GIS and Spatial Analysis in Veterinary Science

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The Use of GIS in Veterinary Parasitology

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6.1 Introduction

During the past few decades the publication of papers of veterinary and human health interest related to the use of geographical information systems (GIS) and/or remote sensing (RS) has followed an exponential trend (Fig. 6.1a). Some key events have marked the curve. Prior to the review published by Hugh-Jones (1989) in *Parasitology Today* on the applications of remote sensing to the identification of habitats of parasites and disease vectors, only a few papers were published. Of these, one-third were related to parasitology and were aimed mainly at the identification of mosquito habitats (malaria and Rift Valley fever). A second major event was the publication in 1991 of an issue of *Preventive Veterinary Medicine* devoted to the applications of remote sensing to epidemiology and parasitology. This clearly raised interest in these new technologies; the average number of publications increased from three papers every 2 years to 17 per year in the first half of the 1990s. In the second half of the 1990s, numbers further increased exponentially, and currently more than 60 papers are recorded per year, 60% of which are related to parasitology and vector-borne diseases. A further breakdown by subject is given in Fig. 6.1b. Papers on four major disease vectors predominate (69% of published papers). These vectors are: (i) mosquitoes (29%), with topics including malaria, Rift Valley fever, Lacrosse encephalitis, dengue, West Nile fever and eastern equine encephalitis; (ii) tsetse (16%) and (mainly) animal trypanosomiasis; (iii) ticks (13%) as vectors of Lyme disease and tick-borne encephalitis in Europe and northern America as well as some African tick-borne diseases; and (iv) snail intermediary hosts (11%) of

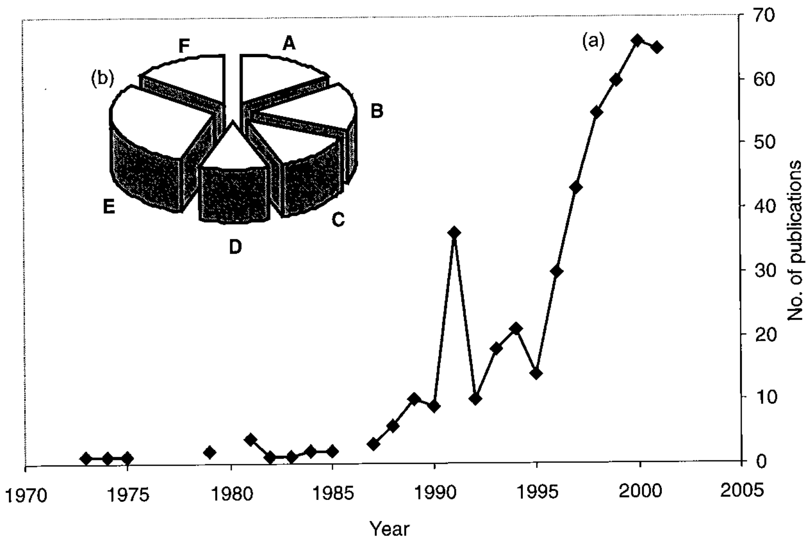

Fig. 6.1. Time distribution of (a) GIS/RS parasitology-related papers and (b) GIS/RS-related parasitology papers on different topics. A, review papers; B, tsetse and trypanosomiasis; C, ticks and tick-borne diseases; D, intermediary snail hosts, schistosomiasis and fasciolosis; E, mosquitoes, malaria, etc.; F, other topics. Data are from CABHealth and VetCD.

schistosomes and liver fluke. Currently *Culicoides* midges, major players on the arboviruses and emerging diseases scene, are a topical subject.

The applications of GIS and RS in epidemiology and parasitology have been reviewed by several authors (44 recorded papers). The most recent in-depth summary of one decade of research was by Hay *et al.* (2000), who reviewed all relevant topics in great detail, providing the scientific community with the latest landmarks in this field.

The use of GIS and RS is now generally accepted by the scientific community as a major tool contributing to the understanding of epidemiological processes *sensu lato*: disease, vector, host, environment. Nevertheless, whilst most people are now aware of the potential of these techniques, many still hesitate to use them for research or decision making. This chapter reviews recent advances towards the more widespread routine use of GIS/RS and of space–time information systems (STIS) in parasitology.

First we will review past trends. To do this we will focus on three case studies. The first is an insect-borne disease: tsetse-transmitted animal trypanosomiasis, with particular reference to West Africa. Secondly, we consider an intermediary host disease, *Fasciola hepatica* in the southern USA and East Africa. Thirdly, we examine a tick-borne disease, East Coast fever in East and southern Africa.

In the second part of the chapter we consider current and future trends, starting with a discussion about the implications of using GIS at an operational level and the need to fully integrate all aspects of time and space to achieve this goal. In this part, a review of literature published since 2000 on topics relevant to GIS and parasitology is given.

6.2 Tsetse-transmitted trypanosomiasis

Arguably, area-wide knowledge of the different factors affecting the interactions between vectors, parasites and hosts is required in order to understand the spatial epidemiology of the disease and to provide a strong basis for rational trypanosomiasis management. Thus, a first step towards understanding those interactions at a macro scale will include the systematic mapping of:

- The distribution and abundance of the different tsetse species (vectors).
- The occurrence (prevalence) and expression (anaemia) of trypanosomes (parasites).
- The distribution and relative importance of cattle breeds and cattle management systems (hosts).

6.2.1 Area-wide mapping

Since the early workers established, 100 years ago, the link between nagana, caused by trypanosomes, and the tsetse vector, considerable efforts have been made to map the distributions of the different tsetse species. This wealth of information, gathered by often anonymous field workers at country level, has regularly been compiled to produce distribution maps on a subregional or continental scale (Nash, 1948; Ford, 1963; Ford and Katondo, 1973).

The maps produced by Ford and Katondo (1973) are still considered to be an international standard. They include nine sheets of 1:5,000,000 maps describing the distributions of the different tsetse species of each group (palpalis, morsitans, fusca) and for each subregion (western, eastern and southern Africa). They have been locally updated by several authors (Katondo, 1984; Moloo, 1985; Gouteux, 1990). A detailed review of past and present tsetse distributions in southern Africa is given by Van den Bossche and Vale (2000) for Malawi, Mozambique, eastern Zambia and Zimbabwe.

Whilst historical tsetse distribution patterns are often well documented on a country scale, the problem of mapping tsetse abundance has been addressed less frequently. Most efforts towards that goal are limited to the monitoring of tsetse populations in areas earmarked for vector eradication before, during and after suppression campaigns; for example, the pastoral zone of Sidéradougou (3000 km^2) of Burkina Faso (Cuisance *et al.*, 1984b). In northern Côte d'Ivoire (134,000 km^2) tsetse surveys carried out between 1978 and 1981 to help define a rational control strategy for the whole area yielded detailed tsetse distribution and abundance maps of all species present (Clair and Lamarque, 1984). In The Gambia (10,000 km^2) an abundance map of *Glossina morsitans submorsitans* was produced (Rawlings *et al.*, 1993). More recently, in Togo (56,000 km^2) a set of national distribution maps at a grid resolution of 0.125° for all species present (*G. m. submorsitans, G. longipalpis, G. tachinoides, G. palpalis palpalis, G. fusca and G. medicorum*) and abundance maps for both riverine species (*G. tachinoides* and *G. p. palpalis*) was produced in the 1990s (Hendrickx *et al.*, 1999a).

Whilst tsetse survey results are well documented, there are few known records of the systematic mapping of trypanosome distribution and prevalence rates. Most studies report results in tabular form according to administrative units (e.g. Awan *et al.*, 1988; Agu *et al.*, 1989). Other examples include some spatial aspects, such as reported by Corten *et al.* (1988) in south-west Zambia, where surveys revealed that the extent of the trypanosomiasis problem covered a wider area than expected from historical fly distribution data alone.

The recorded fly abundance was expected to reflect disease risk (Clair and Lamarque, 1984; Cuisance *et al.*, 1984a). Therefore, trypanosomiasis surveys were often not conducted. In parts of the northern Côte d'Ivoire area, Camus (1981a) conducted prevalence surveys in 191 herds of the 1200 herds monitored by the Société pour le Développement de la Production Animale. Sixteen cattle were sampled from each herd. Herds were classified as either positive or negative. Results were summarized in a table and some spatial variation of disease prevalence was shown. No link was made with tsetse maps. An analysis of contemporary zootechnical data showed a significant difference between positive and negative herds. In the Gambia example (Rawlings *et al.*, 1993), a series of integrated trypanosomiasis control measures was proposed, adapted to the different levels of *G. m. submorsitans* abundance. In a later study, Snow *et al.* (1997) showed positive correlations between the recorded tsetse abundance figures and disease prevalence in cattle, small ruminants and equids.

Only a few studies were aimed at area-wide trypanosomiasis mapping. In Togo, in addition to the entomological surveys mentioned above, herds were systematically sampled at the same spatial resolution. After transformation, results yielded detailed countrywide raster maps of parasite distributions and prevalence as well as of herd anaemia (Hendrickx *et al.*, 1999b). This work was later extended to western Burkina Faso along the Mouhoun river system. Data on disease prevalence and the prevalence of anaemic cattle were combined to map epidemiological patterns, and this showed clearly the changing risk levels according to the importance of drainage systems (Hendrickx and Tamboura, 2000).

In southern Africa, point measurement maps were produced, summarizing trypanosomiasis surveys conducted in the 1990s in Malawi (159 sampling sites), Mozambique (274 sampling sites), Zambia (128 sampling sites) and Zimbabwe (62 sampling sites) (Van den Bossche and Vale, 2000).

In western and central Africa, the International Livestock Centre for Africa (1979) produced cattle breed maps for different countries with details for the larger administrative regions. Maps combined with pie charts depict the presence of dominant cattle breeds. In addition, information is provided on breed performance and husbandry systems. No maps are given of the latter.

In northern Côte d'Ivoire, Camus *et al.* (1981b) studied, as part of the same investigation into trypanosomiasis prevalence mentioned above, breed distributions and the effect of increasing zebu pressure on sedentary taurine herds after the droughts of the 1970s. Cattle were classified as either Baoulé (West African Shorthorn taurine), N'dama (West African Longhorn taurine), zebu or taurine × zebu crosses. Data were gathered from the SODEPRA (Société de Développement des Productions Animales) extension workers. Schematic maps are given of distributions of sedentary cattle of individual breeds for reproductive females and males. Densities are shown as dots representing 500 and 5000 head respectively.

In The Gambia, the ITC (International Trypanotolerance Centre) team involved in the examples given above have developed a low-cost rapid appraisal method whereby results of field surveys are combined with two socioeconomic questionnaires, including topics on farming systems and village economics and livestock and tsetse (Snow *et al.*, 1995).

Finally, during the Togo study mentioned above an exhaustive countrywide cattle survey yielded distribution and breed maps for cattle (Hendrickx *et al.*, 1999b). Cattle breeds were characterized as either trypanosusceptible (zebu), trypanotolerant (West African Shorthorn Somba) or crossbreds (Colour Plate 12). Results obtained using a phenotypic key were validated using microsatellite technology (to measure zebu introgression) on a subsample.

6.2.2 Remote sensing to assist disease mapping

The influence of climatic variables on the distribution and abundance of tsetse has long been recognized, at both the local (Nash, 1937) and the regional (Nash, 1948) level, through years of field study. Nowadays, the increased availability of satellite imaging allows us to draw up much improved vector distribution maps (Hay *et al.*, 1997). Satellite images offer several advantages over field surveys: the data are free from any human bias, make remote places accessible, are continuously produced and show real-time information.

Rogers and Randolph (1993) pioneered the application of NOAA (National Oceanic and Atmospheric Administration, USA)-derived NDVI (normalized difference vegetation indices, a measure of the amount of vegetation activity) data plus ground-measured temperature and elevation data to predict the distribution of *G. morsitans* and *G. pallidipes* in Kenya and Tanzania. Taking the historical fly distribution (Ford and Katondo, 1973) as a reference, satellite-derived predictor variables were selected and an accuracy of 84 and 79% correct predictions was obtained when predicting the presence of *G. morsitans* and *G. pallidipes* respectively.

For West Africa, Rogers *et al.* (1996) carried out a similar exercise and produced distribution limits of eight tsetse species encountered in Burkina Faso and Côte d'Ivoire at 0.167° resolution. The satellite data in this study comprised Fourier-processed NDVI, channel 4 (linked to ground temperature) and CCD (cold cloud duration, linked to rainfall) values. As before, historical records served as the reference for fly distribution. Selecting the ten best predictor variables, the percentage of correct predictions of the abundance of *G. tachinoides*, *G. palpalis*, *G. m. submorsitans* and *G. longipalpis* was 74, 87, 67 and 71%, respectively.

In Togo, Hendrickx *et al.* (1995) and Rogers *et al.* (1994) introduced discriminant analysis of satellite data to identify tsetse habitat in an attempt to minimize the use of ground-collected data and to optimize the application of satellite imaging. Hendrickx *et al.* (2001b) used non-linear discriminant analysis models in combination with Fourier-processed AVHRR–NOAA (AVHRR = Advanced Very High Resolution Radiometer) predictor data to produce spatial predictions of fly distribution for *G. m. submorsitans, G. longipalpis, G. tachinoides, G. p. palpalis, G. fusca* and *G. medicorum*. The results yielded presence/absence accuracies greater than 90%. Low-, medium- and high-abundance models were also produced for both riverine species, *G. tachinoides* (70% correct) and *G. p. palpalis* (56% correct). Three other aspects linked to vector prediction were also studied: (i) the effects on accuracy of using a spatial subsample to predict the remainder of the country; (ii) the effects on accuracy of the number of predictor variables included in the models; and (iii) the accuracy of using training sets to predict the presence of flies in non-adjacent areas. Not surprisingly, decreasing the size of the training set systematically reduced the accuracy of the predictions. The effect of the number of predictor variables was less straightforward. It was shown that accuracy increased to a maximum with an increasing number of predictor variables for sampled grids included in the training set. However, for grids not included in the training set predictions were always maximized with fewer predictor variables compared with results obtained in grids included in the training set. This highlighted the risk of overfitting models to restricted subsamples. Finally, it was clearly shown that one should be cautious when using training sets to predict the presence of flies in non-adjacent areas. The huge discrepancies observed between the prediction of fly presence in Togo using data from Côte d'Ivoire and Burkina Faso and the observed Togo maps clearly suggested that, whilst training set quality may certainly play a role, multivariate conditions at the grid level were (are) far too different between these two areas to produce results that are accurate enough. This work was later extended to western Burkina Faso in ecoclimatically drier areas complementary to the prevailing conditions in Togo. The aim was to map fly ecology patterns along the Mouhoun river system (Colour Plate 13) as a contribution to the understanding of riverine fly fragmentation patterns at their distribution limits.

The Togo approach developed for georeferenced trypanosomiasis management was extended to Burkina Faso. Results included maps of epidemiological patterns and fly ecology patterns for the Mouhoun river in western Burkina Faso (Hendrickx and Tamboura, 2000).

In southern Africa, Robinson *et al.* (1997a,b) analysed the historical distribution of *G. m. centralis*, *G. m. morsitans* and *G. pallidipes* in the common fly belt of Malawi, Mozambique, Zambia and Zimbabwe (Ford and Katondo, 1973) using NDVI, ground-measured temperatures, rainfall and elevation. Multivariate techniques included were linear discriminant analysis, maximum likelihood classification and principal component analysis. For each species, the best predictor variables were selected and the discriminant functions were applied to produce 84–92% correct predictions. Interestingly, the analysis successfully identified the geographical limits of both subspecies of *G. morsitans* present.

As for field surveys, remote sensing has been used mainly to assist in mapping the vectors whose distribution and abundance depend on ecovariables. The sole example of predicting trypanosome distribution and prevalence rates is the above-mentioned Togo study. Using techniques similar to those described for the spatial prediction of tsetse flies, models were produced for the prevalence of *Trypanosoma congolense* and *T. vivax* (Hendrickx *et al.*, 2000). In addition, prediction maps were also produced for average herd packed cell volume (PCV, a measure of anaemia, the most important symptom of trypanosomiasis). For trypanosomiasis, the highest prediction accuracy was obtained (83 and 89% for the two species of *Trypanosoma* respectively) when, in addition to remote sensing, a set of anthropogenic predictor variables was used. Not surprisingly, since many other causes may affect anaemia, the accuracy of PCV predictions was significantly lower than the accuracy of prediction of trypanosomiasis.

6.2.3 Integrated spatial data analysis and management in a GIS environment

To date, different approaches have been explored to use GIS towards a better understanding of the epidemiology and impact of tsetse-transmitted trypanosomiasis in order to assist rational disease management. Such studies have been conducted at the continental, subregional, national and local levels.

At the continental scale, Reid and Ellis (1995) performed GIS simulations using data on tsetse distributions, human population, cattle densities and protected or conservation areas with the aim of identifying the possible environmental implications of eventual trypanosomiasis control. Maps were generated depicting the areas where trypanosomiasis control may, from an ecological perspective, be encouraged, i.e. areas of agricultural intensification, banned, i.e. areas of high ecological integrity, or recommended with caution, i.e. areas of agricultural extensification. In a further study Reid *et al.* (2000) modelled, also at the continental level, the effect of an expanding human population and associated agriculture on the distribution of tsetse fly species. The spatial model included a combination of fine-resolution human population data, field data and the distribution of different types of tsetse. Results suggest that many of the 23 species of tsetse fly will begin to disappear by the year 2040, and that the area of land infested and the number of people in contact with flies will also decline. However, an area of Africa larger than Western Europe will remain infested by tsetse and under threat of trypanosomiasis for the foreseeable future.

At the subcontinental scale, Wint *et al.* (1997) conducted a series of studies in eastern, western and southern Africa. The rationale here was to select areas where trypanosomiasis control would yield high agricultural benefits, by integrating data on tsetse fly distributions, the pattern of human habitation, cropping areas and cattle densities. Tentative farming systems were defined on the basis of ecozone-related, geographic clusters of typical combinations of farmer densities, the proportion of land brought into the cultivation cycle and cattle numbers. These different farming systems were next matched with the tsetse distributions, to allow the likely outcome of any tsetse control, expressed in terms of expected changes in the amount of cropping and livestock to be predicted. In the case of missing field data, multivariate analysis models and NOAA satellite data were used to compensate for these shortfalls. The results are believed to aid the prioritization of areas particularly in the eastern and western parts of Africa. The results obtained have been embedded in the Food and Agriculture Organization (FAO) Programme Against African Trypanosomiasis (PAAT) information system (http:// www.fao.org/paat/html/home.htm).

At the regional scale, data layers from the PAAT information system have been used, together with other data, to assist in the area-wide planning of tsetse control in West Africa (Hendrickx *et al.*, 2004). On the basis of the results of a livestock production systems analysis and a series of hypotheses concerning riverine fly ecology, different approaches for integrated vector control have been suggested and pathways for future research proposed.

In southern Africa (Malawi, Mozambique, Zambia, Zimbabwe) Doran and Van den Bosche (2000) developed a strategy to identify priority areas for control on the basis of detailed knowledge of socioeconomic, institutional, technical and environmental (SITE) variables. To be fully operational, this decision-making process must be seen as a dynamic process in which potential and existing control activities need to be filtered by each SITE criterion on an ongoing basis. Whilst it is not yet applied in practice, this system is the only one that includes a strong time factor.

At a national level, Robinson (1998) integrated data from eastern Zambia on tsetse distribution, agricultural land use intensity, net stocking rates and arable potential in order to identify areas where tsetse control may be appropriate for relieving direct disease pressure and areas where control could potentially relieve land pressure. This approach was refined in a second paper (Robinson *et al.*, 2002).

In Togo, Hendrickx *et al.* (1999b) developed a GIS-based decision support system using the various data layers on vectors, parasites and hosts described elsewhere in this chapter. Different decision tree models were developed that were adapted to the prevailing mapped livestock production systems. The system was used to plan a national extension campaign focused on disease management and the involvement of private veterinary practitioners and auxiliaries ('barefoot vets'). This also included some areas earmarked for vector control. In these selected priority areas an additional study was conducted to model soil fragility, a crucial factor in the development of sustainable mixed farming.

Finally, a series of fine-scale studies were conducted at the local level using high-resolution satellite imaging. De Wispelaere (1994) integrated SPOT (Satellite Pour l'Observation de la Terre)-derived data on vegetation and land use to discern *G. m. submorsitans* habitat on the Adamawa plateau in Cameroon. Kitron *et al.* (1996) used Landsat imagery in the remote Lambwe Valley (Kenya) to predict favourable fly habitat. De La Rocque (2001b) combined high-resolution satellite imaging with entomological, disease prevalence, hydrography, landscape patterns, land-use and animal husbandry data in an attempt to identify major discriminating factors of tsetse presence and trypanosomiasis risk at a resolution of 30 metres in Sidéradougou, Burkina Faso. Currently targeted vector control activities focus on epidemiological hotspots (personal communication, S. De La Rocque). In addition, the combined experience of the Togo and Burkina Faso projects (see also above) serves as a basis to further study fly fragmentation and dispersion patterns on the Mouhoun river in western Burkina Faso.

In the Didessa Valley (Ethiopia) Erkelens *et al.* (2000) used a series of environmental variables and Landsat TM (Thematic Mapper) imagery to map priority areas for tsetse control on the basis of a cost–benefit approach addressing the following questions: (i) where does trypanosomiasis have a negative effect on (agricultural) development? (ii) In which areas will control measures have the highest impact/economic benefit? Currently, different ongoing projects in the area are further refining this approach.

6.3 Snails and liver flukes

6.3.1 Hard-copy maps

Prior to the 1990s, few attempts were made to map fasciolosis. Interestingly, most of these early studies did not focus on habitat mapping of the intermediary hosts but rather on observed disease data; that is, they looked at the problem from a veterinary perspective.

In this pre-GIS period, Ollerenshaw (1966) published crude choropleth maps for England and Wales at the county level showing predicted and observed disease in sheep. Forecasts were made using climatic conditions occurring in the previous 6 months excluding winter, a method derived from a pioneering model developed in Anglesey, Wales (Ollerenshaw and Rowlands, 1959). On the basis of a visual comparison between the expected incidence and the observed cases it was concluded that a 'reasonable correlation' could be shown. Some years later, Boray (1969) published a sketch map of south-east Australia that divided the area into five endemic areas of fluke, defined by temperature–rainfall regimes. The approach used was very crude and was mainly based on the extrapolation of disease prevalence results from a limited number of tracer studies.

In 1980 Watt published choropleth maps of Victoria, Australia, showing the prevalence of condemned bovine livers (slaughterhouse data) at the shire level. High-prevalence areas were visually correlated with high-rainfall and irrigation areas (see Chapter 1). The last significant study of this pre-GIS era involved small-area mapping of the intermediary hosts. Maps produced by Wright and Swire (1984) show a broad visual association between snail habitat and gley soil classes. The distribution of snails is shown to be patchy within given wet soil classes and the associated wetland plants.

6.3.2 Digital spatial data

On the basis of previous work, which concluded that a developed climate forecast model did not account for local variations in observed prevalence of fasciolosis, Zukowski *et al.* (1991) used a raster GIS to overlay snail habitats traced on to an aerial photograph and digitized US Geological Survey (USGS) soil maps of the coastal area of Louisiana, USA. As a first step, snail habitat was associated with certain soil types on a primary study farm. These results were confirmed when the association was extended to another 12 maps. In a further study, Zukowski *et al.* (1993) found a good association between the proportion of high-risk soil types and snail habitats; this relationship was less clear for disease risk.

Malone *et al.* (1992) used a more complex GIS approach to produce a composite risk index for 25 farms in the Red River Basin, Louisiana. The risk index included data from digitized USGS soil data updated using multispectral scanner (MSS) images, slopes, and length of pasture/water course per hectare. A significant regression was found between the weighted risk index and measured egg counts per farm, a measure of disease in live animals. The importance of GIS in quantifying local risk at farm level was further stressed by Malone and Zukowski (1992).

In Africa, a series of studies attempted to relate the distribution and abundance of *Fasciola* to NDVIs derived from low-resolution meteorological satellite data. In East Africa, Malone *et al.* (1998) used a set of digital agroecological data layers from the FAO and a climate forecast computer model that had been developed previously for crop productivity models to construct forecast index maps, i.e. abundance estimates, for *F. hepatica* and *F. gigantica* for different crop production system zones. The calculated risk forecast for both species combined was shown to be significantly correlated with average monthly NDVI values, and less so with available disease prevalence data. This approach was also applied separately to Ethiopia (Yilma and Malone, 1998) using the NDVI rather than a forecast index. The spatial association between the predicted and observed distributions of *Fasciola* was mainly based on visual map interpretation.

More recently, Fuentes *et al.* (2001) made an attempt to predict human fasciolosis in the northern Altiplano of Bolivia. Best results were obtained when fasciolosis was predicted using 1.1 km NDVI data. Nevertheless, whilst the model correctly predicted abundance ranges in known fasciolosis hotspots, it failed to identify the absence of disease in areas where the intermediary snail host was known to be absent. Little detail was given about the statistical techniques used. Finally, Cringoli *et al.* (2002) report the mapping of *F. hepatica* and *Dicrocoelium dendriticum* in the southern Appennines of Italy, using faecal samples from cattle and sheep. The GIS analysis of point distribution maps revealed a homogeneous distribution for *D. dendriticum* and a focal distribution for *F. hepatica.*

No attempt was made to use these training data to forecast the spatial distribution of liver flukes in the area.

6.4 Tick-transmitted East Coast fever

6.4.1 The pre-GIS era

Early studies focused mainly on the relationship between the distributions of cattle and East Coast fever. Robson *et al.* (1961) showed that in Tanzania, East Coast fever was confined to areas of tsetse absence and cattle presence. In north-west Tanzania, Yeoman (1966a) produced maps of cattle density and East Coast fever outbreaks in the study area. It was possible to draw a line separating endemic (ticks always present) and epidemic (ticks only present in favourable years) areas and map the spatial development of the epidemic over a 4-year period. The relationship between endemicity/epidemicity and rainfall isolines was also studied (Yeoman, 1966b). No direct relationship was found between the number of ticks on cattle and the annual variation in rainfall.

6.4.2 The ecoclimatic index, CLIMEX and the prediction of tick distributions

In the 1980s the idea of ecoclimatic matching for predicting the potential distribution and relative abundance of species by matching climates inside and outside sampled areas was first applied to animal disease vectors. Sutherst and Maywald (1985) calculated an ecoclimatic index (EI) for *Rhipicephalus appendiculatus* for selected sites worldwide on the basis of the distribution of the tick in Kenya. A reasonable correlation was obtained between the observed and predicated distributions. The absence of this tick in West Africa despite predicted climatic suitability was noted. Implementation of ecoclimatic matching was through a specifically developed software package, CLIMEX (http://www.ento.csiro.au/climex/climex.htm)

In the early 1990s, the International Livestock Research Institute (ILRI) initiated the use of CLIMEX to forecast tick distributions. Norval and Perry (1990) determined CLIMEX values for the period 1972–1986 at a single weather station in south-east Zimbabwe. Though this paper did not involve a spatial study as such, the authors explained the spread and subsequent disappearance of ticks by a run of favourable years as determined by EI values. A first spatial data set was depicted by Lessard *et al.* (1990), who used the ARCINFO software to map the disease (theileriosis), the vector (*R. appendiculatus*) and the hosts (cattle and buffalo) for Africa, with a special focus on East and southern Africa. Interpolated climatic data at a resolution of 625 km^2 were used to train CLIMEX predictions for all pixels. A vegetation map based on average monthly NDVI values was also included. In this paper the authors discuss biological processes only briefly. The discussion was taken further by Perry *et al.* (1990), who mapped CLIMEX dry and heat stresses and discussed tick distribution in relation to such climatic stresses in East and southern Africa, and by Norval *et al.* (1991), who identified similar EI and NDVI values between the Kenyan and Ethiopian highlands. The absence of ticks in south-west Ethiopia despite favourable conditions was related to the presence of tsetse (the tsetse corridor). These different results (Colour Plate 14) were summarized by Perry *et al.* (1991a), who also reproduced some of the earlier CLIMEX map outputs in greater detail, showing the sensitivity and specificity of CLIMEX EI for *R. appendiculatus* according to grid cell. The authors showed a visual correlation between NDVI values greater than or equal to a value of 0.150 and tick presence.

In southern Africa, historical data on East Coast fever outbreaks (at administrative region resolution) which occurred between 1901 and 1960 were visually related by the use of a CLIMEX-generated map of climatic suitability for *R. apendiculatus* (Lawrence, 1991). This built on the results published by Mayward and Sutherst in 1987. It was concluded that the CLIMEX favourability map overestimated tick suitability areas.

6.4.3 Remote sensing, an added value for mapping tick distribution patterns

The growing availability of remote sensing products since the late 1980s and early 1990s has opened new avenues for understanding and predicting area-wide tick distributions.

Early exploratory studies covering Zimbabwe explored the relationship between mean monthly NDVI and ecoclimatic zones. NDVI was related to rainfall and it was shown that commercial grazing lands averaged a higher NDVI value than adjacent communal areas (Kruska and Perry, 1991). On the basis of an extensive georeferenced data set that included ecoclimatic data, cattle distributions, boundaries between commercial and communal land, EI for ticks and East Coast fever outbreaks, Perry *et al.* (1991b) and Kruska and Perry (1992) reported (no analysis given) a visual relationship between ticks, disease outbreaks, EI and agro-ecoclimatic zones. The boundaries between commercial and communal lands were obtained from Landsat MSS images, and Thiessen polygons were used to convert cattle numbers at dip-tanks into area distribution values.

By relating seasonally variable tick mortality rates to remotely sensed vegetation data for Burundi, Uganda, Tanzania, Zimbabwe and South Africa, a major breakthrough in the understanding of area-wide tick distributions and abundance was achieved (Randolph, 1993). By showing that meteorological satellite sensor data (i.e. NDVI) seem to be a reliable marker for tick performance, taking regional heterogeneities into consideration, a sound biological justification was provided for using this type of variable in a purely statistical GIS framework to define the environmental characteristics of sites where ticks do occur and others where they do not (Randolph, 2000). Using discriminant analysis and NDVI, temperature and altitude as predictor variables, the spatial distribution of *R. appendiculatus* was modelled for Zimbabwe, Kenya and Tanzania (Rogers and Randolph, 1993) (Colour Plate 14).

6.4.4 Towards mapping disease risk

Whilst the relationship between spatial tick distribution patterns and remotely sensed and ground-measured ecoclimatic data has been shown, this relationship is less clear for the disease. As was shown for trypanosomiasis (Hendrickx *et al.*, 1999b), anthropogenic factors, such as husbandry systems, grazing management, vector control and treatment against the disease, are mostly not related to ecoclimatic spatial settings and therefore blur the picture.

Most efforts towards mapping East Coast fever were conducted by ILRI teams to aid in decision support in the planning of 'infect-and-treat' immunization campaigns. The aim was to infect young cattle with a live strain of *Theileria parva*, the causative agent of East Coast fever, and to administer at the same time a curative drug treatment. This approach provides protection for up to 3 years (Perry and Young, 1995). Since, in most cases, studies with this goal involve several visits to the same farms over a period of time, the collection of samples for laboratory analysis and the implementation of socioeconomic questionnaires, these studies usually cover limited areas. Results are therefore difficult to extrapolate.

Delehanty (1993) used a GIS to map agroecological and socioeconomic variables of livestock farmers in the Uasin Gishu district in west Kenya. The aim was to identify areas where immunization may be most applicable. In his discussion, the author mainly addresses the difficulty of extrapolating from data-rich to data-poor areas. In the Coast Province of Kenya, Deem *et al.* (1993) showed an East Coast fever gradient in three out of four coastal agroecozones. In a later study, Gitau *et al.* (2000) analysed epidemiological patterns in a series of contrasting agroecological and grazing strata in the Muranga district in highland Kenya. It was concluded, as in the previous studies, that the link between East Coast fever and agroecozone may be a key to understanding the spatial patterns of East Coast fever outbreaks.

Duchateau *et al.* (1997) developed a spatial logistic regression model to predict the presence and absence of East Coast fever using the georeferenced data set of Kruska and Perry (1992). Results included maps of outbreak probabilities for Kenya and residual distribution patterns. Much attention was given to reducing the size, whilst retaining the maximum amount of information, of the spatial predictor variable database, which included ground-measured climatic data, remotely sensed NDVI and land cover data. This was achieved using principal components analysis and subsequent varimax rotation of the principal components that were obtained. The same data set was revisited by Pfeiffer *et al.* (1997) using three spatial regression models. The spatial models selected the same variables as in the previous study.

Recently, ILRI has put effort into collating the results of different longitudinal and cross-sectional epidemiological studies conducted in the framework of their East Coast fever immunization activities and covering a series of different settings (from both the agroecozone and the animal husbandry point of view) in coastal and highland Kenya. Currently, efforts are under way to improve these results (personal communication, B.D. Perry).

6.5 About GIS, semantics and teamwork

The acronym 'GIS' can be interpreted in two ways (see Chapter 3). First, as geographical information *systems*, which encapsulates the different commercial software packages; secondly, as geographical information *science*, which recognizes the fact that almost every process in nature displays some pattern in the space domain. While the first interpretation involves only the systems that are used to store data and to perform some elementary operations on the data, the latter includes the multidisciplinary techniques for the description of the spatial patterns of natural processes.

As GIScience evolves, one could argue that GISystems will never meet the full requirements of every end-user: a geologist may need a totally different tool-set from that of a parasitologist. Although the toolsets become larger as new versions of GIS software systems emerge, GIS system developers recognize that it is impossible to fulfil everyone's needs and are therefore developing and commercializing application programming interfaces (APIs) to enable the end-user to develop her or his own specific tools without having to deal with data file formats or elementary GIS operations (e.g. point-in-polygon operations, buffering, overlays). However, because IT standards develop rapidly and because the traditional educational background of the majority of environmental scientists is not focused on IT-related problem-solving, this may strengthen the general feeling that GIS is nice, but ...

In addition, most GIS-related research focuses on 'where?' and

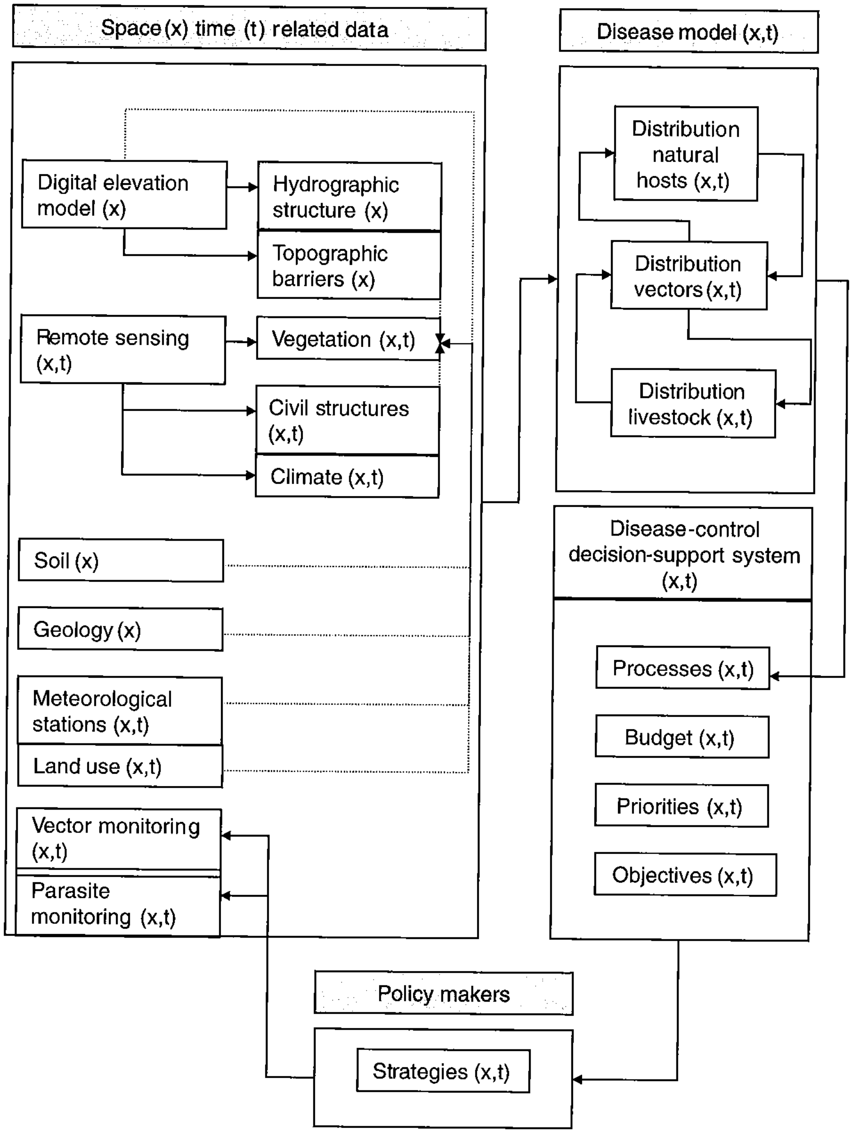

Fig. 6.2. Structural framework of an STIS decision-support system.

'what?', and often completely ignores 'when?'. Because this time domain is equally important in most environmental processes, it has been suggested that 'GIS' should be replaced by 'STIS', standing for space–time information science/systems (Kyriakidis and Journel, 2001). STIS aims to model processes in order to support our decisions and is now emerging in many university departments (Fig. 6.2). Also, STIS recognizes that all data feature some degree of error/uncertainty and that our knowledge is imprecise or not exhaustive and tries to incorporate this uncertainty throughout any analysis (Heuvelink, 1998; Biesemans *et al.*, 2000). Although knowledge of the confidence level of the model results is vital in making decisions, uncertainty propagation is often (if not almost always) neglected.

The list of techniques encapsulated by this new concept of STIS is massive and reaches far beyond the capabilities of currently available GIS software packages. It is therefore an advantage to form multidisciplinary groups to tackle the problems involved. This idea of 'scientific clustering' is nowadays embraced by many governmental organizations, which assign research funds only if such clusters are formed.

STIS reasoning offers a series of advantages. First, it is an important step towards the integrated management of our natural resources. Secondly, it increases awareness of the techniques used in other scientific research fields. Thirdly, STIS reasoning stimulates the integration of uncertainty analysis in expert systems; therefore, in the decision-making process uncertainty and/or error should no longer be considered to be bad.

But there are not only advantages in STIS reasoning. The major disadvantages are that the level of complexity is rising and it is a demanding task to keep pace with technological developments. Further, there is a lack of standards, which does not favour the portability of STIS/GIS data and the software modules that operate on this type of data.

Obviously, one can pinpoint many subjects in which STIS science and technology can be improved. However, it is clear that the disadvantages are best regarded as topics for further research and development rather than fundamental concerns. It may be that the only real disadvantage or pitfall in STIS reasoning is that some might link complexity with accuracy. Complex models may be 'better' than simple models, but this should certainly not be used as a rule of thumb. It all depends on the manner of implementation, and thus the manner of reasoning. If one takes this attitude, it is clear that STIS reasoning is a major step forward: it initiates and consolidates a more holistic approach in the decision-support cycle.

6.6 STIS: from theory to practice

Whilst it is clear that the proposed expansion of the GIS concept to STIS opens new avenues for collaborative research, we may ask what products we may expect and how far the parasitologist is from the routine use of these tools.

6.6.1 Mapping

Mapping is a crucial step towards understanding the spatial epidemiology of parasitic diseases. Vector and host distributions are directly related to ecoclimatic conditions. Therefore, populations can be described in great detail using a variety of ground-measured and remotely sensed environmental and geographical correlates. Apart from simple presence/absence modelling, the mapping of spatial patterns may also address population density and time-dependent seasonal fluctuations or longer-term trends. The latter includes the likely impact of climate change.

The collection of field data on parasites, vectors or (intermediary) hosts, including the identification of gathered samples, is notoriously time-consuming and expensive. Different approaches have been developed to allow the extrapolation of point field survey data to continuous probability maps of presence/absence or abundance. Although in some studies the distribution of sampling points may be dense enough to produce usable point density maps without need for further interpolation or extrapolation, as in the study on liver flukes in southern Italy (Cringoli *et al.*, 2002), in most cases it is not.

One way round this problem is to establish correlations between distribution data and landscape categories. These techniques were already in use prior to the RS/GIS era; for example, the mapping of ixodid ticks, including *Ixodes persulcatus*, in Siberia and the Soviet Far East by Korenberg (1973) and Korenberg and Lebedeva (1976). On the basis of historical and field-collected transect data, tick populations were related to landscape types at a local and regional scale. Ten main types and 26 regional subtypes of habitat were identified in Asiatic Russia. Further subdivisions were characterized by the relative proportions of the different tick species found in each area. The aim of these maps was to link discrete tick populations with foci of tick-borne encephalitis and rickettsiosis and to conduct epidemiological forecasting, also based on seasonal activity patterns.

Such techniques have since been refined and now include the use of high-resolution satellite imagery (Landsat, SPOT) to fingerprint landscape types using various supervised and unsupervised classification techniques. The most recent examples include the mapping of *Culiseta melurna*, the vector of eastern equine encephalomyelitis in Massachusetts, USA (Moncayo *et al.*, 2000) and a study of the transmission and intermediary hosts of alveolar echinococcosis in Tibet (Danson *et al.*, 2002).

Whilst the cost of high-resolution satellite data, as used in the studies listed above, limits their use to relatively small areas, other techniques, relying on data from meteorological satellites, have been developed for area-wide mapping. Using this approach, distribution maps at a resolution of between 8 and 1 km are now routinely produced. Point measurements of the variable to map (e.g. a vector) are related to gridded environmental predictor variables. Various statistical techniques are then used, including regression models and discriminant analysis, to calculate the probability of presence in non-sampled grids, thus creating a continuous distribution map based on scattered point observations.

This approach has been adapted to a wide range of (vectors of) diseases and geographical settings relevant to the veterinary parasitologist. Recent examples include the mapping of fasciolosis in Bolivia (Fuentes *et al.*, 2001), the mapping of tsetse in South Africa (Hendrickx *et al.*, 2002) and the mapping of *Culicoides* midges in the Mediterranean basin (Baylis *et al.*, 2001; Wittmann *et al.*, 2001).

In addition to mapping the distribution of parasites, vectors and intermediary hosts, similar approaches have also been used to map the distribution of livestock. Currently, distribution data at a grid resolution of 5 km are available for Europe, Asia and Africa on the World Wide Web (Wint *et al.*, 2001). Data on North, Central and South America have been processed and will soon be available to the user community, as will be regular updates and improvements of existing maps.

Whilst it is not the purpose of this chapter to discuss statistical methods (see elsewhere in this book), it is important to discuss briefly some issues related to training data, i.e. observed or historical data used to feed spatial prediction models. Ideally, the sampling procedure should follow the following steps: (i) define homogeneous ecoclimatic strata in the area under consideration; (ii) randomly select grids to sample within each stratum; and (iii) sample the variable to be modelled according to the same standard procedure in each selected grid.

Ecoclimatic strata may be defined by clustering the available ground-measured and remotely sensed environmental correlates using standard statistical software. A dendrogram should be used to determine the number of relevant clusters to include. Whilst this is relatively straightforward, deciding how many grids to sample is far less so. If the total area is large enough and the sampled grids are carefully selected, as few as 1% of the grids under consideration may be sufficient (Lark, 1994). Often the final number sampled will be a compromise between statistical relevance and the funding, infrastructure and manpower available.

Some additional tools are available to upgrade observed training data before predicting continuous spatial distribution patterns. Recently geostatistics have been used to achieve this goal (Hendrickx *et al.*, 2002). For example, we have modelled the distribution of *G. austeni* in KwaZulu Natal, using a geostatistics (indicator kriging) approach (Colour Plate 15) and multivariate logistic regression. In the latter, a model was fitted using the presence/absence of *G. austeni* and a set of environmental covariates including NOAA–AVHRR Local Area Coverage satellite images at 1.1 km resolution (Colour Plate 15).

6.6.2 Spatial epidemiology and the time dimension

The previous section dealt with the development of individual data layers; here some recent developments towards understanding the spatial epidemiology of vector-borne and/or parasitic diseases are highlighted, with emphasis on studies including a time dimension.

In a series of studies conducted in China (Yang *et al.*, 2000, 2002) the impact of flooding on the habitat and distribution of the intermediary snail host of schistosomiasis has been studied in great detail. Ground validation indicated that such an ecology-based approach, taking into consideration specific environmental conditions associated with the extent of annual floods, correctly predicted potential snail habitats and contributed to the understanding of seasonal habitat differences, a key factor in integrated disease control. In an additional study, Seto *et al.* (2002) identified two key factors hampering the development of predictive models of the spatial distribution of schistosomiasis: (i) different subspecies of *Oncomelania hupensis*, the intermediary snail host, are adapted to distinct habitats ranging from mountainous to floodplain habitats; and (ii) environmental changes resulting from the construction of the Three Gorges Dam and global warming threaten to increase snail habitats. The understanding of these factors is a prerequisite for accurate risk mapping and the identification of priority areas for schistosomiasis control.

In Burkina Faso, historical tsetse distribution records and high-resolution satellite imaging (SPOT) time series analysis made it possible to link changes in the distribution and density of two riparian tsetse species, *G. palpalis* and *G. tachinoides*, and increased human activity as depicted by land use changes and cattle densities. Results identified anthropogenic and environmental factors affecting riparian tsetse populations either positively or negatively (De La Rocque *et al.*, 2001a). Such indicators are essential in predicting the human impact on riparian tsetse populations in the region; little is known about this, but such knowledge is a key to current area-wide tsetse suppression plans.

The study of historical outbreaks of Rift Valley fever in Kenya between 1950 and 1998 revealed that outbreaks followed periods of abnormally high rainfall in otherwise dry habitats (Linthicum *et al.*, 1999). More than three-quarters of these events have been linked to the warm phase of the El Niño southern oscillation phenomenon. During these abnormal rainfall periods, dry dambos (distinct mosquito habitats) are flooded, resulting in the hatching of transovarially infected mosquito eggs – the start of a new epidemic. The mapping of ecological conditions using satellite recordings of vegetation shows increased greenness up to 5 months before outbreaks, indicating the forecasting potential of this type of approach.

An analysis of the seasonal variation in abundance of larvae and nymphs of ticks in seven European countries showed that, at sites within foci of Western type tick-borne encephalitis, larvae consistently started feeding and questing several months earlier in the year compared with sites where the disease did not occur, when nymphs are also active (Randolph *et al.*, 2000). Such synchronization between live stages is necessary for outbreaks to occur (Randolph *et al.*, 1999). Using satellite-derived time series of land surface temperature, it was shown that this behavioural pattern was associated with a higher than average rate of autumnal cooling relative to the peak midsummer land surface temperature. It was concluded that this link between satellite signals and biological processes is a key to predictive risk mapping (Randolph *et al.*, 2000). Such information is crucial in the testing of different 'what if?' temperature scenarios linked to anticipated global climate change patterns to predict the spread or decline of this disease (Randolph and Rogers, 2000).

Other teams have also used multivariable GIS models to study the spatial epidemiology of tick-borne disease outbreaks. In the north-central USA (Guerra *et al.*, 2002) results showed that the presence and abundance of *Ixodes scapularis* varied, even when the host population was adequate. Using different modelling techniques, risk maps were produced indicating suitable habitats and areas of high probability where ticks are likely to become established should they be introduced, thus highlighting both the explanatory and predictive capability of such models. This is an important feature, given the upsurge of these emerging diseases. In Italy a multivariable GIS model was developed to link the probability of tick (*I. ricinus*) occurrence with the probability of occurrence of infected tick nymphs at 50/50 metre resolution (Rizzoli *et al.*, 2002).

6.6.3 Decision-support systems

Spatial decision-support systems take spatial analysis one step further: from understanding epidemiological patterns to planning integrated control schemes.

As seen in Section 6.4.4 of this chapter, a leading field in this domain is African tsetse-transmitted trypanosomiasis, where decision-support tools have been developed at various scales. Data feeding these systems originated from: (i) extensive pluridisciplinary field surveys on vectors, hosts, parasites and socioeconomics; (ii) a wide range of contemporary ecogeographical environmental correlates; and (iii) access to various historical databases. Decisions are made by ranking identified sets of key variables. The different approaches used in these models have been reviewed in Section 6.2.2 of this chapter. Nevertheless, it is important to note here that, except for the Sidéradougou study, in which historical data on land use and tsetse distribution changes are part of the decision-making procedure, and for SITE criteria (see Van den Bossche and Vale, 2000), in which continuous data influx is considered a condition *sine qua non* for success, none of the systems that have been developed include a time component dealing with seasonal variation and medium-term forecasting.

No other examples are known to us of multidisciplinary information systems intended to aid in planning the integrated control of animal parasitic diseases over a large area. Most other existing information systems focus on vector-transmitted 'emerging' infectious diseases (West Nile fever, bluetongue, Rift Valley fever) or human parasitic diseases (malaria, schistosomiasis).

In Mpumalanga province, South Africa, a GIS-based information system was implemented for use in planning malaria control (Booman *et al.*, 2000). The system functioned in three steps: (i) data collection – a simplified reporting system to allow improved malaria reporting at the village and town levels; (ii) data analysis – the definition of high-risk areas and the stratification of malaria risk within these areas; and (iii) disease control – the planning and implementation of more efficient disease control. In the Republic of Korea (Claborn *et al.*, 2002) a GIS-based information system was used to compare the costs of malaria chemoprophylaxis with the costs of larvicidal treatment of potential mosquito breeding areas around two US military camps.

In China, mathematical models are being developed to describe the transmission of schistosomiasis using georeferenced field data and remote sensing inputs (Spear *et al.*, 2002). Though still at an experimental stage, it is expected that such models will produce sufficiently precise predictions to discriminate among competing control options.

The advent of diseases that may have an impact on public health has boosted the funding of research towards web-based forecasting systems. It is clear that other fields, such as veterinary parasitology, will greatly benefit from these developments.

A leading example in this field is the NASA-based website on the spread of West Nile virus in the USA (see http://www.gsfc.nasa.gov/topstory/20020828phap.html and http://www.gsfc.nasa.gov/topstory/20020204westnile.html). Data on virus occurrence in migratory birds, human cases of disease, the monitoring of mosquito populations, and satellite-derived forecasts are combined to produce updated risk maps. 'The idea is to let the satellite capture where the disease is spreading from year to year and make some predictions about where the disease is going. Computer models can determine which areas have the right combinations of temperatures and moisture levels most suitable for mosquitoes and transmission. Then, efforts and resources can target those high-risk areas. The goal of the programme is to extend the benefits of NASA's investments in Earth system science, technology and data toward public-health decision making and practice.'

In Australia, the National Arbovirus Monitoring Program operates a web-based information system, http://www.namp.com.au, which maps risk areas for bluetongue, Akabane virus and ephemeral fever virus. The aims are to: (i) facilitate international trade in Australian livestock (export certification); (ii) act as an early warning system for bluetongue; and (iii) assist producers and exporters in risk management. Risk models are based on seroconversion data from a network of sentinel animals and data on *Culicoides* midges from insect traps located near these animals. Efforts are also under way to develop disease-forecasting systems (Cameron, 2000). Results obtained with such information systems are of particular interest in Europe and the Mediterranean Basin, where bluetongue is currently emerging following the invasion of *Culicoides imicola*, a major vector of the disease (Wittmann *et al.*, 2001).

6.7 Discussion

Current trends show that systems based on spatial data analysis and the use of remote sensing are now applied to a wide variety of diseases and geographical areas. This is particularly the case with respect to the use of meteorological satellite data to predict spatial distribution patterns of parasites, vectors, intermediary hosts and hosts, not only in the tropics but also at subtropical and temperate latitudes (Green and Hay, 2002).

Developed methods are now robust enough to be included more routinely in spatial epidemiology studies and for decision support. Though meteorological satellite data are freely downloadable from the Internet (e.g. NOAA–AVHRR data; see http://www.saa.noaa.gov) data processing to transform raw data into usable formats remains a bottleneck. We have recently developed software (AVIA-GIS NOAA TOOLS 1.0: see http://www.avia-gis.com) that allows the user to process downloaded data and to produce composite images in different formats compatible with commercial GIS software. Apart from the parasitologist's knowledge of epidemiological processes and creativity, the sole remaining limit now is hard disk space and computing memory: typically, gigabytes of meteorological data are needed to produce time series covering several years of information.

An increasing number of studies also consider time in addition to spatial analysis. Examples that have been cited include the analysis of historical trends, the impact of recurrent natural phenomena such as floods and El Niño, and the seasonal variation of vector populations. Nevertheless, many obstacles still have to be overcome before operational parasitic disease forecasting systems can be produced. It is anticipated that the current efforts deployed to monitor and forecast emerging diseases, e.g. West Nile virus in the USA and arboviruses in Australia, will further boost the development of such systems.

Another opportunity to develop such tools arises from the increasing (and not unrelated) interest in monitoring global changes. These include not only climate changes but also changes related to globalization: increases in mobility and trade, population shifts towards densely populated areas, increasing numbers of livestock in close contact with human populations, and changes in consumption patterns. All these factors have a major impact on the epidemiology of animal diseases and can be measured and monitored in space and time.

It is suggested that parasitic and vector-borne diseases are more likely to be affected by global climate change (Harvell *et al.*, 2002). Human-induced climate change is having measurable effects on ecosystems, communities and populations and therefore will most likely affect free-living stages and vectors or intermediary hosts. Greater overwintering success of free-living stages and effects on stages in hypobiosis will have a direct impact on parasite populations, resulting in increased disease severity and changing epidemiological patterns. Shifts in the geographic range and abundance of vectors and intermediary hosts may occur: known vectors of disease may invade new territory and existing (potential) vector populations may now reach the critical size that will allow disease transmission. An increase in temperature will also affect parasite development and transmission rates, resulting in the spread of disease as a result of the increased vectorial capacity of endemic vectors. But in some cases the opposite may also be true: changing habitats and climatic conditions may cause vector extinction or disrupt fragile epidemiological pathways. In any case, one will have to remain cautious and avoid oversimplification when interpreting results, as was recently shown by a study on the lack of a relationship between the spread of malaria and meteorological trends in the East African highlands (Hay *et al.*, 2002).

Both the variety of subjects and the increasing use of the time dimension in spatial analysis suggest that GIS and RS are now widely used and accepted. Most of the tools and ingredients are now available to further promote the emergence of STIS reasoning in veterinary parasitology, provided scientists from different disciplines are prepared to share data and experience. More than ever, such technologies and collaborative networks are needed to help understand and cope with a changing world.

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