewed*.

An indicator of the "centre" of data which is not affected in this way and which is therefore more likely to give a value typical of the whole data set is the *median* (m). This is a number so chosen that at least half the data have a value not smaller than m , and, simultaneously, at least half the data have a value not greater than m . The median value of the data in Table 1 is 1.37 kg, while for Table 3 the median parturition is 2. Of course, to discover the "middle" value in a set of data one has to write all the values in the correct order, and this can be time consuming unless it is done automatically by using a (micro) computer. In most practical contexts it will make little difference which of the indicators is used, and the mean is the most frequently chosen.

4. THE EPIDEMIOLOGICAL APPROACH TO INVESTIGATING DISEASE PROBLEMS

4.1 INTRODUCTION

In Chapters 1 and 2 we described the need for an epidemiological approach to the investigation of disease problems. We also implied that such investigations usually have the basic objective of describing and quantifying disease problems and of examining associations between determinants and disease. With these objectives in mind, epidemiological investigations are normally conducted in a series of stages, which can be broadly classified as follows:

1. A diagnostic phase, in which the presence of the disease is confirmed.
2. A descriptive phase, which describes the populations at risk and the distribution of the disease, both in time and space, within these populations. This may then allow a series of hypotheses to be formed about the likely determinants of the disease and the effects of these on the frequency with which the disease occurs in the populations at risk.
3. An investigative phase, which normally involves the implementation of a series of field studies designed to test these hypotheses.
4. An experimental phase, in which experiments are performed under controlled conditions to test these hypotheses in more detail, should the results of phase 3 prove promising.

5. An analytical phase, in which the results produced by the above investigations are analysed. This is often combined with attempts to model the epidemiology of the disease using the information generated. Such a process often enables the epidemiologist to determine whether any vital bits of information about the disease process are missing.

6. An intervention phase, in which appropriate methods for the control of the disease are examined either under experimental conditions or in the field. Interventions in the disease process are effected by manipulating existing determinants or introducing new ones.

7. A decision-making phase, in which a knowledge of the epidemiology of the disease is used to explore the various options available for its control. This often involves the modelling of the effects that these different options are likely to have on the incidence of the disease. These models can be combined with other models that examine the costs of the various control measures and compare them with the benefits, in terms of increased productivity, that these measures are likely to produce. The optimum control strategy can then be selected as a result of the expected decrease in disease incidence in the populations of livestock at risk.

8. A monitoring phase, which takes place during the implementation of the control measures to ensure that these measures are being properly applied, are having the desired effect on reducing disease incidence, and that developments that are likely to jeopardise the success of the control programme are quickly detected.

The following two sections are concerned with describing ways in which epidemiological investigations can be designed and implemented, and the data produced analysed.

4.2 TYPES OF EPIDEMIOLOGICAL STUDY

There are three main types of epidemiological study:

- *Prospective studies*, which look *forward* over a period of time and normally attempt to examine associations between determinants and the frequency of occurrence of a disease by comparing attack rates or incidences of disease in groups of individuals in which the determinant is either present or absent, or its frequency of occurrence varies.

- *Retrospective studies*, which look *backward* over a period of time and normally attempt to compare the frequency of occurrence of a determinant in groups of diseased and non-diseased individuals.

- *Cross-sectional studies*, which attempt to examine and compare estimates of disease prevalence between various populations and subsets of populations at a *particular point* in time.

Frequently, however, these approaches may be combined in a general study of a disease problem. In such studies, other morbidity and mortality rates may be compared as well as other variables such as weight gain, milk yield etc, depending on the objectives of the particular study.

4.2.1 Prospective studies

There are, essentially, two approaches to a prospective study. The first, which is similar to that used in controlled experiments, can be used when the investigator has control over the distribution of the determinant that is to be studied. The individual animals selected for the study are assigned to groups or *cohorts*. (For this reason, prospective studies are often called cohort studies). The determinant to be studied is then introduced into one cohort and the other cohort is kept free of the determinant as a control. The two cohorts are observed over a period of time and the frequencies with which disease occurs in them are noted and compared.

Often, however, the investigator has no control over the distribution of the determinant being studied. In such a case he will select the individuals that have been or are exposed to the determinant concerned, while another group of individuals that do not have, or have not been exposed to, that determinant is used as a control. The frequency of

occurrence of the disease in the different groups is then observed over a period of time and compared.

In prospective studies, the cohorts being compared should consist, ideally, of animals of the same age, breed and sex and should be drawn from within the same herds or flocks, since there may be many differences in the way that different herds or flocks are kept and managed, which may be expected to have an effect on the frequency of occurrence of the disease being investigated. If such cohorts can be selected, prospective studies can demonstrate accurately the association between determinants and disease, since the cohorts will differ from each other merely in the presence or absence of the particular determinant being studied. This will only be possible if the investigator has control over the distribution of the determinant being selected. Even then, such conditions are often very difficult to fulfil in the field, where the investigator is dependent on the cooperation of livestock owners who may be unwilling to alter their management systems to fit in with the study design. If the investigator has no control over the distribution of the determinant being studied, the study design becomes more complicated and the investigation may have to be repeated to take into account the variations in the many different factors involved.

Prospective studies have the disadvantage that if the incidence of the disease is low, or the difference one wishes to demonstrate between groups is small, the size of the study groups has to be large. (Methods for analysing the results of prospective studies and for estimating the size of cohorts needed are described in Chapter 5). The problem of low disease incidence can sometimes be overcome by artificially challenging the different cohort groups with the disease in question. However, this may not be acceptable under field conditions, since livestock owners take grave exception to having their animals artificially infected! For these reasons, prospective studies are normally performed on diseases of high incidence and where the expected difference in disease frequencies between the groups studied is likely to be large.

4.2.2 Retrospective studies

Retrospective studies are often referred to as *case-control studies*. In such studies, the normal procedure is to look back

through records of cases of a particular disease in a population and note the presence or the absence of the determinant being studied. The case group can then be compared with a group of disease-free individuals in which the frequency of occurrence of the determinant has been determined. Note that in a case-control study one is, in effect, comparing the frequency of occurrence of the determinant in two groups, one diseased (cases) and one not (controls).

Retrospective studies have various advantages and disadvantages when compared with prospective studies. The principal advantage of retrospective studies is that they make use of data that have already been collected and can, therefore, be performed quickly and cheaply. In addition, because diseased individuals have already been identified, retrospective studies are particularly useful in investigating diseases of low incidence.

The main disadvantage is that the investigator has no control over how the original data were collected, unless he or she collected them. If the data are old, it may not be possible to contact the individuals who had collected them, and thus there is often no way of knowing whether the data are biased or incomplete (see also Section 4.7 on some other disadvantages in using already generated data in epidemiological work).

The second major disadvantage is that although one knows the frequency of occurrence of the determinant in the case group, one does not know its frequency of occurrence in non-diseased individuals from the *same population*. The latter is normally determined by sampling from a population of non-diseased individuals at the time that the study is being carried out. There is no way of knowing the extent of the similarity between the two different populations from which the case and control groups are taken. Consequently, there is no way of ascertaining the distribution within these populations of undetermined factors which could affect the frequency of the disease. Great caution has to be exercised, therefore, in making inferences about associations between determinants and disease frequencies from retrospective studies.

A third disadvantage is that historical data on cases of disease that are sufficiently accurate to merit further study, are hard to come by in veterinary medicine. The opportunities for doing case-control studies are thus rather lim-

ited. They are much more common in human medical studies.

In spite of the fact that classic case-control studies are rarely performed in veterinary epidemiology, retrospective data are often used in livestock disease studies. The advantages and disadvantages of using such data are discussed later on in this chapter.

Methods for analysing case-control study data and for calculating the sizes of case and control study groups are described in the following chapter.

4.2.3 Cross-sectional studies

Cross-sectional studies are, in fact, surveys. They take place over a limited time period and, in epidemiological studies, are normally concerned with detecting disease, estimating its prevalence in different populations or in different groups within populations, and with investigating the effect of the presence of different determinants on disease prevalence. They can, of course, be used to provide data on a large number of other variables present in livestock populations. Two types of cross-sectional study are commonly performed.

Censuses

A census in effect means sampling every unit in the population in which one has an interest. If the population is small, this is the most accurate and effective way of conducting a survey. Unfortunately, in most instances the populations studied are large and censuses become difficult and expensive to undertake. A further drawback with censuses in large populations is that, because of the practical constraints of staff and facilities, each individual unit within a population can be allocated only a limited amount of time and effort. Consequently, the amount of data that can be obtained from each unit sampled is limited.

Sample surveys

Sample surveys have the advantage of being cheaper and easier to perform than censuses. Because the population is being sampled, the actual number of units being measured is relatively small, and as a result more time and effort can

be devoted to each unit. This enables a considerable amount of data to be collected on each sample unit.

The question is, how closely do the results of the survey correspond to the real situation in the population being sampled? If undertaken properly, sample surveys can generate reliable information at a reasonable cost; if they are performed improperly, the results may be very misleading. This is also true of censuses.

4.3 SAMPLING TECHNIQUES IN EPIDEMIOLOGICAL STUDIES

Epidemiological studies usually involve sampling from livestock populations in some way in order to make inferences about a disease or diseases present in these populations. The units sampled are referred to as *sample units*. Sample units may be individual animals or they may be the units that contain the animals to be investigated, such as herd, ranch, farm, or village.

The *sample fraction* is the number of units actually sampled, divided by the total number of units in the population being sampled.

Various methods can be used to sample a population. The more common techniques used in epidemiological studies are described in the following sections.

4.3.1 Random sampling

The rationale behind random sampling is that units are selected independently of each other and, theoretically, every unit in the population being sampled has exactly the same probability of being selected for the sample. It is, in fact, akin to the process of drawing lots. Random sampling removes bias in the selection of the sample and thereby removes one of the main sources of error in epidemiological studies.

The first step in random sampling is to construct a list of all the individual sample units in the population being sampled. This is known as the *sample frame*. Each unit in the sample frame can then be assigned an identification number which is normally the numerical order in which they appear in the sample frame. A computer program can be used to generate random numbers or a table of the out-

put from such a program. (A random number table is given in Appendix 1). As each number is produced, the unit to be sampled can be identified from the sample frame. Random numbers are selected from a random number table by starting anywhere in the table and then reading either horizontally across the rows or vertically down the columns.

Example: Suppose we are interested in detecting the presence of brucellosis in a dairy herd of 349 cows. We decide that, for our purposes, we wish to be 90% sure of detecting the disease and we estimate, although we do not know, that the prevalence of brucellosis in the herd is not likely to be less than 8% (see Section 4.4 on estimating sample sizes). From Table 10 we see that in order to be 90% sure of detecting the disease at this level of prevalence in a herd of 349 cows, we need a random sample of 27 animals. The animals in the herd are not tagged, but the herdsman is able to identify each animal by name. We can, therefore, construct a sample frame of the animals in the herd by listing their names. If, for any reason, two or more animals had the same name, we could further identify them by a number (e.g. Daisy 1, Daisy 2 etc). A similar procedure can sometimes be used to establish the identity of certain unnamed animals in a herd by identifying them as the first calf of Emma, the second calf of Flora etc.

To select the animals to be sampled we could simply write the name of each animal in the herd on a piece of paper, place the name cards in a hat and then draw out 27 cards. Alternatively, we could use a random number generator or table to produce a set of three-digit numbers. Rejecting all numbers greater than 349, we continue until we have 27 three-digit numbers. A series of such numbers might for instance read 001, 088, 045, 008, 016, 344 etc. We would then select the first, the eighty-eighth, the forty-fifth, the sixteenth, the three-hundred-and-fourty-fourth etc animal from the sample frame. Since we now know the names of the animals to be sampled, we can identify them in the herd and include them in the sample. As a simple alternative, we could run the herd through a chute and select the animals as they come through, taking the first, sixteenth, thirty-fourth etc animal for the sample.

Note that if the population to be sampled was between 10 and 99, we would use two-digit numbers to select the sample; if it was between 100 and 999, three-digit numbers would be used; for populations between 1000 and 9999, and

between 10 000 and 99 999, four-digit and five-digit numbers, respectively, would be selected. Any number in these categories greater than the size of the population being sampled is rejected. If during the sampling procedure the same unit is selected a second time, the number that led to that selection is also rejected.

If we were selecting animals from the same herd for the purposes of a prospective study, we could use random numbers to identify them in the sample frame and then assign each animal in turn to the appropriate group. Thus, in the above example, if we wanted to select three groups from the herd, the first cow on the list would be assigned to group 1, the eighty-eighth cow on the list to group 2, the forty-fifth cow on the list to group 3, the eighth cow to group 1, the sixteenth cow to group 2, the three-hundred-and-forty-fourth cow to group 3 and so on. There are many ways of selecting random samples, but the principles are substantially the same as those outlined above.

Apart from removing bias in the selection of the sample, random sampling has other advantages, the main being that we can easily calculate an estimate of the error for the values of a population parameter estimated by a random sample. This is done by the use of a statistic known as the *standard error* (see Section 4.4). Having calculated the error, we can adjust the size of the sample according to how precise we require our sample estimate to be. It is possible to calculate estimates of errors in other forms of sampling, but the calculations involved are more complex. For this reason, random sampling is normally the method of choice when circumstances permit.

The main disadvantage of random sampling is that it cannot be attempted if the size of the population is not known. In most instances, a sample frame must be constructed before sampling can begin. This sample frame must contain all the sample units in the population, and the sample units must be identifiable by some means or other in the population which is being sampled. Sample frames are notoriously difficult to construct, certain sample units may occur in the frame more than once, thus increasing their chance of selection, or certain sectors of the population to be sampled may be omitted. Moreover in Africa, where records of individually identifiable animals are seldom available, sample frames of individual animal units can rarely be constructed. For this reason, simple random

sampling based on individual animals as sample units is rarely attempted in Africa.

Furthermore, random sampling is impossible where the type of unit being sampled does not permit the population size to be determined beforehand. If, for instance, events such as births or deaths are being sampled, there is simply no way of knowing with absolute precision how many births or deaths there will be in a population over the study period.

4.3.2 Multi-stage sampling

A way round the problem of constructing sample frames of individual animal units is to use a technique known as *multi-stage sampling*. As the name implies, this involves sampling a population in different stages, with the sample unit being different at each stage. If it is not possible to construct a sample frame of individual animals, then herds, farms or villages in which livestock are kept can be used as units. Lists, particularly of farms or villages, are frequently compiled for administrative purposes by governments, and it is relatively easy to construct a sample frame from such lists. This would be the first stage of the process. The sample units are then selected at random from the sample frame. Once the farm or village units have been selected, it may prove possible to construct a sample frame of the animals within the units and sample these in turn.

Alternatively, all the animals within a village, farm or herd can be sampled. This technique is known as *cluster sampling*. The herd, farm or village is the sample unit and the animals contained within the sample unit are the cluster. Since one of the main expenses of sampling is often for travel, the advantages of sampling all the animals in the herd, village or farm during one visit are obvious. For this reason, cluster sampling is often the method of choice in epidemiological studies in Africa.

An alternative method of cluster sampling is to define the target population as all the livestock of a particular type within a region demarcated by well defined geographical boundaries. An areal sampling method is then used whereby the region is divided into small units, with all the animals in each unit being defined as a single cluster. The advantage of this procedure is that the investigator knows how many areal units there are in total, since he has defined

them, and this in turn enables him to construct easily a sample frame. The disadvantage is that it may be difficult to find all the animals in a given small area, or even to be sure to which areal unit a particular animal belongs.

Cluster sampling has some advantages and disadvantages when compared with simple random sampling. These are discussed in detail in the next chapter but it may be useful to include a brief summary here.

The first advantage of cluster sampling is one of a saving in travel costs. Much less travelling is involved in sampling animals on a cluster basis than if animals are selected at random from a target population. Provided that the complete collection of animals in each cluster is included in the sample, it is not too difficult to calculate an estimate of the variable being investigated and the corresponding standard error. (It is not very difficult even if only a subset is used).

However, since the variation in disease prevalence is likely to be greater between clusters than within clusters, examining animals within clusters will give less information than examining animals from different clusters. This is particularly so in the case of infectious diseases. The more infectious the disease, the more likely it is that in any particular cluster of animals either none or most of the animals will be infected. Because of this, cluster sampling will almost always increase the standard error – sometimes very considerably – and hence the uncertainty involved in the estimation of the particular variable being considered.

One implication of this is that the minimum number of cases required for a reliable estimate of disease prevalence or incidence in the target population as a whole will be several times larger than that required in simple random sampling. The sample size in a cluster sample has to be correspondingly larger, therefore, to produce an estimate of the same reliability. If, as a result, the procedures for measuring a particular variable become time consuming and/or costly, the time and money spent may outweigh the benefits of reduced travel costs and increased administrative convenience gained by cluster sampling.

4.3.3 Systematic sampling

Systematic sampling involves sampling a population systematically i.e. if a $1/n$ sample is required, every n th unit in

that population is sampled. For example, if a 10% ($1/10$) sample is required, every 10th unit in the population is sampled. If a 5% ($1/20$) sample is required, every 20th unit in the population is sampled.

The main advantage of systematic sampling is that it is easier to do than random sampling, particularly if the sample frame is large. It also enables sampling a population whose exact size is not known. This is impossible in random sampling. Thus systematic sampling is used to sample such events as births or deaths, whose total number cannot be known before the study begins, or livestock populations at abattoirs or dips where, again, the population size may not be determinable at the outset.

The main disadvantage of systematic sampling is that if the sample units are distributed in the sample frame or in the population periodically, and this periodicity coincides with the sampling interval, the sample estimate may be very misleading. Estimating the standard error is thus more difficult and depends on making the assumption that there is no periodicity in the data.

4.3.4 Purposive selection

Purposive selection involves the deliberate selection of certain sample units for some reason or other. The reason may often be that they are regarded as being “typical” of the population being sampled. For example, a herd or series of herds may be selected because they are representative of a certain production system. Purposive selection is also used to select particular sample units for a particular purpose e.g. high-risk sentinel herds along a national or geographic boundary or along a stock route.

The main advantage of purposive selection is the relative ease with which sample units can be selected. Its main disadvantage is that sample units are frequently selected not because they are representative of a particular situation but because they are the most convenient to sample. Even if the sample units are selected as being representative of a general population or situation, they often tend to reflect the opinions of the individual selecting them as to what he or she considers to be representative, rather than the actual case. In addition, if the samples are selected on the basis of being typical of the average situation, they only represent

those units close to the population mean and tell one little about the variation in the population as a whole.

In spite of these drawbacks, purposive selection may in certain instances be the only method available. If there are difficulties of communication, sample units may have to be selected purposively on the basis of their accessibility. Alternatively, if the measurement procedures are long or complicated, involve some form of damage to an animal or upset local beliefs or prejudices, e.g. when taking blood or biopsies, a sample may have to be purposively selected on the basis of the livestock owner's willingness to cooperate.

4.3.5 Stratification

This involves treating the population to be sampled as a series of defined sub-populations or strata. Suppose, for example, that we wished to sample a population of 4000 goat flocks in order to estimate the prevalence of a particular disease in an area, and that this population consisted of:

- 200 large-sized flocks containing 51 animals or more;
- 800 medium-sized flocks containing between 20 and 50 animals; and
- 3000 small-sized flocks containing 19 animals or less.

If we took a 1% random sample of all flocks, we might find that this would give us a sample consisting of, say, 1 large flock, 9 medium-sized flocks and 30 small flocks. Suppose, however, that one of the determinants we were interested in was the influence of flock size on the prevalence of the disease. We would obviously want to know more about the larger flocks than our present system of sampling would tell us. We could, therefore, divide the population to be sampled into strata according to flock size, and sample each stratum in turn.

We could also take larger samples from those strata that we are particularly interested in and smaller from those that we are not. For example, we might decide to take a 5% random sample from the large-flock stratum, a 2% sample from the medium-flock stratum and a 0.5% sample from the small-flock stratum. This might give us 10 large flocks, 16 medium flocks and 15 small flocks. Note that the actual sample size has increased from 40 to 41 only, although if we were cluster sampling more animals would be involved. This technique is known as *stratification with a variable sampl-*

ing fraction, and its usefulness lies in that it allows us to concentrate the facilities at our disposal on those sections of the population that are of particular interest to us.

Many different systems of stratification are possible, depending on the purpose of the study being undertaken. Common variables for stratification include area, production system, herd size, age, breed and sex.

4.3.6 Paired samples

Variations in the sample groups due to host and management characteristics can sometimes be overcome by pairing individuals in the different sample groups according to common characteristics (age, breed, sex, system of management, numbers of parturitions, stage of lactation etc) and then analysing the paired samples (see Chapter 5). This technique is useful in that it often greatly increases the precision of the study.

4.3.7 Sampling with and without replacement

There are essentially two different options for selecting clusters. We may select them in such a way that each cluster has an equal probability of being selected, or that some clusters have a higher probability of being selected than others.

If the first option is chosen, the natural method of selection is simple random sampling. If, however, the clusters have different probabilities of being selected, it then becomes rather difficult to devise a sampling method which allows the clusters to be chosen with the intended probability. In addition, the correct method to calculate unbiased estimates of the standard errors of any estimates which include "between-cluster" variability is rather complicated and requires a powerful computer with a special program. If such resources are not available, it will be advisable to select clusters with *replacement* i.e. choose from the complete set of clusters without discarding any previously selected. This will mean that sometimes the same cluster will appear more than once in the sample, though this will happen rarely if the total number of clusters is large compared to

the sample being selected. (The interested reader should consult Chapters 9 and 10 in Cochran (1977) for further details).

There are many variations and combinations of sampling possible even within one particular study. Detailed descriptions of all the possible permutations involved are beyond the scope of this manual, and the ensuing discussions in this and the next chapter will focus on simple random and cluster sampling.

4.4 SAMPLE SIZES

This section is concerned with estimating sample sizes for cross-sectional studies. The approach used will depend on whether we are measuring a categorical or a numerical variable. Categorical (discrete) variables are probably more frequent in epidemiology, particularly dichotomies, and we shall illustrate the problem of estimating sample size for such variables in the following subsections. Techniques available for estimating sample sizes in cross-sectional studies involving numerical (continuous) variables, and in cohort and case-control studies, are described in Chapter 5.

4.4.1 Sample sizes for estimating disease prevalence in large populations

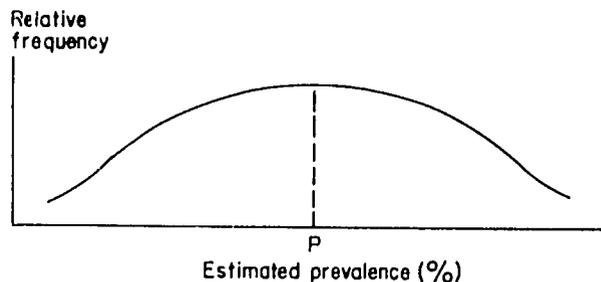
Suppose that we wish to carry out a survey to investigate the distribution of disease in a large animal population. How big a sample should we aim for? Since the cost of finding and examining each animal (i.e. *the unit sampling cost*) is likely to be quite high, the total sampling cost, and hence the sample size, will be an important determinant of the total cost of the survey. So how do we decide how many animals we need to examine? The answer to this question largely depends on four subsidiary questions:

- To what degree of accuracy do we require the results?
- What sampling method have we used?
- What is the size of the smallest subgroup in the population for which we require accurate answers?
- What is the actual variability in the population surveyed of the variable we wish to measure?

Clearly the last of these questions will cause the greatest problem, since if we knew the exact answer to this we would have no need to carry out the survey in the first place! Let us now consider these questions one by one.

Suppose that a disease is distributed in a population with a prevalence of P , and that we have decided to estimate P by means of a survey using a particular sampling method. We carry out the survey and obtain an estimated prevalence p . If we repeated the whole survey a second time using the same sampling method and the same sample size, we would get a different estimate p of the prevalence P . If it were possible to go on repeating the survey many times with the same sample size, we would get a whole series of estimates from which we could draw a histogram. This would resemble Figure 7 if n , the sample size, was large.

Figure 7. Distribution of different estimates of disease prevalence in a large-sized sample.



$P = \text{True prevalence (\%)}$

It can be shown that the average of all the estimates p_1, p_2 etc will be almost exactly the true prevalence P , and that 68% of the estimates will differ from the true value by less than the quantity $\sqrt{PQ/n}$, called the *standard error of the estimated prevalence (SE)*, where:

- $P = \text{true prevalence (\%)}$,
- $Q = 100 - P$, and
- $n = \text{size of the sample}$.

Similarly, 95% of the estimates would differ from the true value by less than twice the standard error, and 99% of the

estimates would be within three standard errors of the true value.

This suggests a method for stating how precise we would like the results to be. We might, for example, say that we would like to be 95% sure of being within 1% of the correct, true prevalence $P(\%)$. This implies that we want twice the standard error to be no greater than 1%, or that the standard error should not be greater than 0.5%. This means that it is always possible to fix a given accuracy level by choosing the sample size so that the standard error of the estimate is controlled.

Requirements for precision can be stated in terms of *absolute or relative accuracy*. If we talk in terms of absolute accuracy we might say that "we want the estimate of the prevalence to be within 1% of the true prevalence" i.e. $p = P \pm 1\%$. For example, if the true prevalence is 3%, we will be requiring an estimate that lies in the range of 2 to 4%. If the true prevalence is 20%, we require the estimated value to fall between 19 and 21%.

If we want to state our requirements in terms of *relative accuracy*, the estimated value must lie within 10% of the true value. For example, if the true prevalence is 20%, this would mean obtaining an estimate in the range of 18 to 22%, since 2 is 10% of 20. If the true value was 5%, we would be demanding an estimate between 4.5 and 5.5%, since 0.5 is 10% of 5. In principle, there is nothing wrong in stating accuracy requirements in this way, but high relative accuracy will not be possible when true prevalence is low (see Table 9).

Table 8 shows the sample sizes required for estimating prevalences at different levels of absolute accuracy from large populations. Note that no sample size is given unless the standard error is smaller than the true prevalence. The entries have been calculated using the formula:

$$n = P(100-P)/SE^2$$

If the sample size is a large proportion of the population, say greater than 10%, then it is better to use the more exact formula:

$$n = \frac{P(100 - P)}{(SE^2 + P(100 - P)/N)}$$

where N is the total size of the population.

Table 8. Sample size (n) for controlling the standard error (SE) of estimated prevalence for different values of the true prevalence (P) in large populations.

P (%)	SE (%)					
	0.1	0.5	1.0	1.5	2.0	2.5
0.5	4975	-	-	-	-	-
1.0	9900	396	-	-	-	-
1.5	13275	591	148	-	-	-
2.0	19600	784	196	87	-	-
2.5	24375	975	244	108	61	-
3.0	29100	1164	291	129	73	47
3.5	33775	1351	338	150	84	54
4.0	38400	1536	384	171	96	61
4.5	42975	1719	430	191	107	69
5.0	47500	1900	475	211	119	76
6.0	56400	2256	564	251	141	90
7.0	65100	2604	651	289	162	104
8.0	73600	2944	736	327	184	118
9.0	81900	3276	819	364	205	131
10.0	90000	3600	900	400	225	144
20.0	160000	6400	1600	711	400	256
30.0	210000	8400	2100	933	525	336
40.0	240000	9600	2400	1067	600	384
50.0	250000	10000	2500	1111	625	400

Example 1: Suppose we wish to be 95% sure that a survey will give an estimated prevalence within 1% of the true value in absolute terms. Two standard errors will then be less than 1% i.e. $2SE < 1\%$ or $SE < 0.5\%$. Table 8 gives the sample sizes required for different prevalence rates and standard errors. However, since the sample size we are looking for will depend on true prevalence, whose value we do not know, that being the reason for the survey, this does not seem to help much. It will be rare, however, to have absolutely no idea what value of the true prevalence to

expect. We will usually be able to make an estimate and say, for example, that "we believe the prevalence is not greater than 8%". If we then choose the sample size, it might turn out to be much too big, since the correct sample size to measure a prevalence of, say, around 2% to the desired accuracy is 784, while the sample size corresponding to a prevalence of around 8% is 2944. However, there is nothing much we can do about this. Lack of prior knowledge will always result in a need for liberal (i.e. overlarge) sample sizes and hence higher costs.

If we do not have the slightest idea what prevalence to expect, we can use the sample size corresponding to the least favourable case (P = 50%) given in Table 8, though if we are demanding a high degree of accuracy the indicated sample size (10 000) may be unrealistically large.

Example 2: We might suspect that the true prevalence is of the order of 20% and would like to be 99% sure that the estimated prevalence is within 2% of the true value. We can be 99% certain that the true value lies within three standard errors of the estimate. Hence, to fulfill the required conditions we must choose the sample size in such a way that $3 SE = <2\%$ or $SE = <2/3 = 0.7\%$ approximately. From Table 8 we see that for $SE = 0.5\%$ and $P = 20\%$, we need a sample of 6400. For $SE = 0.7\%$, it seems, we will need around 4000. (In fact the exact sample size as calculated from the formula $n = P(100-P)/SE^2$ is only 3265).

Table 9 gives sample sizes required to estimate prevalence in a large population when the desired precision is stated in terms of relative accuracy. In this case the sample sizes are such as to ensure that the standard error will not be greater than the stated percentage of the true prevalence. The entries in the table have been calculated using the formula:

$$n = \frac{(100 - P) \times 10\,000}{P \times SE^2}$$

If the sample size required represents a very high proportion of, or is greater than, the sampled population itself, the more accurate formula

$$n = \frac{N(100 - P) \times 10\,000}{NP SE^2 + (100 - P) \times 10\,000}$$

should be used to calculate the sample size. (N is the size of the population being sampled).

Table 9. Sample size (n) to control the standard error (SE) of estimated prevalence relative to the true value of the prevalence.

P (%)	SE as a percentage of P		
	1.0	5.0	10.0
0.5	1 990 000	79 600	19 900
1.0	990 000	39 600	9 900
1.5	656 667	26 267	6 567
2.0	490 000	19 600	4 900
2.5	390 000	15 600	3 900
3.0	323 333	12 933	3 233
3.5	275 714	11 029	2 757
4.0	240 000	9 600	2 400
4.5	212 222	8 489	2 122
5.0	190 000	7 600	1 900
6.0	156 667	6 267	1 567
7.0	132 857	5 314	1 329
8.0	115 000	4 600	1 150
9.0	101 111	4 044	1 011
10.0	900 000	3 600	900
20.0	40 000	1 600	400
30.0	23 333	933	233
40.0	15 000	600	150
50.0	10 000	400	100

The sample sizes calculated in the two different exercises were obtained assuming that the sample was to be chosen by simple random sampling i.e. that animals were sampled individually. If we use a different sampling method, these sample sizes will no longer be appropriate. For example in cluster sampling, which increases the variability of any estimates made, we should assume that, to be on the safe side, we will need to examine four times as many animals as for a simple random sample.

If we require an accurate estimate of prevalence not only for the complete population but also within well defined subgroups, as in a stratified survey, we need to choose the sample size sufficiently large *within each subgroup*. Suppose, for instance, that the population is distributed in six regions. Then, in our first example, if we require to estimate a true prevalence of 2% with an SE of 0.5% for each region, we would need a sample size of 784 *in each region*, assuming that we take simple random samples within the regions.

4.4.2 Sample sizes needed to detect the presence of a disease in a population

It may sometimes be important to discover whether a disease is at all present in a population. This population may be a single herd or a much larger group in, say, a well defined geographical region. Here the problem is no longer one of having a sample large enough to give a good estimate of true prevalence, but rather of knowing the minimum sample size required to find at least one animal with the disease. This will clearly need a much smaller sample than would be required for an accurate estimation of prevalence. Again the answer will depend on the true, but unknown, value of the prevalence of the disease in the target population. For small populations, e.g. individual herds, the answer will depend on the size of the population (Table 10). For populations of over 10 000, the sample sizes in the last column of the table will be approximately correct.

The values in Table 10 were calculated from the formula:

Probability of detection =

$$1 - (N-M)/N \times (N-M-1)/(N-1) \times \dots \times (N-M-n+1)/(N-n+1)$$

where: N = size of population,

M = total number of infected animals, and

n = sample size.

Where the indicated prevalence did not correspond to a whole number of animals, the value was rounded up to the next whole number (e.g. 3% of 75 = 2.25 animals; this was rounded up to 3). The sample sizes indicated in Table 10 are appropriate only for simple random sampling and would be much larger if cluster sampling was used. The determination of sample sizes required to estimate continuous variables is discussed in Section 5.3.2.

4.5 METHODS FOR OBTAINING DATA IN EPIDEMIOLOGICAL STUDIES

In epidemiological studies we can obtain data on a particular variable in two main ways. We can actually measure the variable or we can ask individuals concerned with livestock to give an estimate of the variable in the livestock populations with which they are concerned. As in estimating sample size, the approach adopted will largely depend on the purposes of the study. If the objective of the study is to obtain broad estimates of the relative importance of various diseases within a livestock population, the degree of precision need not be great. Consequently, the sample size may be small and the quality of the data generated does not need to be high. If, on the other hand, we are interested in studying the epidemiology of a particular disease in detail, accurate estimates of prevalence or incidence may be needed, the sample size will have to be large, and the data generated must be of high quality.

4.5.1 Interviews and questionnaires

Interviews and questionnaires are frequently used in epidemiological studies and can be a valuable means of generating data. In countries with good postal services, data can be collected cheaply and quickly by circulating questionnaires. Because of literacy and communications difficulties, this approach is of little use when one is soliciting information from traditional livestock owners, but it can be helpful in obtaining information from extension officers, veterinarians and other individuals concerned with traditional livestock production. It should be noted, however, that questionnaires involving a considerable effort in filling in are likely to have a high non-return rate, and the sample size may have to be adjusted accordingly. Furthermore, high non-return rates can introduce substantial bias in the estimates calculated from the returns.

Epidemiological studies often involve visiting the sample units and collecting the relevant data by questioning the owners and/or carrying out the appropriate measurement procedure on the animals concerned. Designing questionnaire formats and interview protocols can be a long and difficult process, particularly where traditional livestock producers are concerned. Remember that ques-

Table 10. *Sample size as a function of population size, prevalence and minimum probability of detection.*

P (%)	Population size							
	50	75	100	300	500	1000	5000	10 000
a) 90% probability of detection								
0.5	50	75	100	271	342	369	439	449
1	45	68	91	161	184	205	224	227
2	45	51	69	95	102	108	113	114
3	34	40	54	67	71	73	76	76
4	34	40	44	52	54	55	57	57
5	27	33	37	42	43	44	45	45
6	27	27	32	35	36	37	38	38
7	22	24	28	31	31	32	32	32
8	22	24	25	27	27	28	28	28
9	18	21	20	22	22	22	22	22
10	18	18	20	22	22	22	22	22
b) 95% probability of detection								
0.5	50	72	100	286	388	450	564	581
1	48	72	96	189	225	258	290	294
2	48	58	78	117	129	138	147	148
3	39	47	63	84	90	94	98	98
4	39	47	52	66	69	71	73	74
5	31	39	45	54	56	57	69	59
6	31	33	39	45	47	48	49	49
7	26	29	34	39	40	41	42	42
8	26	29	31	34	35	36	36	36
9	22	26	28	31	31	32	32	32
10	22	23	25	28	28	29	29	29
c) 99% probability of detection								
0.5	50	75	100	297	450	601	840	878
1	50	75	99	235	300	368	438	448
2	49	68	90	160	183	204	223	226
	48	59	78	119	131	141	149	151
	45	59	68	94	101	107	112	113
5	39	51	59	78	83	86	89	90
6	39	44	53	66	70	72	74	75
7	34	39	47	58	60	62	64	64
8	34	39	43	51	53	54	55	56
9	29	35	39	45	47	48	49	49
10	29	32	36	41	42	43	44	44

tioning a traditional livestock producer about the numbers or performance of his animals is akin to questioning other individuals about their bank accounts! Considerable time and patience are needed to obtain the trust and cooperation of such individuals. Wherever possible, a trusted intermediary should be employed. Nevertheless, as most traditional livestock producers live in close proximity to their animals and normally come from sections of the population with a vast experience of keeping livestock under African conditions, they are obviously an extremely useful and valuable source of information.

The success or failure of this type of epidemiological study depends as much on the design of recording forms as it does on the overall survey, the actual field work and the analysis. The latter will be impossible unless the material recorded is intelligible. Much thought should therefore be given to the design of forms and their efficiency should be tested in pilot trials. The forms should be orderly, with related items grouped together (calf number, date of birth, place of birth), convenient to use (the form should fit on a clip board), and technical words not likely to be understood by field staff avoided, as should any ambiguities in the terms used. The form should have a title and provisions for the identification of both the officer completing the form and the data source. It should also have a reference number which relates to the survey design (e.g. 06/04/93 might indicate the sixth visit to farm 93 in stratum 4). Completed forms should be checked for errors as soon as possible, so that appropriate corrections can be made while the memory of the interviewer is still fresh and the sample unit accessible.

Some additional points to bear in mind in the design of interviews and questionnaires include:

i) Explain the purposes of the interview to the interviewee. People are generally much more cooperative when they know why they are being questioned.

ii) Being normally very polite, livestock owners tend to answer questions with the answer that they think the interviewer wishes to hear, rather than giving the correct answer. The use of leading questions which give the interviewee a clue as to the answer expected or desired, should therefore be avoided.

iii) Human memories are short, and there is a tendency to concentrate events into a more limited time period

than was actually the case. So if livestock owners are asked about events that occurred in their animals over the last year, they tend to report events that happened over the last 2 or 3 years. This obviously exaggerates data on disease frequencies.

iv) Do not make interviews or questionnaires too long, or else the interviewee will get bored and the quality of his answers will suffer. To avoid this, the most important questions should be asked at the beginning.

v) Questions requiring subjective answers generate data that are extremely difficult to analyse. They should be avoided whenever possible, even though they may give valuable insights.

vi) Long, complicated questions tend to lead to misunderstanding and wrong answers.

4.5.2 Procedures involving measurements

If a high degree of precision is required in the study, the variable being investigated will normally have to be measured in some way. This may involve taking a biological specimen from an animal for a diagnostic test, weighing the animal, measuring milk yield, or measuring climatic variables such as rainfall, temperature etc.

Before measuring begins, it is important to understand exactly what is being measured and what are the advantages and disadvantages of the method used. This applies particularly to diagnostic tests. If the procedure is complicated or involves complex equipment, the person using it must master all its aspects before the survey begins, to ensure that an acceptable level of consistency in the measurements is being obtained. The equipment used during a field investigation should be calibrated and checked for accuracy before the start of each series of measurements and should be regularly maintained.

4.5.3 Errors due to observations and measurements

Earlier in this chapter we discussed statistical techniques available to calculate the size of a sample that would give a population estimate with the precision required if:

- The study is performed exactly as it was originally designed; and

- All the statistical assumptions are fulfilled.

However, this does *not* take into account errors due to variations between observers and those inherent in the measurement procedures used. These errors may, in fact, be more important than the errors generated by faulty sampling procedures.

Errors due to variations between observers

Many epidemiological studies are conducted with the help of enumerators, usually field services staff, who visit the sample units and carry out the procedures required. If interviews are being conducted by such staff, answers may be received which could be subject to different interpretations by different individuals. To keep errors to a minimum, strict control should be maintained over the interview protocols and the interviewees monitored from time to time.

Variations between different observers may occur when some degree of subjective judgement is involved, as may be the case in the diagnosis of a disease. Criteria need to be established by which a diagnosis is arrived at and adhered to by all those engaged in the study. Such considerations are of particular importance in retrospective studies.

An additional problem frequently encountered is that of bias on the part of the observer. If an individual wishes to prove a particular point he may, quite unintentionally, be biased in recording his observations. This problem can be avoided by the use of a "blind" technique whereby the observer is kept ignorant of the distribution of the determinant in the groups being studied, merely being required to record a set of observations about those groups.

Errors due to measurements

Errors inherent in the procedures by which a variable is being measured are common in epidemiological studies. For example, if two weighing scales are being used in a study, one scale may consistently give a higher reading than the other. Obviously, careful checking and monitoring of such apparatus before and during the study will reduce errors of this kind.

Further errors may occur when diagnostic tests are being used to determine the presence or absence of an infec-

tious agent. The terms used to describe the reliability of diagnostic procedures are:

Repeatability, which is the ability of a diagnostic test to give consistent results.

Accuracy, which is the ability of a test to give a true measure of the variable being tested. Accuracy is normally measured by two criteria:

– *Sensitivity*, which is the capability of that test to identify an individual as being infected with a disease agent when that individual is truly infected with the disease agent in question. In other words, it gives the proportion of infected individuals in the sample that produce a positive test result.

– *Specificity*, which is the capability of that test to identify an individual as being uninfected with a disease agent when that individual is truly not infected with the disease agent in question. In other words, it gives the proportion of uninfected individuals in the sample that produce a negative test result.

These two terms are illustrated in Table 11.

Table 11. *Estimated and true prevalences of a disease agent illustrating the terms specificity and sensitivity.*

	Number of individuals infected	Number of individuals not infected	Total
Positive test result	a	b	a+b
Negative test result	c	d	c+d
Total	a+c	b+d	N

Notes. The estimated prevalence is $(a+b)/N$; the true prevalence is $(a+c)/N$.

The sensitivity of the test is $a/(a+c)$ and its specificity is $d/(b+d)$.

Example 1: Suppose that we tested a sample of 1000 animals for the presence of a disease agent using a test of 90% sensitivity and 90% specificity. The results of the testing procedure are shown in Table 12.

Table 12 is somewhat artificial in that it gives the column totals, which we are trying to estimate. However, if the

Table 12. Results of using a diagnostic test of 90% sensitivity and 90% specificity in a sample of 1000 animals in which the true prevalence of infection is 10%.

	Number of individuals infected	Number of individuals not infected	Total
Positive test result	90	90	180
Negative test result	10	810	820
Total	100	900	1 000

disease was distributed through the population in this way and we used a test that was 90% sensitive and 90% specific to estimate the extent of this distribution, we would arrive at an estimated prevalence of 180/1000, which would be an overestimate of the true prevalence of 100/1000. Of the 180 animals that the test identified as positive, 90 were, in fact, not infected with the disease, while of the 820 animals that the test identified as negative, 10 were, in fact, infected with the disease.

Example 2: Suppose we used the same diagnostic test on a similar sample of animals but the true prevalence of the infection in the sample was 1%. The results of this test are given in Table 13.

Table 13. Results of using a diagnostic test of 90% sensitivity and 90% specificity in a sample of 1000 animals in which the true prevalence of infection is 1%.

	Number of individuals infected	Number of individuals not infected	Total
Positive test result	9	99	108
Negative test result	1	891	892
Total	10	990	1 000

The true prevalence of the infection in this case is $10/1000 = 1\%$, while the estimated prevalence of infection is $108/1000 = 10.8\%$. Of the 108 animals that the test diag-

nosed as positive, 92% (i.e. 99/108) were, in fact, not infected with the disease agent in question. This leads us to another useful statistic, the *diagnosibility* of a test, which is the proportion of test-positive individuals that are truly infected with the disease agent.

In our first example the diagnosibility was $90/180 = 50\%$ while in the second it was $9/108 = 8.3\%$. Note that the diagnosibility of a diagnostic test declines as the prevalence of a disease decreases. This means that sensitivity and specificity errors in diagnostic tests produce relatively much greater errors in prevalence estimates of diseases with low true prevalence than would be the case in diseases of high prevalence.

It is obviously desirable to use a test that is as sensitive and specific as possible, so that the numbers of false positives and false negatives in the sample are reduced. The sensitivity and specificity of a test can be determined by administering the test to a number of animals and then comparing its results with the results obtained from a series of detailed diagnostic investigations on the animals concerned. In order for the results to be valid, however, the animals selected for the evaluation must be representative of the population to which the test is to be applied.

Once the sensitivity and specificity of a test are known, a correction factor can be applied to the prevalence estimate to take into account the sensitivity and specificity of the test:

$$\text{True prevalence} = \frac{(\text{Estimated prevalence} + \text{Specificity} - 1)}{(\text{specificity} + \text{sensitivity} - 1)}$$

where all values are expressed as decimals.

For our example 2 (Table 13):

$$\begin{aligned} \text{True prevalence} &= (0.108 + 0.90 - 1) / (0.90 + 0.90 - 1) \\ &= 0.008 / 0.80 = 0.01 \text{ or } 1\%. \end{aligned}$$

Note that although we can now correct the prevalence estimate, we still have no idea which of the individual animals are truly negative, falsely negative, truly positive and falsely positive. This problem can occur when diagnostic tests are being used in a test-and-slaughter policy for controlling a particular disease. Such policies are normally only implemented after a vaccination campaign has reduced the disease to a low prevalence, when the diagnosibility of a test is likely to be low. In addition, vaccination it-

self often has an adverse effect on test sensitivity and specificity. We can see from our second example that if we slaughtered all the test positives, 92% of the animals being slaughtered would not be actually infected with the disease agent.

While it is relatively easy to make a test more sensitive, often by lowering the criteria by which a test result is deemed positive, this normally results in the test becoming less specific. Tests which are highly specific are often complicated, time consuming and, consequently, expensive. As such they can rarely be employed on a large scale.

A way round this problem is to apply two separate and independent testing procedures. Initially, a screening test of high sensitivity is needed to ensure that as many infected animals as possible are detected. Once the initial screening test has been performed, all positive reactors can be re-examined by a second test of high specificity. Since only the positive reactors have to be examined and not the entire sample, this cuts down the cost of using a highly specific test.

Example: Suppose we were attempting to eradicate a disease of 1% prevalence from a population of 10 000 animals by a process of test and slaughter. If we first use a test of high sensitivity (95%) but low specificity (85%), our initial results would be as illustrated in Table 14.

Table 14. *Results of a diagnostic test of 95% sensitivity and 85% specificity used to examine a population of 10 000 animals for the presence of a disease with true prevalence of 1%.*

	Number of individuals infected	Number of individuals not infected	Total
Positive test result	95	1 485	1 580
Negative test result	5	8 415	8 420
Total	100	9 900	10 000

We then subject the 1580 test-positive animals to a further test of the same sensitivity but a higher specificity (Table 15).

Table 15. *Results of a diagnostic test of 95% sensitivity and 98% specificity applied to the 1580 test-positive animals identified in Table 14.*

	Number of individuals infected	Number of individuals not infected	Total
Positive test result	90	30	120
Negative test result	5	1 455	1 460
Total	95	1 485	1 580

This test indicates that we would need to slaughter 120 as opposed to 1580 animals. Admittedly, a few false negatives might have slipped through the testing procedure, but it is hoped that these would be picked up on subsequent testing.

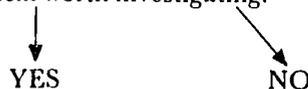
4.6 BASIC CONSIDERATIONS IN THE DESIGN OF EPIDEMIOLOGICAL INVESTIGATIONS

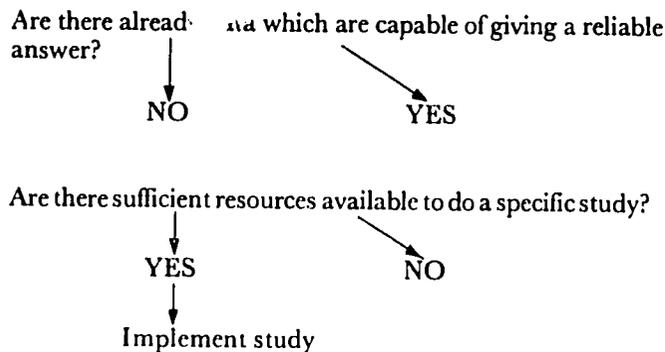
In this chapter we have illustrated some of the many problems that can be encountered in the design and implementation of epidemiological studies, and it may be useful at this point to summarise the basic considerations.

4.6.1 Objectives and hypotheses

A good way to approach the planning of a field study is to take the view that we are, in effect, buying information. We must make sure, therefore, that the study produces the information required at the lowest possible cost. We should also ask ourselves if that information can be obtained from other, cheaper sources. The processes involved in such considerations could be schematised as follows:

Is the problem worth investigating?





The first step is to write out clearly the objectives of the study and the data that will need to be generated in order to attain them. Throughout the entire planning process, constant reference should be made to these objectives in order to ensure that the procedures being planned are of relevance. If it is found that the resources available may not permit the achievement of the original objectives, the objectives may have to be redefined or additional resources found.

Objectives can often be defined by constructing a hypothesis. An epidemiological hypothesis should:

Specify the population to which it refers i.e. the population about which one wishes to make inferences and therefore sample from. This is referred to as the target population. Sometimes, for practical reasons, the population actually sampled may be smaller than the target population. In such cases the findings of the study will relate to the sampled population, and care must be exercised in extrapolating inferences from the sampled population to the target population.

Frequently, inferences may be required about different groups within the target population. For example, one may want to estimate not only the overall prevalence of a specific disease, but also the prevalences or incidences of the disease in various groups or subsets of the population. To obtain estimates with the accuracy required, the samples taken from these groups must be large enough, and this will obviously affect the design of the study.

A further problem may occur when defining the actual units to be sampled within a population. If, for example, the sample unit was a calf, at what age exactly does a calf

cease being a calf? Alternatively, suppose the sample unit is a herd. What exactly is meant by the term "herd"? If a live-stock owner has only one animal, does that constitute a herd? Obviously, the sample unit must be precisely defined and appropriate procedures designed to take care of borderline cases.

Specify the determinant or determinants being considered. Can such disease determinants as "stress", "climate" and "management" be defined accurately? How are these determinants to be quantified and what measurements would be used in their quantification? What are the advantages and disadvantages of these methods of measurement? How accurate are they?

Specify the disease or diseases being considered. The criteria by which an animal is regarded as suffering from a particular disease must be carefully defined. Will the disease be diagnosed on clinical symptoms alone? If so, what clinical symptoms? Are there likely to be problems with differential diagnoses? Will laboratory confirmation be needed? If so, are there adequate laboratory facilities available? Will they be able to process all the samples submitted? Will diagnostic tests be used? How accurate are these tests? Remember that studies based solely on diagnostic tests may provide data about the rates of infection present in the population being sampled, but they may not indicate whether the infected animals are showing signs of disease or not. Additional data on mortalities and morbidities may have to be generated.

What rates are to be calculated? Remember that incidence and attack rates cannot normally be obtained by a cross-sectional study. If estimates on economic losses due to particular diseases are required, various production parameters may have to be recorded. How are these to be measured? How good and how accurate will these measurements be?

Specify the expected response induced by a determinant on the frequency of occurrence of a disease. In other words, what effect would an increase or decrease in the frequency of occurrence of the determinant have on the frequency of occurrence of the disease? Remember that the determinant must occur prior to the disease. This may be difficult to demonstrate in a retrospective study.

Make biological sense. In epidemiological studies we are interested in exploring relationships between the frequency of occurrence of determinants and the frequency of occurrence of disease. We are particularly interested in determining whether the relationship is a causal one i.e. whether the frequency of occurrence of the particular variable being studied determines the frequency of occurrence of the disease. We analyse such relationships by the use of statistical tests which tell us the probability of occurring by chance of the relative distributions of the determinant and the disease in the studied populations. If there is a good probability that the distributions occur by chance, the result is not significant and the distributions of the variable and the disease are independently related. If there is a strong probability that the distributions did not occur by chance, the result is significant and the distributions of the variable and the disease are related in some way. Note that a *statistically significant result does not necessarily imply a causal relationship*.

Example: Suppose that the frequency of occurrence of variable A is determined by the frequency of occurrence of variable B, which also determines the frequency of occurrence of disease D. What is the relationship between variable A and disease D?



Note that although this arrangement would produce a statistically significant relationship between variable A and the disease D, the relationship is not a causal one, since altering the frequency of occurrence of variable A would have no effect on the frequency of occurrence of the disease, which is determined by variable B.

Variables that behave in this way are known as *confounding variables* and can cause serious problems in the analysis of epidemiological data. For this reason, any hypothesis that is made about the possible association of a determinant and a disease should offer a rational biological explanation as to why this association should be.

Finally, remember that common events occur commonly and that often the simplest explanation for a disease phenomenon is the right one. Complicated hypotheses should not be tested until the simplest ones have been ruled out. For example, the presence of ticks on supposedly dipped animals is more likely to be due to a failure to dip the

animals or to improper dipping procedure, rather than to the appearance of a new strain of acaricide-resistant ticks.

These considerations emphasise the need for careful and detailed planning of an epidemiological study. They also illustrate the need to obtain as comprehensive and detailed knowledge as possible about the subject being investigated and the techniques used in the investigation. The time spent reading relevant literature is therefore usually well spent. Extensive literature searches can often be performed quickly and easily by using modern information-processing techniques.

Do not be afraid to ask advice from experts. Such advice is essential when one is conducting investigations or employing techniques outside one's particular area of expertise. Remember that the time to ask for advice is *before* the study has begun. Whenever possible, consult a statistician on the statistical design of the study in order to ensure that the data generated will be sufficient and can be analysed in the appropriate way to fulfil the objectives of the study

4.7 THE USE OF EXISTING DATA

Collecting specific epidemiological data involves a considerable amount of time and effort in both the planning and implementation stages. Because of this, the possibility of using existing data should be explored before generating new ones.

4.7.1 Advantages and disadvantages

The main advantages of using existing data are:

- Data collection is expensive; using existing data is cheaper although not cost free.
- Time is often essential; analysis of existing data sources gives answers more quickly.
- By using data from various sources, it may become possible to monitor the progress of a disease through different populations and to establish linkages between disease events, so that the sources of disease outbreaks can be traced and populations likely to be at risk of the disease identified.
- The use of existing data sources will help strengthen them or induce the need for change.

- Since the original data collection was performed in ignorance of the ongoing study, there may be a reduced chance of bias in favour or against any hypothesis being tested.

The main disadvantages encountered in the use of existing data include:

- Data sets are often incomplete. For example, national reports based on compilations of regional reports are almost invariably incomplete and frequently very late in appearing, as some regions are late in reporting. Parts of data sets may have been lent out and not returned.

- The data may have been collected for other purposes than those of the present study. For example, data collected initially for administrative or accounting purposes are unlikely to help identify the associations between a disease and its determinants.

- Existing data may be inconsistent or of unknown consistency. Observers change and so do recording systems. Changes in administrative procedures or policy may alter the type and method of data collection and complicate analysis. Random errors of counting or in reading instruments may cancel each other out in the long term, but errors are often not random. Scales may be consistently misread due to confusion over units and graduations. Different observers may consistently under- or overestimate livestock numbers, weights and ages and differ in their diagnosis of the same disease condition. Calculations of epidemiological rates are often prejudiced by ignorance of the size of the population at risk and of the time over which events were observed.

- The data may not be relevant. Records for Friesians will not be useful in estimating production losses in zebus. Although data may be readily available from commercial producers, they will not relate to the majority of rural enterprises. Since livestock production is dependent on weather, among other factors, data from a series of years need to be examined to obtain representative estimates of means and scatter. Even if such data are available from apparently similar farming systems, checking is necessary to identify any changes that might have occurred in the provision of services, health control, markets and in prices, before taking historical data as being a good estimate of animal health and production at present.

- The method used to collate and analyse the data may not be adequate for epidemiological purposes. If this is the case, the data may have to be obtained in the original form, if still available, and reanalysed. This may be a time-consuming process. Moreover, it may not be possible to subject the original data to the appropriate analysis.

There are nearly always some serious limitations in the value of existing data for epidemiological purposes. This does not mean that the data may not be useful; if the limitations are understood, the probability of their misinterpretation will be reduced.

4.7.2 Sources of data

In Africa, epidemiological data can be obtained from the following potential sources:

Livestock producers. Little or no recorded data are generated directly by traditional livestock producers. Where livestock development projects, government, parastatal, or commercial farming are operating, records may be kept. Such records can often furnish data on production parameters, births, deaths, purchases and sales, husbandry practices, the frequency of occurrence of specific diseases, particularly those that produce distinct and easily recognisable symptoms, and disease control inputs such as vaccinations, dipping, treatments, diagnostic tests etc.

The quality of such data fluctuates widely. Staff may change, and individual animal records may be lost or destroyed on removal of the animals. Historic records may give no indication of the population at risk. If record cards of different groups of animals (e.g. infertile and milking cows) are kept separately, care should be taken that *all* available records are, in fact, examined. If data on disease are being collected, it is necessary to know the diagnostic criteria used and who made the diagnosis, so that the likely problem of differential diagnoses can be assessed. When diagnosis is attempted by farm staff, there is often a tendency not to record common conditions, such as mastitis, neonatal mortalities and lameness, whereas the incidence of dramatic diseases or sudden death is given undue prominence. Cross-checking with records on veterinary inputs may help to reveal serious discrepancies.

The main disadvantage of the data generated by livestock producers is that the data often relate to specific

populations of livestock which may be atypical in terms of breed, husbandry practices and disease control inputs, to the general livestock populations of the country.

Veterinary offices, clinics, treatment and extension centres. The data produced from such sources are likely to be in the form of case books, treatment records, vaccination and drug returns, outbreak reports etc. The main problem with such data lies in relating them to a source population. They are frequently incomplete and may contain significant omissions, particularly with regard to those diseases that are either treated by livestock owners themselves or for which treatment is unavailable. Veterinarians may vary considerably in their diagnostic ability and preferences. As a result, increases or decreases in the occurrence of specific diseases which may be reflected in the records may not, in fact, be due to actual increases or decreases in disease incidence but rather to the replacement of one veterinarian by another, or to a greater efficiency in overcoming operational constraints, or to the provision of additional drugs, equipment and facilities. An increased awareness on the part of livestock owners to a particular disease problem or more selective diagnosis and treatment may also lead to an apparent increase in recorded incidence.

Probably the most useful data from such sources are those related to notifiable disease outbreaks, on which detailed reports have to be compiled. If the report forms have been properly designed and the investigative procedures specified, such data may allow the appropriate rates to be calculated. However, owners may be reluctant to report such diseases in their livestock, especially if they know that restrictions are likely to be imposed.

Diagnostic laboratories. The data generated by diagnostic laboratories often provide precise diagnoses of disease conditions but can be highly selective. The relative frequencies with which specific diagnoses are reported often reflect the standard and range of laboratory facilities, and the interests or expertise of the field staff and laboratory workers, rather than the actual situation in the field. Unless the laboratory has a field survey capacity, incidence and prevalence rates cannot be established, since the data on diagnoses obtained cannot be related to a source population. Nevertheless, such data are often useful in highlighting disease problems which are of particular concern to the indi-

viduals submitting the specimens. The minimum knowledge that disease x was confirmed in location y at time z provides some basis on which to build.

Research laboratories, institutions and universities. Most of the data generated by these institutions are likely to come from experiments and may be difficult to relate to the situation in the field. Nevertheless, if research is being conducted into a particular disease, the data generated are likely to provide valuable insights into the epidemiology of the disease in question. Such institutions are also good sources of reference and advice.

Slaughter houses and slaughter slabs. The data generated from these sources are normally in the form of findings at meat inspection, and may be recorded in a limited and highly administrative format. Major variations in the sensitivity and specificity of diagnoses may occur between different inspectors. The data only pertain to certain sections of livestock populations, being highly biased since mostly healthy young adults are examined. Significant omissions are common, and relatively rare pathological conditions are not usually differentiated, but the data may provide information on congenital abnormalities and chronic disease conditions which produce distinctive lesions. Slaughter houses and slaughter slabs are frequently used as a starting point for epidemiological investigations since they have facilities for conducting examinations and taking specimens that are not available elsewhere.

Marketing organisations. Data from marketing organisations provide information on sales and offtake and sometimes also on livestock movements. Information on the latter might be used to trace back disease outbreaks to their sources. Unfortunately, this is rarely the case in Africa, since animals are seldom individually identified and therefore their movements cannot be accurately recorded.

Control posts and quarantine stations. Records from these facilities can provide information about livestock movements and outbreaks of notifiable diseases.

Artificial insemination services. Records from AI services may be of assistance in providing some information about fertility. The data are normally collected in the form of non-return rates i.e. the proportions of first, second, third inseminations etc for which no further insemination is requested.

Such rates often give an overestimate of the true reproductive performances in the populations concerned. Many AI services often include a facility for the investigation of infertility problems. Data from such a facility can be of interest but are difficult to relate to a source population.

Insurance companies. Since these companies now offer insurance cover for high-value animals, and may offer limited cover for animals of lower value, they need to calculate and monitor risks, which reflects the interest of the epidemiologist. As such their records may be useful but only limited data may be available.

The time required to identify and analyse existing records should not be underestimated, while their value needs to be carefully weighed against the cost. A quick but comprehensive survey of such material should indicate whether it will provide the required answers.

4.8 MONITORING AND SURVEILLANCE

One of the most important activities in veterinary epidemiology is the continuous observation of the behaviour of disease in livestock populations. This is commonly known as monitoring or surveillance. The term *surveillance* refers to the continuous observation of disease in general in a number of different livestock populations, while *monitoring* normally refers to the continuous observation of a specific disease in a particular livestock population.

4.8.1 Epidemiological surveillance

Surveillance activities involve the systematic collection of data from a number of different sources. These may include already existing data sources as well as new ones that have been created for specific surveillance purposes. The data are then analysed in order to:

- Provide a means of detecting significant developments in existing disease situations, with particular reference to the introduction of new diseases, changes in the prevalence or incidence of existing diseases, and the detection of causes likely to jeopardise existing disease control activities, such as the introduction of new strains of disease agents, changes in systems of livestock management,

changes in the extent and pattern of livestock movements, the importation of livestock and their products, and the introduction of new drugs, treatment regimes etc.

- Trace the course of disease outbreaks with the objective of identifying their sources and the populations of livestock likely to be at risk.

- Provide a comprehensive and readily accessible data base on disease in livestock populations for research and planning purposes.

The prime objective of such activities is, however, to provide up-to-date information to disease control authorities to assist them in formulating policy decisions and in the planning and implementation of disease control programmes. Although a detailed discussion on the design and implementation of surveillance systems is beyond the scope of this manual, it may be useful to review briefly some of the considerations involved.

The success of any surveillance or monitoring system depends largely on the speed and efficiency with which the data gathered can be collated and analysed, so that up-to-date information can be rapidly disseminated to interested parties. As a result of recent advances in data processing techniques, particularly in the field of computing, the development of comprehensive and efficient surveillance and monitoring systems at a reasonable cost is now within the reach of most veterinary services.

The capacity of epidemiological units to employ these modern techniques means that such units may be able to offer data-processing services to institutions and organisations in return for the use of their data. This has removed one of the main constraints on the development of such systems in the past, which was the reluctance of various data-generating sources to make their data available to those responsible for surveillance. Such cooperation depends on a clear identification of the information needs of reporting organisations and fulfilling these rapidly and efficiently.

Modern computerised data processing allows complicated analytical procedures to be carried out on large volumes of data quickly and easily. However, they must be used with a great deal of caution and only on data which justify them. If used on incomplete or inaccurate data whose limitations are not understood, they may produce results which are at best confusing or misleading. For this reason, the analysis of surveillance or monitoring data

should be kept simple and the limitations of the information produced should be clearly stated.

A further consideration is that of confidentiality. Any surveillance or monitoring system will contain a certain amount of confidential data. If such data get into the wrong hands and are used indiscriminately without due regard to their probable limitations, serious problems may result. Appropriate safeguards need to be designed, therefore, to ensure that information is distributed to interested parties on a confidential and need-to-know basis.

4.8.2 Epidemiological monitoring

Epidemiological monitoring may include the use of existing routine data sources as well as of specific epidemiological field studies. Monitoring of a specific disease in a population is, in effect, a specialised form of a longitudinal study. The design of any individual monitoring programme will depend largely on the disease or control programme being monitored e.g. monitoring a vaccination programme would require different types of data than monitoring a tick

control programme by dipping. The following objectives should be borne in mind in the design of monitoring systems:

- If control measures are being employed, the monitoring programme should provide a means to ascertain whether these measures are being carried out promptly and efficiently as specified in the programme design, and if not, why not.
- The monitoring programme should provide a means to ascertain whether the control measures being applied are having the desired and predicted effect on disease incidence. This normally implies a prompt and comprehensive disease-reporting system. The system should not be passive, but should include a component that is actively concerned with searching out disease outbreaks.
- The monitoring programme should provide a means for a rapid detection of developments which might jeopardise the control programme, or, in instances where no control measures are being implemented, which might warrant the introduction of control activities.

5. STATISTICAL METHODS IN THE ANALYSIS OF EPIDEMIOLOGICAL DATA

5.1 INTRODUCTION

In this chapter readers will be introduced to some of the simpler statistical techniques used in the analysis and interpretation of epidemiological data. At this stage, it may be of use to make a few general points about analysing epidemiological data.

- *Look at the data* to gain an insight into the problem being studied. Some of the useful methods for setting out data were outlined in Chapter 3.
- If data generated by other investigators are being used, find out as much as possible about how the data were generated. This may reveal significant omissions or biases in the data which may influence the analysis.
- Do not ignore anomalies in the data; investigate them. Often such anomalies provide valuable clues to a deeper understanding of the problem being investigated.
- Avoid the temptation to use complicated statistical techniques if the quality of the data does not warrant it. Above all, avoid using such techniques to try and establish relationships between variables unless you can satisfy yourself that there are valid biological reasons for such relationships.
- Be cautious about making inferences from sampled to target populations. Your own experience should normally tell you whether such inferences are valid or not. If

any inference is made, the populations involved should be clearly defined and the fact that an inference is being made clearly stated.

- When setting out findings, display the data used and the analyses undertaken in a simple, clear and concise form. A series of simple tables or graphs is preferable to one complicated table or graph. Long, complicated data sets should be placed in an appendix. Any limitations in the data presented should be clearly stated.

- Look at the data during the study, not just when it has been completed. This may enable the study design to be modified so as to include lines of inquiry which appear promising and to disregard those which do not.

- Finally, remember that a “negative” result, i.e. one that does not prove the hypothesis, is often as valuable as a “positive” one. Do not be afraid to record negative findings.

5.2 ESTIMATING POPULATION PARAMETERS

5.2.1 Estimating a population mean

Using the data in Table 1, we calculated that the mean weight of a sample of 150 chickens randomly selected at a large market was 1.3824 kg. Since the chickens were selected at random, the same data can be used to derive general statements about the population from which the sample was drawn. In particular, we would like to know how precise will be the information that we can obtain about the mean weight of all the chickens offered for sale in the market on the day we selected the sample.

Although our intuition tells us that the mean weight of the sample ought to be something like the mean weight for the whole population from which it was drawn, the sample mean will hardly ever have exactly the same value as the population mean. There are many millions of different possible samples of 150 chickens which could result from a total of 4000, and each possible sample of 150 chickens will have its own mean value. These means will mostly be different from one sample to another. We cannot know for sure in any particular case how close the mean value of the sample is to the population mean in which we are interested.

Furthermore, statistical methods of analysis cannot remove this uncertainty. Nevertheless, the theory of statistical inference does provide us with the means to measure it. For example, we will be able to say that "we can be 95% certain that the true population mean weight lies in the interval 1.3521 to 1.4127 kg" or that "we can be 99% sure that the true population mean weight lies in the interval 1.3425 to 1.4223 kg". Such statements about a population mean will always be possible provided that the information was obtained in a reasonably large random sample – a sample size greater than 50 ought to be enough.

There are four steps involved in the calculation of intervals. We will work through these steps using the example of chicken liveweights, and then state them in general terms.

- First, we have to calculate the mean chicken weight in the sample (1.3824 kg), which we shall use as an estimate of the population mean.

- We then calculate the *standard error of the estimated mean* using the rule:

$$\text{Standard error} = (\text{standard deviation of the sample}) \times \sqrt{\frac{1-f}{n}}$$

where: n = sample size, (150), and

f = *sampling fraction* i.e. the proportion of the total population which was sampled, in this case $f = 150/4000$.

In Chapter 3 we calculated the standard deviation of the sample as 0.1931 so that:

$$SE = 0.1931 \times \sqrt{\frac{1 - 150/4000}{150}} = 0.0155 \text{ kg}$$

- Third, we have to decide how sure we wish to be that the interval we state will actually include the true value. Generally, 90%, 95% or 99% confidence is demanded, and the resulting interval is called a 90% (or 95% or 99%) *confidence interval*. There is a special multiplier corresponding to each of these levels of confidence (Table 16).

Table 16. *Multipliers to give 90%, 95%, 99%, and 99.9% confidence that a stated interval includes the true population mean value.*

Confidence	90%	95%	99%	99.9%
Multiplier	1.64	1.96	2.58	3.30

- Fourth, we calculate the interval from the formula:

Estimated mean \pm multiplier \times standard error of estimated mean.

For a 95% confidence interval, we have:

$$1.3824 \pm 1.96 \times 0.0155$$

or 1.3824 ± 0.0303 .

or $1.3824 - 0.0303$ to $1.3824 + 0.0303$

i.e. 1.3521 to 1.4127 kg.

To sum up, the four stages in the calculation of a confidence interval for the true value of a population mean are:

- i) Calculate an estimated mean of the sample.
- ii) Calculate the standard error of the estimate.
- iii) Decide on the level of confidence required.
- iv) Calculate the interval from the formula:

Estimated mean \pm multiplier \times standard error.

The actual formulae used to calculate the estimate (step i) and its standard error (step ii) will depend on how the data were collected. The above calculations are appropriate for a simple random sample taken from a population which consists of a single group. In reality, however, we often use cluster samples.

We will illustrate now what difference cluster sampling would make to the estimation of the population mean. Table 17 gives the weights of chickens offered for sale by five traders selected at random from 132 chicken traders in the market.

The total and mean weights of chickens sold by each trader are given in Table 18.

The population mean will again be estimated by dividing total weight by the number of chicken sampled i.e.: $207.36/150 = 1.3824$ kg

Table 17. Weights (kg) of chickens offered for sale by five traders.

Trader 1									
1.40	1.09	1.74	1.48	1.82	1.09	1.52	1.41	1.83	1.22
1.34	1.68	1.25	1.65	1.14	1.33	1.06	1.71	1.17	1.51
Trader 2									
1.36	1.34	1.03	1.24	1.06	1.12	1.15	1.57	1.38	1.40
1.39	1.31	1.50	1.10	1.45	1.34	1.38	1.35	1.49	1.58
1.25	1.42	1.64	1.57	1.53	1.18	1.39	1.34	1.13	1.23
Trader 3									
1.17	1.88	1.30	1.27	1.01	1.63	1.47	1.23	1.48	1.48
1.37	1.42	1.22	1.47	1.31	1.05	1.61	1.41	1.17	1.45
1.43	1.22	1.40	1.14	1.53	1.25	1.02	1.30	1.35	1.37
1.69	1.37	1.11	1.30	1.05	1.19	1.36	1.63	1.44	1.29
Trader 4									
1.35	1.59	1.94	1.51	1.78	1.37	1.11	1.38	1.53	1.44
Trader 5									
1.47	1.39	1.55	1.76	1.43	1.37	1.67	1.36	1.31	1.41
1.36	1.26	1.17	1.15	1.79	1.46	1.35	1.29	1.50	1.26
1.36	1.41	1.36	1.32	1.08	1.28	1.33	1.29	1.42	1.50
1.32	1.39	1.20	1.68	1.20	1.35	1.56	1.57	1.37	1.27
1.25	1.38	1.56	1.60	1.74	1.40	1.11	1.60	1.21	1.44

Table 18. Total and mean weights of chickens sold by each trader.

Trader	No. of chickens (X)	Total weight (Y) (kg)	Mean weight (kg)
1	20	28.44	1.4220
2	30	40.22	1.3407
3	40	53.84	1.3460
4	10	15.00	1.5000
5	50	69.86	1.3972
Total	150	207.36	

The standard error has to be calculated differently, however, as follows:

Let $f = 5/132$, the sample fraction of traders sampled.

Let $m = 5$, the number of traders sampled.

Let $n = 150$, the total number of chickens sampled.

Then the standard error (SE) is given by:

$$SE = m/n \sqrt{(1-f)/m \times W/(m-1)}$$

where:

$$W = R^2 \sum X^2 - 2R \sum XY + \sum Y^2$$

The estimated mean (R) = $207.36/150 = 1.3824$

$$\sum X^2 = 20^2 + 30^2 + 40^2 + 10^2 + 50^2 = 5500$$

$$\sum Y^2 = 28.44^2 + \dots + 69.86^2 = 10430.6472$$

$$\sum XY = 20 \times 28.44 + \dots + 50 \times 69.86 = 7572.0$$

Thus:

$$W = (1.3824)^2 \times 5500 - (2 \times 1.3824 \times 7572) + 10430.6472 = 6.2453$$

So:

$$SE = 5/150 \sqrt{0.9621/5 \times 6.2453/4} = 0.0183$$

This is an increase of 20% on the standard error we calculated using simple random sampling. As a result, the 95% confidence interval would be:

Estimated mean \pm multiplier \times standard error of estimated mean

i.e. $1.3824 \pm 1.96 \times 0.0183$

or 1.3824 ± 0.0359

or 1.3465 to 1.4183 kg.

The interval span now is $1.4183 - 1.3465 = 0.0718$ kg or 71.8 g, compared to the 60.6 g spanned by the interval calculated using a simple random sample. This demonstrates that if the sample is clustered, our knowledge of the population mean will be less precise. There are two reasons for this. First, with a simple random sample we fix the sample size in advance. When we choose a number of traders, we do not know in advance how many chickens they will have for sale, and this introduces an extra element of uncertainty. Second, it may happen that one of the chosen traders specialises in either unusually large or unusually small chickens. The sample will then contain a disproportionately large number of heavy or light chickens and, for that reason, it will be more variable than a single random sample.

On the other hand, before we can take a simple random sample we have to know how many chickens there are offered for sale, which may not be easy to establish. It will be much easier to count the number of traders. The chickens in a simple random sample are also likely to be distributed over a large number of traders, and it will take much more time to find and weigh them than to weigh all the chickens of a few traders.

For these and other reasons discussed in the previous chapter, some degree of clustering will be required in most practical surveys. Remember that clustering will nearly always increase the standard error and hence the uncertainty involved in the estimation of population means and proportions. This is especially true for variables associated with infectious diseases.

Although confidence intervals can always be calculated from the formula used above, how to calculate the standard error will not always be obvious. Indeed, if a survey is carried out using a complex sampling method, it may not be simple even to obtain an estimate of the mean. The possible options are so numerous and some of the corres-

ponding formulae so complex that it is not appropriate to attempt to discuss them here. It is better to consult a statistician with some knowledge of sampling theory, or relevant textbooks (e.g. Ra \ddot{u} , 1968; or Yates, 1981).

5.2.2 Sample size needed to estimate a population mean

We are now in a position to establish a method for judging how large a sample we may need to estimate a population mean with a given precision, at least when random sampling is used. We will demonstrate the principle by working through a hypothetical example, after which we will define the general procedure.

Example: Suppose we were to return to the market on another day and tried to estimate the mean chicken liveweight in such a way that we would be 95% confident that the estimated mean value will not differ from the true mean value by more than 0.02 kg.

From the previous section we know that, for a simple random sample, we can be 95% confident that the true mean value lies inside the interval:

Sample mean $\pm 1.96 \times$ standard error of the sample mean.

In other words, we can be 95% sure that the difference between the sample mean and the true mean is not greater than $1.96 \times$ SE.

In our present example we require that this difference should not be greater than 0.02 kg. If we find the sample size for which $1.96 \times$ SE = 0.02 kg, we will know that any sample at least this large will meet the specification.

For a simple random sample, the standard error of the sample mean is:

$$SE = S \sqrt{\frac{1-f}{n}}$$

where: S = standard deviation of chicken weights,

n = sample size, and

f = fraction of the population being sampled.

We therefore have to solve the equation:

$$1.96 \times S \sqrt{\frac{1-f}{n}} = 0.02$$

If it turns out to be less than 10% it can be ignored, and we will assume for the moment that this is the case. The equation then simplifies to:

$$1.96 \times S / \sqrt{n} = 0.02$$

$$\text{or } 1.96^2 \times S^2 = (0.02)^2 \times n$$

$$\text{or } n = \frac{1.96^2 \times S^2}{(0.02)^2}$$

The next problem is that we do not know the value of S . If we have no idea what this value is, we cannot estimate the required sample size, and we will have to take the largest sample we can afford with the resources available for the study. In our present example, we can use the value of S calculated in Section 3.6, since it seems reasonable to assume that the variability in the weights of the chickens offered for sale will not change dramatically from one market day to the next. Thus writing 0.1931 for S in the above equation, we get:

$$n = \frac{1.96^2 \times 0.1931^2}{0.02^2} = 358.11$$

and a sample size of about 360 is indicated.

If only 3000 chickens are available on the day we carry out the study, this sample would be a large proportion (greater than 10%) of the total, and it is then appropriate to use a more exact formula:

$$n = \frac{3000 \times 1.96^2 \times 0.1931^2}{3000 \times 0.02^2 + 1.96^2 \times 0.1931^2} = 320$$

In general, the two formulae can be stated thus:

$$\text{Approximate formula: } n = \frac{\text{multiplier}^2 \times S^2}{d^2}$$

$$\text{Exact formula: } n = \frac{N \times \text{multiplier}^2 \times S^2}{N \times d^2 + \text{multiplier}^2 \times S^2}$$

where:

d = maximum difference to be tolerated between the sample mean and the true mean, and

N = total population size.

The multiplier, chosen from Table 16, depends on the level of confidence required to ensure that the specification will be met.

Note that to apply any of the formulae provided above, the value of S has to be known *before the study is carried out*. If it is the first study of a particular variable under the prevailing conditions, it may not be possible to suggest a plausible value for S . In that case there is no way of deciding what sample size will be required to provide a given precision with a given level of confidence.

Note further that the formulae are relevant *only when the sampling units are chosen by simple random sampling*. If a clustered sample is used, the estimated sample size should be increased by a factor of four to give a rough estimate of the total number of units which will need to be sampled to meet the specification.

5.2.3 Estimating a population proportion or rate from a simple random sample

In many ways, estimating a population proportion or rate is similar to estimating a population mean. Proportions and rates play a central role in epidemiological investigations, and there are one or two rather special pitfalls to avoid in their estimation. The following discussion will be confined to estimating point prevalence (P) and attack rate (A).

Let us first estimate a prevalence whose true value in the whole target population is P , a fraction between 0 and 1. For example, suppose that 850 animals were chosen at random and 62 were found to be diseased. The sample prevalence (p), which will be used as an estimate of the population prevalence (P), will then be:

$$p = 62/850 = 0.0729$$

The standard error (SE) of this estimated prevalence can be obtained from the formula:

$$SE = \sqrt{\frac{(1-f) p (1-p)}{n}}$$

where:

n = the sample size, which, in random sampling, is fixed before the sample is taken, and

f = fraction of the total population sampled.

$$\text{Thus: } SE = \sqrt{\frac{(1-f) \times 0.0729 \times 0.9271}{850}}$$

If f is less than, say, 10%, little information is lost by ignoring the factor $(1 - f)$. SE then is 0.0089.

We can indicate how precise we believe the estimate to be by constructing a confidence interval using the multipliers in Table 16. For example, a 95% confidence interval for the true prevalence would be given by:

Estimated prevalence $\pm 1.96 \times$ standard error of the estimate

i.e. $0.0729 \pm 1.96 \times 0.0089$

or 0.0729 ± 0.0174 .

Hence we would be 95% confident that the true prevalence lay between the limits 0.0555 and 0.0903. It is more common to state the limits in percentage terms i.e. 5.55% and 9.03%. If these limits are too far apart for the purposes of the study, the sample size is too small. (See Section 4.4).

The attack rate (A) for a population can be estimated in a similar way. For example, suppose that we chose 1500 healthy animals at random from a population of, say, 18 000 animals and, by the end of the observation period, we find that 437 of these have suffered the relevant disease. The estimated attack rate (a) would be:

$$a = 437/1500 = 0.2913 \text{ or } 29.13\%.$$

The sampling fraction is $1500/18\ 000 = 0.0833$, which is just over 8%. The standard error of the estimate is:

$$SE = \sqrt{\frac{a(1-a) \times (1-f)}{1500}} = \sqrt{\frac{0.2913 \times 0.7087 \times 0.9167}{1500}} = 0.0112$$

If we had ignored the factor $(1-f)$, we would have calculated the standard error to be 0.0117, which supports the previous statement that the factor can be safely ignored if less than 10% of the total population has been sampled.

Note that the correct estimation of a population proportion or rate from a simple random sample depends on the occurrence of a sufficient number of cases in the sample. However large is the number of animals examined, if fewer than five cases are discovered in total, reliable estimation is not possible.

5.2.4 Estimating a rate or proportion from a cluster sample

Table 19 shows the numbers of sampled and diseased ani-

mals on 12 farms chosen at random from 943 farms containing the total population at risk.

Table 19. Results of a survey of 12 farms chosen at random from 943 farms available.

Farm	Total No. of animals (n)	Number diseased	Proportion diseased
1	183	22	0.120
2	92	12	0.130
3	416	37	0.089
4	203	23	0.113
5	107	17	0.159
6	388	32	0.082
7	79	36	0.456
8	243	29	0.119
9	314	24	0.076
10	83	17	0.205
11	113	59	0.522
12	294	26	0.088
Total	2515	334	

If we ignore the fact that the data were collected in a clustered fashion, we would reach the following conclusions:

- i) The estimated prevalence $p = 334/2515 = 0.133$
- ii) The standard error of the estimate is:

$$SE = \sqrt{\frac{p(1-p)(1-f)}{2515}}$$

A minor problem here is that we do not know f , the fraction of the available animals belonging to the complete population of the 943 farms. However, since we have chosen 12 of the 943 farms, i.e. 1.3%, we can guess that the 2515 animals sampled is well under 10% of the total and, therefore, can safely ignore the factor $(1-f)$:

$$SE = \sqrt{p(1-p)/2515} = \sqrt{0.133 \times 0.867/2515} = 0.0068$$

- iii) A 95% confidence interval for the true population prevalence would then be:

$$0.133 \pm 1.96 \times 0.0068$$

This procedure would be incorrect. Because of the clustered nature of the sample, the standard error must be calculated in a different way. This point is frequently misunderstood, especially when estimating rates and proportions.

The correct approach involves three steps:

i) Estimate the prevalence:

$p = \text{total with disease} / \text{total examined}$

$p = 334/2515 = 0.133$, as before.

(It is not uncommon to find the prevalence for the population being sampled by calculating the mean of the prevalences of the sampled herds, thus:

$$p = (0.120 + 0.300 + \dots\dots\dots 0.522 + 0.088) / 12 = 0.180$$

If this were done, the estimate of the true prevalence would be 18% rather than the 13.3% estimated earlier. Note that the mean of the sampled herd prevalences will give a misleading impression unless the herds are all of a similar size or the herd prevalences are roughly equal. Neither is true here.)

ii) To obtain the standard error we need first to calculate three quantities.

– The sum of squares of the herd sizes (H):

$$\Sigma H^2 = 183^2 + 92^2 + \dots\dots\dots 113^2 + 294^2 = 688\,191$$

– The sum of squares of the number of cases (C) in each herd:

$$\Sigma C^2 = 22^2 + 12^2 + \dots\dots\dots 59^2 + 26^2 = 10\,998$$

– The sum of the products obtained by multiplying each herd size by the number of cases (HC):

$$\Sigma HC = 183 \times 22 + 92 \times 12 + \dots\dots\dots 113 \times 59 + 294 \times 26 = 72\,575$$

These three quantities are combined, together with the estimated prevalence (p), into a single value (W) by the formula:

$$W = p^2 (\Sigma H^2) - 2p (\Sigma HC) + (\Sigma C^2)$$

$$W = (0.133)^2 \times 688\,191 - (2 \times 0.133 \times 72\,575) + 10\,998$$

$$W = 3866.45$$

The standard error of the estimated prevalence can then be calculated by:

$$SE = \frac{m}{\text{Total number of animals in sample}} \times \sqrt{(1-f) \times \frac{W}{m(m-1)}}$$

where: m = number of clusters in the sample (12 in our example), and

f = fraction of clusters sampled.

Since f in this case is small enough, it can be ignored and the standard error will be:

$$SE = 12/2515 \times \sqrt{\frac{3866.45}{12 \times 11}} = 0.0258$$

iii) The correct 95% confidence interval for the true prevalence then is:

$$0.133 \pm 1.96 \times 0.0258 \text{ i.e. } 0.0824 \text{ to } 0.1836$$

Note that if the data were analysed ignoring the clustered nature of the sampling, we would conclude, erroneously, that we could be 95% confident that the prevalence of the disease in the whole population was between 12% and 14.6%. If the sample is analysed correctly, the prevalence is between 8.2% and 18.4%, which is a much wider interval.

This has occurred because the clustering has increased the standard error by a factor of almost four. Such large increases in the standard error can be expected whenever the prevalence or attack rate varies noticeably from herd to herd, and will be particularly troublesome for highly infectious diseases when a herd is likely to be in one of two conditions, either completely free of infection or almost entirely infected.

The implication is that when a cluster sample is taken, the minimum number of cases required for a reliable estimation of prevalence or an attack rate will be several times larger than the 5 suggested as being sufficient in a simple random sample. The minimum would be 20 cases, but if all of them were in the same herd there would be problems.

It may be better, therefore, to confine the analysis to an estimation of the proportion of infected *herds* rather than animals. If the herds are sampled in such a way that each herd is considered as a single unit, there will be no clustering involved, and we can use the procedure applicable for the estimation of a proportion based on a simple random sample.

The problem just discussed is only one example of the way in which the actual sampling process can affect the statistical analysis and the conclusions based on it. There is a wide range of possible sampling schemes, each of which

may require a different formula both for estimating the prevalence or attack rate and calculating the standard error of the estimate. A detailed account of these possibilities can be found in Yates (1981), Raj (1968) or Cochran (1977). The latter two books are rather mathematical; Raj (1972), although less comprehensive, may be easier to understand.

5.3 FORMULATING AND TESTING STATISTICAL HYPOTHESES IN LARGE-SIZED SAMPLES

One of the common aims of an epidemiological study is to compare two different populations of the same species. For example, we may wish to know whether a given disease is equally prevalent under two different management systems or prophylactic regimes; or we may want to test the possible economic benefits of anthelmintics by investigating whether treated animals gain weight more rapidly than those left untreated.

5.3.1 Testing for a difference in two means

Let us suppose that an experiment was carried out to compare the weight gains of 50 pigs treated with anthelmintics with the gains of 63 untreated pigs of the same strain and age, kept under the same management system over the same time period. The mean weight gains and the standard deviation of the weight gains were calculated for each group (Table 20). On average, the treated pigs gained more weight than those in the untreated sample. Could this be due to the specific, individual characteristics of the pigs chosen, by chance, for each sample? How can we decide whether this apparent improvement is just a chance effect?

Table 20. *Weight gains of two groups of pigs of which one was treated with an anthelmintic.*

	Treated group	Untreated group
Number of animals	50	63
Mean weight gain (kg)	6.0	5.3
Standard deviation	1.6	1.9

First we must estimate the mean extra gain in a treated pig. This *mean difference* (MD) is easily calculated as:

$$MD = 6.0 - 5.3 = 0.7 \text{ kg}$$

As usual, we will also need to calculate the standard error of the estimated mean difference (SE_{MD}). We can do this by using the formula:

$$SE_{MD} = \sqrt{\frac{(n_t - 1) S_t^2 + (n_u - 1) S_u^2}{n_t + n_u - 2}} \times (1/n_t + 1/n_u)$$

where:

n_t, n_u = numbers of treated and untreated animals, and

S_t, S_u = standard deviations of weight gains in the respective groups.

Thus we have:

$$SE_{MD} = \sqrt{\frac{49 \times (1.62)^2 + 62 \times (1.9)^2}{50 + 63 - 2}} \times (1/50 + 1/63) = \sqrt{0.1129} = 0.34$$

Note that this is the correct method of calculating SE_{MD} only if the two samples are chosen by simple random sampling. A more general method will be given later.

We now set up a *working hypothesis*, called by statisticians the *null hypothesis*, usually hoping that we can show it to be false. When comparing two means or proportions, the working hypothesis will always be that the two means or proportions in the two populations are equal. To test the hypothesis we need to know the value of the *test statistic Z*, which is calculated by dividing the estimated mean difference by its standard error:

$$Z = MD/S_{MD}$$

$$Z = 0.7/0.34 = 2.059.$$

The next step depends on the *experimental hypothesis*, called by statisticians the *alternative hypothesis*, which we are trying to prove. There are two possibilities. The first is that we know in advance which mean or proportion is likely to be the larger; in our example, we expect, or at least hope, that the treated animals will do better. This is called a *one-sided alternative hypothesis*.

To illustrate why the hypothesis is one-sided, let us plot the two mean weight gains on a line, thus:

Untreated	Treated
5.3	6.0

The mean for the treated group is *on the right* of the mean for the untreated group i.e. it has a larger value. If it had been on the left, i.e. was smaller than the mean for the untreated animals, there would have been no possibility of the experiment supporting the hypothesis that the treatment produced higher weight gains on average. In other words, the result we are testing for can be obtained only if the mean for the treated animals appears on the "correct" side of the mean for the untreated group.

There will be occasions when this restriction is not appropriate. For example, there may be two types of management operating in a particular area, and we may wish to test whether the attack rate of a disease *differs* with the management regime. This will be true if the rates are sufficiently different, no matter whether the rate under the first management system lies to the left (i.e. is smaller) or to the right (i.e. is larger) of the rate under the second system. This is a *two-sided experimental hypothesis*, and an example is given in the next section.

If the sample of treated pigs does not have a higher mean, the analysis ends with the statement that there is no evidence that anthelmintics aid weight gain. If the treated sample does better, we need to assess whether the apparent improvement could easily be explained by sampling fluctuations or whether the evidence is so strong that a chance mechanism is an unlikely explanation. The key to the problem is the value of the test statistic Z which has to be compared with a set of fixed numbers, known as *critical values* of the test statistic (Table 21).

Table 21. *Critical values of Z for comparing means or proportions.*

Hypothesis	Significance level			
	10%	5%	1%	0.1%
One-sided	1.28	1.64	2.33	3.09
Two-sided	1.64	1.96	2.58	3.30

N.B. This table should be used only if the sample sizes are sufficiently large.

In our example we have used a one-sided experimental hypothesis, since we are investigating whether anthelmintics will increase the rate of weight gain. We will therefore consult the first row of Table 21. The first number in the row is smaller than the value of the test statistic produced by the data. If the test statistic were less than 1.28, we would say that the difference in mean weight gain is not significant. If it were greater than 1.28 but smaller than 1.64 we would say that the difference in mean weight gain is significant at the 10% level but not at the 5% level, and so on. In the present case Z is 2.059, which is greater than 1.64 but less than 2.33, so we can say that the difference in mean weight gain is significant at the 5% level but not at the 1% level. The larger the value of the test statistic, the more significant is the result.

It is an unfortunate perversion of historical statistics that has led to the 5% significance level being "more significant" than the 10% significance level. The significance level is the probability that any apparent difference is due entirely to chance features of the sample. Clearly, the smaller this probability is, the stronger is the support for the experimental hypothesis. If there is a 5% probability that the apparent difference is a random effect, we can be 95% confident that the difference is a real effect. If there is a probability that the difference in a random sample is 1%, there is a 99% confidence that it is a real effect. It is because of this correspondence between significance and confidence levels that the values in Table 16 are identical to those in the bottom row of Table 21.

If our hypothesis test indicates that there is evidence of a difference, a 95% confidence interval for the size of the difference can be estimated as usual by:

$$\text{Mean difference} \pm 1.96 \times \text{SE}_{\text{MD}} \text{ i.e. } 0.7 \pm 1.96 \times 0.34.$$

Hence we could say that we are 95% confident that the use of anthelmintics in pigs in this experiment is associated with an increase in weight gain between 0.034 and 1.366 kg per animal over the relevant time period.

5.3.2 Testing for a difference in two proportions

Our second example shows how to test for a difference between two proportions. Suppose that two very large

herds are managed under different husbandry systems. Random samples of 45 animals from the first herd, and of 58 animals from the second, were chosen as sentinel groups just before the rainy season began, and the attack rate for a common wet-season complaint was recorded for each group (Table 22).

Table 22. Attack rates of a common wet-season complaint in two sample groups of animals managed under different husbandry systems.

	No. of susceptible animals	No. of infected animals	Attack rate
Herd 1	45	18	18/45
Herd 2	58	15	15/58

The estimated attack rate for the first herd is $P_1 = 18/45 = 0.4000$ and for the second herd it is $P_2 = 15/58 = 0.2586$. The test statistic (Z) appropriate to the working hypothesis of equal attack rates in the two herds, is obtained thus:

$$Z = \frac{\text{Difference between sample attack rates} - 1/2(1/n_1 + 1/n_2)}{\sqrt{\bar{P}(1-\bar{P})(1/n_1 + 1/n_2)}}$$

The difference between the sample attack rates is calculated by subtracting the smaller estimated attack rate from the larger; n_1 and n_2 are the two sample sizes; and \bar{P} is obtained by dividing the total number of infected animals by the sample size i.e. $\bar{P} = 33/103 = 0.3204$.

Substituting for all these values from Table 22 we get:

$$Z = \frac{(0.4000 - 0.2586) - 1/2(1/45 + 1/58)}{\sqrt{0.3204 \times 0.6796 \times (1/45 + 1/58)}} = 1.31$$

If there is no prior reason to suspect that the attack rate will be higher under one of the two management systems studied, but we simply wish to investigate whether there is a difference, the correct experimental hypothesis is that the herd attack rates may be different. This is a two-sided hypothesis, since either system might give a higher attack rate, and we will test the hypothesis by comparing Z with its critical values in the second row of Table 21. Since the calculated value of Z , 1.31, is less than the first tabu-

lated value, 1.64, we would conclude that the apparent difference in attack rates could be due entirely to random differences in the chosen samples and that the herd attack rates could be the same in the two herds.

If the test indicates a likely difference, we can calculate an approximate 95% confidence interval for the difference as follows:

$$(P_1 - P_2) \pm [\text{multiplier} \times \sqrt{\frac{P_1(1-P_1)}{n_1} + \frac{P_2(1-P_2)}{n_2}} + 1/2(1/n_1 + 1/n_2)]$$

where the multiplier is chosen from Table 16. Despite having found no real evidence of a significant difference, if we carry out the calculation, we get the interval:

$$(0.4000 - 0.2586) \pm [1.96 \times \sqrt{\frac{0.4 \times 0.6}{45} + \frac{0.2586 \times 0.7414}{58}} + 1/2(1/45 + 1/58)]$$

i.e. - 0.061 to 0.343

This interval includes the value 0 which indicates the possibility that there is no real difference, a conclusion we have already reached by testing the hypothesis.

The procedures described for testing whether a mean of a variable, or the proportion of cases, varies between two herds are correct under the assumption that both samples have been collected by simple random sampling. It is not difficult to extend them to more complex sampling schemes, provided that we have an estimate of the relevant quantity for each herd and have also correctly calculated the standard errors of these estimates. We can calculate the standard error of the difference (SE_D) by:

$$SE_D = \sqrt{(\text{SE from first herd})^2 + (\text{SE from second herd})^2}$$

Note that there is a plus sign under the square root symbol. The test statistic (Z) can be calculated by:

$$Z = \frac{\text{Estimate for first herd} - \text{Estimate for second herd}}{SE_D}$$

If the sample sizes are fairly large, a test can be carried out by comparing this value with the critical values in Table 21.

5.3.3 Sample size for detecting differences between two proportions in prospective and cross-sectional studies

The detection of a difference between two proportions is often one of the purposes of an epidemiological study. The proportions might be prevalences in a cross-sectional study, attack rates or incidence rates in a cohort study, and so on. Unfortunately, the sample size required will depend on the true values of both proportions, as well as on the significance level at which the test will be carried out and the confidence we require that the difference will be detected.

An approximate formula for the calculation of the sample size (n) required from *each* group is:

$$n = \frac{[C_1 \sqrt{2\bar{P}(1-\bar{P})} + C_2 \sqrt{P_1(1-P_1) + P_2(1-P_2)}]^2}{(P_2 - P_1)^2}$$

where: P_1, P_2 = true values of the proportions in the two populations we wish to compare;

\bar{P} = $1/2(P_1 + P_2)$;

C_1 = critical value corresponding to the significance level required (chosen from the bottom row of Table 21); and

C_2 = critical value corresponding to the chance we are willing to accept of failing to detect a difference of this type (chosen from the top row of Table 21).

Example: Suppose we are going to try a new farm management method in the hope that it will reduce the incidence of a common disease. We intend to take a sample of animals managed under a "standard" system and another of animals managed under a new system. From previous experience we expect the first group to suffer an attack rate of approximately 20% (i.e. $P_1 = 0.2$). We wish to discover whether this attack rate could be reduced to 15% (i.e. $P_2 = 0.15$).

Let us suppose that we would like the difference to be significant at the 5% level ($C_1 = 1.96$) and that we are willing to accept only a 1% probability that the difference will not be detected ($C_2 = 2.33$). Then we find that $n = 2120$, which means that the *total* sample is $2 \times 2120 = 4240$ ani-

mals. We can reduce this by increasing to 5% the probability that we fail to detect the difference, and then we get $n = 1494$ with a total sample of nearly 3000.

The size of the sample depends mostly on the magnitude of the difference we want to detect. If we reduce P_2 to 0.1, so that we are now trying to detect the difference between attack rates of 20% and 10%, we find that $n = 328$ and the total sample size drops from 2984 to 656.

The formula given above will slightly underestimate the sample size for studies in which the animals are not paired, and may overestimate it slightly for studies where they are. However, given the degree of arbitrariness which will usually be involved in assuming values for the true proportions, it is to be expected that the indicated sample size will never be better than a rough approximation.

5.3.4 Sample size for detecting differences between two proportions in retrospective studies

The procedure for estimating the sample sizes required in case-control studies is similar to that described in the previous section. However, there is one important exception: unlike in cohort studies where one is comparing the proportions of *disease* in two groups – one with and one without the determinant – in case-control studies one is comparing the proportions with the *determinant* in two groups – one with the disease (cases) and one without the disease (controls).

The formula for the sample size required in these studies is the same as that given in Section 5.3.3, with the exception that P_1 and P_2 now refer to the proportions with the determinant in the two populations we wish to consider.

5.3.5 Testing for differences in prevalence between several groups simultaneously

We may want to consider the question of whether several herds or other groups of animals suffer from the same prevalence of a given disease. The technique will be demon-

strated using an example involving three groups, but it is easily extended to as many groups as may be required. From Table 23 we see that the sample prevalences from the three herds are not exactly equal – we would not expect that even if the herd prevalences were the same, because of fluctuations in random sampling.

Table 23. *Prevalences of a disease in samples of animals taken from three different herds.*

	Herd 1	Herd 2	Herd 3	Total
Size of sample	68	52	73	193
No. of infected animals	12	11	20	43
Sample prevalence	0.176	0.212	0.274	0.223

The question we would like to resolve is whether the differences are sufficiently large in the samples to indicate a real difference in the herds from which they were drawn. To answer this, we must first present the data in the slightly different form of Table 24, in which each animal of the overall sample contributes to one and only one of the cells of the table. Such a table of frequency counts is often called a *contingency table*.

We now calculate the numbers which we would expect to see in the different cells of the table if a total of 43 infected animals and 150 animals free of infection were to be found in samples of 68, 52 and 73, respectively, from three herds with the same disease prevalences. These numbers are called *expected frequencies* (Table 25), and they have been calculated using the following simple rule:

The expected frequency e_{ij} of the cell in the i -th row and the j -th column of a table is obtained by multiplying the total of the i -th row, r_i , by the total of the j -th column, c_j , and dividing the product by the grand total, N . Symbolically, we can write:

$$e_{ij} = (r_i \times c_j) / N$$

Example: The expected frequency of the cell in the first row and second column in Table 25 is:

$$e_{1,2} = \frac{r_1 \times c_2}{N} = \frac{150 \times 52}{193} = 40.4$$

This is very similar to the observed frequency $O_{1,2}$ of the same cell in Table 24, which was 41.

Table 24. *Contingency table based on the data from Table 23.*

	Herd 1	Herd 2	Herd 3	Total
No. of animals not infected	56	41	53	150 (r_1)
No. of animals infected	12	11	20	43 (r_2)
Total	68 (c_1)	52 (c_2)	73 (c_3)	193 (N)

Table 25. *Expected frequencies for Table 24.*

	Herd 1	Herd 2	Herd 3	Total
No. of animals not infected	52.8	40.4	56.7	150
No. of animals infected	15.2	11.6	16.3	43
Total	68.0	52.0	73.0	193

Note: The row and column totals of the expected frequencies will be the same as for the original contingency table of observed frequencies, except for small rounding errors. For example, the total for row 1 seems to be 149.9 instead of 150, but this is because we have rounded all the expected frequencies to one decimal place.

The next step is to calculate a measure of the deviation of the observed frequency from the expected frequency for each cell. We do this by squaring the difference between the observed and expected frequencies and dividing the result by the expected frequency of the cell. Thus:

$$\text{Deviance} = \frac{(\text{Observed frequency} - \text{Expected frequency})^2}{\text{Expected frequency}}$$

Using this formula the deviance for the cell in the first row and first column of Table 24 is:

$$(56 - 52.8)^2 / 52.8 = 0.19$$

Table 26 shows deviances for all the cells in Table 24.

Table 26. Deviances for Table 24.

	Herd 1	Herd 2	Herd 3	Total
Not infected	0.19	0.01	0.24	0.44
Infected	0.67	0.03	0.84	1.54
Total	0.86	0.04	1.08	1.98

The working hypothesis will be that the herd prevalences are effectively the same. The experimental hypothesis is that there is some difference between herds. The test statistic is the total deviance, 1.98. As usual, this will have to be compared with a set of critical values which, in turn, depend on a quantity called *degrees of freedom* (df). For any table, this quantity is calculated as follows:

$$df = (\text{number of rows} - 1) \times (\text{number of columns} - 1)$$

For Table 26: $df = (2 - 1) \times (3 - 1) = 1 \times 2 = 2$

The critical values of the test statistic, called the *chi-square statistic*, can be found in Table 27.

Table 27. Critical values of the chi-square statistic.

df	Significance level			
	10%	5%	1%	0.1%
1	2.71	3.84	6.63	10.83
2	4.61	5.99	9.21	13.82
3	6.25	7.80	11.34	16.27
4	7.78	9.49	13.28	18.47
5	9.23	11.07	15.09	20.52
6	10.64	12.59	16.81	22.46

The value resulting from our contingency table is 1.98 with 2 degrees of freedom. If we consult the second row of Table 27, we see that 1.98 is smaller than the 10% value, 4.61, and conclude that there is not sufficient support in the data for the experimental hypothesis and that, until further data are obtained, we must assume that the herd prevalences could be equal. If the chi-square value had been between 5.99 and 9.21, for example, we would find that there was a difference in the herd prevalences at the 5% signifi-

cance level. The test may not be valid if some of the expected values are rather small. A useful guideline is that the expected values for each of the cells should be at least 5.

A similar analysis can be carried out on sample attack rates or any other rate or proportion based on simple random samples from different groups of animals. The problem with the chi-square test is that, if a difference is indicated, it is rather difficult to estimate the extent of the difference without the help of a statistician.

Let us test once again whether the two attack rates given in Table 22 are equal, using this time a chi-square test. Table 28 is a two-by-two contingency table based on Table 22. The figures in parentheses give the expected values for each cell.

Table 28. Two-by-two contingency table based on Table 22.

	Herd 1	Herd 2	Total
No. of animals not infected	27 (30.6)	43 (39.4)	70
No. of animals infected	18 (14.4)	15 (18.6)	33
Total	45	58	103

When the contingency table has only 2 rows and 2 columns, a slight modification has to be made in the calculation of the chi-square statistic. The deviance for each cell is calculated by finding the difference between the observed and expected value as before, but now always subtracting the smaller of these values from the larger. Before the difference is squared, it is reduced by 0.5. The remainder of the calculation is carried out exactly as before.

One point to note in a 2 x 2 table is that the difference between observed and expected frequency (ignoring signs) is the same for all four cells. In our example it is 3.6 for each cell. This has to be reduced by 0.5 i.e. $3.6 - 0.5 = 3.1$. For each cell the reduced value is squared and divided by the expected value to obtain the deviance. The four deviances are then summed to give the value of the chi-square statistic thus:

$$\frac{3.1^2}{30.6} + \frac{3.1^2}{14.4} + \frac{3.1^2}{39.4} + \frac{3.1^2}{18.6} = 1.74$$

Comparing this value with the first row of Table 27, we see that it is not significant and we reach the same conclusion as we did in Section 5.3.2, namely that the evidence does not give sufficient grounds to reject the hypothesis that the attack rates are equal in the two herds. In fact there is an exact correspondence between this chi-square test and the test carried out in Section 5.3.2. The value of Z we obtained there was 1.31 which is $\sqrt{1.74}$. The value of Z which arises from that test will always be equal to the square root of the chi-square test based on the corresponding 2 x 2 contingency table. Furthermore, the values in the lower row of Table 21 are the square roots of the values in the first row of Table 27. As a result, the two tests are exactly the same.

5.3.6 Testing for differences in several means simultaneously

It is likewise possible to test the working hypothesis that several sample means are equal against the experimental hypothesis that there are some real differences. The technique is known as the *analysis of variance* (ANOVA) and can be found in most general statistical textbooks. A description of the technique is beyond the scope of this manual. The important point to realise is that it is not correct to compare the means of several different samples two at a time using the procedure described in Section 5.3.1.

5.4 FORMULATING AND TESTING HYPOTHESES IN SMALL-SIZED SAMPLES

All the procedures that have been recommended for comparing two groups depend on having a reasonably large sample size. The following points should be noted carefully:

- i) When comparing two prevalences or attack rates, there must be at least five cases observed in both groups of animals for the test to be valid.
- ii) When comparing ratios or proportions or rates across several groups by means of the chi-square test, *all* the expected values should be greater than 5.
- iii) When comparing two means, the combined sample size should be greater than 40. If it is less

than 40, the same calculations are carried out, but the value of the test statistic, usually called the *t-statistic*, should be compared with the critical values given in Table 29 and not with those in Table 21.

Table 29. *Critical values of the t-statistic.*

df	One-sided test			Two-sided test		
	5%	1%	0.1%	5%	1%	0.1%
1	6.31	31.80	318.00	12.70	63.72	637.00
2	2.92	6.96	22.31	4.30	9.92	31.61
3	2.35	4.54	10.20	3.18	5.84	12.88
4	2.13	3.75	7.17	2.78	4.60	8.61
5	2.02	3.36	5.89	2.57	4.03	6.87
6	1.94	3.14	5.21	2.45	3.71	5.96
7	1.89	3.00	4.79	2.36	3.50	5.41
8	1.86	2.90	4.50	2.31	3.36	5.04
9	1.83	2.82	4.30	2.26	3.25	4.78
10	1.81	2.76	4.14	2.23	3.17	4.59
12	1.78	2.68	3.93	2.18	3.05	4.32
15	1.75	2.60	3.73	2.13	2.95	4.07
20	1.72	2.53	3.55	2.09	2.85	3.85
25	1.71	2.48	3.45	2.06	2.79	3.73
30	1.70	2.46	3.39	2.04	2.75	3.65
40	1.68	2.42	3.31	2.02	2.70	3.55

Like the chi-square statistic, the critical values of the t-statistic depend on the quantity known as "degrees of freedom" which, for this test, are calculated as the sum of the two sample sizes minus 2.

Example: Suppose that the experiment with anthelmintics had been carried out on two smaller groups comprising 23 treated and 19 untreated pigs. The mean weight gains for the two groups were 6.1 and 5.4 kg, respectively, and the sample standard deviations were 1.72 and 1.64. Then, using the formula already given, the standard deviation of the mean difference is:

$$S_{MD} = \sqrt{\frac{22 \times 1.72^2 + 18 \times 1.64^2}{40}} (1/23 + 1/19)$$

$$S_{MD} = 0.522$$

The difference in the two means is $6.1 - 5.4 = 0.7$ kg. The test statistic is $0.7/0.522 = 1.34$. The degrees of freedom are $23 + 19 - 2 = 40$. We now compare the value of the test statistic, 1.34, with the last row of Table 29, and see that weight gain is not significant at the 5% level. We can not conclude, therefore, on such evidence that treatment by anthelmintics will cause a general weight increase. It could simply be that, by chance, naturally faster growing animals were chosen to receive the drugs.

5.5: MATCHED COMPARISONS

The sensitivity of statistical hypothesis tests carried out to compare two treatments, or a treatment with a control, can be greatly increased if, instead of choosing two independent samples receiving different treatments, the two samples are chosen in pairs so that the two animals in each pair are as alike as possible. Consider again the study of the use of anthelmintics in pigs. This could have been carried out by matching pigs for sex, initial body weight etc. Let us suppose that this has been done for 10 pairs of pigs to give the results in Table 30.

Table 30. *Weight gains in 10 matched pairs of pigs.*

Pair	Treated (Y)	Untreated (X)	Difference (d)
1	6.1	5.7	0.4
2	5.2	5.3	-0.1
3	5.4	4.8	0.6
4	5.9	5.2	0.7
5	6.3	6.4	-0.1
6	6.0	6.3	-0.3
7	5.7	5.1	0.6
8	5.1	4.8	0.3
9	6.2	5.1	1.1
10	5.9	5.0	0.9
Mean	5.78	5.37	0.41
Standard deviation	0.4185	0.5774	0.4606

The analysis for such paired comparisons is carried out by considering the individual differences, d , between

the two animals of each pair. The test statistic is calculated from the formula:

$$t = \frac{\bar{d}}{(S_d/\sqrt{n})}$$

where: \bar{d} = sample mean,
 S_d = sample standard deviation of the differences, and
 n = number of pairs.

Note that when adding the differences to calculate \bar{d} it is important to take into account whether the difference is positive or negative. From Table 30 we see that $\bar{d} = 0.41$, $S_d = 0.4606$ and $n = 10$. Hence, the test statistic is:

$$t = \frac{0.41}{(0.4606/\sqrt{10})} = 2.81$$

with $10 - 1$ degrees of freedom. If we now consult Table 29, we see that the corresponding 1% significance value for a one-sided test is 2.82. There has been, therefore, a significantly higher weight gain in the treated animals.

If we had ignored the pairing and carried out the test presented earlier in this section, we would have obtained a value of $t = 1.82$ with 18 degrees of freedom, which just fails to be significant at the 5% level. Matching the animals has sufficiently increased the precision of the measurement of the difference in weight gain to affect the inference we make from the experiment.

Similar gains in precision can be obtained in case-control studies carried out to examine possible determinants of disease. Suppose that 100 cases and their paired controls were examined for the presence or absence of a suspected determinant, and this determinant was found to be:

- present in both the case and control individuals in 70 pairs;
- present in the control but absent in the case individuals in 5 pairs;
- absent in both the case and control individuals in 10 pairs;
- absent in the control but present in the case individuals in 15 pairs.

These results could be summarised in tabular form as was done in Table 31.

Table 31. Results of a paired case-control study of the effect of a suspected determinant on the occurrence of a disease.

Controls	Cases		Total
	Factor present	Factor absent	
Factor present	70	5	75
Factor absent	15	10	25
Total	85	15	100

It would be wrong to analyse this table as though it was a contingency table. An appropriate test would be the McNemar's test, which can be carried out as follows:

- Find the difference, D , in the frequencies of the two categories for which the case and its control are *not* in agreement with respect to the factor. Thus, for Table 31, $D = 15 - 5 = 10$.
- Find the sum, S , of the same two frequencies. $S = 15 + 5 = 20$.
- The test statistic is $(D - 1)^2/S = 81/20 = 4.05$. This statistic should always be compared with the critical values of the chi-square statistic with one degree of freedom (see Table 27).

Since 4.05 is greater than 3.84, the result of the test is that there is a difference at the 5% significance level between the cases and the controls with respect to the presence or absence of the factor.

If the pairs are ignored, the data can be presented in a contingency table (Table 32).

Table 32. Two-by-two contingency table of the results of a case-control study.

	Factor present	Factor absent	Total
Cases	85	15	100
Controls	75	25	100
Total	160	40	200

Using the procedure given earlier for analysing such tables, the expected frequencies are as shown in Table 33.

The total deviance is $4.5^2/80 + 4.5^2/80 + 4.5^2/20 + 4.5^2/20 = 2.53$ with one degree of freedom. This is not significant at the 5% level.

Table 33. Two-by-two contingency table of expected frequencies of disease, derived from Table 32.

	Factor present	Factor absent	Total
Cases	80	20	100
Controls	80	20	100
Total	160	40	200

5.6 A WORD OF WARNING

There is no such thing as a working or null hypothesis that is *exactly* true. It is most unlikely, for example, that the use of anthelmintics in pigs bred in an environment where helminths are endemic will have no effect on weight gain whatsoever. The result of a hypothesis test will depend on:

- The extent to which the null hypothesis is incorrect;
- The natural variability in the population studied; and
- The size of the sample observed.

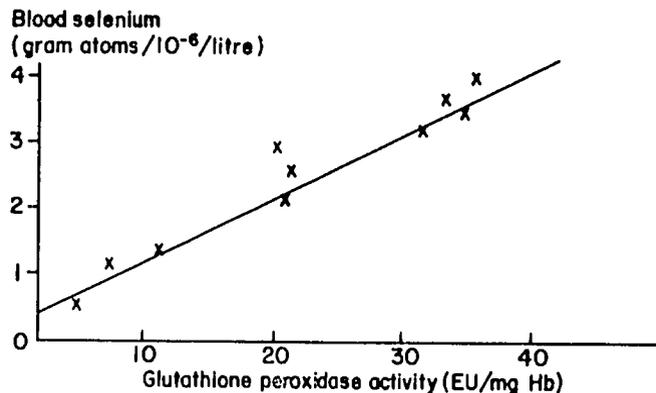
It is always possible to obtain a statistically significant result by choosing the sample size large enough. Even if, on average, a prophylactic induced an extra weight gain of only 1/10th of a gram per year, a large enough sample would cause the null hypothesis of no gain to be rejected. It follows that no study is complete without giving some estimate of the *magnitude* of the effects it claims to have detected. Only then will it be possible to judge the economic value of a treatment, change in husbandry method etc.

5.7 LINEAR CORRELATION AND REGRESSION

In epidemiological studies we are very often interested in exploring a relationship between two variables. For example, selenium is an essential nutritional element in the ovine diet, and disorders arise as a result of selenium deficiency. It is therefore of interest to have some measure of blood selenium levels. Unfortunately, the direct assessment of selenium concentration is lengthy and requires expensive and unusual equipment. The whole-blood selenium concentration (gram atoms per million per litre) is closely related, however, to glutathione peroxidase activ-

ity (enzyme units per milligram of haemoglobin), as can be seen in Figure 8.

Figure 8. Plot of whole-blood selenium concentration against glutathione peroxidase activity in 10 randomly selected sheep.



The measured values which were used to construct this graph are given in Table 34.

Table 34. Whole-blood selenium concentration (Y) and glutathione peroxidase activity (X) in 10 randomly selected sheep.

Sheep	Y	X
1	2.6	22.1
2	3.1	32.8
3	1.3	10.1
4	3.2	35.4
5	2.0	21.2
6	0.4	4.8
7	2.7	21.2
8	3.8	37.9
9	1.2	8.3
10	3.6	35.1

The points in the graph have a suggestively linear form, and it is possible to draw a straight line which comes close to passing through them. We have drawn in this line in the figure. Before explaining how to calculate it, we will discuss a measure of the degree to which the relationship

between two variables can be described by a straight-line graph. This measure is called the product-moment coefficient of linear correlation or, sometimes, the Pearson's correlation coefficient (r).

To obtain this coefficient, we first have to calculate a quantity known as the sample covariance of the two variables X and Y from the formula:

$$\text{cov}(X, Y) = \frac{\sum XY - n\bar{X}\bar{Y}}{n - 1}$$

where: n = number of pairs (X,Y) studied, and

$\sum XY$ = the sum of products obtained by multiplying together the two observations of each pair and adding the products. From Table 34 we have:

$$\sum XY = 22.1 \times 2.6 + 32.8 \times 3.1 + \dots + 35.1 \times 3.6 = 667.45$$

$$\bar{X} = 22.89$$

$$\bar{Y} = 2.39$$

$$n = 10$$

$$\text{cov}(X, Y) = \frac{667.45 - 10 \times 22.89 \times 2.39}{9} = 13.38$$

The correlation coefficient is then calculated as:

$$r = \frac{\text{cov}(X, Y)}{S_x S_y}$$

where:

S_x = sample standard deviation of the observed values of X, and

S_y = sample standard deviation of the observed values of Y.

For this example, $S_x = 12.20$ and $S_y = 1.13$, so that:

$$r = \frac{13.38}{12.20 \times 1.13} = 0.971$$

The value of r lies always between -1 and 1 . A value close to 0 implies that the two variables are not linearly related, while a value close to 1 or -1 means that it is possible to draw a straight line in such a way that it will come close to the plotted data points, as in Figure 8.

A positive correlation implies that the variables X and Y tend to increase or decrease together, while a negative correlation implies that as one increases the other decreases. The value of r^2 gives the proportion of the variation

in one variable which is due to variation in the other. However, a high statistical correlation between two variables does not necessarily mean that one is the cause of the other. The correlation between two variables may be due to the fact that they have a common cause rather than that they are directly related.

In our example, $r^2 = 0.94$ and we can say that 94% of the variation in enzyme activity is "due to" or is "explained by" the variation in blood selenium concentration in the observed animals. This suggests that it ought to be possible to get good information about blood selenium from the measurement of enzyme activity, a result already indicated by the rather good fit of the straight line to the sample points in Figure 8.

Any straight line can be represented by the formula:

$$Y = a + bX$$

where:

- Y = the variable plotted on the vertical axis,
- X = the variable plotted on the horizontal axis, and
- a, b = constants which define a particular straight line.

In our case a is the value of Y when X = 0, i.e. the point where the line crosses the Y axis, and b describes the slope of the line. If there is an exact linear relationship between X and Y, all pairs of points will lie on a single line and there will be only one possible value for a and one for b. When the points do not lie exactly on a straight line, there are several possible ways to define what is meant by the "best-fitting line" or the line that runs "closest" to the points. The values of a and b, which give the line known as the *least squares regression line*, are usually calculated using the formulae:

$$b = \frac{\text{cov}(X, Y)}{S_x^2} = \frac{13.8}{12.2^2} = 0.09$$

$$a = \bar{Y} - b\bar{X} = 2.39 - 0.09 \times 22.89 = 0.33$$

For the data in Table 34 we then have the *fitted regression line*:

$$Y = 0.33 + 0.09X$$

Given any enzyme activity score (X) we can now estimate the corresponding value of the blood selenium concentration (Y) using the regression formula. For example,

if a sheep has an enzyme activity of 32.8, we would predict that its blood selenium concentration is $Y = 0.33 + 0.09 \times 32.8 = 3.28$. The observed concentration for an animal in this sample with this enzyme activity level was 3.10. The value 0.09 is the estimated *slope* or *gradient* of the regression line and indicates the change in selenium concentration which corresponds to a change of one unit of enzyme activity.

As always, whenever we make an estimate, we would like to know how good that estimate may be. We can obtain a 95% confidence interval for the blood selenium of any animal with an enzyme activity X as follows:

$$Y \pm \text{multiplier} \times S_r \times \sqrt{1 + 1/n + (X - \bar{X})^2 / (n-1) S_x^2}$$

where:

- S_r = the residual standard deviation calculated by:

$$S_r = \sqrt{\frac{(n-1)}{(n-2)} \left[S_y^2 - \frac{(\text{Cov}(X, Y))^2}{S_x^2} \right]}$$

- The multiplier is chosen from Table 29 with n-2 degrees of freedom.

In this example $X = 32.8$ and we can say with 95% confidence that the selenium content lies in the interval:

$$3.28 \pm 2.31 \times 0.29 \times 1.083$$

i.e. 2.55 to 4.01.

This interval may seem too wide to be useful. Part of the problem is that the estimation of the regression line is based on observations of only 10 animals. If a regression line is to be used in this way, it ought to be based on a much larger sample.

5.8 TIME SERIES

An epidemiologist will frequently be interested in examining the manner in which certain variables vary over time.

Example: Table 35 gives hypothetical values of neonatal deaths per month in a large pig-breeding project over 9 years. At first glance it appears that there may have been a general increase in the number of deaths per month between the beginning of 1974 and the end of 1982, and that there were seasonal variations during the year.

Table 35. Hypothetical neonatal mortalities in piglets by month and year.

Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1974	359	361	363	455	472	545	598	729	874	587	483	380
1975	336	361	366	465	522	534	651	598	794	782	449	347
1976	308	329	354	391	467	633	846	950	989	830	676	531
1977	368	373	396	393	483	561	860	906	1095	780	764	543
1978	352	370	384	426	481	619	819	929	1090	805	711	559
1979	380	409	423	428	476	656	826	886	1058	803	725	543
1980	403	412	414	432	485	605	837	959	1152	773	784	515
1981	405	400	396	432	552	667	892	971	1076	821	789	570
1982	432	437	462	460	543	700	961	994	1042	890	780	573

A common approach to the analysis of such data is to try to examine separately the two major likely causes of variation – the gradual general increase or decrease (*trend*) from one year to another, and seasonal variations within each year. There are several different methods for doing this, but they will all give similar results to the method outlined below.

The first step is to estimate the *linear trend*. This can be done by fitting a linear regression line to the monthly means calculated over complete calendar years:

Year (X)	1	2	3	4	5	6	7	8	9
Mean (Y)	517.2	517.1	608.7	626.8	628.7	634.4	647.6	664.2	691.2

Note that the years 1974–1982 have been coded simply as 1, 2, etc.

We then calculate the least squares regression line of mean deaths on year number to get the trend line:

$$Y = 513.2 + 20.38X$$

The slope of the line, 20.38, tells us that the monthly deaths are increasing at an average rate of just over 20 each year. In other words, the number of deaths in a given month will be about 20 more than the number in the same month in the previous year. This does not necessarily imply that the death rate is increasing: the increase in the number of deaths could simply be a response to an increase in the total number of births.

Having obtained a measure of the rate of increase, the trend, it would now be useful to have some information

about the magnitude of the seasonal effects. These can be estimated by considering the extent to which the observed deaths for each month differ from the corresponding value on the trend line.

The first step is to calculate the value of the trend line corresponding to each calendar month. We will exemplify the procedure by carrying out the calculations for all the months of January in the sample. Note first that the trend line was calculated using mid-year averages centered on the end of June each year. The value corresponding to each month should be centered in the middle of that month. For example, the middle of January 1974 is five and a half months or $5.5/12 = 0.46$ years before the end of June 1974. Since the value "1.0 years" on the time axis corresponds to the end of June, $1.0 - 0.46 = 0.54$ will correspond to mid-January, and the corresponding trend value will be:

$$Y = 513.2 + (20.38 \times 0.54) = 524.2$$

The number of deaths in January 1974 was 359. The ratio of the observed number of deaths to the number predicted by the trend line in the middle of the month is called the *specific seasonal*, and its value for January 1974 is $359/524.2 = 0.68$.

The point on the time axis corresponding to January 1975 is $2 - 0.46 = 1.54$ and the corresponding trend value is:

$$Y = 513.2 + (20.38 \times 1.54) = 544.6$$

The number of deaths observed in January 1975 was 336 and the specific seasonal is $336/544.6 = 0.62$. Proceed-

ing in this manner, we can calculate the specific seasonals for any month. The specific seasonals for January in each of the study years are:

Year	1974	1975	1976	1977	1978	1979	1980	1981	1982
Specific seasonal	0.68	0.62	0.55	0.63	0.58	0.61	0.62	0.61	0.63

Averaging the specific seasonals for a given month over all the years in which it appears gives the *typical seasonal* for that month. The typical seasonal for January will be:

$$\frac{0.68+0.62+0.55+0.63+0.58+0.61+0.62+0.61+0.63}{9} = 0.61$$

The combined use of the typical seasonal and the trend line allows us to "predict" the number of deaths to be expected in January 1983. The trend line value will be:

$$Y = 513.2 + 20.38 \times 9.54 = 707.6$$

The value of the seasonal tells us that the number of deaths in any January is only about 61% of the value suggested by the trend line. The prediction would be to expect about $707.6 \times 0.61 = 432$ deaths in January 1983. The accuracy of such a prediction depends on how stable both the trend and the seasonal effects are. The farther into the future we try to predict, the less faith we should have in the quality of the prediction.

6. AN INTRODUCTION TO THE USE OF ECONOMICS IN THE PLANNING AND EVALUATION OF DISEASE CONTROL PROGRAMMES

6.1 INTRODUCTION

6.1.1 Basic philosophy

Economics is a social science dealing with the production and distribution of goods and hence of wealth. It analyses how scarce resources are allocated between different uses and groups within the economy. Originally, economic thought was developed under the name “political economy” and examined the production and distribution of wealth in a society composed of landlords, peasants and artisans. With the advent of industrialisation, thinkers looked at the economic relationship between capitalists, workers and landlords. This approach was the one taken by Marx and underlies Marxist economics. Modern economics in the “capitalist” societies looks at the economic interactions between producers and consumers, who meet in the market place and try to satisfy their needs. Its aim is to analyse objectively the “positive” i.e. the verifiable or factual aspects of the economic relationships in society, and thus to derive generally applicable theories. It does not concern itself directly with the “normative” aspects which

relate to value judgements about how the economic process ought to function.

The study of economics is conventionally divided into two areas. *Micro-economics* analyses the behaviour of individual producers and consumers, focussing on the factors influencing their levels of production and consumption and the mix of goods involved. *Macro-economics* analyses the economy as a whole, and deals with such topics as national income, balance of payments, overall savings and investment.

Development economics has emerged as a branch dealing with the specific problems of the less developed countries. It tries to analyse and explain the particular situation of these countries and to examine economic policies, such as price control, subsidies and taxes, and the channelling of investment funds into certain areas, which can help overcome their problems and improve their people’s standard of living. The topics covered include an analysis of the causes and symptoms of poverty, of the dichotomy between the agricultural and the industrial sector in Third World countries, and of the extent of the bias in actual development towards urban areas. Development economics examines the questions of choice of technology, unemployment and underemployment, migration and land reform, from an economic point of view and also studies the roles of trade and commodity markets.

Project appraisal, the economic analysis of projects before they are undertaken (*ex-ante* analysis), and *project evaluation*, the assessment of projects after they have been undertaken (*ex-post* analysis), are practical applications of economic principles to decision-making based on a social benefit-cost

analysis. This consists of setting out costs and benefits over a number of years and comparing them according to certain prescribed conventions so as to determine whether the project would be profitable. Budgeting and accounting are also techniques of applied economics.

6.1.2 Application of economics in disease control policy

Economics contributes to the improvement of policy formulation and decision-making for animal health projects and programmes at four levels:

- Economic theory explains the behaviour of producers and consumers, and the effect of this on the price structure and on the output of the economy as a whole. In the livestock sector, it explains how economic factors influence producers, how they decide what and how much to produce, what prices are acceptable to them, why production is expanded or contracted, how much they invest etc. It also explains the economic factors underlying demand for livestock products, how these affect the amount and mix of products bought, and how prices are fixed in different circumstances (micro-economics).

- The economic aspects of the different livestock production systems can be described by collecting relevant information and using it as well as the knowledge derived from economic theory to analyse how producers and consumers interact. A particular livestock production system can be described in economic terms by looking at the value of output, the cost of the inputs, calculating the income received by the producers, butchers, traders and other middlemen, and examining the final price paid by the consumers.

- Having characterised the production systems involved, as well as the interactions between the consumers and producers, it becomes possible to examine and predict the likely economic effects of any changes introduced into the sector. Such changes would include both changes affecting prices of inputs or outputs, which would affect the incomes of consumers and, therefore, demand, and changes in the technical coefficients of output due to introducing improved inputs, changing the animal health picture etc.

- Finally, the techniques of economic analysis make it possible to arrange this information so as to provide the basic yardsticks for ranking and hence comparing different programmes, projects or measures, and assessing their overall economic feasibility.

Thus, for an animal health project, economic theory can help explain producers' behaviour, describe the production systems involved, then help to predict and quantify the effect of the project on output, prices, demand and incomes, and, finally, provide a framework for arranging this information in the form of a *benefit-cost* analysis. Then, having ranked and compared the alternatives, a decision can be made whether to implement the project or not.

Obviously, decisions cannot be taken on the basis of economic considerations alone. First, the technical feasibility of any proposed measure must be examined by the relevant specialists (veterinarians, animal husbandry experts, sociologists, management experts etc). Second, its overall compatibility with the stated policies and goals of the livestock sector must be ensured, and, third, its feasibility from an organisational and social point of view needs to be verified.

In this manual, the methodology of the benefit-cost analysis is examined in some detail with regard to long-term decisions on animal health programmes. Let us consider some of the basic economic principles before applying them.

6.2 PRICES APPROPRIATE FOR USE IN ECONOMIC ANALYSES

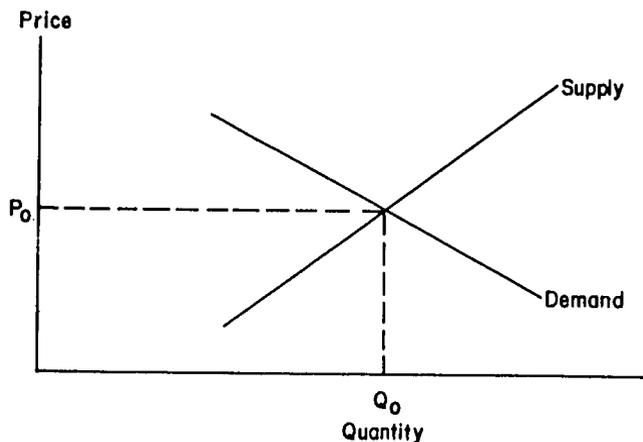
6.2.1 Theoretical aspects

Supply and demand

Prices are the "labels" or weights used in economic decision-making. As such, an understanding of how they are derived and what they represent is crucial. Money is the "unit" in terms of which prices of goods are given in a cash economy, although barter can fix their relative values. For example, if a kilogram of meat costs US\$ 3 and a yard of cloth US\$ 1.50, 2 yards of cloth could be exchanged for 1 kg of meat in the absence of money, or both could be paid for in cowries, manillas or some other acceptable currency.

Historically, price theory began with the concept of goods having either a scarcity value or a value because of the labour needed to produce them. Modern economics sees prices as being determined by the interaction of supply and demand, reflecting both the balance of the price producers are willing to accept, taking into account their production costs, and the price consumers are willing to pay for a certain quantity of goods. For most goods, the quantity offered increases with increasing price, but the quantity demanded decreases. This process is illustrated in Figure 9.

Figure 9. *The equilibrium of supply and demand.*



If supply equals demand, the market is said to be "in equilibrium" at price P_0 . This price is also referred to as the *market-clearing price*, and it represents the point at which all that is offered is bought. At a higher price, supply exceeds demand, since producers are willing to offer more and consumers are reluctant to purchase. The converse is true if the price is lower than the market-clearing price, in which case consumers are eager to buy but producers are reluctant to sell or produce, and, consequently, the quantity demanded exceeds that supplied. If the individuals were bargaining in a real market place, they would continue to offer each other prices until they arrived at a mutually agreeable price, or else the consumer would decide not to buy or the producer not to sell.

Example: Suppose that a government fixes a maximum price for meat with the objective of ensuring that low-income consumers can afford the commodity. If this price is below the market-clearing price, producers would like to charge more, demand outstrips supply, and a black market develops where meat is sold at prices nearer to, or even exceeding, the market-clearing price to those consumers who can afford it. Conversely, if a government fixes a minimum price which is above the market-clearing price, supply will tend to outstrip demand at that price and suppliers will be forced to sell off their goods cheaply, avoiding the government regulations. This commonly happens when there is a fixed minimum wage for labour: if many people are looking for employment, a large number will end up accepting jobs below the minimum wage.

In fact, if a government wants its price-setting policies to be effective, it will often need to pay a subsidy to compensate producers, if the price is too low, or consumers, if it is too high. The government would need sufficient knowledge of the supply and demand curves for the product, i.e. the lines illustrating what quantity is demanded or supplied at which price, in order to work out at what price (P_1) the quantity supplied would be equal to that demanded at a minimum price (P_2) and representing the amount the government would like people to consume. The government can then pay producers a subsidy equivalent to the difference between P_1 and P_2 , so that the supply rises to the level equal to the quantity demanded at the minimum price, and the market clears.

The discussion of price theory has raised several points which need to be considered when deciding which prices to use in various economic studies. These can be summarised as follows:

- Since for most goods the quantity demanded falls as the price rises, governments can stimulate demand for an item by setting a low price. Conversely, they can lower demand by setting a high price. A low price can be supported by a subsidy, a high price may be enforced by a purchase tax. For example, the consumption of milk may be encouraged by setting a low price for consumers, backed up by a subsidy to producers. Similarly, new inputs into production systems, such as fertilisers, improved breeds of livestock, ploughs etc, may be encouraged by subsidising their cost to whoever is prepared to use them. In the absence of a

support for artificially high or low prices, black markets tend to emerge.

- Different consumers may pay different prices for the same goods. For example, because of the costs of transport, goods may cost more in isolated rural areas or if they are imported from another region or country. Products may be more expensive when bought in retail outlets with high overheads, while items sold in large quantities are usually cheaper. If a good passes through many hands before it is sold to the final consumer, it will be more expensive since every middleman on the way expects to make some profit. These are all concrete reasons for price variations.

- A more subtle effect is that of the individual consumer's bargaining power. In the market, one person may be better or worse at negotiating a price than another. On a wider scale, the price an individual will pay may depend on such things as his or her influence in society, whether the seller wishes to gain favour, or considers the purchaser rich and capable of paying a good price. All these effects are intensified in a black market.

- A variety of prices exists for each item affected by a government subsidy or tax. These include:

- The price paid by the consumer, which may include a purchase tax or is the portion of the cost after the subsidy has been removed.
- The price received by the producer, which is the price before purchase tax is added or, in the case of a subsidy, the equivalent to the price paid by the consumer plus the government subsidy.
- The cost to the government of the subsidy or the revenue brought in by the tax.
- The cost to the nation, which is roughly equivalent to the price paid to the producer. A government tax or subsidy is a transfer between tax payers who pay the subsidy or tax and those who benefit from it, either by receiving the subsidy or using the facilities financed with the money collected from the tax.

The concept of elasticity

The concept of supply and demand as discussed in the previous section has been much simplified. In practice there are often deviations from the general rule of price increases leading to a fall in demand and a rise in supply. In order to

be able to measure precisely how supply and demand respond to changes in prices, the concept of *elasticity* was developed, which is expressed by the following formula:

$$\text{Price elasticity of supply (or demand)} = (-) \frac{\text{The percentage change in quantity}}{\text{The percentage change in price}}$$

Elasticity should be expressed as a positive number. A minus sign is placed before the equation in the case of the price elasticity of demand, since demand falls as price increases, making the overall result positive. Thus, if the demand or supply changes by the same percentage as price, the elasticity is 1. If a price increases by 10% and elasticity is 2, supply will increase by 20%. Goods are said to be *inelastic* if the demand for them changes very little with price, in which case the calculated elasticity is less than 1. Such goods are generally necessities, for which demand is very stable. For luxuries, demand is generally more elastic.

In some cases producers have a target income rather than trying to maximise their profits, and once this income is reached, they cease to supply more goods. Thus, beyond a certain point, price increases may lead to a reduction in supply. This has been alleged to be the case with some nomadic cattle keepers, who only sell their animals to meet their fixed cash needs for such items as school fees, taxes, clothing, veterinary expenses etc.

The concept of elasticity can also be applied to changes in income:

$$\text{Income elasticity of demand} = \frac{\text{The percentage change in quantity}}{\text{The percentage change in income}}$$

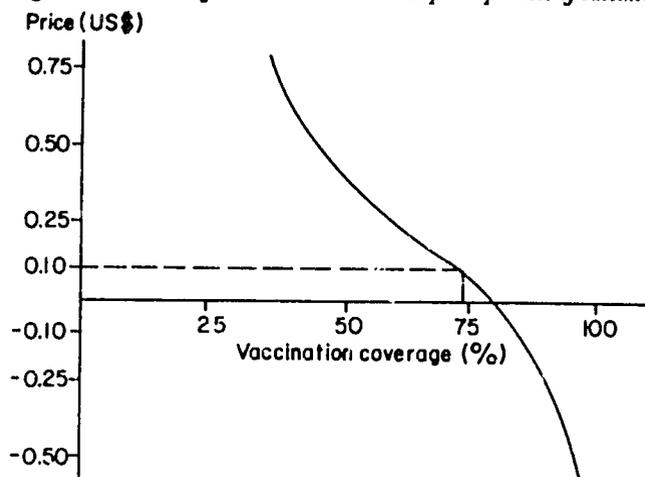
Changes in income must be taken into account when trying to project how the demand for livestock products will evolve over the years. Generally, the demand for a good increases with increasing incomes. However, as people get wealthier they reduce the consumption of goods that are considered inferior, such as very cheap cuts of meat and/or clothing.

The concept of elasticity thus has the following practical applications in the formulation and assessment of animal disease control policy:

- It assists in the general understanding of the livestock sector, particularly in determining what the future supply and demand are likely to be in response to changes in prices and incomes.

• It is crucial in determining what prices to charge producers for various veterinary treatments. Figure 10 illustrates a hypothetical relationship between the demand for vaccination and its price.

Figure 10. Demand for vaccination at various prices per dose of vaccine.



The elasticity of demand varies, being very elastic as the price of an individual vaccination falls from US\$ 0.50 to about US\$ 0.10 and relatively inelastic at US\$ 0.75 per vaccination. Therefore, to ensure a vaccination coverage of about 80%, it will be necessary to provide the vaccination free of charge. To increase the coverage further, livestock owners would actually have to be paid or coerced. If vaccinations cost more than US\$ 0.90 each, less than 5 to 10% of the livestock would be vaccinated. Suppose that a coverage of 75% is thought necessary for a voluntary vaccination campaign to be effective, then the maximum amount that can be charged by the veterinary service is US\$ 0.10. If the vaccine costs US\$ 0.12 per dose and the average cost of distributing and administering the distribution is US\$ 0.27, it will be necessary to subsidise the campaign to the extent of US\$ 0.29 per dose. The vaccine might be cheaper if purchased in bulk, and the cost per dose for distribution and administration might go down as more animals are presented at each vaccination session.

However, experience has shown that this analysis of livestock producers' response to opportunities for vaccina-

tion may not always correspond to reality. In some cases, producers avoid having their animals vaccinated when the vaccination is free but present them when a fee is imposed. This does not reflect a failure of economic theory to cope with reality, rather the belief of producers that free vaccinations may be inferior to those that are charged for. Their decision is thus quite rational from the economic point of view: it is not worth their while to spend time getting their animals together for a free vaccination of no value, whereas it is worth paying for one that confers a real benefit.

Prices of factors of production and of durable goods

So far we have analysed prices as though they were for consumer goods that were purchased outright. Prices for durable goods and the various inputs of production are slightly more complex. There are three factors of production to be considered:

- Labour, which can be divided into various grades;
- Land, which includes natural resources; and
- Capital, which covers both money itself and production goods such as livestock and machinery.

A fourth factor, entrepreneurship or management, is sometimes added to cover management and risk taking.

The factors of production are subject to the laws of supply and demand in the same way as other goods, but the demand for them is described as *derived demand*, since it depends on the demand for the products the factors are used to make. Given sufficient information about the production conditions, prices and the demand for final products, input-output models can be constructed for the whole economy to determine the demand for the different factors of production.

The many inputs of production and most durable goods can usually be bought in two ways:

- Outright purchase, which confers on the owner all the incomes that can be earned from using a particular input or all the benefits from a particular durable good.
- Renting or hiring, which enables the purchaser to use the item for a stated period of time.

Thus a durable consumer good, such as a television, can be owned or rented. Machines used for production (tractors, draught oxen, harvesting equipment) can be hired or owned. Labour is usually rented out by an indi-

vidual by the hour or week against a fixed wage. Capital in the sense of machinery and buildings can be owned or rented. Money in the sense of cash can either be owned, in which case the owner reaps the income it can earn, or rented in return for a payment per unit of the time that it is used. This "rental" is conventionally referred to as borrowing and the payment per unit of time is the interest. Similarly, land or mineral rights can be owned or rented for a period of time.

Underlying all investment or project appraisals is the concept that the various inputs or factors of production at the disposal of an individual or a nation should be used so as to earn that individual or nation the highest possible income. Thus, just as an individual should not borrow money at an interest of 10% per annum to finance an investment from which he expects a profit of 8% per annum, a nation should not invest resources in projects with a return of 8% when alternatives yielding 10% exist.

6.2.2 Opportunity cost and the choice of prices in economic analysis

In a project appraisal or budget, the main economic input lies in the choice of prices, since it is assumed that the technical inputs which give the main physical components of costs and benefits have been derived by the professionals responsible for ensuring the technical feasibility of the project. In the same way as all the assumptions necessary for deriving the physical parameters must be clearly stated, so the *origin* or *derivation* of every price or group of prices chosen must be given as well as the *justification* for using them. A simple rule determining which prices can be used in a particular analysis is that the prices chosen should approximate, as far as possible, to the *opportunity cost* of the relevant items to the individual, firm, institution or country from whose point of view the analysis is being made.

Opportunity cost and shadow prices

The opportunity cost of making a particular economic choice is given by the cost of whatever alternative production or consumption had to be foregone as a result of that choice. The allocation of labour in a village production sys-

tem means that new projects introducing new work patterns need to take into account opportunity costs.

Example: The labour needed to grow fodder crops could be valued at the government's minimum wage rate of, say, US\$ 5 a day. After consideration, this rate might be found artificially high, so a black market wage rate of US\$ 3 per day might be applied. We may also look at the problem from the point of view of opportunity cost and ask the question, What would the farmer be doing with his time if he were not cultivating his fodder crop? If the answer is that he would be doing nothing but lying in the shade sleeping, the opportunity cost – unless he is very tired – may be nil. If the answer is that he would be drinking beer with his friends, it may be that the opportunity cost is negative – by not drinking he saves money and has fewer hangovers. Alternatively, his drinking may be a way of finding out information on marketing issues, pasture availability, local politics etc. Most often, however, the opportunity cost will be expressed in terms of another crop or of time spent trading or on craftwork or some other remunerative occupation. In order to assess the true cost of transferring the farmer's labour to fodder crop production, the cost of the *income foregone* from the alternative occupation must be estimated.

The opportunity cost of capital, i.e. of using money or investment funds, is the rate of return or interest rate that can be earned in alternative uses.

From the concept of opportunity cost, the idea of *shadow prices* can be derived. Shadow prices are used with the broad objective of bringing prices to values nearer their true opportunity cost and thus, in project analysis, they lead to the selection of projects which use up the different resources at rates reflecting the real cost to society. Shadow prices can be defined as artificial prices calculated for certain items in order to ensure that their real opportunity cost is taken into consideration when making decisions. These shadow prices may be different from the money actually received or paid for the items at the time they are used.

Shadow prices are generally used in the following circumstances:

- Where market prices do not reflect real opportunity costs. This is often the case when prices are fixed by the government or are affected by speculators indulging in monopolistic trading.

- To accomplish particular policy objectives by encouraging the use of some items by setting artificially low prices for them and discouraging that of others by setting artificially high prices.

Thus, in project appraisal, shadow prices will present the costs and benefits of the projects at prices that: a) reflect, as far as possible, the real opportunity costs of the choices being made and the policies being proposed; and b) follow government policy by making those projects that use a higher proportion of the inputs whose use or production the government wishes to encourage, seem relatively more profitable. This is because shadow prices give such inputs an artificially low cost and such outputs an artificially high value.

Shadow prices are most commonly used in the case of two commodities:

- *Labour*, which can be rather difficult to value in monetary terms, as was illustrated by the example given above. Moreover, governments often want to encourage projects that use a high proportion of local labour while maintaining a relatively high minimum wage rate. A low shadow price for labour would make such projects appear relatively cheaper compared to projects substituting other inputs for local labour.

- *Foreign exchange*. Foreign exchange is a market commodity just like any other. It is accumulated by exporting and receiving aid in hard currencies and spent on imports, foreign debt repayments etc. A low price for foreign exchange means that the value of the local currency is high. This is often felt to give the country prestige and to imply a strong economy. It also makes the repayment of international loans artificially cheap. As with any other market, an artificially low price will lead to demand exceeding supply. Imports are artificially cheap, but exports are artificially expensive and hence not competitive, resulting in a shortage of foreign exchange. So governments end up restricting imports by imposing quotas, licences or banning certain commodities. One way to ensure the selection of a project that saves foreign exchange is to use a high shadow price for it.

Shadow prices can be used for any commodity if the need arises. For instance, if the objective of government policy is to raise the living standard of a particular group of people in a country, shadow prices can be used to give a

higher value to incomes gained by that group as compared to those of another group. A comprehensive system of shadow pricing based on world market prices has been devised by Little and Mirrlees (1977).

An example of the application of shadow prices is given in Table 36, which presents a comparison of costs of different techniques used for the control of tsetse in Nigeria. A shadow price for foreign exchange was calculated, based on the prevailing black market rate for the Naira (N). The shadow price calculated for labour was 1 N per day. This was partly based on the actual rate paid locally outside the civil service and on an estimate of alternative earnings in the rural sector. Since the shadow price for labour was lower than the market price of 2 N per day, its effect was to lower costs. The shadow price for foreign exchange was N 2.10 per pound sterling instead of N 1.40, thus increasing costs.

Given a choice of techniques between insecticidal spraying by ground teams and by helicopter at market prices, the difference in cost per km², N 357 and N 400 respectively, was not large. However, 90% of the field costs for the helicopter consisted of foreign exchange as compared to 34% for ground spraying. In addition, 43% of ground-spray costs were payments for local labour while only 3% of the costs of helicopter spraying were used for this purpose. Taking the shadow prices into account, the resulting costs were N 354/km² for ground spraying and N 552/km² for helicopter spraying.

Generally, it is not recommended that individuals working within a government framework attempt to use a variety of shadow prices that they have calculated themselves. Ideally, the ministry in charge of planning and appraisal should give clear guidelines as to which shadow prices are acceptable. In the absence of this, individuals should make their initial calculations at market prices, and only if they feel that there is a strong case, should they apply their own shadow prices, stating clearly what these are and how they have been derived. Because the issue of shadow pricing is a complex one, the advice of a professional economist should be sought before attempting to assign shadow prices to goods and resources.

Table 36. Comparison of costs for ground and helicopter spraying against tsetse flies - Nigeria, 1978.

Component of costs/km ²	Ground spraying	Helicopter spraying
Field costs		
Breakdown of average field costs (%)		
Insecticide*	16.7	35.4
Labour**	43.2	2.7
Flying time*	-	52.0
Junior staff	17.2	3.2
Senior staff	2.5	1.3
Vehicle running and maintenance	3.4	2.6
Depreciation of equipment*	17.0	2.8
Total	100.0	100.0
Average field cost of newly reclaimed area (N)		
Without shadow prices	87.0	238.0
With shadow price for labour and foreign exchange	82.0	342.0
Adjustments and overheads to average field costs (N)		
Barrier resprays	5.0	0.2
Resprays of reinvasions and residual foci	35.0	109.0
Costs of staff not included above (administrative, headquarters, junior and senior staff outside spraying season)	100.0	24.0
Share of all other costs of running units and headquarters	130.0	29.0
Total*		
Without shadow prices	270.0	162.2
With shadow prices for labour and foreign exchange used in respray operations	272.0	210.0
Final cost		
Without using shadow prices	357.0	400.2
Using shadow prices	354.0	552.0

* Foreign exchange costs.

** Local labour costs.

Choice of prices for financial and economic analyses

In economic studies, a distinction is made between *financial* and *economic* analyses. Financial analyses examine the monetary implications of any particular activity by an individual person, enterprise or institution, looking at the actual expenses and receipts from the point of view of the individual or firm concerned. The prices used in these analyses are usually market prices.

Economic analyses study the effect of a particular activity on the whole economy. The prices used should approximate to their opportunity cost, so they may be shadow prices. Since the analysis is undertaken from the point of view of the whole economy, all prices are net of purchase taxes and subsidies.

As a study undertaken from the point of view of an individual person (firm or institution) examines the implications of a particular activity to that individual, the prices used must be those that the individual faces. Thus to a farmer who ends up buying all the supplementary feed for his cattle on the black market, the application of the government's subsidised price makes no sense. Supplying supplementary feed at subsidised prices costs the government the handling and distribution expenses plus the value of the subsidy. Whereas if a trader is involved, the feed brings him a profit if he sells it at a higher price, less his own costs of transport, handling, storage etc. These are all *financial* viewpoints.

From the nation's (*economic*) point of view, the cost of the supplementary feed is probably best estimated using the price paid by the livestock producer, if the feed is sold on the open market. In economic evaluations involving most agricultural and livestock products, the so called "farm-gate price", which is the price paid to the producer, should be used. The retail price paid by consumers includes the profits of middlemen, transport and handling charges etc, which do not form part of the real value of the product. Where the farm-gate price is artificially fixed, a shadow price reflecting the black market price may be used. World market prices for particular items should only be applied if these prices are being used throughout and if the government or agency for whom the evaluation is being undertaken desires this.

The distinction between economic and financial analyses will be used throughout the rest of this manual. Up to now, the word "economic" has been used to cover both aspects. Used on its own without contrasting it to the word "financial", it will continue to be the general term covering all studies of this nature.

6.2.3 Adjusting for inflation – price conversions and price indexes

Dealing with inflation falls naturally into a general discussion on prices but the reader is also referred to the relevant sections in Chapter 8 on benefit-cost analysis. The relationship of inflation to interest rates is discussed in Section 6.3, as is the principle of compounding, which will be of use in estimating the effect of an annual rate of inflation on prices over a number of years.

For the purposes of project appraisal, making budgets or other economic or financial activities, it is often necessary to convert prices at current levels (i.e. for the year in which they occur) to constant values i.e. to those in a chosen base year.

Since any cost (C) is obtained by multiplying the quantity (Q) by the price (P) i.e.

$$C = P \times Q$$

it follows that, if for any year two out of the three items (C, P or Q) are known, and the price for the base year is known, costs can be converted to their value in the base year. Most commonly, it will be necessary to convert the cost of a particular item or undertaking in year n to that in the base year 0. Since the item or undertaking is the same, it follows that:

$$Q_0 = Q_n$$

so that

$$C_0 = C_n \times P_0/P_n$$

i.e. the costs in the year n are converted to costs in the base year by multiplying them by the ratio obtained when prices in the base year (P_0) are divided by those in year n (P_n). Sometimes this ratio is given in the form of a *price index* for a fixed quantity of goods.

Usually the price level in the base year 0 is assigned the number 100, so that price changes will show up as per-

centages of prices in year 0. Thus as the price changes, the price ratio for each year n (P_n/P_0) is calculated and multiplied by 100. Similarly, to convert costs from year n to a base year, they should be divided by the price index and multiplied by 100.

Example: Suppose that milk cost F 180 per litre in 1981 and F 250 in 1983, then the ratio 250/180 multiplied by 100 will give a price index of 139 if the base year is 1981. To create this index a constant quantity (1 litre) was used. Thus the quantity of milk bought for F 15 000 in 1981 would cost 15 000 x 139/100 or F 20 850 in 1983. Conversely, expenditure on milk of F 25 000 in 1983 would have cost 25 000/39 x 100 or F 17 986 in 1981. Often price indices are presented in a series for a fixed quantity. Thus if the 1982 price was given as F 215, the complete series would be as follows:

	Base year 1981	Base year 1983
1981	100	72
1982	119	84
1983	139	100

The base year in this series is given by 100. Using such a series makes it possible to convert costs from any year to those of any other, but most conveniently to the base year. Frequently an economist evaluating a project will be confronted with a series of expenditure figures extending over many years. If detailed information is not available, price indices published by government statistical services can be used in the analysis or else such indices can be put together from the existing information on prices and quantities. Until costs over a number of years have been converted to constant prices, it is meaningless to compare them, since any decreases or increases could be due to price changes.

Any project manager, planner or individual planning his finances must make it a priority to collect not only information on costs but also on prices. Ideally all quantities, prices and expenses should be recorded. In fact, since the objective is to compare expenditure or receipts at constant prices, a record of total costs and unit prices would be sufficient. Expenditure and receipts could then be converted to the base year by making price indices out of the price series. This is the most practical approach. An alternative approach is to note all quantities purchased or sold. When the moment for comparing expenditure and receipts comes,

these can be converted to current costs for all items since the quantities and current prices are known.

In many cases price indices actually cover a mixed sample of goods of a particular category. Examples of these include consumer price indices, share indices, construction goods indices, industrial price indices etc. In each case, the same principle applies. As before, the quantity must be fixed, but this quantity is a fixed selection of goods, usually called a "basket".

Table 37 gives an example of a price index created to convert costs to constant prices for the evaluation of a tick control project in Malawi. The last year of the project, 1981/2, was chosen as the base year, with prices increasing to that level.

6.3 COMPOUND INTEREST, DISCOUNTING, ANNUAL RATES OF GROWTH AND ANNUAL LOAN REPAYMENTS

This section explains the formulae needed for calculating annual rates of growth, inflation and compound interest and for discounting, which is, in effect, deducting compound interest. These are all based on a single, simple formula which is explained below.

6.3.1 Simple vs compound growth (or Interest) rates

If a given number (a livestock population, a sum of money, a price) is said to increase at a percentage rate per annum (population growth, interest or inflation rates), this increase could be interpreted as simple or compound growth. Table 38 illustrates these two types of growth for a sum of money (US\$ 100) growing at an interest rate of 10% over 5 years.

Simple growth is calculated by applying the percentage rate only to the initial sum, so that the numerical value of annual growth is always the same. Thus *simple interest* is paid only on the sum initially invested (US\$ 100) and is fixed at 10% of this (US\$ 10).

Table 37. *Price indexes calculated for a tick control project in Malawi (base year 1981/82).*

Year	Blantyre low-income consumer price index	Salaries in the veterinary and livestock departments	Construction work: dip tanks and staff housing	Vehicles
68/69	32.6	40	18	12
69/70	33.7	40	19	13
70/71	37.0	40	20	14
71/72	39.4	40	23	15
72/73	40.9	46	27	17
73/74	44.1	46	32	20
74/75	50.9	48	42	24
75/76	57.2	48	51	36
76/77	59.7	48	55	41
77/78	62.9	64	57	48
78/79	68.7	82	65	59
79/80	71.7	84	71	71
80/81	90.0	89	87	87
81/82	100.0	100	100	100

Compound growth is calculated by applying the percentage rate each year to the initial sum *plus* the previous year's growth, so that the annual growth rate also increases each year. Thus *compound interest* is paid not only on the principal but also on the interest that has accumulated. In the example given, the interest payments over the 5 years increase from US\$ 10 to US\$ 15.

In practice, almost all forms of annual increase are calculated on a compound basis. Interest is always paid on the full amount of money in the account, so simple interest would generally only apply if the individual removed the previous year's interest (US\$ 10), leaving the original sum (US\$ 100) in the bank. Human and livestock population growth rates apply each year to the whole of the population existing in the previous year, so the growth rate is again compound. The same is true of the annual inflation rate.

If the present value (PV) and the annual rate of increase (i) are known, the future value (FV) can be calculated from the formula:

$$FV = PV (1 + i)^n$$

Table 38. Simple vs compound interest.

Year	Simple interest			Compound interest		
	Sum at start of year	Interest at 10%	Total at end of year	Sum at start of year	Interest at 10%	Total at end of year
1	100	10	110	100	10	110
2	100	10	120	110	11	121
3	100	10	130	121	12	133
4	100	10	140	133	13	146
5	100	10	150	146	15	161

By manipulating this formula, three further formulae can be derived, enabling the calculation of either the present value (PV), the annual rate of increase (i) or the number of years (n), provided that the three other values are known.

Examples

1) Calculation of future values

The current rate of inflation on housing is estimated at 6% per annum. An individual's house is currently valued at US\$ 30 000. How much could he expect to sell it for in 5 year's time?

The three known values are: $n = 5$
 $i = 0.06$
 $PV = 30\,000$

The formula for calculating future values is:

$$FV = PV(1+i)^n$$

Thus:

$$FV = 30\,000 \times (1.06)^5 = 40\,147$$

The individual could expect to sell his house for just over US\$ 40 000.

2) Calculation of present values

In 1983, a country estimates that in order to provide sufficient beef for its population in 1990 at least 300 000 head of cattle must be slaughtered annually. The number of cattle present in the country in 1983 is unknown, but an annual

growth rate in the national herd of 3.5% and an offtake of 12% are considered to be reasonable values. What would the minimum cattle population in the country need to be in 1983 to be able to satisfy demand in 1990?

With offtake at 12%, 300 000 would have to represent 12% or less of the 1990 cattle population for the demand to be satisfied. Thus:

$$FV = 300\,000 / 0.12 = 2\,500\,000$$

$$n = 1990 - 1983 = 7$$

$$i = 0.035$$

The formula for calculating present values is:

$$PV = \frac{FV}{(1+i)^n}$$

Thus:

$$PV = \frac{2\,500\,000}{(1 + 0.035)^7} = 1\,964\,977$$

To satisfy demand in 1990, the minimum cattle population in the country in 1983 should be 1.965 million.

3) Calculation of growth rate or rate of increase

In a census carried out in 1980, the human population in a region was given as 5 350 071. In 1970, the result was 3 897 136. What is the annual rate of growth of the population?

$$PV = 3\,897\,136$$

$$FV = 5\,350\,071$$

$$n = 1980 - 1970 = 10$$

The formula for calculating growth rate is:

$$i = \sqrt[n]{FV/PV} - 1$$

Thus: $i = \sqrt[10]{5\ 350\ 071/3\ 897\ 136} - 1 = 0.03219$

The annual rate of growth is 3.22%.

4) Calculation of n

If the interest rate is 12%, for how long must money be invested to double its face value?

$$FV/PV = 2$$

$$i = 0.12$$

The formula for calculating n is:

$$n = \frac{\text{Log}(FV/PV)}{\text{log}(1 + i)}$$

Thus: $n = \frac{\text{log}(2)}{\text{log}(1 + 0.12)} = 6.116$

It will take 6.12 years to double the face value of money invested at 12%.

6.3.2 Discounting and compounding tables

Discounting is the process of converting future values to present values. It is used in project appraisal, when considering a stream of future costs and benefits in order to determine what their total present value would be. Items for different years are "discounted" separately by calculating their present value and then the total present value of all items is calculated by adding these together. In order to simplify the process, tables exist giving the conversion factors for a range of i's and n's – usually 2% to 50% and 1 to 50 years – worked out to three decimal places. For the reader's convenience discounting and compounding tables are given in Appendix 1.

Table 39 compares the future values of US\$ 1000 invested in year 0 and earning interest from years 1 to 10, to the present values of the same sum received in each of years 0 to 10.

We can see in the table that US\$ 1000 received in 10 years' time has a present value of only US\$ 386 at a discount rate of 10%. If, however, the sum of US\$ 1000 was in-

Table 39. *Discounting and compounding present and future values.*

Year	Future value of US\$ 1000 at 10%	Present value of US\$ 1000 at 10%
	$FV = PV(1 + i)^n$	$PV = FV/(1 + i)^n$
0	1000	1000
1	1100	909
2	1210	826
3	1331	751
4	1464	683
5	1611	621
6	1772	564
7	1949	513
8	2144	467
9	2358	424
10	2594	386

i = interest rate; r = discount rate.

vested in year 0, it would be worth US\$ 2594 in 10 years' time at 10% interest. The conversion factor is the same:

$$(1 + 0.10)^{10} = 2.5937$$

$$\frac{1}{(1 + 10)^{10}} = 0.3855$$

$$FV = 1000 \times (1.10)^{10} = 2594$$

$$PV = \frac{1000}{(1.10)^{10}} = 386$$

Table 40 shows how discount factors are used to discount the present value of a stream of incomes.

Compounding is the process of converting present values to future values. Compounding tables exist showing the future values of money invested now for different i's and n's.

The different values of i or n can be estimated by looking down the column giving the appropriate ratio for FV/PV in the compounding table or PV/FV in the discounting table. Using Table 3 in Appendix 1 and applying this to Example 3 we find that for $FV/PV = 1.3728$ and $n = 10$, the value in the row for 10 years closest to 1.3728 is 1.344, and this occurs under 3%, so that i can be estimated as being just over 3%.

In Example 4, $FV/PV = 2$ and $i = 12\%$. Looking down the column for 12%, the closest value to 2 is 1.974 in the row for 6 years, so n can be estimated at just over 6.

Compounding tables can be applied to any form of compound growth, not just interest rates.

Table 40. *Discounting a stream of incomes using present value tables.*

Year	Undiscounted values of benefits less costs	10% discount factor	Discounted values of benefits less costs
1	-12 500	.909	-11 362
2	-4 000	.826	-3 304
3	6 500	.751	4 881
4	6 500	.683	4 440
5	6 500	.621	4 036
6	6 500	.564	3 666
7	5 750	.513	2 950
8	5 750	.467	2 685
9	5 750	.424	2 438
10	8 750	.386	3 378
Total	35 500	Present value	13 808

6.3.3 Estimating present and future values using annuity tables

So far, the discussion has been in terms of the present value of US\$ 1 received at a given future date or of the future value at a given date of US\$ 1 invested today. The present value of an annuity table (see Appendix 1, Table 2) gives the present value of US\$ 1 received or spent *annually* at a given rate of discount i and for a given number of years n . Similarly another annuity table (see Table 4, Appendix 1) gives the future value of US\$ 1 invested annually at a rate i for n years.

Such tables are derived by making a year-by-year cumulative total of the compounding or discounting factors, as illustrated in Table 41.

Annuity tables can greatly facilitate the process of discounting if the same figure appears for a number of years in the stream of figures to be discounted. In Table 42 the fig-

ure for years 3 to 6 inclusive is identical at 6500. Since the present value of an annuity is a simple cumulative total of the discount factors, we can take the figure for year 6, which gives the total annuity over 6 years, and subtract from it that for year 2, which gives the total for the 2 years not to be included, to obtain a discount factor of 2.619 for years 3 through 6. The same process is applied for years 7 through 9. This considerably reduces the work that was necessary to arrive at the total present value of the same costs in Table 40.

Annuity tables giving present and future values of an annuity can be found in Appendix One.

Table 41. *Derivation of tables for calculating present and future values of an annuity of 1 at 10%.*

Year	Discount factor	Present value of an annuity	Compounding factor	Future value of an annuity
1	.909	0.909	1.10	1.10
2	.826	1.736	1.21	2.31
3	.751	2.487	1.33	3.64
4	.683	3.170	1.46	5.11
5	.621	3.791	1.61	6.72

6.3.4 Loan repayments

The average amount that must be repaid annually to repay the interest and principal on a loan at an i rate of interest over n years can be calculated using the average capital recovery or amortization factor, which can be derived as follows:

The lender needs to fix *annual* repayments at a rate of interest i over n years at a value such that:

$$PV \text{ (all repayments)} = \text{amount lent.}$$

These repayments are a form of annuity, being an annual and equal amount. From Table 41 we can see that at an interest rate of 10% over 5 years, an annuity of US\$ 1000 would have a present value of US\$ 3791. Thus to repay a loan of US\$ 3791 at 10% in equal annual installments over 5 years, US\$ 1000 would have to be repaid annually. Similarly, to repay a loan of US\$ 1000 at 10%, five equal annual

Table 42. *Discounting a stream of costs using present-value and present-value-of-an-annuity tables.*

Year	Undiscounted values of benefits less costs	10% discount factor	Discounted value of benefits less costs
1	-12 500	.909	-11 362
2	-4 000	.826	-3 304
3	6 500	2.619*	17 023
4	6 500		
5	6 500		
6	6 500		
7	5 750	1.404**	8 073
8	5 750		
9	5 750		
10	8 750	.386	3 378
Total	35 500	Present value	13 808

Present value of an annuity at 10% for:

* Year 6 - Year 2 = 4.355 - 1.736 = 2.619

** Year 9 - Year 6 = 5.759 - 4.355 = 1.404

installments would be necessary. Each installment would be:

$$1000 \times (1/3.791) = \text{US\$ } 263$$

The factor 1/3.791 is the reciprocal of the present value of an annuity table (Appendix 1, Table 2) and is referred to as the capital recovery or amortization factor (Appendix 1, Table 5).

6.3.5 Interest or discount rates and inflation

Market interest rates that are actually paid in the economy include inflation since to make money by investing it, the rate of interest being paid must be higher than the rate of inflation. Often this is not the case. If, for example, the rate of inflation is 15% while the rate of interest is only 12% per annum, the *real rate of interest* is negative (-3%). The real rate of interest is defined as the market rate of interest less the rate of inflation; discount rates should usually reflect the real rate of interest.

7. ESTIMATING THE COSTS OF DISEASES AND THE BENEFITS OF THEIR CONTROL

7.1 INTRODUCTION

This chapter deals with the methods whereby the costs of livestock disease as well as the costs of its control and the benefits arising from it can be assessed. Disease is only one of the many factors influencing the level of productivity in a production system and often cannot be considered in isolation. In order, therefore, to evaluate effectively animal disease control programmes, the economics of the livestock production systems involved must be clearly understood.

7.2 ECONOMIC ASPECTS OF LIVESTOCK PRODUCTION SYSTEMS

7.2.1 Inputs and outputs

Describing the economic aspects of a livestock production system essentially involves the determination of the costs and quantities of the various inputs and outputs of that system. Two distinctions can usefully be made in the analysis of inputs or costs. Firstly, costs can be listed by item and the various factors of production (land, labour, capital) they apply to and, secondly, they can be classified by their degree of variability into variable and fixed costs.

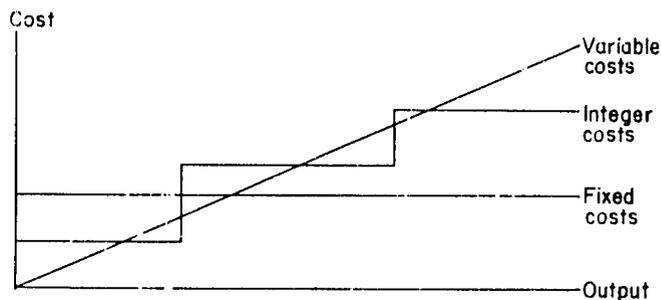
Variable costs vary in the short run and directly with the amount of output produced, declining to zero if the output is zero.

Fixed costs vary only in the long run and are still incurred if output is nil. They are sometimes called overheads and cover such annual cost items as permanent labour, rent and rates, maintenance and running, and depreciation on durable goods which last for more than 1 year.

Sometimes an intermediate category of items is defined. These are *integer costs*, which vary with output in the medium term, such as large capital items.

The relationship of these costs to output is illustrated in Figure 11.

Figure 11. Variable, fixed and integer costs and their relationship to output.



A great deal of literature exists on the use of farm budgets for planning, control, analysis, and decision-making at the producer level. In farm budgets a distinction is made not only between economic and financial analyses,

but also between financial and cash-flow analyses. In *financial analyses*, the actual financial position of the farmer is analysed. *Depreciation*, which reflects the annual reduction in value of durable goods or capital items, must be calculated. Several formulae exist, of which the simplest is:

$$\text{Annual depreciation} = \frac{\text{Replacement cost} - \text{Salvage value}}{\text{Years of productive life}}$$

Here salvage value refers to the residual value of the machine when it is scrapped.

A similar approach can be used in calculating the replacement cost of livestock. The cull value is the salvage value. The replacement cost is the price of a new animal. The formula above gives the so-called "straight-line depreciation" and must be included in fixed costs in a financial budget. A financial budget also includes the value of produce consumed at the farm.

Cash-flow budgets cover cash depreciation receipts and payments. They exclude home consumption, and depreciation but include loan receipts and repayments. If the latter were included in financial budgets as well as depreciation on equipment, for whose purchase loans had to be taken out, there would be an element of double counting.

In Table 43 the main costs of livestock production are classified into variable and fixed cost items corresponding to the various factors of production.

Budgets are distinct from benefit-cost analyses as set out in Chapter 8, in that they are a form of *annual analysis* applicable to the individual farm, firm or institution. As such they are useful for decision-making on a year-to-year basis but not for sector planning and project analysis and will therefore not be discussed in detail here. In contrast, a benefit-cost analysis can be undertaken from an individual or a national point of view and covers a *number of years*.

Distinguishing between the variable and the fixed costs of production is important in the analysis of disease control projects, because changes in production levels due to disease losses or the removal of production constraints affect costs at different levels as well as output. Usually a reduction in mortality and morbidity will affect only the producer's variable costs, since these vary with the levels of output and thus usually with the number of animals. The variable costs most often affected are feed and veterinary costs.

Table 43. A two-way classification of the main costs of livestock production.

Factor of production	Variable cost items	Fixed cost items
Labour	Daily paid or casual labour wages, travel allowances, production-related bonuses	Wages and salaries of permanent staff
Land and buildings	Seed, fertilizer, insecticide	Maintenance of buildings; Rent and rates; Mortgage repayments or loan and interest repayments on borrowings in cash-flow budgets
Capital Livestock	Fodder, concentrates, health care	The net cost of replacing livestock is subtracted from gross output in farm budgets
Machinery	Fuel and oil ¹	Maintenance and running of vehicles and machinery; Depreciation (financial and economic analyses); Interest (sometimes included); Loan repayments (cash flow only)

¹ Theoretically these are variable, but are often included with maintenance in fixed costs in farm budgets, since, unlike other variable costs, it is difficult to allocate them to individual crop or livestock enterprises.

7.2.2 Factors influencing output and offtake

In most herd- or flock-based production systems where farmers rear their own replacement stock the choice between *present* and *future* consumption, between *current income* and *investment*, presents itself clearly. All producers choose to some extent between saving and investing for future consumption or consuming now. The livestock producer can make this choice at two levels:

- Livestock products, such as eggs, meat or milk, can be sold or consumed by the family or, in the case of milk,

given to young animals, thus increasing their nutritional intake and probably having an effect on their survival.

- Animals can be kept or slaughtered. Females are almost always retained, though, in some systems, some are sold for meat before culling becomes necessary. Males can be retained for breeding, sold or kept in the herd as a reserve of cash, or to assist in maintaining a balanced herd.

The choice between keeping or slaughtering animals can be illustrated using the following production parameters (expressed throughout as percentages):

GP – gross productivity per 100 animals	AF – proportion (%) of adult females in herd
O – annual offtake rate	CR – calving rate
G – annual rate of growth	LB – live births (AF x CR x 100) per 100 animals
CM – calf mortality	CS – calf survivals
AM – adult mortality	(LB – CM)

Gross productivity can be expressed as births minus deaths. This gives the increase in numbers which can then be allocated between growth and offtake, i.e.:

$$GP = CS - AM = O + G$$

Without making any distinction between sexes in the surviving calves, this equation gives a rough estimate of the growth potential (from GP) of the herd at different offtake rates. It emphasises the trade-off between offtake now (O) and investment leading to growth (G) and hence offtake later i.e. the choice between present and future consumption. At this level gross productivity is fixed by the basic production parameters of calving rates and mortality. How the increase in numbers is allocated between offtake and growth is decided by the producer. While the equation is useful to make a crude initial estimate of the production potential of a livestock system, for more accurate estimates the reader is referred to Appendix 2, where livestock models are discussed.

7.2.3 The relationship between livestock prices and output

The prices which consumers or producers find acceptable for a particular item are related to the incomes or other

benefits that buyers expect to gain from that item. In theoretical terms it can be stated that, in a free market the price of any input item which lasts for several years will approximate to the present value of the incomes expected from the use of that item over the years of its working life.

For livestock this explains, for example, why a female calf generally has a higher value than a male calf. A heifer's price rises as soon as she is in calf and her fertility is proven. As a cow ages, its value declines. An example of how prices are expected to vary throughout an animal's life is given in Table 44.

Table 44. Derivation of price at different ages for male cattle destined for slaughter in a nomadic production system in Mali (1980 prices, MF 1000 = £ 1 or MF 420 = US\$ 1).

Age (years)	Mortality per year (%)	Survival per year (%)	Probability of survival to age 7 (1) ^a	Present value of selling price at age 7 discounted at 12% (2)	Actual price (1) x (2)
0-1	30	70	0.51	54	28
1-2	10	90	0.73	61	44
2-3	5	95	0.81	68	55
3-4	4	96	0.85	76	65
4-5	4	96	0.88	85	75
5-6	4	96	0.92	96	88
6-7	4	96	0.96	107	103
7-8	4	100	1.00	120	120

^a The probability of a 0 to 1 year-old animal of surviving to year 7 is $0.7 \times 0.9 \times 0.95 \times 0.96 \times 0.96 \times 0.96 \times 0.96 = 0.51$.
The probability of a 1 to 2 year-old animal of surviving to year 7 is $0.9 \times 0.95 \times 0.96 \times 0.96 \times 0.96 \times 0.96 = 0.73$ etc.

In the nomadic production system in Mali the purchased inputs are nil, so the price in each year can be seen as the product of both the expected probability of an animal surviving until it is slaughtered at 7 years and the present value in each year of the slaughter prices. This gives a good approximation to the actual price and helps explain the ob-

served fact (Crotty, 1980) that prices, even per kilogram live weight, are considerably lower for young animals.

7.3 ESTIMATING THE COST OF DISEASE

The quantification of the losses due to individual animal diseases follows on from the disease investigation work undertaken. Once the actual disease prevalence and/or incidence and the nature and magnitude of the losses experienced in infected herds at the regional and national levels have been defined, the economic portion of the analysis proceeds to:

- Organise, classify and present the information on disease losses.
- Quantify losses in monetary terms, choosing prices that reflect the economic or financial nature of the analysis being undertaken.
- Identify and attempt to quantify the indirect losses attributable to a disease.

7.3.1 Quantifying the direct losses due to disease

Direct losses are those production losses directly attributable to the presence of disease. Depending on the information available, and the needs of the study, these losses can be estimated at various levels of detail, matching the complexity of the methods used to the sophistication of the data. Two main approaches exist for quantifying disease losses:

- Given a knowledge of the production parameters of the livestock systems, and the effect of disease on them, a livestock model can be built which looks at the values of output when the disease is present and when it is absent. Such a model would, by its nature, either involve projections over a number of years or the calculation of losses for a static livestock population in equilibrium.

The methods outlined in the following sections produce annual approximations as to the effect of a disease in depressing certain production parameters. Except in so far as price reflects future output, the dynamic effects through reduced fertility and delays in reaching maturity are not really included. A dynamic evaluation, either in the context

of a static herd of fixed size or of a growing livestock population, will give the most accurate estimate of disease losses. For a given disease, the values of all production parameters in the absence and presence of that disease can be entered. The difference in output with and without the disease is then calculated using the model. This type of evaluation relies on a detailed knowledge of the production system and of the effects of the disease. Small differences in the various parameters can then be estimated and valued. The use of models is discussed further in Appendix 2.

- Estimates can be made of the *annual level of losses* associated with the disease. These can then be extrapolated over the period being studied, in line with the expected changes in livestock populations in the affected production systems and with the expected behaviour of the disease.

In calculating disease losses on an annual basis, two methods can be distinguished. Figure 12 gives a diagrammatic representation of these methods and lists the information required.

7.3.2 Methods for estimating annual losses

Method I: Losses estimated as a function of the value of the animal

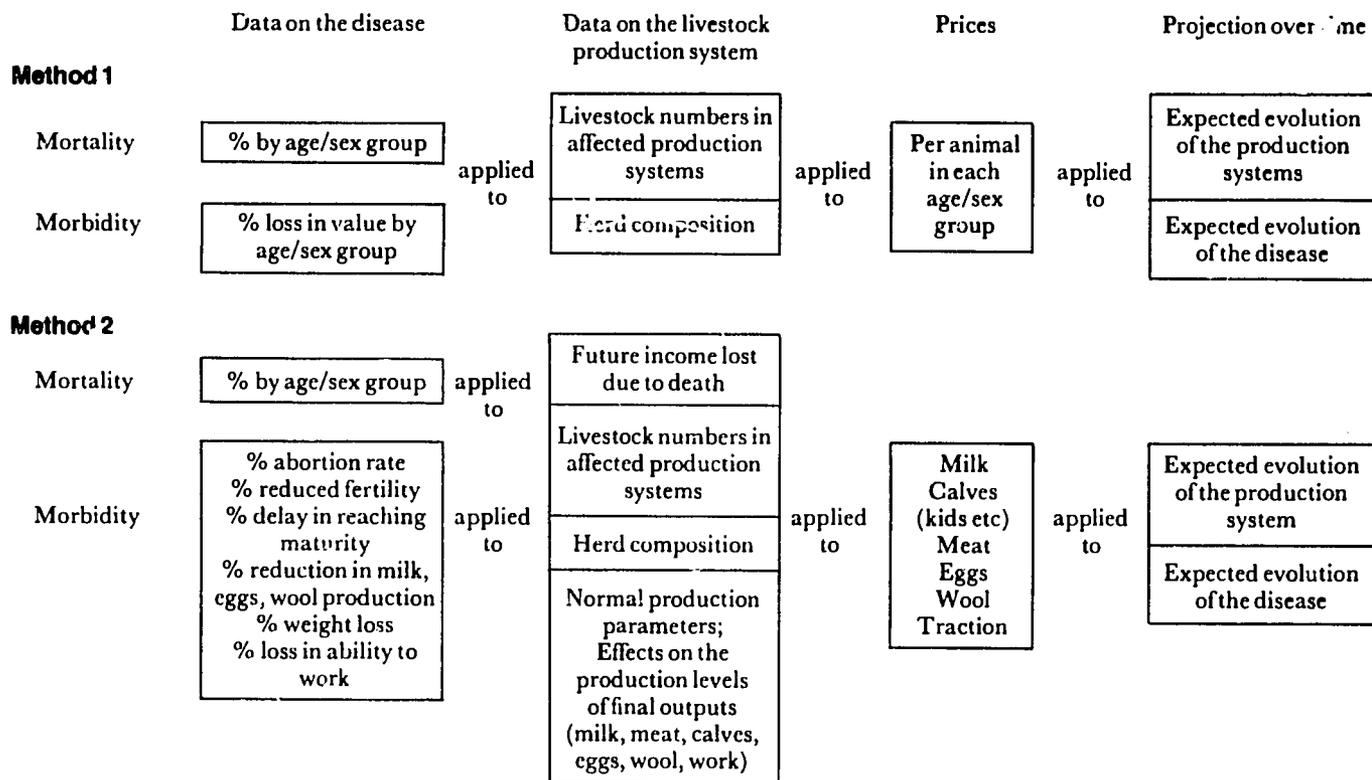
Mortality: Since Method I is based on the concept that price reflects the expected future income from an animal, the cost of mortality can be calculated by applying the price by age/sex category to the number of animals in each category, and to the percentage mortality in each category, if it is known how this varies between different age/sex categories.

The result is a weighted average cost per mortality. In Table 45 this has been calculated for the zebu cattle in Malawi. If the price for each age category is unknown, the age of the average animal or median age group can be applied to the price at that age, as an approximation (see Table 46). Usually some of the meat value of an animal can be salvaged after its death, or through emergency slaughter; this value should be deducted from the cost of mortality.

Morbidity: Similarly, if there are no detailed data on the effects of morbidity, its cost can be estimated as an overall lowering of output, expressed as a percentage of:

- all future output from the affected animal, by using its price; or

Figure 12. Conceptualisation of the process of putting money values on disease losses year by year.



- annual output from the average animal or the herd, in terms of milk, meat etc.

In Table 46 the losses due to trypanosomiasis in Mali have been estimated for two categories of cattle – transhumant and sedentary. The morbidity and mortality losses can be calculated on an annual basis and adjusted for future years to reflect:

- The growth of the animal population affected.
- Any change in the animal population away from or towards more susceptible animals.
- Any change in the disease picture, following from animal health measures, changes in management practices, cycles of disease occurrence etc.

Method II: Losses itemised in terms of the effect of disease on the final output of milk, wool, meat, young animals and draught power

Mortality: This can either be calculated as above, or the present value of expected output less costs is calculated for the age/sex group or for the average animal.

Morbidity: If this is known, the losses due to disease can be calculated via the observed effects of disease, such as:

- infertility
- abortion
- delays in reaching maturity (for reproduction or sale)

- lowered production of milk, eggs, wool etc.
- lowered draught power (which may affect the ability of a healthy animal or a pair of animals to work)
- lowered weight of fattened or culled animals etc.

Table 45. Calculation of the average cost of mortality in zebu cattle in Malawi (1981 prices, K 1.4 = £ 1).

Category	% mortalities	Unit value (K) ¹	Weighted price (K)
Calves	25	25	6.2
Cows/Heifers	55	110	60.5
Bulls	6	160	9.6
Work oxen and feeder steers	14	110	15.4
Total			91.7

Note: This calculation assumes that mortality is evenly distributed between all age/sex categories.

¹ K = Kwacha (Malawian currency).

The majority of the effects are most conveniently calculated in terms of lowered output. In some cases (delays in reaching maturity or slaughter weight) the loss may be more easily evaluated in terms of wasted inputs. A more sophisticated estimate would include the time value of the delay in reaching maturity calculated by discounting to obtain the present value of the costs and receipts involved. Losses in the final output can be evaluated on an annual basis and then adjusted for changes in animal numbers or in the disease picture as outlined above.

In the following example this approach was used to evaluate a sheep scab control project in Lesotho in terms of meat and wool lost. The prices quoted are in maloti (M). The total number of sheep in Lesotho is 1 200 000. The value of wool produced per sheep per year is 2.1 kg at M 1.74/kg = M 3.65. The cost of mortality per sheep is M 40 and the price received for an average animal slaughtered is M 50.

Example: Calculation of total annual losses attributable to sheep scab in Lesotho, using different assumptions.

Assumption A:

Annual incidence = 5.5% = 66 000 sheep
 Mortality in infected flocks = 25% = 16 500 sheep
 Remaining infected animals subject to losses = 75% = 49 500 sheep

Wool loss in infected sheep = 80%
 Weight loss in infected sheep = 10%

Losses due to mortality	Cost
Current annual wool loss (M 3.65/sheep)	16 500 x 3.65 = M 60 225
Value of dead sheep (M 40/sheep)	16 500 x 40 = M 660 000
<i>Losses in remaining infected sheep</i>	
80% loss in annual wool production (M 2.92/sheep)	49 500 x 2.92 = M 144 540
Reduction in value of annual meat offtake due to 10% weight loss in 14% of sheep (M 5 per slaughtered sheep)	49 500 x 0.14 x 5 = M 34 650
Cost of total annual losses	M 899 415

Assumption B:

Annual incidence = 1.4% i.e. 1/4 of level under A
 Other losses as in A
 Cost of total annual losses: 1.4/5.5 x 899 415 = M 224 854

Assumption C:

Annual incidence = 0.1% = 1200 sheep
 Mortality in infected flocks = 0
 Number of infected animals = 1200 sheep
 Wool loss in infected animals = 50%
 Weight loss in 14% of infected animals = 5%

	<i>Cost</i>
50% loss of annual wool production (M 1.82/sheep)	1200 x 1.82 = M 2184
Reduction in value of annual meat: offtake due to 5% weight loss in 14% of the infected sheep (M 2.5 per slaughtered sheep)	1200 x 0.14 = M 420
Cost of total annual losses	M 2604

Two points are worth noting at this stage. First, the choice as to which method is used depends almost entirely on the sophistication of the data available. The first method is used for quick estimates or if little is known about the actual losses. The second method is suitable for more careful calculations when the epidemiology of the disease is better understood or specific investigations have been made.

The second point, namely that it is very easy to overestimate losses from an individual disease and hence the benefits of disease control projects, applies particularly to evaluations based on Method II. Focussing on a particular disease leads to a tendency to see it as perhaps more important than it actually is and to isolate it as the only cause of a particular production loss although a number of other factors, such as other diseases, nutrition and management, are involved. When evaluating losses due to diseases, it is extremely important to keep in mind what the ceiling or limit is on such losses. This ceiling should be identified and, if possible, quantified in general terms. For example, in a given production system overall annual mortality will frequently not exceed 10% of all animals. Some of these deaths will be due to accidents, starvation and the balance to a disease or, more often, to a combination of diseases and nutritional and management factors. Thus a single disease can only be responsible for a limited number of mortalities.

Similarly, within that system, output can only rise to a finite level, which is determined by the limits of the particular species and breed producing under the best possible conditions. The danger when itemising the effects of infertility, abortion, weight loss, lowered milk yield etc is that a slight overestimate of each item may accumulate, or double counting may occur when quantifying linked effects (e.g. abortion and milk loss), so as to attribute to a single disease responsibility for eliminating a vast proportion of an animal's total maximum production.

Table 46. Hypothetical losses associated with untreated cases of bovine trypanosomiasis: Sedentary and transhumant cattle, Mali (1980 prices, MF 1000 = £ 1 or MF 420 = US\$ 1).

a) Calculation of cattle values

	Sedentary herds		Transhumant herds	
	Male	Female	Male	Female
Average age	3-4	3-4	2-3	4-5
Value at average age (MF)	60 000	75 000	55 000	100 000
Ratio males/females (%)	30	70	33	67
Weighted average value (MF)	70 000		85 000	

b) Possible outcomes of infections - high- and low-level possibilities

Effect	% affected	Sedentary herds		% affected	Transhumant herds	
		High level	Low level		High level	Low level
Rapid death within a year*	4	2 800	1 900	10	8 500	5 700
High weight and production loss**	20	7 000	4 900	30	12 800	8 900
Low weight and production loss***	65	6 800	4 500	60	7 600	5 100
Recovery within a year; no loss	11	0	0	0	0	0
Totals	100	16 600	11 300	100	28 900	19 700

Assumptions used for high- and low-level estimates:

- * High level = complete loss
Low level = 1/3 of value salvaged.
- ** High level = 50% loss in value of the animal
Low level = 35% loss in value of the animal.
- *** High level = 15% loss in value of the animal
Low level = 10% loss in value of the animal.

7.3.3 Losses due to disease acting as a constraint on production

As well as causing *direct* losses, diseases can act as constraints on production by partly determining the producer's efforts to avoid as far as possible the risks of disease in his animals. Disease control policy may bring about changes in the location of production or in the production methods used.

If a disease control policy removes a constraint, the benefits resulting from such changes are called *indirect benefits*. The losses thus avoided are called *indirect losses*. Indirect losses are particularly important in cases where the existence of a disease poses an almost absolute constraint on certain types of production or on the use of certain animals in particular areas.

For example in eastern Africa, tick-transmitted diseases, particularly East Coast fever, may prohibit the introduction of improved, exotic breeds of cattle except under extremely efficient tick control programmes. Tsetse-transmitted trypanosomiasis poses a constraint on both agricultural and livestock production at several levels, often by limiting access to, and the full exploitation of, valuable land resources.

Quantifying such effects can be complex, but it is possible. It principally involves the estimation of *changes* in the income of the producer groups involved, which would arise if the disease threat were removed and the producers were able to improve existing systems of production or adopt new ones. These *income changes* can then be related to the effects of the disease control policy.

7.3.4 Other losses due to animal diseases

Zoonoses. While the effects of zoonoses on human production or output in terms of lost income and the costs of treatments can be quantified, the costs of mortality and human suffering are difficult to evaluate. As well as these direct losses, indirect losses may exist where the fear of contracting a disease limits human activity.

Trade effects. Outbreaks of some diseases, particularly foot-and-mouth disease, will have a major effect on the availability of export markets to a country. An estimate of costs

can be made by assuming that after an initial loss of exports, an alternative market offering lower prices can be found.

7.3.5 Secondary effects, externalities and intangible effects

Secondary effects are effects arising upstream (e.g. in the feed industry) or downstream (e.g. in processing and marketing) of the affected production process, as the dependent industries also expand. These effects are seldom evaluated, and should be reflected in the prices of the products directly affected. They can be quantified by calculating the value added at every stage of the production process affected. This "method of effects" is widely used in francophone countries and, from the theoretical point of view, is analogous to calculating and using shadow prices to estimate the opportunity cost.

Externalities occur when the production or consumption activities of one group of individuals affect another without the results being reflected in the market, in costs or in receipts.

For example, pollution of a river by effluent from a firm causes damage which is not paid for by that firm. The shade given by a tree planted and owned by one individual is shared by others free of cost. One farmer's failure to vaccinate his livestock may put at risk the livestock of the whole community.

Externalities are said to be "internalised" when the costs or benefits involved are paid for in some way. For example, the firm could be required by law to install a plant for treating its effluent and rendering it harmless. The owner of the tree could charge people for sitting under it. Failure to vaccinate livestock could be subject to fines imposed by the community.

In a financial analysis, if the externalities are not "internalised", they are not reflected in the costs to individuals, since no one actually pays for them. In an economic analysis some estimate of their effect should be attempted where possible. For example, the cost of pollution of a river can be measured in terms of its effect on fish mortality or on human health. Failure to vaccinate has a quantifiable effect on the direct losses due to the disease.

Intangible effects of disease are effects that exist but are very difficult to quantify. An example is the effect of a disease risk to people and animals on the quality of human life. People's welfare and behaviour may be modified if they no longer need fear certain diseases (e.g. rabies or brucellosis) or losing their whole herd to rinderpest. Some aspects of this could perhaps be quantified, but generally it is acceptable to state that such effects exist and that they should be taken into consideration. This approach may also be the most practical way of dealing with some externalities.

7.4 THE COSTS OF CONTROLLING DISEASE

7.4.1 Introduction

The costs of animal disease control will obviously vary not only with the disease and the type of control policy adopted, but also with the country and region in which the programme is being implemented. The reasons for this are easy to identify: different institutional frameworks, different salaries of those involved, different terrain and different production systems leading to very different transport costs. Nevertheless, it is possible to make some generalisations about the types of cost incurred and the components of these costs.

Non-medicinal prevention

This covers preventive care within the daily routine of an animal production system. The cost is the producer's time spent observing the animals, ensuring that they have a clean environment etc. Non-medicinal prevention can include attempts to contain particular diseases by controlling livestock movements, policing borders and building fences. At a more modest level, they include the costs of protective measures undertaken at markets, the disinfection of vehicles used for transporting livestock and their products etc.

Medicinal measures and the eradication of diseases

The direct actions taken against a particular disease may include:

- Identification of a disease through diagnosis and surveys.
- Treatment of the disease, which usually entails diagnosis, treatment and follow-up. Treatment is a function of the reported incidence of the disease, which in itself often reflects the distribution of veterinary facilities and personnel, and the capacity of the veterinary service to treat a particular problem. Treatments continue to be necessary for as long as the disease remains in the population.
- Prophylaxis or vaccination. This is repeated at specified intervals once the population to be protected has been determined, either as a result of an epidemiological study and/or the producer's decision as to which animals he can afford to protect.
- Vector control, which may be repeated at determined intervals if necessary.
- Use of disease-resistant animals, which may be considered a form of disease control policy requiring experimentation, surveys and follow-up. The costs continue over the whole period during which the animals are used and are calculated in terms of the difference in productivity between resistant animals and the alternative which would have been used.

Eradication normally involves an intensification of one or more of the methods outlined above, which may be combined with a test and slaughter programme. It always involves intensive surveillance and investigative work. The initial costs of eradication are high but should be substantially reduced once the objective has been achieved.

In examining and comparing different disease control policies, two aspects should be emphasised:

- The overall level of costs and their relation to the funds available.
- The *timing* of expenditures over the years. Treatments and prophylaxis typically involve costs over a number of years, while eradication demands a much higher level of expenditure but for a much shorter period. Surveillance and diagnostic work must accompany all policies. In all cases the present values of the costs, i.e. the sum of the discounted costs, need to be compared, not the simple sum of costs.

7.4.2 The components of disease control costs

Tables 47, 48, and 49 give examples of how the costs of disease control work are allocated between different items. The examples vary from eradication through vector control, as in the case of tsetse-transmitted trypanosomiasis in Nigeria, to eradication through identification and elimination of diseased animals, as in the case of brucellosis control

Table 47. Breakdown of costs of sheep scab control by dipping, Lesotho.

Item	% of total costs
Dipping chemicals	38.2
Dip tank construction and repair	5.4
Dipping certificate books	0.2
Vehicle purchase	1.6
Vehicle running	9.0
Purchase and maintenance of mules and saddlery	0.2
Information and publicity	0.3
Subsistence allowances	4.7
Field staff salaries	20.5
Administration and senior staff	17.6
Miscellaneous	2.3

in the U.K., and control of arthropod-related diseases by dipping, as in the case of sheep scab in Lesotho.

The major components of general costs usually are:

- staff costs, including administrative costs,
- labour costs, and
- vehicle depreciation and running costs.

Added to this are costs linked to the specific nature of the project, such as:

- dip tanks and dipping chemicals,
- insecticides,
- vaccines or drug treatments,
- syringes, needles, cool boxes etc, and
- incentive payments or compensation.

In the case of more routine work, especially vaccination, it is often useful to distinguish between:

- The cost of *administering* the treatment or vaccination, sometimes called the *cost of intervention*, which includes all the costs involved in running the veterinary service and of the facilities used for the relevant treatments or vaccinations (Table 50).

- The cost of *specific equipment*, such as drugs, syringes, needles etc, necessary for a particular treatment or vaccination.

Table 48. Breakdown of costs¹ of tsetse eradication by ground spraying, Nigeria (1977/78 prices, N = £ 0.70 = US\$ 1.43).

Year	Land reclaimed (km ²)	Cost/km ² (N)	% of total costs					
			Insecticide	Labour	Junior staff	Senior staff	Vehicle running	Depreciation
1973/4	13 300	48.3	17.2	42.4	15.5	2.8	3.8	18.3
1974/5	8 390	73.2	18.8	41.7	13.8	2.5	3.9	19.3
1975/6	7 622	113.0	16.1	44.7	20.9	2.6	2.1	13.6
1976/7	6 148	159.2	14.0	48.8	18.4	2.9	2.0	13.9
1977/8	1 271	293.8	13.5	25.4	30.0	1.6	6.4	23.1
Average			16.7	43.2	17.2	2.5	3.4	17.0

¹ All costs calculated at constant (1977/8) prices; the increase is not due to inflation.

Table 49. Breakdown of costs of brucellosis control, U.K., 1973.

Item	Cost (£'000)	% of total cost
Headquarters staff	89	0.5
Divisional staff	1 656	9.3
Local vet. inspector's costs	1 848	10.4
Blood tests at the Central Veterinary Laboratory	63	0.4
Divisional blood tests	200	1.1
Milk ring tests	53	0.3
Computer	53	0.3
Mileage	17	0.1
Incentive payments	12 027	67.5
Compensation (reactors and contacts)	1 137	6.4
Vaccine (S 19)	203	1.1
Local vet. inspector's costs (Free calfhood vaccination scheme)	483	2.7
Total	17 829	100.0

7.4.3 The importance of fixed and variable costs in planning disease control policy

As in any costing exercise, in costing disease control measures it is essential to distinguish clearly between variable and fixed costs. Variable costs include the cost of:

- drugs for treatments, vaccinations, insecticides or acaricides;
- syringes, needles and other small equipment; and
- staff travel and subsistence allowances.

Fixed costs or overheads in disease control include:

- vehicle running (this can be regarded as a semi-variable);
- permanent staff salaries;
- office running and administration;
- depreciation on vehicles, equipment and buildings; and
- office rents, rates, water and electricity.

Table 50. Estimate of the costs of veterinary services distributed over the number of vaccinations and treatments administered, Mali (1980 prices, MF 1000 = £ 1 = US\$ 2.38).

Costs	MF '000	%
Total costs		
Recurrent costs		
Salaries	42 727	32.0
Office supplies	2 136	1.6
Fuel, maintenance and oil	17 957	13.5
Borrowed transport	6 000	4.5
Transport of livestock to veterinary offices	6 870	5.1
Subtotal	75 690	56.7
Depreciation on capital assets		
Personal and official vehicles	17 279	12.9
Buildings	15 750	11.8
Office furniture and equipment	1 680	1.3
Subtotal	34 709	26.0
Costs of administration		
Cost of national headquarters	23 100	17.3
Total	133 499	100.0
Unit costs		
Proportion of costs attributable to vaccination campaigns:		
40% of all transport costs	19 242	
30% of other costs	25 618	
Total	44 860	
Remainder of costs attributable to treatments and castrations:	88 615	

The unit cost of administering vaccinations was 30 MF = 44 860 000 divided by the number of vaccinations, 1 486 000.

The unit cost of treatment/castration was 160 MF = 88 615 000 divided by the number of treatments and castrations, 553 000.

The main objective in allocating costs into these categories is to make sure that the elements that contribute to the fixed costs are used to their maximum capacity. Projects frequently waste enormous sums of money because

highly paid staff or expensive equipment are not fully utilised. A good example of this is given in Table 48 for Nigeria. Due to a shortfall in the money available in the recurrent account, a severe reduction in funds for tsetse eradication was experienced. Fixed costs or overheads, mainly junior and senior staff salaries, continued to be paid, since they could not be avoided without dismantling the tsetse control service. Equipment already purchased

continued to depreciate--another overhead. The "savings" were made in the areas of avoidable expenditure, the variable costs of insecticides, labour and, to some extent, vehicle running. This meant that spraying was severely curtailed. Costs at constant prices, i.e. excluding the effects of inflation, rose from about N 50 to about N 300/km² of infested area reclaimed. The share of fixed costs in the total costs increased from 34% to 53%.

8. ECONOMICS AND DECISION-MAKING IN DISEASE CONTROL POLICY

8.1 INTRODUCTION

This chapter deals with the ways of comparing costs and benefits, so as to be able to decide whether a particular project, programme or measure should be undertaken or not. The economic analysis of a project is undertaken *last*, summarising all the available information and putting monetary values on it. Before this is done, the project's feasibility must be established from three points of view.

- *Technical.* The types of expenditure, numbers of staff and timing must all be adequate to ensure that the project fulfils its objectives.

- *Social.* The project must be acceptable to the farmers and livestock owners involved and must respond to the needs they have.

- *Institutional and management aspects.* For the project to function successfully in the institutional setup provided, the organisation and management planned must be viable.

The economic analysis needs to look at the project from the points of view of the nation (*economic appraisal*) and of all the individuals concerned (*financial appraisal*). A project can be profitable from the point of view of the national economy while still offering inadequate incentives to the livestock producers or the civil servants involved.

The techniques for *evaluating* a project *after* its implementation (ex-post analysis) are exactly the same as

those used for its *appraisal* undertaken *before* its implementation (ex-ante analysis). The appraisal looks at the *expected* profitability of the project. The evaluation monitors the *actual* performance and compares it with the expected performance.

8.2 THE PRINCIPLES OF PARTIAL ANALYSIS

When deciding whether to implement any measure, be it a minor change on an individual farm or a major disease control programme, the underlying principle for laying out the costs and benefits is the same: the situation *with* the change is compared to that *without* the change. Itemised under each heading will be:

Costs	Benefits
Extra costs incurred	Costs saved
Revenue foregone	Revenue gained

This approach is called *partial analysis*. It can be applied on an annual basis, using budgets to guide short-term decisions, or it can be applied to long-term projects, using benefit-cost analysis.

In the partial analysis of disease control programmes, the extra costs of introducing a new programme over time are compared to the benefits of a reduction in the direct and indirect losses due to a disease plus the costs saved as a result of the change in the control policy. In Table 51 the approach has been used to analyse different disease control policies.

Table 51. *Partial analysis of the costs and benefits of different disease control policies.*

Project/policy	Costs	Benefits
Do nothing	Unchecked morbidity and mortality.	No downside risk of making matters worse.
Treatment of diagnosed cases	Surveillance, treatment and diagnosis costs.	Reduction in morbidity and mortality.
Control of the disease	Annually recurring cost of a systematic programme depending on the nature of control.	Reduction in morbidity and mortality, plus the costs of the previous programme, if any, that are saved.
Eradication of the disease	Once-and-for-all cost of the programme, which includes survey, diagnosis and followup.	As above, with morbidity and mortality eliminated and costs of a previous programme saved in perpetuity.

When listing costs and benefits over time it is important to realise that the situation “without” the project is not likely to have remained static: otherwise there is a danger that all change taking place will be attributed to the project. Figure 13 illustrates the errors in estimation that can arise as a result.

In each example the vertically shaded area “B” represents the benefits due to the project. If it was erroneously assumed that the situation without the project was static, fixed at the output level of O_a prevailing when the project started, the whole of “A” plus “B” would be taken as the value of benefits, a considerable overestimate represented by the horizontally shaded area “A”.

8.3 THE PRINCIPLES AND CRITERIA OF BENEFIT-COST ANALYSIS

Benefit-cost analysis is based on discounting the benefits and costs attributable to a project over time and then comparing the present value of costs (PVC) with the present

value of benefits (PVB). The present value of benefits is the sum of the discounted values of benefits in each year. Thus:

$$PVB = \sum_{t=1}^{t=n} \frac{B_t}{(1+i)^t}$$

and similarly:

$$PVC = \sum_{t=1}^{t=n} \frac{C_t}{(1+i)^t}$$

where: n = number of years being considered

t = each individual year

i = the discount rate expressed as a decimal fraction

$t = n$

\sum = the sum of all expressions B_t or $C_t/(1+i)^t$,

$t = i$ for every value of t from $t = 1$ to $t = n$.

8.3.1 The role of the discount rate

In benefit-cost studies, the discount rate chosen should theoretically reflect the *real rate of interest* (or of return) on investments. It can be one of the following:

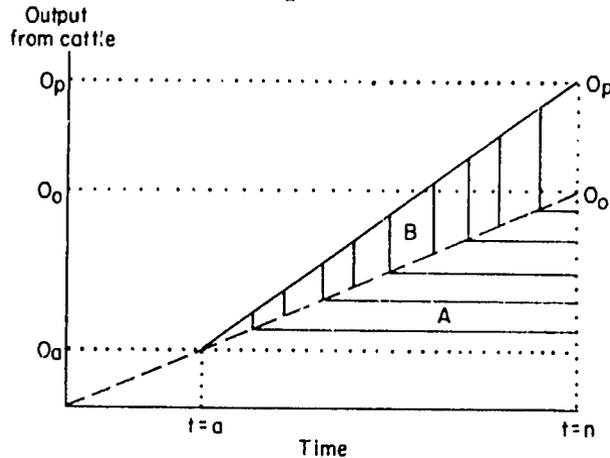
- A rate comparable to the real rate of interest that could be earned if the sum involved was put into a bank or invested in another project; or
- A *social time preference rate* (STP), reflecting the preference society has for present as opposed to future consumption, or the relative value it puts on the consumption of future generations; or
- An *accounting rate of interest* (ARI), which is such rate that all the available investment funds are used up if all the projects earning less than that rate of return are rejected and the remaining projects are implemented.

The discount rate can thus be thought of as a “price” set on the use of money. It is in fact the *opportunity cost of capital*. Discounting should be regarded as a process whereby future values are converted to present values by deducting the minimum acceptable return (or interest) earned in an alternative investment.

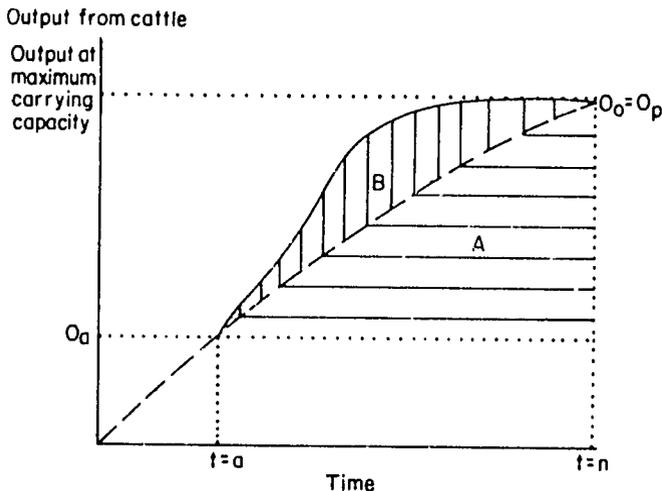
The discount rates usually chosen for projects in developing countries range from 3 to 12%. Generally, the agency responsible for project evaluation or the central

Figure 13. Estimating benefits over time with and without a project and with and without a production ceiling.

A. Without production ceiling



B. With production ceiling



Legend: — Production over time with project
 - - - Production over time without project
 t = a Year project starts
 t = n End of time period considered
 O_a = Output in year a
 O₀ = Output in year n without project
 O_p = Output in year n with project

planning office of the country concerned will fix the rate it considers suitable. Otherwise the evaluator is best advised to use 10% or 12%, or to try out two rates of, say, 8% and 12% to see how much the choice of discount rates affects the overall result.

It should be noted that since the process of discounting makes future receipts and expenditures look progressively smaller relative to present incomes, the choice of a high discount rate will penalise projects with high initial expenditures and a low level of benefits over a long period. Disease eradication projects often fall into this category. This problem should be acknowledged while realising that a reasonably high discount rate does often need to be applied in order to reflect the opportunity cost of capital.

8.3.2 Dealing with Inflation

The objective of a benefit-cost analysis is to assess the profitability or economic feasibility of an investment from today's point of view. As long as relative prices do not change, *inflation is not included* and estimates are made on the basis of today's prices, so all prices may be converted to constant values for a single base year. This further explains why the *real* and not the *market* rate of interest is used as a discount rate, since the prices chosen do not reflect inflation.

For an *ex-ante* appraisal, the current year, generally year 0, is used as a base year. In an *ex-post* evaluation, the prices at the time the project was appraised, which is generally year n, are mostly used. Price indices can then be used to convert all benefits and costs to year n or year 0 values. If a change in relative prices is expected, the price of those items which are getting cheaper or more expensive over time can be decreased or increased as necessary, bearing in mind that the changes in their level should be calculated *relative* to the prices of other goods which are fixed, *not* in simple monetary terms. Thus, if over a year all prices go up 10% and the price of a particular good goes up 15%, then, in constant terms, the price has increased by 5% only. In practice, such calculations are fairly complex and, unless reliable information about an expected price change at a very different rate from that for other items exists, it is simpler and safer to use present-day price levels.

8.3.3 Layout of a benefit-cost analysis

Table 52 shows how a benefit-cost analysis can be set out and gives the notation used for the mathematical formulation of the decision criteria.

In setting out benefits, it is often convenient to divide them under different headings, such as direct losses due to disease saved, indirect losses and costs of previous policy avoided etc. Further subdivision can be made into, say, meat or milk production, losses due to infertility or weight loss etc. The sum of benefits in each year is called *gross benefits*.

Sometimes it is convenient to deduct production costs, which may be the variable costs of production or the cost incurred by the producers themselves, from each source of benefit. Benefits are then described as *net benefits*. Often this is done implicitly, since benefits are calculated in terms of *extra income* due to producers. For example, in a disease control project, a reduction in mortality will mean that more animals are produced and sold for meat and more milk is produced. Thus extra production will involve producers in extra variable costs for feed, veterinary care etc. If these are deducted from output, which is then seen as extra income, the benefit items listed would be net benefits, which would

Table 52. *The layout of a benefit-cost analysis.*

a) Undiscounted values							
Years	Individual benefits BI_t	Sum of benefits B_t	Capital costs CC_t	Operation and maintenance costs OM_t	Production costs PC_t	Sum of Costs C_t	Incremental benefit (Cash flow) $B_t - C_t$
0							
1							
2							
·							
·							
n							
b) Discounted values							
	$\frac{BI_t}{(1+i)^t}$	$\frac{B_t}{(1+i)^t}$	$\frac{CC_t}{(1+i)^t}$	$\frac{OM_t}{(1+i)^t}$	$\frac{PC_t}{(1+i)^t}$	$\frac{C_t}{(1+i)^t}$	$\frac{B_t - C_t}{(1+i)^t}$
0							
1							
2							
·							
·							
n							
Totals	$\sum_{t=1}^n \frac{BI_t}{(1+i)_t}$	$\sum_{t=1}^n \frac{B_t}{(1+i)_t}$	$\sum_{t=1}^n \frac{CC_t}{(1+i)_t}$	$\sum_{t=1}^n \frac{OM_t}{(1+i)_t}$	$\sum_{t=1}^n \frac{PC_t}{(1+i)_t}$	$\sum_{t=1}^n \frac{C_t}{(1+i)_t}$	$\sum_{t=1}^n \frac{B_t - C_t}{(1+i)_t}$

be compared to the rest of costs, called *total costs*. If the extra costs are separately listed as production costs, the comparison would be between gross benefits and *gross costs*.

Rather than discounting all the benefits and costs, usually it is sufficient to discount the gross or the net benefits and the gross or the total costs, or the annual incremental benefit if an internal rate of return is required (see following section). Discounting individual benefit and cost sources is only useful if it is desired to examine the share of the individual sources of benefits in the total benefit. To do this the individual present values:

$$\sum_{t=1}^n \frac{BI_t}{(1+i)^t}$$

must be expressed as a percentage of the present value of the gross (GB) or net benefits (NB):

$$\sum_{t=1}^n \frac{GB_t \text{ (or NB}_t)}{(1+i)^t}$$

8.3.4 The decision-making criteria

After the discounting has been completed, the present value of the benefits (PVB) is compared to the present value of all the costs (PVC). Obviously for a project to be considered profitable at a given discount rate, the present value of benefits should exceed that of costs i.e. $PVB > PVC$, or, if a discount rate is found such that the present value of the benefits is *equal* to the present value of costs, the discount rate should exceed the opportunity cost of capital. In other words, when "interest" is deducted by discounting at a rate high enough for $PVB = PVC$, then that interest or rate of return should be higher than the minimum acceptable return (r) earned in an alternative use of money. Thus if $PVB = PVC$, then $i > r$, where i is discount rate used to calculate PVC and PVB, and r is the minimum acceptable discount rate.

From this, three decision-making criteria emerge:

- The *net present value* (NPV). This is sometimes called "net present worth", and it is obtained by subtracting the present value of costs from that of benefits i.e. $NPV = PVB - PVC$, mathematically:

$$NPV = \sum_{t=1}^n \frac{B_t - C_t}{(1+i)^t}$$

where: t = individual years,

n = number of years over which the project is evaluated,

B = the sum of benefits in a given year,

C = the sum of costs in a given year, and

i = the discount rate expressed as a decimal.

For a project to be acceptable, $PVB > PVC$ i.e. the net present value should be *positive*.

The net present value gives a good idea of the total profit, in present value terms, of the project. Difficulties arise when net present values are used to rank projects, since a large project with a relatively low net present value would look as profitable as a far smaller project with a relatively high net present value in comparison to its overall level of costs and benefits.

- The *benefit-cost ratio* (B/C), which is obtained by dividing the present value of benefits by the present value of costs i.e. $B/C = PVB/PVC$ or, mathematically:

$$B/C = \frac{\sum_{t=1}^n \frac{B_t}{(1+i)^t}}{\sum_{t=1}^n \frac{C_t}{(1+i)^t}}$$

For a project to be acceptable, the benefit-cost ratio should be greater than 1.

The benefit-cost ratio is a very useful criterion for ranking projects of different sizes, and it is relatively easy to calculate. However, the ratio will be different when net benefits are compared to total costs from that obtained when gross benefits are compared to gross costs.

- The *internal rate of return* (IRR), which is that discount rate i for which $PVB = PVC$. In mathematical terms, the IRR is that i for which:

$$\sum_{t=1}^n \frac{B_t - C_t}{(1+i)^t} = 0$$

If $i > r$, i.e. IRR exceeds the minimum acceptable rate or the opportunity cost of money, the project is acceptable.

The internal rate of return is a useful criterion for comparing projects, especially since it can be expressed as an annual percentage rate of return. An internal rate of return cannot be calculated if:

- the annual incremental benefit or cash flow, $B_t - C_t$, is always ≥ 0 for every year, since in that case it would be impossible for the sum

$$\sum_{t=1}^n \frac{B_t - C_t}{(1+i)^t} \text{ to equal zero.}$$

- the annual cash flow, $B_t - C_t$, changes from negative to positive more than once over the years. In this case an IRR may exist for every change of sign.

An IRR can only be calculated for those cases where costs exceed benefits in the first years of the project. These cases are by far the most common.

Tables 53 and 54 give examples of how these three criteria can be obtained. The internal rate of return can

only be calculated by trying out different discount rates until an NPV closer to 0 than that for the discount rates immediately above and below it is obtained. The method is illustrated in Table 53 and described below:

- Check that the *undiscounted* sum of the benefits exceeds that of the costs. If not, the project will not be profitable at any discount rate. From Table 53, the sum of benefits is 58 000 and the sum of costs is 46 250.
- Check that costs exceed benefits for some years. In Table 53, costs exceed benefits in years 1,2 and 3.
- Check that the annual cash flow ($B_t - C_t$) changes from negative to positive only once. In Table 53, it changes from negative to positive after year 3 and never thereafter.
- Calculate the NPV at the usual discount rate. Check if this is positive or negative. In Table 53, NPV is -3264 at 12%.
- If the NPV is positive, try a higher discount rate. If the NPV is negative, try a lower one. Continue until you ar-

Table 53. Derivation of the benefit-cost ratio, the net present value and the internal rate of return using a 12% discount rate.

Year	Capital	Operations and maintenance	Production costs	Sum of costs	Discount factor	PVC	Sum of benefits	Discount factor	PVB	PVB-PVC
1	10 000	-	-	10 000	.893	8 929	-	.893	-	-8 929
2	5 000	-	-	5 000	.797	3 986	-	.797	-	-3 986
3	5 000	750	600	6 350	.712	4 520	2 000	.712	1 424	-3 096
4	-	1 500	1 200	2 700	.636	1 716	4 000	.636	2 542	826
5	-	1 500	1 200	2 700	.567	1 532	5 500	.567	3 121	1 589
6	3 000	1 500	1 200	5 700	.507	2 888	8 000	.507	4 053	1 165
7	-	1 500	1 200	2 700	.452	1 221	8 000	.452	3 619	2 397
8	-	1 500	1 200	2 700	.404	1 090	8 000	.404	3 231	2 141
9	3 000	1 500	1 200	5 700	.361	2 055	8 000	.361	2 885	829
10	-	1 500	1 200	2 700	.322	869	14 500	.322	4 669	3 799
Total	26 000	11 250	9 000	46 250		28 807	58 000		25 543	-3 264

At 12% discount rate: Net present value = 25 543 - 28 807 = -3264
Benefit-cost ratio = 25 583 / 28 807 = 0.89

At 10% discount rate: NPV = -1850

At 8% discount rate: NPV = -116

At 6% discount rate: NPV = 2008

Internal rate of return = 7.891%.

Table 54. Present value of costs and benefits of sheep scab control in Lesotho in 1974/5 (prices in 1981/2 maloti).

a) Discounted at 10%

Year	Costs (M)	Benefits (M)
1975/76	307 796	0
1976/77	700 427	0
1977/78	391 809	552 650
1978/79	463 818	1 675 243
1979/80	297 348	
1980/81	329 525	
1981/82	242 982	
1981/82	242 982	
Total	2 733 705	2 818 203

Benefit-cost ratio = 1.03

Net present value = M 84 498

b) Discounted at 12%

Year	Costs (M)	Benefits (M)
1975/76	302 378	0
1976/77	675 836	0
1977/78	371 462	523 950
1978/79	431 901	1 532 650
1979/80	271 492	
1980/81	296 222	
1981/82	214 089	
1981/82	214 089	
Total	2 563 380	2 576 717

Benefit cost ratio = 1.01

Net present value = M 13 337

Note: To calculate internal rate of return we need to find an NPV closer to 0 than the above values:

NPV at 12.5% = -M 3062

NPV at 12.3% = +M 4829

Using the formula given above:

$$\text{IRR} = 12.3 + \frac{(12.5 - 12.3) \times 4829}{4829 + 3062} = 12.42$$

Thus the internal rate of return for the sheep scab control programme in Lesotho was 12.42%.

rive at an NPV of the opposite sign to the previous one. In Table 53, at a discount rate of 10%, the NPV is -1850. At a discount rate of 6%, the NPV is 2008.

- Calculate IRR using the following formula:

$$\text{IRR} = \text{Lower DR} + \frac{(\text{Difference between the DRs}) \times (\text{NPV at the lower DR})}{(\text{The sum of the absolute values of the two NPVs})}$$

From Table 53:

- Lower DR = 6%; NPV = 2008
The absolute value of 2008 is 2008.
- Higher DR = 10%; NPV = -1850
The absolute value of -1850 is 1850.

Thus:

$$\text{IRR} = 6 + \frac{(10 - 6) \times 2008}{2008 + 1850} = 8.08$$

The actual IRR is 7.891%. The closer the two discount rates used are, the more accurate is the result obtained.

8.3.5 Dealing with risk and uncertainty

Risk and uncertainty can be dealt with by applying the probability of a particular outcome, or by doing a *sensitivity analysis* to see how different values or outcomes affect the overall results. Contingency allowances can also be used, especially for estimating costs.

A sensitivity analysis is usually undertaken if there is a great deal of uncertainty as to the values of particular parameters, but no probability can be attached to their attaining certain values. The analysis uses different values for the relevant item in the calculations to illustrate how sensitive the results are to the assumptions made about the value of a particular parameter.

The items for which different values are most commonly tried are:

- *Discount rates.* Several discount rates may be tried, if an internal rate of return is not being calculated. This is especially important for projects (e.g. disease eradication projects) which have high initial capital costs and benefits extending far into the future. Such projects can be said to be disadvantaged by the use of high discount rates, since the high initial costs are then given a relatively higher value in comparison to the future benefits.

- *Prices.* Several prices, which may be shadow prices or various market prices, may be tried out. A full recalculation of the project with the new price is not necessary; one can simply determine the percentage of costs or benefits which are accounted for by that item each year. The percentage is the same for both the discounted and undiscounted costs and benefits in a particular year. The overall total for costs or benefits cannot be used, unless the percentage accounted for by that item is *constant* from year to year. Having determined the percentage of the total (say X%) accounted for by that item, and if the percentage change in price is Y%, then the total cost (TC) for that year is multiplied by:

$$1 + (X/100 \times Y/100)$$

where Y can obviously be positive or negative, since it can represent an increase or a decrease.

- *Estimates of benefits.* Since the extent of the benefits realised by a project are often open to doubt, it is useful to make high- and low-level estimates of benefits (optimistic versus pessimistic projections). These give an upper and lower limit within which the real performance of the project is expected to fall. Some indication of this nature is necessary in almost all cost-benefit studies.

Alternatively, a break-even analysis can be done to determine what level benefits must reach to cover costs. The analysis uses the present value of costs to estimate the present value of benefits needed to cover the costs.

If either the level of benefits is totally unknown or else the same level of benefits can be attained by several differ-

ent methods, the *cost effectiveness* of the different methods can be analysed by comparing the present values of costs.

- *Estimates of costs.* Uncertainty in estimating costs can be dealt with by trying different assumptions or sets of prices, or by making contingency allowances.

Once the present values of benefits and costs have been determined, the effects of increasing or decreasing these by certain percentages can be examined. Thus at its simplest, sensitivity analysis may consist of, say, looking at the effect of a 10% cost overrun or a 20% shortfall in expected benefits.

8.3.6 The scope of a benefit-cost analysis

The number of years covered by a cost-benefit analysis depends on:

- The requirements of the project, its duration and how long it will take before investments and subsidies stop and the project shows a return.

- The feasibility of estimating costs and benefits with any accuracy beyond a certain number of years.

- The fact that by using a discount rate the value of future income is reduced to very small amounts after a number of years. At a 10% discount rate after 12 years, an item is worth less than a third of its face value; after 25 years less than a tenth; and after 50 years less than a hundredth (see Appendix 1, Table 1).

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APPENDIX ONE: TABLES

Table 1. *Discount factors.*

The present value of 1 received or spent in a given future year 'n' at a given discount 'i'.
Discount factor: $1/(1 + i)^n$

Yrs	%	2	4	5	6	8	9	10	12	14	15	16	18	20	25	30	35	40	45	50
1	.980	.962	.952	.943	.926	.917	.909	.893	.877	.870	.862	.847	.833	.800	.769	.741	.714	.690	.667	
2	.961	.925	.907	.890	.857	.842	.826	.797	.769	.756	.743	.718	.694	.640	.592	.549	.510	.476	.444	
3	.942	.889	.864	.840	.794	.772	.751	.712	.675	.658	.641	.609	.579	.512	.455	.406	.364	.328	.296	
4	.924	.855	.823	.792	.735	.708	.683	.636	.592	.572	.552	.516	.482	.410	.350	.301	.260	.226	.198	
5	.906	.822	.784	.747	.681	.650	.621	.567	.519	.497	.476	.437	.402	.328	.269	.223	.186	.156	.132	
6	.889	.790	.746	.705	.630	.596	.564	.507	.456	.432	.410	.370	.335	.262	.207	.165	.133	.108	.088	
7	.871	.760	.711	.665	.583	.547	.513	.452	.400	.376	.354	.314	.279	.210	.159	.122	.095	.074	.059	
8	.853	.731	.677	.627	.540	.502	.467	.404	.351	.327	.305	.266	.233	.168	.123	.091	.068	.051	.039	
9	.837	.703	.645	.592	.500	.460	.424	.361	.308	.284	.263	.225	.194	.134	.094	.067	.048	.035	.026	
10	.820	.676	.614	.558	.463	.422	.386	.322	.270	.247	.227	.191	.162	.107	.073	.050	.035	.024	.017	
11	.804	.650	.585	.527	.429	.388	.350	.287	.237	.215	.195	.162	.135	.086	.056	.037	.025	.017	.012	
12	.788	.625	.557	.497	.397	.356	.319	.257	.208	.187	.168	.137	.112	.069	.043	.027	.018	.012	.008	
13	.773	.601	.530	.469	.368	.326	.290	.229	.182	.163	.145	.116	.093	.055	.033	.020	.013	.008	.005	
14	.758	.577	.505	.442	.340	.299	.263	.205	.160	.141	.125	.099	.078	.044	.025	.015	.009	.006	.003	
15	.743	.555	.481	.417	.315	.275	.239	.183	.140	.123	.108	.084	.065	.035	.020	.011	.006	.004	.002	
16	.728	.534	.458	.394	.292	.252	.218	.163	.123	.107	.093	.071	.054	.028	.015	.008	.005	.003	.002	
17	.714	.513	.436	.371	.270	.231	.198	.146	.108	.093	.080	.060	.045	.023	.012	.006	.003	.002	.001	
18	.700	.494	.416	.350	.250	.212	.180	.130	.095	.081	.069	.051	.038	.018	.009	.005	.002	.001	.001	
19	.686	.475	.396	.331	.232	.194	.164	.116	.083	.070	.060	.043	.031	.014	.007	.003	.002	.001	.000	
20	.673	.456	.377	.312	.215	.178	.149	.104	.073	.061	.051	.037	.026	.012	.005	.002	.001	.001	.000	
21	.660	.439	.359	.294	.199	.164	.135	.093	.064	.053	.044	.031	.022	.009	.004	.002	.001	.000	.000	
22	.647	.422	.342	.278	.184	.150	.123	.083	.056	.046	.038	.026	.018	.007	.003	.001	.001	.000	.000	
23	.634	.406	.326	.262	.170	.138	.112	.074	.049	.040	.033	.022	.015	.006	.002	.001	.000	.000	.000	
24	.622	.390	.310	.247	.158	.126	.102	.066	.043	.035	.028	.019	.013	.005	.002	.001	.000	.000	.000	
25	.610	.375	.295	.233	.146	.116	.092	.059	.038	.030	.024	.016	.010	.004	.001	.001	.000	.000	.000	
30	.552	.308	.231	.174	.099	.075	.057	.033	.020	.015	.012	.007	.004	.001	.000	.000	.000	.000	.000	
35	.500	.253	.181	.130	.068	.049	.036	.019	.010	.008	.006	.003	.002	.000	.000	.000	.000	.000	.000	
40	.453	.208	.142	.097	.046	.032	.022	.011	.005	.004	.003	.001	.001	.000	.000	.000	.000	.000	.000	
45	.410	.171	.111	.073	.031	.021	.014	.006	.003	.002	.001	.001	.000	.000	.000	.000	.000	.000	.000	
50	.372	.141	.087	.054	.021	.013	.009	.003	.001	.001	.001	.000	.000	.000	.000	.000	.000	.000	.000	

Table 2. Present value of an annuity.

The present value of 1 received or spent annually at a given rate of interest 'i' for a given number of years 'n'.
Present value of an annuity factor: $\Sigma 1/(1 + i)^n$

Yrs	2	4	5	6	8	9	10	12	14	15	16	18	20	25	30	35	40	50
1	.9804	.9615	.9524	.9434	.9259	.9174	.9091	.8929	.8772	.8696	.8621	.8475	.8333	.8000	.7692	.7407	.7143	.6667
2	1.942	1.886	1.859	1.833	1.783	1.759	1.736	1.690	1.647	1.626	1.605	1.566	1.528	1.440	1.361	1.289	1.224	1.111
3	2.884	2.775	2.723	2.673	2.577	2.531	2.487	2.402	2.322	2.283	2.246	2.174	2.106	1.952	1.816	1.696	1.589	1.407
4	3.808	3.630	3.546	3.465	3.312	3.240	3.170	3.037	2.914	2.855	2.798	2.690	2.589	2.362	2.166	1.997	1.849	1.605
5	4.713	4.452	4.329	4.212	3.993	3.890	3.791	3.605	3.433	3.352	3.274	3.127	2.991	2.689	2.436	2.220	2.035	1.737
6	5.601	5.242	5.076	4.917	4.623	4.486	4.355	4.111	3.889	3.784	3.685	3.498	3.326	2.951	2.643	2.385	2.168	1.824
7	6.472	6.002	5.786	5.582	5.206	5.033	4.868	4.564	4.288	4.160	4.039	3.812	3.605	3.161	2.802	2.568	2.263	1.883
8	7.325	6.733	6.463	6.210	5.747	5.535	5.335	4.968	4.639	4.487	4.344	4.078	3.837	3.329	2.925	2.598	2.331	1.922
9	8.162	7.435	7.108	6.802	6.247	5.995	5.759	5.328	4.946	4.772	4.607	4.303	4.031	3.463	3.019	2.665	2.379	1.948
10	8.983	8.111	7.722	7.360	6.710	6.418	6.145	5.650	5.216	5.019	4.833	4.494	4.192	3.571	3.092	2.715	2.414	1.965
11	9.787	8.760	8.306	7.887	7.139	6.805	6.495	5.938	5.453	5.234	5.029	4.656	4.327	3.656	3.147	2.752	2.438	1.977
12	10.58	9.385	8.863	8.384	7.536	7.161	6.814	6.194	5.660	5.421	5.197	4.793	4.439	3.725	3.190	2.779	2.456	1.985
13	11.35	9.986	9.394	8.853	7.904	7.487	7.103	6.424	5.842	5.583	5.342	4.910	4.533	3.780	3.223	2.799	2.469	1.990
14	12.11	10.56	9.899	9.295	8.244	7.786	7.367	6.628	6.002	5.724	5.468	5.008	4.611	3.824	3.249	2.814	2.478	1.993
15	12.85	11.12	10.38	9.712	8.559	8.061	7.606	6.811	6.142	5.847	5.575	5.092	4.675	3.859	3.268	2.825	2.484	1.995
16	13.58	11.65	10.84	10.11	8.851	8.313	7.824	6.974	6.265	5.954	5.668	5.162	4.730	3.887	3.283	2.834	2.489	1.997
17	14.29	12.17	11.27	10.48	9.122	8.544	8.022	7.120	6.373	6.047	5.749	5.222	4.775	3.910	3.235	2.840	2.492	1.998
18	14.99	12.66	11.69	10.83	9.372	8.756	8.201	7.250	6.467	6.128	5.818	5.273	4.812	3.928	3.304	2.844	2.494	1.999
19	15.68	13.13	12.09	11.16	9.604	8.950	8.365	7.366	6.550	6.198	5.877	5.316	4.843	3.942	3.311	2.848	2.496	1.999
20	16.35	13.59	12.46	11.47	9.818	9.129	8.514	7.469	6.623	6.259	5.929	5.353	4.870	3.954	3.316	2.850	2.497	1.999
21	17.01	14.03	12.82	11.76	10.02	9.292	8.649	7.562	6.687	6.312	5.973	5.384	4.891	3.963	3.320	2.852	2.498	2.000
22	17.66	14.45	13.16	12.04	10.20	9.442	8.772	7.645	6.743	6.359	6.011	5.410	4.909	3.970	3.323	2.853	2.498	2.000
23	18.29	14.86	13.49	12.30	10.37	9.580	8.883	7.718	6.792	6.399	6.044	5.432	4.925	3.976	3.325	2.854	2.499	2.000
24	18.91	15.25	13.80	12.55	10.53	9.707	8.985	7.784	6.835	6.434	6.073	5.451	4.937	3.981	3.327	2.855	2.499	2.000
25	19.52	15.62	14.09	12.78	10.67	9.823	9.077	7.843	6.873	6.464	6.097	5.467	4.948	3.985	3.329	2.856	2.499	2.000
30	22.40	17.29	15.37	13.76	11.26	10.27	9.427	8.055	7.003	6.566	6.177	5.517	4.979	3.995	3.332	2.857	2.500	2.000
35	25.00	18.66	16.37	14.50	11.65	10.57	9.644	8.176	7.070	6.617	6.215	5.539	4.992	3.998	3.333	2.857	2.500	2.000
40	27.36	19.79	17.16	15.05	11.92	10.76	9.779	8.244	7.105	6.642	6.233	5.548	4.997	3.999	3.333	2.857	2.500	2.000
45	29.49	20.72	17.77	15.46	12.11	10.88	9.863	8.283	7.123	6.654	6.242	5.552	4.999	4.000	3.333	2.857	2.500	2.000
50	31.42	21.48	18.26	15.76	12.23	10.96	9.915	8.304	7.133	6.661	6.246	5.554	4.999	4.000	3.333	2.857	2.500	2.000

Table 3. *Compound interest factors.*

The future value of 1 invested at a given rate of interest 'i' for a given number of years 'n'.
Compounding factor: $1 \times (1 + i)^n$

Yrs	%	2	4	5	6	8	9	10	12	14	15	16	18	20	25	30	35	40	45	50
1		1.020	1.040	1.050	1.060	1.080	1.090	1.100	1.120	1.140	1.150	1.160	1.180	1.200	1.250	1.300	1.350	1.400	1.450	1.500
2		1.040	1.082	1.103	1.124	1.166	1.188	1.210	1.254	1.300	1.323	1.346	1.392	1.440	1.563	1.690	1.823	1.960	2.103	2.250
3		1.061	1.125	1.158	1.191	1.260	1.295	1.331	1.405	1.482	1.521	1.561	1.643	1.728	1.953	2.197	2.460	2.744	3.049	3.375
4		1.082	1.170	1.216	1.262	1.360	1.412	1.464	1.574	1.689	1.749	1.811	1.939	2.074	2.441	2.856	3.322	3.842	4.421	5.063
5		1.104	1.217	1.276	1.338	1.469	1.539	1.611	1.762	1.925	2.011	2.100	2.288	2.488	3.052	3.713	4.485	5.378	6.410	7.594
6		1.126	1.265	1.340	1.419	1.587	1.677	1.772	1.974	2.195	2.313	2.436	2.700	2.986	3.815	4.827	6.053	7.530	9.294	11.39
7		1.149	1.316	1.407	1.504	1.714	1.828	1.949	2.211	2.502	2.660	2.826	3.185	3.583	4.768	6.275	8.172	10.54	13.48	17.09
8		1.172	1.369	1.477	1.594	1.851	1.993	2.144	2.476	2.853	3.059	3.278	3.759	4.300	5.960	8.157	11.03	14.76	19.54	25.63
9		1.195	1.423	1.551	1.689	1.999	2.172	2.358	2.773	3.252	3.518	3.803	4.435	5.160	7.451	10.60	14.89	20.66	28.33	38.44
10		1.219	1.480	1.629	1.791	2.159	2.367	2.594	3.106	3.707	4.046	4.411	5.234	6.192	9.313	13.79	20.11	28.93	41.08	57.67
11		1.243	1.539	1.710	1.898	2.332	2.580	2.853	3.479	4.226	4.652	5.117	6.176	7.430	11.64	17.92	27.14	40.50	59.57	86.50
12		1.268	1.601	1.796	2.012	2.518	2.813	3.138	3.896	4.818	5.350	5.936	7.288	8.916	14.55	23.30	36.64	56.69	86.38	129.7
13		1.294	1.665	1.886	2.133	2.720	3.066	3.452	4.363	5.492	6.153	6.886	8.599	10.70	18.19	30.29	49.47	79.37	125.3	194.6
14		1.319	1.732	1.980	2.261	2.937	3.342	3.797	4.887	6.261	7.076	7.988	10.15	12.84	22.74	39.37	66.78	111.1	181.6	291.9
15		1.346	1.801	2.079	2.397	3.172	3.642	4.177	5.474	7.138	8.137	9.266	11.97	15.41	28.42	51.19	90.16	155.6	263.3	437.9
16		1.373	1.873	2.183	2.540	3.426	3.970	4.595	6.130	8.137	9.358	10.75	14.13	18.49	35.53	66.54	121.7	217.8	381.8	656.8
17		1.400	1.948	2.292	2.693	3.700	4.328	5.054	6.866	9.276	10.76	12.47	16.67	22.19	44.41	86.50	164.3	304.9	553.7	985.3
18		1.428	2.026	2.407	2.854	3.996	4.717	5.560	7.690	10.58	12.38	14.46	19.67	26.62	55.51	112.5	221.8	426.9	802.8	1478.
19		1.457	2.107	2.527	3.026	4.316	5.142	6.116	8.613	12.06	14.23	16.78	23.21	31.95	69.39	146.2	299.5	597.6	1164.	2217.
20		1.486	2.191	2.653	3.207	4.661	5.604	6.727	9.646	13.74	16.37	19.46	27.39	38.34	86.74	190.0	404.3	836.7	1688.	3325.
21		1.516	2.279	2.786	3.400	5.034	6.109	7.400	10.80	15.67	18.82	22.57	32.32	46.01	108.4	247.1	545.8	1171.	2448.	4988.
22		1.546	2.370	2.925	3.604	5.437	6.659	8.140	12.10	17.86	21.64	26.19	38.14	55.21	135.5	321.2	736.8	1640.	3549.	7482.
23		1.577	2.465	3.072	3.820	5.871	7.258	8.954	13.55	20.36	24.89	30.38	45.01	66.25	169.4	417.5	994.7	2296.	5146.	11223
24		1.608	2.563	3.225	4.049	6.341	7.911	9.850	15.18	23.21	28.63	35.24	53.11	79.50	211.8	542.8	1343.	3214.	7462.	16834
25		1.641	2.666	3.386	4.292	6.848	8.623	10.83	17.00	26.46	32.92	40.87	62.67	95.40	264.7	705.6	1813.	4500.	10819	25251
30		1.811	3.243	4.322	5.743	10.06	13.27	17.45	29.96	50.95	66.21	85.85	143.4	237.4	807.8	2620.	8129.	24210	69349	>100t
35		2.000	3.946	5.516	7.686	14.79	20.41	28.10	52.80	98.10	133.2	180.3	328.0	590.7	2465.	9728.	36449	>100t	>100t	>100t
40		2.208	4.801	7.040	10.29	21.72	31.41	45.26	93.05	188.9	267.9	378.7	750.4	1470.	7523.	36119	>100t	>100t	>100t	>100t
45		2.438	5.841	8.985	13.76	31.92	48.33	72.89	164.0	363.7	538.8	795.4	1717.	3657.	22959	>100t	>100t	>100t	>100t	>100t
50		2.692	7.107	11.47	18.42	46.90	74.36	117.4	289.0	700.2	1084.	1671.	3927.	9100.	70065	>100t	>100t	>100t	>100t	>100t

>100t indicates that the number exceeds 100 000.

Table 4. *Future value of annuity.*

The future value of 1 invested annually at a given rate of interest 'i' for a given number of years 'n'.
 Future value of an annuity factor: $\Sigma(1 + i)^n$

Yrs	%	2	4	5	6	8	9	10	12	14	15	16	18	20	25	30	35	40	50
1	1.02	1.04	1.05	1.06	1.08	1.09	1.1	1.12	1.14	1.15	1.16	1.18	1.2	1.25	1.3	1.35	1.4	1.5	
2	2.060	2.122	2.153	2.184	2.246	2.278	2.310	2.374	2.440	2.473	2.506	2.572	2.640	2.813	2.990	3.173	3.360	3.750	
3	3.122	3.246	3.310	3.375	3.506	3.573	3.641	3.779	3.921	3.993	4.066	4.215	4.368	4.766	5.187	5.633	6.104	7.125	
4	4.204	4.416	4.526	4.637	4.867	4.985	5.105	5.353	5.610	5.742	5.877	6.154	6.442	7.207	8.043	8.954	9.946	12.19	
5	5.308	5.633	5.802	5.975	6.336	6.523	6.716	7.115	7.536	7.754	7.977	8.442	8.930	10.26	11.76	13.44	15.32	19.78	
6	6.434	6.898	7.142	7.394	7.923	8.200	8.487	9.089	9.730	10.07	10.41	11.14	11.92	14.07	16.58	19.49	22.85	31.17	
7	7.583	8.214	8.549	8.897	9.637	10.03	10.44	11.30	12.23	12.73	13.24	14.33	15.50	18.84	22.86	27.66	33.39	48.26	
8	8.755	9.583	10.03	10.49	11.49	12.02	12.58	13.78	15.09	15.79	16.52	18.09	19.80	24.80	31.01	38.70	48.15	73.89	
9	9.950	11.01	11.58	12.18	13.49	14.19	14.94	16.55	18.34	19.30	20.32	22.52	24.96	32.25	41.62	53.59	68.81	112.3	
10	11.17	12.49	13.21	13.97	15.65	16.56	17.53	19.65	22.04	23.35	24.73	27.76	31.15	41.57	55.41	73.70	97.74	170.0	
11	12.41	14.03	14.92	15.87	17.98	19.14	20.38	23.13	26.27	28.00	29.85	33.93	38.58	53.21	73.33	100.8	138.2	256.5	
12	13.68	15.63	16.71	17.88	20.50	21.95	23.52	27.03	31.09	33.35	35.79	41.22	47.50	67.76	96.63	137.5	194.9	386.2	
13	14.97	17.29	18.60	20.02	23.21	25.02	26.97	31.39	36.58	39.50	42.67	49.82	58.20	85.95	126.9	187.0	274.3	580.9	
14	16.29	19.02	20.58	22.28	26.15	28.36	30.77	36.28	42.84	46.58	50.66	59.97	71.04	108.7	166.3	253.7	385.4	872.8	
15	17.64	20.82	22.66	24.67	29.32	32.00	34.95	41.75	49.98	54.72	59.93	71.94	86.44	137.1	217.5	343.9	541.0	1311.	
16	19.01	22.70	24.84	27.21	32.75	35.97	39.54	47.88	58.12	64.08	70.67	86.07	104.9	172.6	284.0	465.6	758.8	1968.	
17	20.41	24.65	27.13	29.91	36.45	40.30	44.60	54.75	67.39	74.84	83.14	102.7	127.1	217.0	370.5	629.9	1064.	2953.	
18	21.84	26.67	29.54	32.76	40.45	45.02	50.16	62.44	77.97	87.21	97.60	122.4	153.7	272.6	483.0	851.7	1491.	4431.	
19	23.30	28.78	32.07	35.79	44.76	50.16	56.27	71.05	90.02	101.4	114.4	145.6	185.7	341.9	629.2	1151.	2088.	6648.	
20	24.78	30.97	34.72	38.99	49.42	55.76	63.00	80.70	103.8	117.8	133.8	173.0	224.0	428.7	819.2	1555.	2925.	9973.	
21	26.30	33.25	37.51	42.39	54.46	61.87	70.40	91.50	119.4	136.6	156.4	205.3	270.0	537.1	1066.	2101.	4096.	14961	
22	27.84	35.62	40.43	46.00	59.89	68.53	78.54	103.6	137.3	158.3	182.6	243.5	325.2	672.6	1387.	2838.	5736.	22442	
23	29.42	38.08	43.50	49.82	65.76	75.79	87.50	117.2	157.7	183.2	213.0	288.5	391.5	842.0	1805.	3833.	8032.	33665	
24	31.03	40.65	46.73	53.86	72.11	83.70	97.35	132.3	180.9	211.8	248.2	341.6	471.0	1054.	2348.	5176.	11246	50499	
25	32.67	43.31	50.11	58.16	78.95	92.32	108.2	149.3	207.3	244.7	289.1	404.3	566.4	1318.	3053.	6988.	15746	75751	
30	41.38	58.33	69.76	83.80	122.3	148.6	180.9	270.3	406.7	500.0	615.2	933.3	1418.	4034.	11349	31349	84702	>100t	
35	50.99	76.60	94.84	118.1	186.1	235.1	298.1	483.5	790.7	1013.	1300.	2144.	3538.	12321	42150	>100t	>100t	>100t	
40	61.61	98.83	126.8	164.0	279.8	368.3	486.9	859.1	1530.	2046.	2738.	4913.	8813.	37611	>100t	>100t	>100t	>100t	
45	73.33	125.9	167.7	225.5	417.4	573.2	790.8	1521.	2953.	4123.	5760.	11247	21938	>100t	>100t	>100t	>100t	>100t	
50	86.27	158.8	219.8	307.8	619.7	888.4	1289.	2688.	5694.	8300.	12105	25739	54597	>100t	>100t	>100t	>100t	>100t	

>100t indicates that the number exceeds 100 000.

Table 5. Annual repayments or capital recovery factors.

The amount that must be repaid annually for every 1 unit borrowed for 'n' years at 'i' rate of interest.

Yrs	Capital recovery factor: $\frac{1}{\sum 1/(1+i)^n}$																			
	%	2	4	5	6	8	9	10	12	14	15	16	18	20	25	30	35	40	45	50
1	1.02	1.04	1.05	1.06	1.08	1.09	1.10	1.12	1.14	1.15	1.16	1.18	1.20	1.25	1.30	1.35	1.40	1.45	1.50	
2	.515	.530	.538	.545	.561	.568	.576	.592	.607	.615	.623	.639	.655	.694	.735	.776	.817	.858	.900	
3	.347	.360	.367	.374	.388	.395	.402	.416	.431	.438	.445	.460	.475	.512	.551	.590	.629	.670	.711	
4	.263	.275	.282	.289	.302	.309	.315	.329	.343	.350	.357	.372	.386	.423	.462	.501	.541	.582	.623	
5	.212	.225	.231	.237	.250	.257	.264	.277	.291	.298	.305	.320	.334	.372	.411	.450	.491	.533	.576	
6	.179	.191	.197	.203	.216	.223	.230	.243	.257	.264	.271	.286	.301	.339	.378	.419	.461	.504	.548	
7	.155	.167	.173	.179	.192	.199	.205	.219	.233	.240	.248	.262	.277	.316	.357	.399	.442	.486	.531	
8	.137	.149	.155	.161	.174	.181	.187	.201	.216	.223	.230	.245	.261	.300	.342	.385	.429	.474	.520	
9	.123	.134	.141	.147	.160	.167	.174	.188	.202	.210	.217	.232	.248	.289	.331	.375	.420	.466	.513	
10	.111	.123	.130	.136	.149	.156	.163	.177	.192	.199	.207	.223	.239	.280	.323	.368	.414	.461	.509	
11	.102	.114	.120	.127	.140	.147	.154	.168	.183	.191	.199	.215	.231	.273	.318	.363	.410	.458	.506	
12	.095	.107	.113	.119	.133	.140	.147	.161	.177	.184	.192	.209	.225	.268	.313	.360	.407	.455	.504	
13	.088	.100	.106	.113	.127	.134	.141	.156	.171	.179	.187	.204	.221	.265	.310	.357	.405	.454	.503	
14	.083	.095	.101	.108	.121	.128	.136	.151	.167	.175	.183	.200	.217	.262	.308	.355	.404	.452	.502	
15	.078	.090	.096	.103	.117	.124	.131	.147	.163	.171	.179	.196	.214	.259	.306	.354	.403	.452	.501	
16	.074	.086	.092	.099	.113	.120	.128	.143	.160	.168	.176	.194	.211	.257	.305	.353	.402	.451	.501	
17	.070	.082	.089	.095	.110	.117	.125	.140	.157	.165	.174	.191	.209	.256	.304	.352	.401	.451	.501	
18	.067	.079	.086	.092	.107	.114	.122	.138	.155	.163	.172	.190	.208	.255	.303	.352	.401	.451	.500	
19	.064	.076	.083	.090	.104	.112	.120	.136	.153	.161	.170	.188	.206	.254	.302	.351	.401	.450	.500	
20	.061	.074	.080	.087	.102	.110	.117	.134	.151	.160	.169	.187	.205	.253	.302	.351	.400	.450	.500	
21	.059	.071	.078	.085	.100	.108	.116	.132	.150	.158	.167	.186	.204	.252	.301	.351	.400	.450	.500	
22	.057	.069	.076	.083	.098	.106	.114	.131	.148	.157	.166	.185	.204	.252	.301	.350	.400	.450	.500	
23	.055	.067	.074	.081	.096	.104	.113	.130	.147	.156	.165	.184	.203	.251	.301	.350	.400	.450	.500	
24	.053	.066	.072	.080	.095	.103	.111	.128	.146	.155	.165	.183	.203	.251	.301	.350	.400	.450	.500	
25	.051	.064	.071	.078	.094	.102	.110	.127	.145	.155	.164	.183	.202	.251	.300	.350	.400	.450	.500	
30	.045	.058	.065	.073	.089	.097	.106	.124	.143	.152	.162	.181	.201	.250	.300	.350	.400	.450	.500	
35	.040	.054	.061	.069	.086	.095	.104	.122	.141	.151	.161	.181	.200	.250	.300	.350	.400	.450	.500	
40	.037	.051	.058	.066	.084	.093	.102	.121	.141	.151	.161	.181	.200	.250	.300	.350	.400	.450	.500	
45	.034	.048	.056	.065	.083	.092	.101	.121	.140	.150	.160	.180	.200	.250	.300	.350	.400	.450	.500	
50	.032	.047	.055	.063	.082	.091	.101	.120	.140	.150	.160	.180	.200	.250	.300	.350	.400	.450	.500	

Table 6. *Random numbers.*

52687	36466	31250	10750	81154	76239	02937	00804	14571	35636	99891	39300	20363	81053
87126	68315	66018	99258	23050	51628	95686	65633	03927	49542	62015	76279	30667	47457
08370	55493	80297	42941	53954	89751	81720	75500	52079	18983	09517	54467	43840	05978
64461	88503	13868	38579	51074	06421	11489	91794	58253	16172	43289	36508	92507	19955
47069	69382	72355	41264	76842	44975	72445	60619	76206	78458	57261	20480	14159	77540
11049	93629	75978	09284	74560	35337	41350	19829	72905	81083	18417	09269	04931	02875
66460	78901	90850	56802	64686	00483	84721	02891	04851	28690	78929	55718	76640	34683
24470	72028	81587	94552	19714	14725	30418	50040	10905	21456	96274	21497	71360	84488
27826	38847	42635	00011	44324	87077	86266	36286	52016	02138	99081	33774	60456	86051
92892	00108	80450	08016	34409	63265	03569	53389	94802	78443	14874	34622	01461	12809
75493	85249	68259	78254	04969	90573	80572	22936	75494	65843	54777	82846	07602	12542
13438	38729	51739	21464	23261	50418	88106	84632	13687	13245	91385	54043	49706	01643
92906	70078	94555	90339	44937	93688	03769	35063	29841	00717	55934	92701	55639	92813
52547	32590	50596	85757	17311	50801	05721	06699	59503	06371	57022	46540	51404	87963
87201	72295	93739	92461	86958	93697	84126	18507	15149	68452	10995	18637	63589	10291
34068	50072	01118	19281	78744	46676	26528	60506	84982	55870	85367	84104	62187	75449
71417	95366	24359	76252	95341	59073	91119	15355	25554	72685	71664	41397	85554	18196
80180	91959	07223	59851	13118	78283	55840	89046	36486	58435	91206	29737	73846	81192
03205	96028	75043	51927	06520	35374	13506	86271	17397	38235	89714	63479	99097	57960
64607	89019	08505	68026	46860	04838	47212	07890	53116	61106	64073	75536	37865	65796

APPENDIX TWO: MODELLING IN VETERINARY EPIDEMIOLOGY AND ECONOMICS

1. INTRODUCTION

One of the major problems in veterinary epidemiology and economics lies in the estimation of the relationships between the many different factors determining a disease process in a livestock population.

There are two approaches to estimating such relationships: the empirical and the theoretical approach. The empirical approach involves going out into the real world to observe and monitor, while the theoretical approach involves attempts to deduce how the system being investigated works and thus the effect that one factor has on another. The latter approach essentially involves building a model of the particular system being investigated. Models are a representation of a system, which allow the behaviour of the system to be simulated under controlled conditions. In engineering, models are often physical (e.g. an aeroplane wing in a wind tunnel) whereas in epidemiology and economics they are invariably mathematical. Thus instead of being represented by physical structures, the system is represented by mathematical relationships.

The difference between the two approaches is best illustrated by a simple example. Suppose that it was necessary to determine the percentage of male calves born in a cattle population. An empiricist would take a sample of calves and count the number of males. A theoretically inclined person might catch a cow and a bull, examine their reproductive system and deduce that since "X" and "Y"

spermatozoa are produced in equal numbers and are of approximately equal viability and motility, the proportion of male calves would be approximately 50%.

In more complex situations, both approaches have weaknesses. If it were necessary to estimate the relationship between foot-and-mouth disease (FMD) vaccination and milk production in dairy cattle in an FMD-endemic area, one would be unlikely to obtain useful results by simply measuring milk production in a sample of vaccinated and unvaccinated herds. This is because milk production is influenced by many factors other than FMD, and these would tend to confuse the results. Worse still, some factors will most likely be related to both FMD vaccination and milk production. For example, farms with better management will tend to have a higher output of milk and to use FMD vaccine. Thus it would be wrong to attribute higher milk production in vaccinated herds to the vaccination alone. The theoretical approach might not be very helpful either for it is unlikely that we shall ever achieve a complete quantitative understanding of either the epidemiology of FMD or of the dairy production system. The solution is to model those parts of the system that are understood, and to estimate those relationships that are not by observation and experiment.

2. TYPES OF MODEL

There are many different types of model based on different techniques with varying degrees of complexity that are used in the fields of veterinary epidemiology and economics. To describe all types of model and the techniques used is beyond the scope of this manual. We will, therefore,

concentrate on two models which are particularly useful in the economic assessment of disease. At this stage, two basic distinctions need to be made.

Models may be either *dynamic or static*. A dynamic model will show the behaviour of a system over time, whereas a static model will only describe the steady-state situation representing the equilibrium that the system should eventually reach. For our purposes, equilibrium can be described as that situation when output and growth have settled at their steady-state or constant values. A dynamic model might show the daily offtake of milk that would be produced by a herd over 20 years, whereas its static counterpart would show only the average daily milk production per head (or per livestock unit) that would be produced when the system had settled to equilibrium. Dynamic models generally involve much more computation than static models and, as such, they normally require a computer for their effective use.

Models may also be *deterministic or stochastic*. A deterministic model will describe the situation which would arise if all the variables had average values, while a stochastic model allows the variables to take values from a range of values according to some probability distribution. For example, we could make a deterministic model of the sex ratio of 100 calves by the formulae:

$$M = pN$$

$$F = (1-p)N$$

where: N = total number of calves,
 M = number of male calves,
 F = number of female calves, and
 p = the probability of a calf being male.

Thus, for 100 calves:

$$M = 0.5 \times 100 = 50$$

$$F = (1 - 0.5) \times 100 = 50$$

A stochastic model of the same system, i.e. based on binomial distribution, would tell us that there is a probability of the number of males being any number from 0 to 100, and that the mean number of males would be $pN = 50$ with a standard error of:

$$\sqrt{Np(1-p)} = \sqrt{25} = 5$$

We may say with 95% confidence that in any sample of 100 calves, the number of males will be within two standard errors of the mean i.e. in the range 40 to 60. Thus,

stochastic models can take into account the effect of chance, but often at a considerable computational cost. Whether the cost is justified depends on how important the effect of chance is seen to be by the user of the model. Generally, if the population to be modelled is large, a deterministic model may give sufficiently good results, as illustrated in Table 1.

Table 1. *Ninety-five percent confidence limits for the percentage of males in calf populations of different sizes.*

Population size	95% confidence limits for % of males
10	18.4-81.6
100	40.0-60.0
1 000	46.8-53.2
10 000	49.0-51.0

A common method for introducing a stochastic, or chance, element into models is the Monte-Carlo technique. Although we shall not be using it in our examples, the technique is worth explaining because it is very simple to apply when dichotomous variables are involved, which is often the case in disease modelling.

If a model is examining individual cows, it is necessary to decide whether their calves will be male or female, as it would be absurd to introduce a calf that was half male and half female. The programme would generate a random number with a value between 0 and 1. If the random number is less than the probability of a calf being male (0.5), the calf would be male, otherwise it would be female. This technique is applicable in many other situations: e.g. Does the cow conceive to the service today? Does an animal become ill with a disease today? If diseased, does the animal die today?

3. EXAMPLES OF MODELS USED IN VETERINARY EPIDEMIOLOGY AND ECONOMICS

We will now describe two models which are particularly useful in the economic assessment of disease control ac-

tivities. The first of these will be a simple dynamic model of a cattle herd and the second will be a static model which relates a series of herd productivity parameters to the quantity of offtake produced per unit of feed resource, under certain conditions.

3.1 The basic parameters required for herd modelling

The main biological parameters required for herd modelling incorporate data on mortalities, fertility and output.

Mortalities. Data on mortalities are normally incorporated in the form of *death rates*. Often age-specific death rates are used, which are death rates occurring in specific age categories (e.g. 0 to 1, 1 to 2, 2 to 3, 3 to 4, 4 to 5 years etc) in a specific time period, usually a year.

Alternatively, different age categories may be used, such as the mortality rate in calves between birth and weaning (calf mortality rate), the mortality rate in young stock between weaning and maturity, and the mortality rate in adults (often given as a constant for the different adult age categories).

Sometimes it is necessary to be even more precise and to use age/sex specific death rates. This is because in certain production systems mortalities may be higher in one sex of the same age category.

Survival rates are also often used. These are obviously 1 minus the death rate, if the rate is expressed as a decimal, or 100 minus the death rate if the rate is expressed as a percentage.

Fertility parameters. Data about fertility are normally incorporated in the form of *parturition rates* (i.e. calving, farrowing, kidding rates etc as appropriate). These are normally expressed as the number of live births occurring in a specified population of females in a specified time period, usually a year. Age-specific parturition rates are sometimes used. In the case of species where multiple births are common, it may also be necessary to specify the number of offspring per parturition.

Sometimes reproductive performance is specified in terms of a *parturition interval* instead of a parturition rate. This is normally expressed in terms of the average time interval between parturitions. In cases of species for which

single births are the rule, the annual parturition interval and the annual parturition rate can be derived from one another by the following formula:

Annual parturition rate = $1/\text{Parturition interval}$ if the parturition interval is given in years; or

Annual parturition rate = $365/\text{Parturition interval}$ if the parturition interval is given in days.

Output. The next category of parameters used in herd models are those determining the physical quantities of output. These are frequently specified in the form of *offtake* (sales, slaughter and culling) and *yields* (milk, wool, eggs etc).

Offtake covers the removal of animals from a herd or flock for all reasons other than mortality and emergency slaughter due to illness. A distinction is often made between culling and the sale of surplus animals, with culling usually referring to sale of old or unproductive animals for slaughter. Offtake is determined by the livestock producer and may vary according to external circumstances. Both offtake and culling can also be expressed in the form of rates and are usually calculated using age and sex categories.

Yields are usually given either in relation to some other parameter (e.g. lactation yield per parturition) or in terms of annual amounts for specific age/sex categories. The average annual milk yield of a dairy animal can be derived from the formula $(12/I)Y$, where Y is the average lactation yield for the particular category of animal and I is the calving interval in months.

The values of offtake and yields are determined by applying prices to the output data. For offtake, prices are normally given in relation to age/sex categories, while for yields they are given in terms of per unit of the appropriate commodity produced.

Once the above parameters have been determined, the composition of the herd or flock must be defined in order to form a basis for the projection. This normally involves defining the number of animals in each age/sex category or setting targets for certain categories. In the latter case, these may be expressed in terms of numbers (e.g. 100 breeding cows) or as ratios (e.g. cow:bull ratio).

3.2 Dynamic herd models

The links between the parameters that are necessary to de-

rive a dynamic herd model are illustrated on the following example.

The model described in Table 2 is a dynamic and deterministic model showing the number of females by age group and the number of male calves produced each year. The parameters required to build this model are the mortality and calving rates for each age group. The survival rate for each group is calculated as $1 - \text{age-specific mortality rate}$. As in most herd models, the parameters used to calculate survival rate, number of births etc expected during a year, are applied to the numbers of animals in the appropriate age/sex categories at the start of the year in question. This generates an end-of-year figure which is shown in the output table for the following year.

We may now calculate the number of immature females in the 1-2 year age group for year 2. This will be the number in the 0-1 age group for year 1, multiplied by the survival rate for the 0-1 age group i.e. $0.92 \times 30 = 27.6$. The decimals are normally rounded off to the nearest whole number since we cannot have 27.6 animals. The same procedure is applied to all other age groups, except that the number moving into the 10+ age group for year 2 will be the sum of the number in the 9-10 age group for year 1 multiplied by the survival rate plus the number in the 10+ age group for year 1 multiplied by the survival rate.

Next we need to calculate the number of calves born in year 1. This will be the sum of the cow numbers in each group from the 3-4 age group onwards multiplied by the calving rate for each group. Half of the calves will be male, and should be entered in a box at the bottom of the table for year 1, and half will be female which will be entered in a box for year 2.

The process can be repeated to calculate herd structures and male calf production for as many years as required. It can also be used to model the herd and flock structures of other livestock species, and the model can be given a stochastic element by applying the Monte-Carlo technique. The last four columns of the table have been left blank for the reader to try the process.

The calculations involved in the model are simple and can be easily programmed into a programmable calculator or computer. The model can be extended to include culling rates, the fattening of male calves, milk production and many other factors. If, for example, we wished to include an

annual culling rate of 10% (0.1) in the age groups over 4 years of age, the number of animals in the 5-6 year age group in year 2 would be the number of animals in the 4-5 year age group in year 1 $\times [1 - (\text{mortality rate} + \text{culling rate})] = 18 \times [1 - (0.05 + 0.10)] = 18 \times 0.85 = 15.3$ or 15.

3.3 Incorporating the effect of disease into herd models

Dynamic herd models are useful in that they allow some of the dynamic effects of disease losses, such as reduction in fertility, to be evaluated on a "with" and "without" basis. They are also useful for simulating the effects of measures designed to improve animal productivity.

For example, the effect of a disease outbreak in a herd may be modelled by applying an increased death rate, an increased culling rate, lowered milk yield, decreased parturition rate etc to different age/sex categories. In order to use the model, we need to determine the effect of disease on various productivity parameters; once this is done, we can model its impact on output. This is much easier than trying to observe the effect on output directly. Information on the effects of disease on productivity parameters can be obtained from surveys or experiments. Normally, the effect of disease is manifested as the difference in the value of a parameter for an infected animal; e.g. a growing animal affected by FMD might suffer a 3-month delay in reaching maturity. The basic parameter values are usually estimated in the "with disease" situation. We therefore need to calculate the mean parameter value when the incidence of disease is 0, so that the model can be run for a "with" and a "without disease" situation, and the output values compared. The general formula is:

$$A_o = A \pm Er$$

where: A = the mean parameter value with the disease,
 A_o = the mean parameter value without the disease,
 E = the disease effect on the parameter, and
 r = the incidence of the disease.

The sign used in the equation depends on whether the disease effect is likely to increase or decrease the mean parameter value.

Example: If the mean age of maturity of animals is 3.8 years in a cattle population with a 15% incidence of trypanosomiasis infection and the effect of the infection is an estimated 0.5-year delay in reaching maturity, then the mean age at maturity without trypanosomiasis would be:

$$3.8 - 0.5 \times 0.15 = 3.725 \text{ years}$$

Most cattle herd models use calving rate as a fertility parameter, but disease effects are frequently expressed as an extension of calving interval. In such circumstances it is necessary to change the calving rate into a mean calving interval before calculating the disease effect. This is done by the following formula:

$$\text{Calving interval} = 1/\text{Calving rate}$$

Example: It is estimated that, in a herd infected with brucellosis, 2% of pregnancies end in abortion. The aborting cows are estimated to suffer a 1-year extension to the calving interval. The calving rate with the disease is 80%. The calving rate without the disease is calculated as follows:

$$\text{Calving interval} = 1/0.8 = 1.25$$

$$\text{Mean calving interval } A_0 = A - Er = 1.25 - 1 \times 0.02 = 1.23$$

$$\text{Calving rate without disease} = 1/1.23 = 0.813 \text{ or } 81.3\%$$

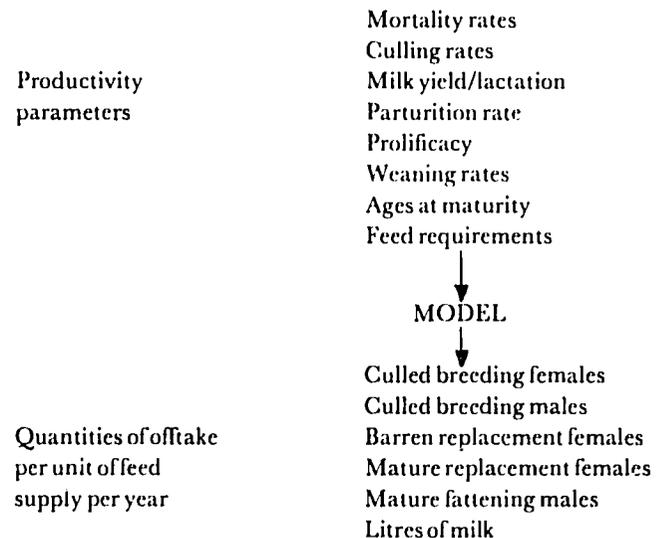
Disease effects on mortality and culling rates are simply additive. Thus, if a disease is estimated to cause 5% mortality in infected animals, and has an annual incidence of 20%, the average annual mortality caused in the whole population will be $0.05 \times 0.2 = 0.01$ or 1%. If the herd mortality rate from all causes is 5% per year, then without the disease, the mortality rate would be $5\% - 1\% = 4\%$.

3.4 Static herd productivity model

The main problem with a dynamic model is that it considers output on a per animal basis. This is a nuisance when we wish to determine the effect of disease on current productivity, because the model changes herd sizes and structures as the various parameters within the model are altered by the effects of the disease. It is then difficult to compare "with" and "without" disease results at the same point in time, because the population structures are different.

This problem can be overcome by the use of a static model, which assumes a herd at equilibrium with a growth rate of 0, so that all animals not needed to replace breeding stock are sold out of the herd as soon as they reach maturity. The model assumes that at equilibrium the system will use all of the available feed resources, and in this case the herd structure and production are implied by a set of parameters. The relationships within the model can be shown to be true for any species, and so we can deduce the effect of a change in any of the production parameters on the value of offtake with absolute certainty, given that certain conditions hold true. The relationships are illustrated in Figure 1.

Figure 1. Illustration of the relationship between productivity parameters and offtake using a static herd productivity model.



Precise account is taken of all the interactions within the system. The value of this is best illustrated by an example. Suppose that a disease kills 10% of all growing animals, but has no other effects, and that it is not possible to purchase replacements at the time of mortality. Then one might calculate the economic loss as being the value of the offtake of mature animals lost. This would be an overestimate, however, because more breeding animals could be

kept on the same feed resource when the mortality was occurring. To calculate how many animals could be kept on the feed resource would be difficult, but the model would take this effect into account.

There are four categories of animals in the model: male and female breeding stock and male and female surplus or fattening animals which are sold out of the herd when they reach maturity. For each of these categories, replacement stock between the ages of weaning and maturity can be found in the herd. The parameters that are used in the model are listed in Figure 1. Having ascertained these parameters, the following steps are generally needed to construct a static model.

1. Work out the number of replacement breeding stock needed annually as follows:
 - Fix the number of breeding cows.
 - Apply a bull/cow ratio to derive the number of breeding bulls.
 - Apply the appropriate death and culling rates to the breeding cow and breeding bull categories and thereby derive the numbers of adult breeding stock required annually. In the case of the adult replacement females, the numbers must be increased by a correction factor to take into account the percentage of these animals assumed to be barren.
2. Work out the maximum number of replacement breeding stock that could be produced as follows:
 - Apply the appropriate parturition rates and numbers of births per parturition to the appropriate breeding female categories in order to derive the number of male and female calves born per annum.
 - Apply the appropriate weaning rate to derive the numbers of calves weaned per annum.
 - Apply the appropriate death rates to each category of weaned replacement breeding stock to derive the number of animals of each sex surviving to maturity.
 - Subtract from this the number of male and female breeding replacements required to derive the proportion of weaned animals of each sex which must be retained as breeding stock.
3. Work out offtake and herd composition as follows:
 - If appropriate, apply a relevant correction factor (to

take into account variations in death rates between surplus and replacement stock) to the surplus numbers of weaned animals of each sex, in order to derive the number of animals that will be sold out of the herd as surplus when they reach maturity.

- Apply the appropriate culling rates to adult breeding stock and the proportion of barren heifers to the number of mature female replacements to derive the total offtake of animals in each of these categories.
- Calculate the total offtake.
- From the above calculations, the number of animals in each of the different categories in the herd can be calculated. The animal numbers can be summed together and the herd composition in percentage terms can be derived.
- Calculate the total annual milk yield by applying the appropriate variations of the formula $(12/I)Y$ to the numbers of breeding cows in the relevant categories.

The steps outlined above do not correspond precisely to the actual steps used in the model demonstrated in Figures 2 and 3, which uses more complex mathematics to arrive at the results more quickly (such as defining the herd structure in terms of the ratios of other classes of stock to females of reproductive age), but the principles are similar.

The model can be taken a stage further. Feed requirements in terms of livestock units can be specified for each of the four categories of mature stock, and the average requirement for the replacement stock can be calculated by assuming a linear growth from no feed requirement to the feed requirement at maturity, making the appropriate allowance for mortality. The mean feed requirement for growing animals tends to be less than half the feed requirement at maturity, since there are more animals in the younger age groups. The whole of the model can then be standardised on one livestock unit, which is not defined in the model. Thus different quantities of grassland, or combinations of concentrates and forage making up the requirements of one livestock unit can be applied to a herd using the production parameters given. The results of the model are then given in terms of the average combination of livestock on one livestock unit of feed resource and the value of output specified in terms of that one unit.

Used in this way, the model can be applied to any species of livestock. It can compare the efficiency of, say, cattle and goats in their utilisation of a feed resource. Moreover, the herd or flock being modelled need not be located solely in one geographical area, so systems where animals are bred in one area and fattened in another can be simulated.

The model has no stochastic element, which means that it gives expected production and tells us nothing about the potential variability in individual herds. It is most useful, therefore, in predicting the behaviour of national herds, where the changes in mean parameter values can be expected to be slow.

We will now illustrate the use of this type of model in detail. The example makes use of a microcomputerised static model whose output is illustrated in Figures 2 and 3. The model programme can be obtained on request from the authors.

Example: Suppose that foot-and-mouth disease is endemic in an extensive cattle production system in, say, Kenya. What would be the estimated annual loss due to the disease? The following parameters for the system were estimated:

Cattle population	2.8 million
Mortality rate in animals over 6 months	4% per annum
Cull rate in cows	5% per annum
Cull rate in bulls	7% per annum
Milk offtake	450 litres/lactation
Calving rate	65% per annum
Calf weaning rate	85% per annum
Age of heifers at first calving	4 years
Age of bulls at maturity	2.5 years
Age of steers at sale	4.5 years
<i>Offtake values</i>	(KSh)*
Culled cows	1800
Culled bulls	2000
Surplus heifers	2500
Mature steers	2200
Milk	2.00/litre

* For the purpose of this exercise the exchange rate is KSh 10 = US\$ 1.

<i>Livestock units</i>	
Breeding female	1.0
Mature fattening female	1.0
Bull	1.25
Mature fattening steer	1.25

The estimated annual incidence of foot-and-mouth disease was 30%, and the effects of the disease were estimated as follows:

- 1% of the animals affected died.
- 2% of the affected cows and bulls were culled.
- Cows produced milk for 6 months after calving. If a lactating cow was affected, 20% of the lactation yield was lost.
- 10% of pregnant cows affected with the disease aborted and had calving intervals extended by 1 year.
- Non-pregnant cows suffered a 1-month extension to the calving interval.
- Calves were weaned at 6 months; 8% of the suckling calves affected died.
- Growing animals suffered an average delay of 6 weeks in reaching maturity.

The parameter values "with" and "without" FMD can be estimated as follows:

Mortality rate

$$\text{Mortality rate due to FMD} = 0.01 \times 0.3 = 0.003$$

$$\text{Mortality rate without FMD} = 0.04 - 0.003 = 0.037$$

Weaning rate

$$\text{Calf mortality rate} = 1 - \text{Weaning rate} = 1 - 0.85 = 0.15$$

$$\text{Incidence of FMD in calves during the 6-month pre-weaning period} = 0.3 \times 0.5 = 0.15$$

$$\text{Calf mortality rate due to FMD} = 0.08 \times 0.15 = 0.012$$

$$\text{Calf mortality rate without FMD} = 0.15 - 0.012 = 0.138$$

$$\text{Weaning rate without FMD} = 1 - 0.138 = 0.862$$

Cull rate

$$\text{Cull rate due to FMD} = 0.02 \times 0.3 = 0.006$$

$$\text{Cull rate without FMD in cows} = 0.05 - 0.006 = 0.044$$

$$\text{Cull rate without FMD in bulls} = 0.07 - 0.006 = 0.064$$

Calving (parturition) rate

$$\text{Pregnancy rate} = \text{Gestation period/Calving interval}$$

$$= \text{Gestation (in years)} \times \text{Calving rate}$$

$$= 0.75 \times 0.65 = 0.4875$$

Non-pregnancy rate = $1 - 0.4875 = 0.5125$

Effect of FMD on mean calving interval in affected animals =

$$(1/12 \times 0.5125) + (1 \times 0.4875 \times 0.1) = 0.0914583 \text{ years}$$

Mean calving interval without FMD =

$$1.5384615 - 0.0914583 \times 0.3 = 1.511024 \text{ years}$$

Mean calving rate without FMD = $1/1.511024 = 0.6618$

Milk: offtake

The cows were in milk for 6 months, so the FMD incidence rate during the lactation period will be half the annual incidence rate i.e. $0.3/2 = 0.15$.

Mean amount of milk lost per lactation =

$$450 \times 0.2 \times 0.15 = 13.5 \text{ litres}$$

Mean amount of milk without FMD =

$$450 + 13.5 = 463.5 \text{ litres}$$

Age at maturity

Incidence of FMD for the growing period in:

$$\text{Heifers} = 4 \times 0.3 = 1.2$$

$$\text{Bulls} = 2.5 \times 0.3 = 0.75$$

$$\text{Steers} = 4.5 \times 0.3 = 1.35$$

Age at maturity without FMD:

$$\text{Heifers} = 4 - 6/52 \times 1.2 = 3.862 \text{ years}$$

$$\text{Bulls} = 2.5 - 6/52 \times 0.75 = 2.413 \text{ years}$$

$$\text{Steers} = 4.5 - 6/52 \times 1.35 = 4.344 \text{ years}$$

These parameters can be fed into the model as indicated in Figures 2 and 3, which show the productivity of cattle "with" FMD and "without" FMD.

Estimating the economic effect of FMD

In order to estimate the effects of FMD we need to compare offtakes in the "with" and "without" situation. To be able to do this we need to determine the total carrying capacity of the area in livestock units, since the model calculates the value of offtake per livestock unit.

The total carrying capacity of the area can be estimated as follows. For each class of stock, the feed requirement will be the product of the number of animals of that type and the feed requirement per animal. Thus from Figure 2:

$$\text{Breeding females} = 0.313806^* \times 2\,800\,000 \times 1 = 878\,657$$

$$\text{Breeding males} = 0.0125522^* \times 2\,800\,000 \times 1.25 = 43\,933$$

Replacement females =

$$0.122716^* \times 2\,800\,000 \times 0.448763^* = 154\,197$$

Replacement males =

$$0.00363414^* \times 2\,800\,000 \times 0.584054^* = 5943$$

Fattening females =

$$0.19721000^* \times 2\,800\,000 \times 0.448763^* = 247\,802$$

Fattening males =

$$0.350082^* \times 2\,800\,000 \times 0.531343^* = 520\,838$$

Total carrying capacity = 1 851 370 LU

The value of production in each situation can then be estimated by multiplying the value of the total offtake per livestock unit carrying capacity (as determined by the model) by the total carrying capacity in livestock units.

The value of the annual production lost because of foot-and-mouth disease is therefore $(769.212870 \times 1\,851\,370) - (730.428550 \times 1\,851\,370) = 71\,804\,126 \text{ KSh}$.

* Determined by the model; see Figure 2.

Figure 2. Static simulation of the productivity of a cattle population located in an area with endemic foot-and-mouth disease (30% annual incidence).

<i>Annual death rates</i>		<i>Mean ages at maturity</i>	
Breeding female	4	Replacement female at first parturition	4
Replacement female	4	Replacement male used for breeding	2.5
Breeding male	4	Surplus female at first parturition	4
Replacement male	4	Fattening males at time of sale	4.5
Fattening male	4		
<i>Annual culling rates</i>		<i>Fertility data</i>	
Breeding female	5	No. of breeding females per breeding male	25
Breeding male	7	Parturition rate (%)	65
		No. of offspring per parturition	1
		Percentage replacement females barren	0
<i>Survival-to-weaning rates</i>		<i>Offtake of milk/lactation (litres)</i>	
Males	85		450
Females	85		
<i>Mean feed requirement (LU)</i>			
<i>Mature animals</i>		<i>Growing animals</i>	
Breeding female	1	Replacement female	0.448763
Breeding male	1.25	Replacement male	0.584054
Surplus female	1	Surplus female	0.448763
Fattening male	1.2	Fattening male	0.531343
<i>Herd structure</i>			
<i>Class of stock</i>		<i>Number/LU carrying capacity</i>	<i>% of herd</i>
Breeding female		0.474598	31.380600
Replacement female		0.185595	12.271600
Breeding male		0.018984	1.255220
Replacement male		0.005496	0.363414
Surplus female		0.225243	19.721000
Fattening male		0.529462	35.008200
<i>Offtake</i>			
<i>Class of offtake</i>	<i>Offtake (Unit/LU/year)</i>	<i>Value/unit (KSh)</i>	<i>Offtake value (KSh/LU/year)</i>
Culled breeding females	0.023730	1800.00	42.713800
Culled breeding males	0.001329	2000.00	2.657750
Barren replacement females	0.000000	0.00	0.000000
Mature surplus females	0.068643	2500.00	171.607000
Mature fattening males	0.107812	2200.00	235.801000
Litres of milk	138.820000	2.00	<u>277.640000</u>
		<i>Total</i>	730.428550

Figure 3. *Static simulation of the productivity of a cattle population in the same area but free from foot-and-mouth disease.*

<i>Annual death rates</i>		<i>Mean ages at maturity</i>	
Breeding female	3.7	Replacement female at first parturition	3.862
Replacement female	3.7	Replacement male used for breeding	2.413
Breeding male	3.7	Surplus female at first parturition	3.862
Replacement male	3.7	Fattening males at time of sale	4.344
Fattening male	3.7		
<i>Annual culling rates</i>		<i>Fertility data</i>	
Breeding female	4.4	No. of breeding females per breeding male	25
Breeding male	6.4	Parturition rate (%)	66.18
		No. of offspring per parturition	1
		Percentage replacement females barren	0
<i>Survival-to-weaning rates</i>		<i>Offtake of milk/lactation (litres)</i>	
Males	86.2		463.5
Females	86.2		
<i>Mean feed requirement (LU/head)</i>			
<i>Mature animals</i>		<i>Growing animals</i>	
Breeding female	1	Replacement female	0.454006
Breeding male	1.25	Replacement male	0.588341
Surplus female	1	Surplus female	0.454006
Fattening male	1.2	Fattening male	0.538336
<i>Herd structure</i>			
<i>Class of stock</i>		<i>Number/LU carrying capacity</i>	
Breeding female			<i>% of herd</i>
Replacement female		0.470112	31.244800
Breeding male		0.158307	10.521400
Replacement male		0.018804	1.249790
Surplus female		0.004798	0.318875
Fattening male		0.221005	21.508800
		0.528965	35.156300
<i>Offtake</i>			
<i>Class of offtake</i>	<i>Offtake (Unit/LU/year)</i>	<i>Value/unit (KSh)</i>	<i>Offtake value (KSh/LU/year)</i>
Culled breeding females	0.020685	1800.00	37.232900
Culled breeding males	0.001203	2000.00	2.406970
Barren replacement females	0.000000	0.00	0.000000
Mature surplus females	0.077844	2500.00	194.611000
Mature fattening males	0.112070	2200.00	246.554000
Litres of milk	144.204000	2.00	288.408000
		<i>Total</i>	769.212870

Table 2. *Dynamic model of a dairy herd.*

Age group (years)	Calving rate	Survival rate	Number of females by age group by year						
			Year 1	Year 2	Year 3	Year 4	Year 5	Year 6	Year 7
0 - 1	0.0	0.92	30	29	35				
1 - 2	0.0	0.96	28	28	27				
2 - 3	0.0	0.96	32	27	27				
3 - 4	0.25	0.95	29	31	26				
4 - 5	0.75	0.95	18	28	29				
5 - 6	0.6	0.95	24	17	27				
6 - 7	0.6	0.95	15	23	16				
7 - 8	0.6	0.95	10	14	22				
8 - 9	0.5	0.92	8	10	13				
9 - 10	0.4	0.75	6	7	9				
10 +	0.4	0.5	3	6	8				
	Male calves		29	36					

LIST OF ABBREVIATIONS

A	attack rate	MD	mean difference
AI	artificial insemination	n	sample size
ARI	accounting rate of interest	N	naira
C	cost	NB	net benefits
df	degrees of freedom	NPV	net present value
DR	discount rate	P	true prevalence
ECF	East Coast fever	p	estimated prevalence
f	fraction of population (clusters) sampled	P _o	market-clearing price
F	franc	PV	present value
FMD	foot-and-mouth disease	PVB	present value of benefits
FV	future value	PVC	present value of costs
GB	gross benefits	Q	quantity
GP	gross productivity	R	estimated mean
i	interest rate (growth rate, rate of increase)	r	correlation coefficient
IRR	internal rate of return	S	standard deviation
K	kwacha (Malawi)	SE	standard error
KSh	Kenya shilling	S _D	standard error of the difference
m	number of clusters in sample	S _{MD}	standard error of the mean difference
M	maloti (Lesotho)	S _d	sample standard deviation of individual differences
MF	Malian franc	STP	social time preference rate

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