Recent advances in the use of geographical information systems with particular relevance to veterinary parasitology.

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1. Abstract

During the past decades the publication of papers interest related to the use of geographical information systems (GIS) and/or remote sensing (RS) and of particular interest to veterinary parasitology veterinary followed an exponential trend. 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 now are aware of the potential of these techniques, many still hesitate to use these tools for research or decision making. This paper reviews recent advances towards more widespread ‘routine’ use of GIS and RS in parasitology. After a brief introduction setting historical trends and milestones, followed by a more detailed review of past work in three chosen fields, tsetse transmitted trypanosomosis, liver fluke and East Coast fever, the authors discuss how Geographical Information Systems-Science (GIS) is currently evolving towards STIS, Space-Time Information Systems-Science, an even more holistic multidisciplinary approach encapsulating not only space but also the time domain. An inventory is made of the different topics addressed during the last two years separately for disease mapping, spatial epidemiology and decision support systems. 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 suggesting that GIS/RS are now widely used for research and decision making purposes. 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 new challenges of a changing world: climate change, globalization and emerging diseases.

2. An historical perspective

During the past 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) followed an exponential trend (Fig.1 - curve).

Some events have marked the displayed 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 have been recorded. Of these, 1/3 were related to parasitology and mainly aimed at identifying mosquito habitats (malaria and Rift Valley fever). A second major event was the publication in 1991 by Preventive Veterinary Medicine of an issue on “Applications of remote sensing to epidemiology and parasitology”. This clearly raised interest in these new technologies and the average number of publications increased from three papers per two years to 17 per year in the first half of the 1990’s. In the second half of the 1990’s numbers further raised exponentially and currently more than 60 papers are recorded per year, 60% of which are related to parasitology and vector born diseases. A further breakdown per subject is given in figure 1 (pie-chart).
Papers on four major disease vectors predominate (69% of published papers): (i) mosquitoes (29%) with topics including malaria, Rift Valley fever, LaCrosse encephalitis, Dengue, West Nile and Eastern equine encephalitis, (ii) tsetse (16%) and (mainly) animal trypanosomosis, (iii) ticks (13%) as vectors of Lyme disease and tick borne encephalitis in Europe and Northern America as well as some African tick born diseases, and (iv) snail intermediary hosts (11%) of schistosomes and liver fluke. Currently culicoides midges, major players on the arboviroses and emerging diseases scene, are an upcoming subject.

The applications of GIS and RS in epidemiology and parasitology have been reviewed by several authors (44 recorded papers). The most recent in dept summary of one decad [399x620]e of research was a special volume of Advances in Parasitology published by Hay and colleagues (2000) in which all relevant topics were reviewed in great detail providing the scientific community with the latest landmark 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 now are aware of the potential of these techniques, many still hesitate to use these tools for research or decision making. This paper reviews recent advances towards more widespread ‘routine’ use of GIS/RS – and Space Time Information Systems (STIS) in parasitology.

First we will review past trends: How has GIS applied to the spatial epidemiology of parasitic diseases evolved from hard copy mapping exercises to interactive decision support tools? To do this we will focus on three case studies: (1) an insect born disease: tsetse transmitted animal trypanosomosis with particular reference to West Africa, (2) an intermediary host disease, Fasciola hepatica in the Southern US and East Africa, and (3) a tick borne disease, East Coast Fever in East and Southern Africa.

In the second part current and future trends will be discussed, 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 (the post Hay et al. 2000 era) on topics relevant to GIS and parasitology is given.

3. GIS and the spatial epidemiology of parasitic diseases
From hard-copy maps to multidisciplinary information systems

3.1 Tsetse transmitted trypanosomosis

Arguably the area-wide knowledge of the different factors affecting the interactions between vectors, parasites and hosts is a prerequisite to understand the spatial epidemiology of the disease and a strong basis for rational trypanosomosis 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 trypanosomosis (parasites);
- the distribution and relative importance of cattle breeds and cattle management systems (hosts).

3.1.1 Area-wide mapping

Vectors. Since the early workers established the link between Nagana, caused by trypanosomes, and the tsetse vector one century ago (cf. Bruce and Kleine reviewed by Hoare 1972), considerable efforts have been made to map the distribution 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 at a sub-regional or continental scale (Newstead 1924, Nash 1948, Potts 1953, Machado 1954, Buxton 1955, Maillot 1957, Rickenbach 1961, 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 distribution of the different tsetse species per group (palpalis, morsitans, fusca) and per sub-region (Western, Eastern and Southern Africa). They have been

Whilst historical tsetse distribution patterns are often well documented at a country scale (e.g. for West Africa Challier et Laveissière 1977 and 1981), the problem of mapping tsetse abundance has less frequently been addressed. 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, e.g. the pastoral zone of Sidéradougou (3,000 km²) - Burkina Faso (Cuisance et al. 1984b). In Northern Côte d’Ivoire (134,000 km²) tsetse surveys carried out from 1978 to 1981 to help define a rational control strategy for the whole area, yielded detailed tsetse distribution and abundance maps of all species present (Clair 1982, Clair and Lamarque 1984). In the Gambia (10,000 km²) an abundance map of G. m. submorsitans was produced (Rawlings et al. 1993). More recently in Togo (56,000 km²) a set of national distribution maps at a 0.125 degree grid resolution 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 1990's (Hendrickx et al. 1999a).

**Parasites.** Whilst tsetse survey results are well documented, few records are known of systematic mapping of trypanosomosis distribution and prevalence rates. Most studies report results in a tabular form per administrative unit (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 Southwest Zambia where surveys revealed that the extent of the trypanosomosis problem covered a wider area than expected from historical fly distribution data alone.

The recorded fly abundance was expected to reflect disease risk (Cuisance et al. 1984a, Clair and Lamarque 1984). Therefore trypanosomosis surveys were often not conducted. In parts of the Northern Côte d’Ivoire area, Camus (1981a) conducted prevalence surveys in 191 herds of the 1,200 herds monitored by the Société pour le Développement de la Production Animale. Sixteen (16) cattle were sampled per herd. Herds were classified as either positive or negative. Results were summarised in a table and some spatial variation of disease prevalence was shown. No link was made with tsetse maps. An analysis of contemporary zootecnic data showed a significant difference between positive and negative herds. In the Gambia example (Rawlings et al. 1993), a series of integrated trypanosomosis control measures were 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 aimed at area-wide trypanosomosis mapping. In Togo in addition to the entomological surveys mentioned above, herds were systematically sampled at the same spatial resolution (0.125 degree grids). After transformation, obtained results yielded detailed country-wide raster maps of parasite distributions and prevalence as well as herd anemia (Hendrickx et al. 1999b). This work was later extended to Western Burkina Faso along the Mouhoun river system. Data one disease prevalence and the prevalence of anaemic cattle were combined to map epidemiological patterns clearly showing changing risk levels according to the impotence of drainage systems (Hendrickx and Tamboura, 2000).

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

**Hosts.** Epstein (1971) discussed the distribution of cattle breeds on a continental scale. In Western and Central Africa ILCA (1979) and FAO (1987) produced cattle breed maps per country. Per country figures are given for each larger administrative region. 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. (1981) studied, as part of the same study on trypanosomosis prevalence mentioned above, breed distributions and the effect of increasing zebu pressure on sedentary taurine herds after the droughts of the 1970's. 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 extension workers. Schematic maps are given of sedentary cattle distributions per breed separately for reproductive females and males. Densities are shown as dots of respectively 500 or 5,000 head. The economic impact of trypanosomosis on those different breeds was further discussed by Camus (1981b).

In the Gambia the ITC (International Trypanotolerance Centre) team involved in the examples given above developed a low cost rapid appraisal methodology where results of field surveys are combined with two socio-economic questionnaires including topics on (i.) farming systems and village economics and (ii.) livestock and tsetse (Snow et al. 1993).

Finally during the same Togo-study mentioned above an exhaustive country wide cattle survey yielded 0.125 degree cattle distribution and breed maps (Hendrickx et al. 1999b). Cattle breeds were characterised as either trypanosusceptible, i.e. Zebu, trypanotolerant, i.e. West African Short Horn Somba or crossbreeds (Fig. 2 – Maps A-B-C-D). Obtained results using a phenotypic key were validated using micro-satellite technology (a measurement of Zebu introgression) on a sub sample (Hendrickx et al. 1996 and Dao 1998).

3.1.2 Remote sensing to assist disease mapping

The influence of climatic variables on the distribution and abundance of tsetse has long been recognised, both at a local (Nash 1937) and regional level (Nash, 1948) through years of field study. Nowadays, the increased availability of satellite imagery allows us to draw up much improved vector distribution maps (Cline 1970, Hugh-Jones 1989, Riley 1989, Epstein et al. 1993, Washino and Wood 1994, Hay et al. 1997). Satellite images offer several advantages over field surveys; 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 NOAA derived NDVI (Normalised Difference Vegetation Indices, a measurement for the amount of vegetation activity) data plus ground measured temperature and elevation data, to predict the distribution of *Glossina morsitans* and *G. pallidipes* in Kenya and Tanzania. Taking the historical fly distribution (Ford & Katondo, 1973) as a reference, satellite derived predictor variables were selected and an accuracy of respectively 84 and 79% correct predictions was obtained when predicting *G. morsitans* and *G. pallidipes* presence.

For West Africa, Rogers et al. (1996) carried out a similar exercise and produced distribution limits of eight different tsetse species encountered in Burkina Faso and Ivory Coast, at a 0.167 degree resolution. The satellite data in this study comprised Fourier-processed NDVI, Channel 4 (linked to ground temperature) and CCD values (Cold Cloud Duration, linked to rainfall). As before, historical records served as the reference fly distribution (Laveissière and Challier, 1977, 1981). Selecting the 10 best predictor variables, a 74 - 87 - 67 and 71% correct description, including all the data in the training set, was obtained when predicting the abundance respectively of *G. tachinoides*, *G. palpalis*, *G. m. submorsitans* and *G. longipalpis*.

In Togo Hendrickx et al. (1993, 1996) and Rogers et al. (1994) introduced discriminant analysis of satellite data to identify tsetse habitat as an attempt to minimise the use of ground collected data and to optimise satellite imagery application. In their final paper Hendrickx et al. (2001) non-linear discriminant analysis models were used in combination with Fourier processed AVHRR-NOAA 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*. Obtained results yielded presence/absence accuracies of >90%. Low-Medium-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: (1) the effects on accuracy of using a spatial sub-sample to predict the remainder of the country, (2) the effects on accuracy of the number of predictor variables included in the model and (3) the accuracy of using training sets to predict fly presence 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 maximised with fewer predictor variables as compared to results obtained in grids included in the training set. This highlighted the risk over overfitting models to restricted
sub samples. Finally it was clearly shown that one should be cautious when using training sets to predict fly presence in non-adjacent areas. The huge discrepancies observed between 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 to different between those two areas to produce accurate enough results. This work was later extended to Western Burkina Faso in eco-climatical dryer areas complementary to the prevailing conditions in Togo. The aim was to map fly-ecology patterns along the Mouhoun river system (Fig.2 – E) as a contribution to the understanding of riverine fly fragmentation patterns at their distribution limits.

The developed Togo approach towards georeferenced trypanosomosis management was further extended to Burkina Faso. Results included maps of (1) epidemiological patterns and (2) fly-ecology patterns on the Mouhoun river in Western Burkina Faso (Hendrickx and Tamboura, 2000).

In Southern Africa Robinson et al. (1997a, 1997b) 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 applied to produce 84 to 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 mainly used to assist in mapping the vectors which distribution and abundance is dependant on eco-climatical variables. The sole example of predicting trypanosome distribution and prevalence rates is the above mentioned Togo study. Using similar techniques as described for tsetse spatial prediction 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 aneamia, the most important symptom of trypanosomosis). For trypanosomosis highest prediction accuracy was obtained (resp. 83% and 89%) using in addition to remote sensing a set of anthropogeneric predictor variables. Not surprisingly, since many other causes may affect aneamia, the accuracy of PCV predictions was significantly lower.

**3.1.3 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 / or impact of tsetse transmitted trypanosomosis in order to assist rational disease management. Such studies were conducted at a continental, sub-regional, national and local level.

At a continental scale Reid & 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 trypanosomosis control. Maps were generated depicting the areas where trypanosomosis control may, from an ecological perspective, be (1) «encouraged», i.e. areas of agricultural intensification, (2) «banned», i.e. areas of high ecological integrity, or (3) «recommended with caution», i.e. areas of agricultural extensification. In a further study Reid et al. modelled, also at a 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 by 2040, many of the 23 species of tsetse fly will begin to disappear as the area of land infested and 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 trypanosomosis for the foreseeable future.

At a sub-continental scale FAO conducted a series of studies in East, West and Southern Africa (FAO 1997). The rationale here was to select areas where trypanosomosis control would yield high agricultural benefits, integrating data on tsetse fly distributions, human habitation pattern, cropping areas and cattle densities. Tentative farming systems were defined, based on ecozone related, geographic clusters of typical combinations of (i.) farmer densities, (ii.) the portion of land brought into the cultivation cycle and (iii.)
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 mount of cropping and livestock. In case of missing field data, multivariate analysis models and National Oceanic and Atmospheric Administration (NOAA) satellite data were used to compensate for these shortfalls. The results are believed to aid the prioritisation of areas in particularly eastern and western parts of Africa. Obtained results have been embedded in the FAO-PAAT\textsuperscript{1} information system (Gilbert et al. 1999).

At the regional scale data layers from the PAAT-IS have been used, together with other data to assist in the area wide planning of tsetse control in West Africa (Hendrickx 2002 and Hendrickx et al. 2003). Based on the results of a livestock production systems analysis and on a series of hypotheses concerning riverine fly ecology different approaches for integrated vector control were suggested and pathways for future research were proposed.

In Southern Africa (Malawi, Mozambique, Zambia, Zimbabwe) Doran and Van den Bosche (2000) developed a strategy to identify priority areas for control based on the detailed knowledge of socio-economic, institutional, technical and environmental variables (SITE). This decision making process to be fully operational must be seen as a dynamic process in which potential and existing control activities would need to be filtered by each SITE criterion on an ongoing basis. Whilst not yet applied in practise this system is the only one including 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 were control could potentially relieve land pressure. This approach was further refined in a second paper (Robinson et al. 2002).

In Togo (Hendrickx 1999) developed a GIS based decision support system using the various data layers on vector, parasites and host described elsewhere in this paper. Different decision tree models were developed adapted to the prevailing mapped livestock production systems. The system was used to plan a national extension campaign focussed on disease management and the involvement of private veterinary practitioners and auxiliaries (bare foot 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 for sustainable mixed farming development (Van Camp et al. 1999).

Finally a series of fine scale studies were conducted at he local level using high resolution satellite imagery. De Wispelaere (1994) integrated SPOT derived data on vegetation and land use to discern \textit{G. m. submorsitans} habitat on the Adamawa plateau in Cameroon. Kitron \textit{et al.} (1996) used Landsat imagery in the remote Lambwe Valley (Kenya) to predict favourable fly habitat. De La Rocque (1997, 2001b) combined high resolution satellite imagery, entomological data, disease prevalence, hydrography, landscape patterns, land-use and animal husbandry data in an attempt to identify major discriminating factors of tsetse presence and trypanosomosis risk at a 30 meter resolution, in Sidéréadougo, Burkina Faso. Currently targeted vector control activities are conducted focussing on epidemiological hotspots (de La Rocque, personal communication). 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 (de La Rocque and Hendrickx, personal communication).

In the Didessa Valley (Ethiopia) Erkelens et al. (2000) used a series of environmental variables and Landsat TM imagery to map priority areas for tsetse control based on a cost-benefit approach addressing both questions: (i) Where does trypanosomosis have a negative effect on (agricultural) development? and (ii) In which areas will control measures have the highest impact/economical benefit? Currently different ongoing projects in the area are further refining this approach.

\footnote{PAAT : Program Against African Trypanosomoses. PAAT Information System: \url{http://www.fao.org/paat/html/home.htm}}
3.2 Snails and liver flukes

3.2.1 Hard copy maps

Prior to the 1990’s few attempts have been 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, i.e. looking at the problem from a veterinary perspective.

In this ‘pre-GIS’ period Ollerenshaw (1960) 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 six months excluding winter, a method derived from a model developed in Anglesey (Ollerenshaw and Rowlands, 1959). Based on 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 deviding the area in five endemic areas of fluke defined by temperature-rainfall regimes. The used approach was very crude and 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. In this book Durr and Gatrell revisit this dataset and confirm this correlation using spatial regression techniques. A last significant study of this ‘pre-GIS’ era involves 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.

3.2.2 Digital spatial data

A first series of studies addressed the fasciolosis problem in Louisiana, USA. Based on previous work where Malone et al. (1987) concluded that a developed climate forecast model did not account for local variations in observed prevalences, Zukowski et al. (1991) used a raster GIS to overlay snail habitats traced onto an aerial photograph and digitised USGS soil maps of the coastal area of Louisiana. As a first step snail habitat was associated with certain soil types on a primary study farm. These results were further confirmed when the association was extended to another 12 maps. In a further study Zukowsky 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 (i) digitised USGS soil data updated using MSS imagery, (ii) slope, and (iii) 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 to quantify local risk at farm level was further stressed in Malone and Zukowski (1992).

In Africa a series of studies attempted to relate Fasciola distribution and abundance to normalised digital vegetation indices, NDVI, derived from low resolution meteorological satellite data. In East Africa Malone et al. (1998) used a set of digital agroecological dat layers from the Food and Agriculture Organisation (FAO) and a climate forecast computer model, previously developed 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 found spatial association between the predicted and observed distribution of Fasciola was mainly based on visual map interpretation. The above described Louisiana and East Africa results were reviewed by the authors in Malone and Yilma (1999).

More recently Fuentes et al. (2001) made an attempt to predict human fasciolosis in the Northern Bolivian Altipano. 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 were the intermediary snail host was known to be absent. Little detail was given on used statistical techniques. Finally Cringoli et al. (2002) report the mapping of *F. hepatica* and *Dicrocoelium dendriticum* in the Southern Apenines, Italy, using faecal samples of cattle and sheep. The GIS analysis of point distribution maps revealed an homogenous 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.

### 3.3 Tick transmitted East Coast fever (ECF)

#### 3.3.1 The pre-GIS era

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

#### 3.3.2 The Ecoclimatic Index (EI), CLIMEX and the prediction of tick distributions

In the late 1980’s the idea of ecoclimatic matching was first applied. Sutherst and Maywald (1985) calculated an ecoclimatic index (EI) for *Ripicephalus appendiculatus* for selected sites world wide based upon the distribution of the tick in Kenya. A reasonable correlation was obtained between the observed and predicated distribution. The absence of the this tick in West Africa despite a predicted climatic suitability was noted.

Based on these encouraging results the approach was further refined. In Zimbabwe Maywald and Sutherst (1987) used a more detailed application of EI with expanded climatic data to explain the distribution of *R. appendiculatus* at four sites in terms of stress indices. In the same study a more detailed map of predicted climatic favourability for *R. appendiculatus* was given for Africa. The absence of the tick from Ethiopia was noted. In another study in Zambia (Sutherst and Maywald, 1987) the same approach was used to predict areas of enzootic instability for theileriosis, i.e. those areas with interrupted transmission and loss of immunity in calves. An EI threshold of <20 was suggested to indicate the tick is not well suited to that environment.

CLIMEX is a software package, developed by CSIRO, [http://www.ento.csiro.au/climex/climex.htm](http://www.ento.csiro.au/climex/climex.htm), for predicting the potential distribution and relative abundance of species by matching climates in and outside sampled areas. In the early 1990’s ILRI, formerly known as ILRAD, initiated using this software to forecast tick distributions.

A first study (Norval and Pery, 1990) determined CLIMEX values for 1972-86 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 run of favourable years as determined by EI values. A first spatial data set was depicted in Lessard et al. (1988, 1990) who used Arc/Info 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 km² 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 only briefly discussed biological processes. Nevertheless the discussion was taken further by (i) 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 (ii) 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 favorable conditions was related to the presence of tsetse (tsetse corridor). These different results (Fig. 3) were summarised in Perry et al. (1991) who also
reproduced some of the earlier CLIMEX map outputs in greater detail showing the sensitivity (Se) and specificity (Sp) of Climex’s EI for *R. appendiculatus* per grid cell. A visual correlation between NDVI values greater or equal to a value of 0.150 and tick presence was shown.

In Southern Africa (Lawrence 1991) historical data on East Coast Fever outbreaks (administrative region resolution) which occurred between 1901 and 1960, were visually related with a CLIMEX generated map on climatic suitability for *R. appendiculatus*. This was building further on the results published by Mayward and Sutherst in 1987. It was concluded that the CLIMEX favourability map overestimated tick suitability areas.

Finally the different CLIMEX outputs were summarised by Andrew et al. (1994) for the African continent with special reference to East and Southern Africa.

### 3.3.3 Remote sensing, an added value for mapping tick distribution patterns

The growing availability of remote sensing products since the late 1980’s – early 1990’s 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 is was shown that commercial grazing lands averaged a higher NDVI value than adjacent communal areas (Kruska and Perry 1991). Based on an an extensive georeferenced data set including eco-climatic data, cattle distributions, boundaries between commercial and communal land, EI for ticks and ECF outbreaks Perry et al. (1991) and Kruska and Perry (1992) reported (no analysis given) a visual relationship between tick, disease outbreaks, EI and agro-ecoclimatic zones. The boundaries between commercial and communal lands were obtained from Landsat MSS imagery and Theissan polygones 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 towards understanding area wide tick distributions and abundance was achieved (Randolph 1993, 1994, 1997). By showing that meteorological satellite sensor data, i.e. NDVI, seem to be a reliable marker for tick performance, given one would take 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 de spatial distribution of *R. appendiculatus* was modelled for Zimbabwe, Kenya and Tanzania (Rogers and Randolph 1993) (Fig. 3).

### 3.3.4 Towards mapping disease risk

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

Most efforts towards mapping ECF were conducted by ILRI teams to contribute to decision support to plan “infection and treat” immunization campaigns (Perry and Young 1995). Since in most cases studies towards that goal involve several visits of the same farms in time, collected samples to be analysed at the laboratory and the implementation of socio-economical questionnaires these studies usually cover limited areas. Results are therefore difficult to extrapolate.

Delehanthy (1993) used a GIS to map agro-ecological and socio-economical variables of livestock farmers in Uasin Gishu district in West Kenya. The aim was to identify areas were immunization might be most applicable. In his discussion the author mainly addressed the difficulty of extrapolating from “data rich” to “data poor” areas. In the Coast Province of Kenya Deem et al. (1993) showed an ECF gradient in 3 out 4 coastal agro-ecozones (AEZ). In a later study Gitau et al. (2000) analyzed epidemiological patterns in a

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2 The aim is to infect young cattle with live strain of Theleeria Parva, the causative agent of East Coast Fever, and administering at the same time a curative drug treatment. This approach provides up to three years protection.
series of contrasting agro-ecological and grazing strata in Muranga district in highland Kenya. It was concluded as for the previous studies that the link between ECF and AEZ may be a key towards understanding spatial patterns of ECF outbreaks.

Duchateau et al. (1997) developed a spatial logistic regression model to predict presence/absence of ECF using the geo-referenced data set of Kruska and Perry (1992). Results included maps of outbreak probabilities for Kenya and residual distribution patterns. Much attention was given to reduce the size, whilst retaining a maximum of information, of the spatial predictor variable data base which included ground measured climatic data, remotely sensed NDVI and landcover. This was achieved using principal component analysis and subsequent varimax rotation of the obtained principal components. The same data set was revisited by Pfeiffer et al. (1997) using three spatial regression models including the autologistic model of Augustin et al. (1996). The spatial models selected the same variables as in the previous study.

Recently ILRI has put efforts into collating the results of different longitudinal and cross sectional epidemiological studies conducted in the framework of their ECF immunization activities and covering a series of different settings (both from an AEZ as an animal husbandry point of view) in coastal and highland Kenya. Results obtained to date are mitigated (Clements & Pfeiffer 2001, Martinez 2002). Currently efforts are under way to improve these results (Perry, personal communication).

4. About GIS, semantics and teamwork

The acronym ‘GIS’ can be interpreted twofold: (1) Geographical Information ‘Systems’, which encapsulates the different commercial software packages and (2) Geographical Information ‘Science’, which recognizes the fact that almost every process in nature displays some pattern in the space domain. While the first interpretation only involves the ‘systems’ to store data and to perform some elementary operations on this data, the latter includes the multidisciplinary techniques for the description of the spatial patterns of natural processes.

As GIS-Science evolves, one could argue that GIS-software systems will never meet the full requirements of every end-user: a geologist might need a totally different toolset as a parasitologist. Although the toolsets become larger as new versions of GIS software systems emerge, GIS system developers recognize the problem that it is impossible to fulfill everyone’s needs and are therefore developing and commercializing API’s (Application Programming Interface) to enable the end-user to develop her/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 and alter at a mind-blasting speed and because the traditional educational background of the majority of environmental scientists is definitely not focused on IT-related problem solving, this may even further strengthen the general feeling that GIS is nice, but ...

In addition most GIS related research focuses on ‘Where? – What?’ and often completely ignores ‘When?’. Because this time domain is equally important in most environmental processes, it has been suggested to expand the acronym ‘GIS’ towards STIS, standing for Space-Time Information Science/Systems (Kyriakidis and Journel, 2001a and 2001b). STIS aims to model processes in order to support our decisions and is now emerging in many university departments, no matter the subject these departments are dealing with (Fig. 4). Also, STIS recognizes that all data features some degree of error/uncertainty and that our knowledge is imprecise or not exhaustive and tries to incorporate this uncertainty throughout the analysis (Heuvelink, 1998, Biesemans, 2000; Goovaerts, 2002). Although the knowledge of the confidence level of the model results is vital information for decision-making, uncertainty propagations are often (if not 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 enhanced by many governmental organizations, which only assign research funds if such clusters are formed.
such STIS reasoning offers a series of advantages such as: (a) it is an important step towards an integrated management of our natural resources, (b) people become aware of the techniques used in other scientific research fields and (c) since STIS reasoning stimulates to integrate uncertainty analysis in the expert systems and thus in the decision making process uncertainty and/or error should not be considered as ‘bad’ or ‘evil’ anymore.

But there are not only advantages involved with STIS reasoning. Major disadvantages include: (a) the level of complexity is rising, (b) computer related technology has become a key tool to analyze environmental problems and the technology (both the hard- and software standards) still evolves fast, making it a demanding task to keep up pace with these developments, (c) there is a lack on standards, which does not favor the portability of STIS/GIS data and the software modules which work with this type of data.

Obviously, one can pinpoint many subjects were the STIS science/technology can be improved, however, it is clear that the upper ‘disadvantages’ are more ‘topics asking for further research and development’ than fundamental disadvantages. Maybe the only real disadvantage or pitfall in STIS reasoning is that some might link complexity with accuracy. Complex models might be ‘better’ than simple models, however this is definitely not a rule of thumb. It all depends on their way of implementation and thus the way of reasoning. If one takes this attitude, it is clear that STIS reasoning is a major step forwards: it initiates and consolidates a more holistic approach in the decision support cycle.

**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 what products may one expect and how far is the parasitologist from routinely using these tools?

**Mapping**

Mapping is a crucial step towards understanding the spatial epidemiology of parasitic diseases. Vector and host distributions are directly related to eco-climatic 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 modeling 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.

Though in some studies, the distribution of sampling points may be dense enough to produce usable point density maps without need for further inter- or extrapolation, e.g. a study on liver flukes in Southern Italy (Cringoli et al. 2002), in most cases it isn’t.

One way around this problem is to establish correlations between distribution data and landscape categories. These techniques were already in use prior to the RS/GIS era, e.g. the mapping of Ixodid ticks, including *Ixodes persulcatus*, in Siberia and the Soviet Far East by Korenberg (1973, 1976), Vershinina et al. (1974), Korenberg and Lebedeva (1976) and Kiselev (1979). Based on 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 tick-borne encephalitis and rickettsiosis foci and to conduct epidemiological forecasting also based on seasonal activity patterns.

Currently such techniques have been further refined and now include the use of high resolution satellite imagery (Landsat, Spot) to fingerprint landscape types using various supervised and unsupervised classification techniques. Most recent examples focus on the mosquito vectors of malaria and the snail intermediate hosts of schistosomiasis. The former in the Republic of Korea (Claborn et al. 2002), India

Whilst the cost of high resolution satellite data, 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 8 to 1 km resolution 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 adopted to a wide range of (vectors of) diseases and geographical settings relevant to the veterinary parasitologist3. Recent examples include the definition of malaria free areas in Tanzania (Oumboo et al. 2002), the mapping of helminth distributions in Cameroon (Brooker et al. 2002), the mapping the distribution of the mosquitoes in Japan (Kobayashi et al. 2002), the mapping of different chromosomal subtypes of Anopheles gambiae in West Africa (Bayoh et al. 2001), the mapping of Rift Valley fever outbreaks in Kenya (Assaf et al. 2001), the mapping of schistosomiasis and its snail intermediary host in Ethiopia and Eastern Africa (Malone et al. 2001 and Kristensen et al. 2001) and in Brazil (Bavia et al. 2001), the mapping of fascioloses in Bolivia (Fuentes et al. 2001), the mapping of tsetse in East and West Africa (Wint 2001) and in South Africa (Hendrickx et al. 2002) and the mapping of Culicoides midges in the Mediterranean Basin (Bavlis 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 (Wint et al. 2002). Currently distribution data at a 5 km grid resolution are available for Europe, Asia and Africa on the world wide web, http://ergodd.zoo.ox.ac.uk/livatl2/index.htm and on CD-Rom (Wint et al. 2001). Data on Northern, Central and Southern America have been processed (Wint 2002a & b) and will be available to the user community soon as will be regular updates and improvements of existing maps.

Whilst it is not the purpose of this paper to discuss statistical methodologies (see elsewhere in this volume), it nevertheless is important to briefly discuss 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: (a) define homogenous eco-climatic strata in the area under consideration, (b) select randomly grids to sample within each stratum, (c) sample the variable to model following the same standard procedure in each selected grid.

Eco-climatic 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 define 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 (Hair et al. 1995) and the sampled grids are carefully selected, as little 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 available funding, infrastructure and manpower.

Some additional tools are available to upgrade observed training data prior to predict continuous spatial distribution patterns. Recently geo-statistics have been used to achieve this goal (Biesemans et al. 2002). Whilst the adopted approach is still experimental and current work aims at improving outputs, results obtained to date are promising (Fig. 5).

3 Since techniques applied to (vectors of) human diseases are also relevant for the veterinary parasitologist, therefore some medical references have also been included in this paper.
Spatial epidemiology and the time dimension.

Whilst the previous part dealt with the development of individual data layers in this part some recent developments towards understanding the spatial epidemiology of vector borne and/or parasitic diseases are highlighted with special emphasis on studies including a time dimension.

In a series of studies conducted in China (Yang H.M. et al. 2000, Yang G.J. et al. 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 understand seasonal habitat differences, a key factor for integrated disease control. In an additional study Seto and colleagues (2002) identified key factors hampering the development of predictive models of the spatial distribution of schistosomiasis: (a) different subspecies of Oncomelania hupensis, the intermediary snail host are adapted to distinct habitats ranging from mountainous to floodplain habitats, (b) environmental changes resulting from the construction of the Three Gorges Dam and global warming threaten to increase snail habitats. The understanding of these factors are a prerequisite for accurate risk mapping and the identification of priority areas for schistosomiasis control.

In Burkina Faso historical tsetse distribution records and Spot (high resolution satellite imagery) time series analysis allowed to link changes in tsetse distribution and density of two riparian species, Glossina palpalis and G. tachinoides, and increased human activity as depicted by land use changes and cattle densities. Results allowed to identify anthropogenic and environmental factors affecting either positively or negatively riparian tsetse populations (de la Rocque et al. 2001a). Such indicators are essential to predict human impact on riparian tsetse populations in the region, a little know subject and a key to current area wide tsetse suppression plans.

The study of historical outbreaks of Rift Valley fever in Kenya from 1950 till 1998 revealed that outbreaks followed periods of abnormal high rainfall in otherwise dry habitats (Linthicum et al. 1999). More than ¾ of these events have been linked to the warm phase of the El Nino 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 (Assaf et al. 2001). The mapping of ecological conditions using satellite recordings of vegetation show increased greenness up to five months prior to outbreaks thus stressing 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 larvae consistently started feeding and questing several months earlier in the year, when nymphs are also active, at sites within Western type tick born encephalitis foci (Randolph et al. 2000). Such a synchronization between live stages is a prior condition for outbreaks to occur (Randolph et al. 1999). Using satellite derived time series of Land Surface Temperature (LST) it was shown that this behavioral pattern was associated with a higher than average rate of autumnal cooling relative to the peak midsummer LST. It was concluded that this link between satellite signals and biological processes is a key to predictive risk mapping (Randolph et al. 2000a). Such information is crucial to test different “what if” temperature scenario’s linked to anticipated global climate change patterns (Houghton et al. 2001) to predict spread or decline (Randolph et al. 2000b) of this disease.

Other teams also used multivariable GIS models to study the spatial epidemiology of tick born disease outbreaks. In the North Central United States (Guerra et al. 2002) results showed that the presence and abundance of Ixodes scapularis varied, even when the host population was adequate. Using different modeling 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. An important feature given the upsurge of these emerging diseases. In Italy a multivariable GIS model was developed linking the probability of tick (Ixodes ricinus) occurrence and the probability of occurrence of infected tick nymphs at a 50/50 m resolution (Rizzoli et al. 2002).
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 the first part of this paper a leading field in this domain is African tsetse transmitted trypanosomosis where decision support tools have been developed at various scales. Data feeding those systems originated from (a) extensive pluri-disciplinary field surveys on vectors, hosts, parasites and socio-economics, (b) a wide range of contemporary eco-geographical environmental correlates and (c) access to various historical data bases. Decisions are made by ranking identified sets of key variables. The different approaches used in these models have been reviewed in the first part. It nevertheless is important to note here that except for the Sideradougou study, where historical data on land use and tsetse distribution changes are part of the decision making procedure, and for SETI, were a continuous data influx in considered a condition sine qua non for success, none of the developed systems include a time component dealing with seasonal variation and medium term forecasting.

No other examples are known to us of multidisciplinary information systems aimed at planning integrated control of animal parasitic diseases over a large area. Most other existing information systems focus on vector transmitted ‘emerging’ infectious diseases (West Nile, Blue Tongue, Rift Valley,) or human parasitic diseases (Malaria, Schistosomosis).

In Mpumalanga province, South Africa, a GIS based information system was implemented to plan malaria control (Booman et al. 2000). The system functions in three steps: (a) data collection: a simplified reporting system allowed for improved malaria reporting at the village and town level, (b) data analysis: the definition of high risk areas and the stratification of malaria risk within those areas, (c) 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 costs of malaria chemo prophylaxis with costs of larvicidal treatment of potential mosquito breeding areas around two U.S. military camps.

In China mathematical models are currently developed to describe the transmission of schistosomosis 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 (re)emerging diseases having a potential impact on public health 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 United States of America4. Data on virus occurrence in migratory birds, human cases of disease and mosquito population monitoring 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 program 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, mapping risk areas for Bluetongue, Akabane Virus and Ephemeral Fever Virus. The aim is to (a) to facilitate international trade in Australian livestock (export certification), (b) act as a Bluetongue early warning system, (c) assist producers and exporters in risk management (NAMP, 2002). Risk models are based on sero-conversion data from a network of sentinel animals and data on Culicoides

4 See also for more information the following online papers : http://www.gsfc.nasa.gov/topstory/20020828phap.html and http://www.gsfc.nasa.gov/topstory/20020204westnile.html
midge from insect traps located near these animals. Currently efforts are also underway towards the
development of disease forecasting systems (Cameron 2000a & b). Results obtained with such information
systems are of particular interest to 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).

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 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 methodologies 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
internet, e.g. NOAA-AVHRR data at http://www.saa.noaa.gov, data processing to transform raw data into
usable formats remains a bottleneck. Recently software has been developed, http://www.avia-gis.com,
which allows the user to process downloaded data and to produce composite images in different formats
compatible with commercial GIS software. Besides the parasitologists 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. Cited examples 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 to
allow the development of operational parasitic disease forecasting systems. It is anticipated that the current
efforts deployed to monitor and forecast emerging diseases, e.g. West Nile Virus in the United States of
America or arboviroses in Australia, will further boost the development of such systems.

Another opportunity to develop such tools is the raising, not unrelated, interest in monitoring global
changes. These include not only climate changes (Houghton et al. 2001), but also changes related to
globalization: increase 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 (Slingenbergh et al. 2002).

It is suggested that parasitic and vector born diseases are more likely to be affected by global climate
change (Harvell et al. 2002). Man 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. A 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 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 critical mass to allow disease transmission. An increase in temperature will also affect parasite
development and transmission rates resulting in disease spread due to 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 non-relationship between malaria spread 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 suggests 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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Legend to the figures:

Figure 1 – GIS parasitology papers over time.
Curve: Time distribution of GIS/RS related papers (Source: CABHealth and VetCD).
Pie-Chart: GIS/RS related parasitology papers per topic (Source: CABHealth and VetCD).
A. Review papers;
B. Tsetse and trypanosomosis;
C. ticks and tick borne diseases;
D. intermediary snail hosts, schistosomiasis and fasciolosis;
E. Mosquitos, malaria a.o.;
F. other topics.

Figure 2
Part 1 (top) – Togo animal husbandry systems.
A. Clustered animal husbandry systems: blue = rural extensive systems, red = market oriented systems, pink = intermediary system (map inlay: source data – cf. Hendrickx et al. 1999b for more detail)
B. Agriculture intensity: percentage land included in the agricultural cycle.
C. Zebu introgression: proportion zebu or crossbreds as compared to indigenous trypanotolerant taurine population. Note that zebu introgression is mainly found in market oriented and intermediary animal husbandry systems.
D. Cattle distribution.
Part 2 (below) – Predicted riverine tsetse distribution patterns in Western Burkina Faso and South-Eastern Mali.
Four distinct classes are shown: (i) tsetse absent, (ii) fragmented tsetse populations = tsetse are only present in suitable habitat islands in otherwise hostil eco-climatic conditions, (iii) linear tsetse populations = tsetse are only found in linear riparian habitats along mainstreams and important tributaries, (iv) ubiquitous = tsetse are present in suitable vegetation of entire drainage system (cf. Hendrickx and Tamboura 2000 for more detail).

Figure 3 (not included here) – The distribution of *Rhipicephalus appendiculatus* in East Africa.
B. Rogers and Randolph (1993): Discriminant analysis output combining ground measured (Temp, altitude) and remoltely sensed (NDVI) data – from Rogers and Randolph (1993)

Figure 4: Structural framework of a STIS decision support systems.

Figure 5: Spatial modelling of the distribution of *Glossina austeni* in KwaZulu Natal using geo-statistics and multivariate analysis.
Training data: observed abundance data in the northern part of KwaZulu Natal: total of 1023 sampled locations, 157 of which harvested *G. austeni* (positives).
a. Geostatistics output. Main objective: extending the number of positive locations to enhance the performance of multivariate techniques. By indicator variograms and indicator kriging the number of positive locations, i.e. p>0.6, could be extended to 841 locations.
b. Logistic regression output. A binary logistic regression model was fitted between the presence/absence of *G. austeni* and the set of environmental co-variables including NOAA-AVHRR Local Area Coverage (LAC) 1KM Level 1B satellite imagery in order to extrapolate a map of potential habitats covering Kwa-Zulu Natal at a 1.1 km resolution.
Space (x) Time (t) related Data

- Digital Elevation Model(x)
- Hydrographic structure(x)
- Topographic barriers(x)
- Remote sensing(x,t)
- Vegetation(x,t)
- Civil structures(x,t)
- Climate (x,t)
- Soil(x)
- Geology(x)
- Meteorological stations(x,t)
- Land Use(x,t)
- Vector monitoring(x,t)
- Parasite monitoring(x,t)

Disease Model(x,t)

- Distribution natural hosts(x,t)
- Distribution vectors(x,t)
- Distribution livestock(x,t)
- Disease-control decision support system(x,t)

- Processes(x,t)
- Budget(x,t)
- Priorities(x,t)
- Objectives(x,t)

Policy makers

Strategies(x,t)