Review article

The impact of remote sensing on the study and control of invertebrate intermediate hosts and vectors for disease

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Abstract. This paper reviews the application of remote sensing to the study and control of invertebrate intermediate hosts and vectors for some of the most prevalent of human diseases worldwide. Examples are also taken from studies involving animal diseases that have considerable adverse effects on human welfare. The current status of remote sensing in epidemiology is assessed and suggestions are made on how, in the future, the two fields might be most profitably combined.

1. Introduction

The potential for the application of remote sensing to epidemiological studies has long been recognized (Cline 1970), though for a variety of reasons this potential has been only partly realized. The problem is well illustrated in Barnes (1991) who documents the fate of the Health Applications Office (HAO), formed by National Aeronautics and Space Administration (NASA) to investigate remote sensing applications to public health in the early 1970s. After many successful pilot studies, further funding was not forthcoming because NASA considered its mandate to have ended, once the feasibility of such projects had been proven. The problem was compounded by other agencies and institutions which had a clearer remit in the field of human health, but which remained sceptical of the techniques (Bos 1990).

The purpose of this review is to survey the many investigations that have used remote sensing techniques for the study of diseases involving invertebrates as intermediate hosts. Such hosts may act simply as passive carriers or specifically as vectors of disease where they introduce or inoculate pathogens directly on to or into a vertebrate through their haematophagous (blood-feeding) habits (Molyneux 1993). Important examples are given in table 1. In addition, these and other invertebrate intermediate hosts transmit a range of diseases of domestic animals, causing significant adverse economic impacts. For each disease a brief explanation of the transmission cycle and intermediate host biology are given to illustrate how surveillance techniques have been used.

Previous reviews of the subject have been orientated towards the medical, veterinary and biological communities (Cline 1970, Hugh-Jones 1989, 1991 a, Riley 1989, Epstein *et al.* 1993, Roberts and Rodriguez 1994, Washino and Wood 1994), while those found in the remote sensing literature are either preliminary, or dated (Rush and Vernon 1975, Jovanovic 1987 a, 1987 b, Wood *et al.* 1992 a, Hacker and Roberts

Table   Major tropical diseases in 1990.

Disease	Prevalence of infection (millions)	Populations at risk (millions)	Distribution
Vector-borne			
Malaria	300–500	2300	Tropics, subtropics
Lymphatic filariasis	90	900	Tropics, subtropics
Leishmaniasis	12	350	Tropics, subtropics
Onchocerciasis	18	90	Africa, Latin America
Trypanosomiasis	25000 new cases/year	50	Tropical Africa
Intermediate host			
Schistosomiasis	200	600	Tropics, subtropics
Dracunculiasis	1–3	63	Tropics (Africa, Asia)

This table shows status of the major human vector-borne and intermediate host transmitted diseases in 1990 and is adapted from WHO (1990, 1994) and Rogers and Packer (1993). The population at risk estimates are based on a world population of approximately 4·8 billion in 1989.

1994, Beck *et al.* 1995). This has allowed common objections concerning complexity, expense, appropriateness and lack of proven operational application to go unchallenged (Barinaga 1993, Kleiner 1995). This review highlights the progress and current status of remote sensing techniques in epidemiology and uses this background to draw conclusions on opportunities for future application and synergy.

2.   Invertebrate intermediate hosts, remote sensing and disease

The prerequisite for all epidemiological applications of remote sensing is a close association between life history variables of a parasite or intermediate host species and environmental features that can be observed remotely (Hugh-Jones 1989, Epstein and Chikwenhere 1994). With this criterion satisfied, remote sensing can provide a relatively homogeneous sample of environmental variables through a wide range of spectral, spatial and temporal resolutions, depending on the choice of sensor and the satellite platform on which it is carried (Cracknell 1991). An overview of the specifications of the satellite sensors most often used in epidemiological studies is given in Hay *et al.* (1996) and summarized in table 2. For the purposes of this review high spatial resolution sensors are arbitrarily defined as those that, when in orbit, are able to resolve pixels smaller than 1×1 km and low spatial resolution sensors as those which can resolve only larger pixels.

Remote sensing is of particular relevance in the technologically developing tropics since it is there that the diseases concerned are most prevalent, the basic information on disease incidence (distribution) and prevalence (abundance) over extensive areas is lacking, and the resources available to deal with disease problems are least. Furthermore, the specificity of many of the disease vectors and the increasing problem of insecticide resistance (Roberts and Andre 1994), coupled with the continued difficulties of chemotherapy and vaccine development (McLaren and Terry 1989, Desowitz 1993, Hide 1994), have resulted in a return to an emphasis on the reduction of vector populations for disease control (Molyneux 1993, Davies 1994, Green 1994, Rogers *et al.* 1994).

Table 2. The spatial, temporal and spectral resolution of the sensors carried by the SPOT, Landsat, NOAA and Meteosat satellites.

Resolution	Spectral[a]	Spatial[b]	Temporal
Satellite Pour l'Observation de la Terre (SPOT)			
High Resolution Visible (HRV)			
Panchromatic mode (HRV-PAN)	Ch 1 (0·51–0·73)	10 m	26 days[c]
Multi-spectral mode (HRV-XS)	Ch 2 (0·50–0·59)	20 m	
	Ch 3 (0·61–0·68)	20 m	
	Ch 4 (0·79–0·89)	20 m	
Landsat-1, -2, -3			
Return Beam Vidicon (RBV) camera	Ch 1 (0·475–0·575)	80 m	18 days
	Ch 2 (0·580–0·680)		
	Ch 3 (0·690–0·830)[d]		
Landsat-1, -2, -3, -4, -5			
Multi-spectral Scanner (MSS)	Ch 4 (0·5–0·6)	79/82 m[e]	16/18 days
	Ch 5 (0·6–0·7)		
	Ch 6 (0·7–0·8)		
	Ch 7 (0·8–1·1)		
Landsat-4, -5			
Thematic Mapper (TM)	Ch 1 (0·45–0·52)	30 m	16 days
	Ch 2 (0·52–0·60)	30 m	
	Ch 3 (0·63–0·69)	30 m	
	Ch 4 (0·76–0·90)	30 m	
	Ch 5 (1·55–1·75)	30 m	
	Ch 6 (10·40–12·50)	120 m	
	Ch 7 (2·10–2·35)	30 m	
National Oceanic and Atmospheric Administration (NOAA)			
Advanced Very High Resolution Radiometer (AVHRR)	Ch 1 (0·58–0·68)	1·1 km	12 h
	Ch 2 (0·72–1·10)		
	Ch 3 (3·55–3·93)		
	Ch 4 (10·30–11·30)		
	Ch 5 (10·50–11·50)		
Meteosat-4, -5, -6			
High Resolution Radiometer (HRR)	Ch 1 (0·40–1·10)	2·5 km	0·5 h
	Ch 2 (10·50–12·50)	5 km	
	Ch 3 (5·70–7·10)	5 km	

[a] The spectral resolutions are the electromagnetic wavelength range in μm. [b] The spatial resolution is given as diameter of the viewing area of the sensor at nadir. [c] A pointing facility can improve the frequency of coverage. [d] Landsat-3 had a fourth RBV channel (0·505–0·750) at 30 m spatial resolution. [e] The spatial resolution is 79 m for Landsat-1 to -3 and 82 m for Landsat-4 and -5; the temporal resolution also changed from 16 to 18 days

3. Disease control

The principal goal of remote sensing in epidemiology is to map the distribution of a disease (often by mapping the distribution of its intermediate host) so that control efforts in endemic situations and intervention strategies in epidemic situations may be most efficiently directed.

Determining the distribution of intermediate hosts is often the first step in an epidemiologically sound approach to disease control. This arises because the basic reproductive rate (or number) of a disease, R_0, which describes the average number of new cases of the disease that will arise from the introduction of an infective host

into a susceptible population (Dietz 1988, Anderson and May 1991, Lord *et al.* 1996), is influenced primarily by factors associated with the invertebrate intermediate host. The standard formula for insect vector-borne diseases is

$$R_o = \frac{a^2 m \ c \ b \ e^{-uT}}{\mu r} \tag{1}$$

where, a is the vector biting rate, m is the ratio of vectors to hosts, c is the transmission coefficient from vertebrate to vector (i.e., the proportion of bites by vectors on infected hosts that eventually give rise to mature infections in the vectors), b is the transmission coefficient from vector to vertebrate, μ, is the vector mortality rate, T, is the incubation period of the infection within the vector (sometimes referred to as the extrinsic incubation period) and r is the rate of recovery of the vertebrate from infection (Rogers 1988). Somewhat different equations describe R_o in tick vectors and those diseases requiring intermediate hosts that do not feed directly on the vertebrate hosts. All of the variables in the above equation are some function of the vector, save r which is a function of the host alone. Given this importance of many aspects of intermediate host biology and behaviour to the transmission dynamics of the diseases they carry, it follows that the distribution and intensity of such diseases is dependent upon the distribution and abundance of the intermediate hosts. Control campaigns should therefore aim to decrease intermediate host population numbers below the threshold of disease transmission (Rogers *et al.* 1994). This occurs when R_o falls to a value of less than one.

4. Malaria and filariasis
4.1. *Disease and vector biology*

Mosquitoes (flies of the family Culicidae, see figure 1(*a*)) have a simple life cycle with the egg, larval and pupal stages passed in still, or slow-moving fresh or brackish water. Soon after emergence the haematophagous adult females seek vertebrate hosts in order to feed. The ingested blood is used in egg production and, following oviposition, females seek further blood-meals to nourish future broods. It is this repeated feeding that facilitates the transmission of parasites between hosts (Bruce-Chwatt 1986). The organisms for which mosquitoes act as vectors include a range of arboviruses (arthropod-borne viruses) such as yellow fever, dengue fever and Rift Valley fever viruses; nematode worms such as *Wuchereria bancrofti* and *Brugia malayi* which cause lymphatic filariasis; and four species of the protozoan genus *Plasmodium* that cause malaria in humans (Mattingley 1969).

Worldwide, mosquitoes are the most important vectors of disease (Godfrey 1978). It is estimated that 2300 million people are at risk from malaria (approximately 42 per cent of the world population), and of these it is estimated between 300–500 million clinical cases are reported each year, 90 per cent of which occur in Africa (WHO 1994). Lymphatic filariasis affects a further 900 million people and, though generally not life-threatening, causes chronic suffering and disability when the adult worms develop in the afferent lymphatic system, leading to painfully swollen and permanently disfigured limbs, often referred to as elephantiasis (Whitfield 1993).

It is the dependence of mosquitoes on fresh and brackish water habitats in the early stages of their life cycle that has allowed remote sensing techniques to be exploited. This is of particular advantage because insecticide is often applied to breeding habitats to kill the larvae during control campaigns.
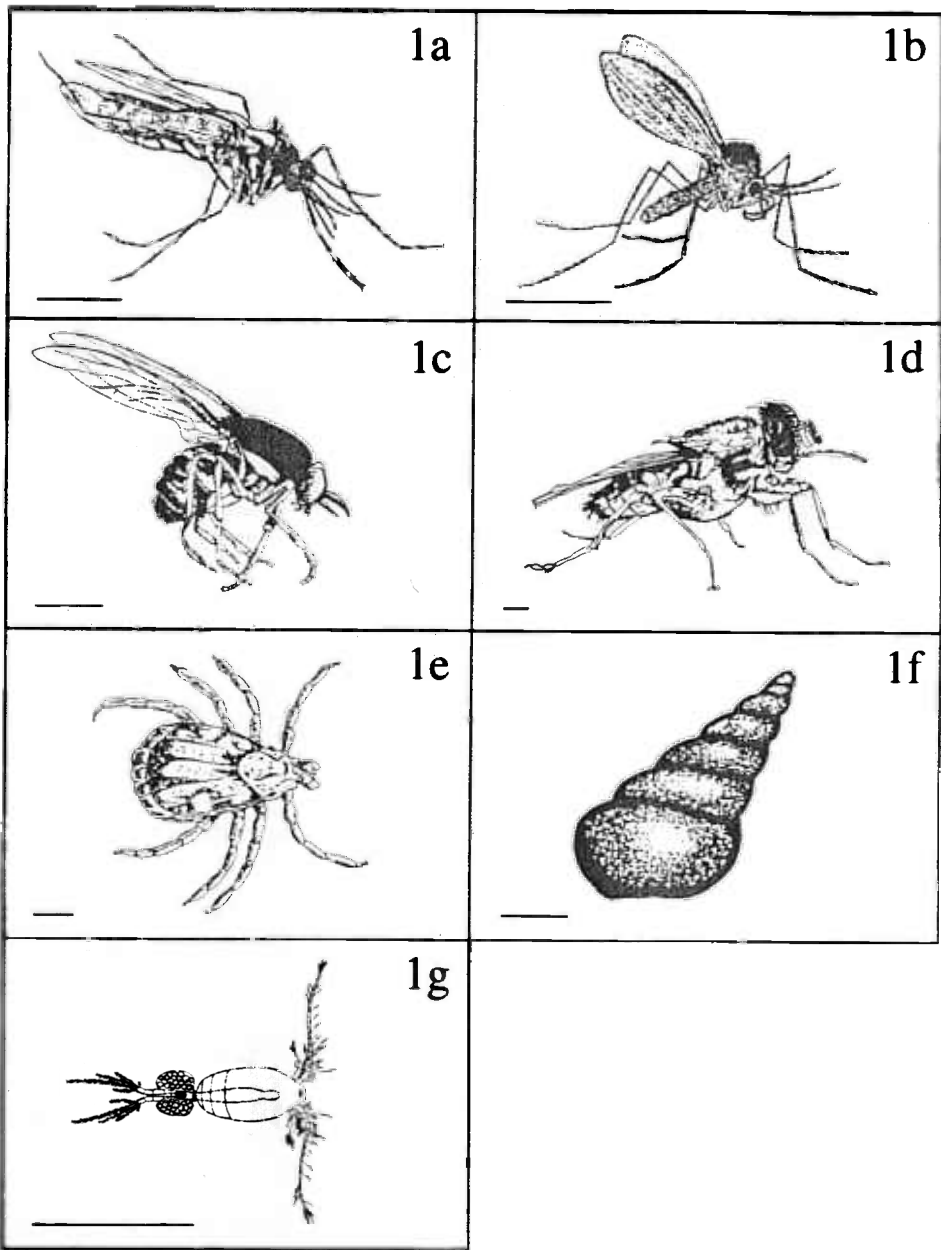
Figure 1.   (a)–(h). Examples of the invertebrate intermediate host and disease vectors species reviewed in the paper. (a) adult female mosquito (family Culicidae, subfamily anophelinae); (b) adult female sandfly (family Psychodidae, subfamily Phlebotaminae); (c) adult female blackfly (family Simuliidae); (d) adult female tsetse fly (family Glossinidae); (e) adult female tick (family Ixodidae); (f) adult aquatic snail (*Oncomelania* spp.); (g) adult female crustacean (*Cyclops* spp). The scale bar in each figure represents 1 mm, except for (g) where it is 0·1 mm. Redrawn in part from Molyneux (1993).

4.2. *Application of high spatial resolution imagery*

In 1971, as part of the HAO initiatives, NASA scientists in combination with personnel from the New Orleans Mosquito Control District (NOMCD) were the first to investigate the use of colour and colour-infrared aerial photography in mapping vegetation assemblages associated with the larval habitat of *Aedes sollicitans*, a saltmarsh mosquito suspected of transmitting the equine encephalitis virus (NASA 1973). Previous work by the NOMCD had shown that the females would always oviposit in areas of the saltmarsh intermittently flooded by freshwater. The floral assemblage dominated by spikerush (*Spartina patens*) and wiregrass (*Juncus roemerianus*) was known to be adapted to the same hydrological regime, and hence was a reliable indicator of *A. sollicitans* larval habitat (Bidlingmayer and Klock 1955). The report documents that such vegetation assemblages were 'extremely accurately' identified at an 80 ha test site near New Orleans, although no statistics were provided.

The first operational use of colour-infrared aerial photography was to map forested and open wetlands, marshes and residential areas for mosquito control in the Saginaw and Bay Counties of Michigan (Wagner *et al.* 1979). These habitats supported populations of nuisance *Aedes* and *Culex* species of mosquitoes that were vectors for a local epidemic of St Louis encephalitis (SLE) in 1975. SLE is an arbovirus causing severe irritation of the central nervous system that proves fatal in approximately 10 per cent of cases (Leake *et al.* 1934, Shope 1980). The known flight range of each mosquito species was used in combination with information on the distance between residential areas and mosquito habitat to identify control priorities for the two counties. The authors stressed the short time in which the environmental inventory was gathered and management priorities identified. Furthermore, the streamlining of subsequent control efforts led to a campaign of relatively low economic and environmental cost, since the area designated for insecticide treatment was considerably reduced in comparison to the more traditional approach of broadcast spraying. For example, Hopkins *et al.* (1975) report that after an outbreak of SLE in Dallas in 1966, the entire county of Texas was sprayed aerially with an organophosphate insecticide (malathion) mist.

The use of colour-infrared aerial photography has been cited as a more cost-effective method than conventional ground survey techniques of obtaining information on the distribution of oviposition habitats of the mosquito *Psorophora columbiae* in Louisiana and Texas rice fields (Fleetwood *et al.* 1981, Welch *et al.* 1989 a, 1989 b). Improvements upon colour-infrared aerial photography were demonstrated by Cibula (1976) and Barnes and Cibula (1979) using an airborne Multi-Spectral Scanner (MSS) that had a spatial resolution of 2.5×2.5 m when flown at an altitude of 1200 m. The greater number of wavelengths at which data were recorded (22 channels from $0.3–13\,\mu m$) enabled a more accurate spectral identification of the *Spartina-Juncas* associations characteristic of favourable egg-laying habitats for *Aedes sollicitans* than aerial infrared photographs. In a similar study Hayes *et al.* (1985) reported that *Culex tarsalis* and *Aedes vexans* larval habitats could be identified along the Niobara River in north-east Nebraska with Landsat-1 and 2 MSS data, using transitional freshwater plant communities associated with seasonal flooding as an indicator. This study demonstrated that such species-habitat correlations could be successfully 'scaled-up' to regional control programmes using relatively high spatial resolution satellite sensor data.

Under the aegis of the NASA Biospheric Monitoring and Disease Prediction

(DI-MOD) Project, various authors have investigated the hypothesis that the spatial and temporal aspects of mosquito population dynamics are controlled by environmental factors that can be observed remotely (Wood *et al.* 1994). In phase I of this project, populations of *Anopheles freeborni* in the rice fields of northern and central California were studied (Pitcairn *et al.* 1988). This species of mosquito represented no significant health risk to the local population, but provided an accessible model for the study of Anopheline vectors in irrigated rice habitat (Wood *et al.* 1991 a, 1991 b, 1992 b). This is important since the cultivation of irrigated rice (a land use occupying an area of 140 million ha globally) provides an ideal habitat for Anopheline mosquitoes, which are the vectors for human malaria transmission in the tropics (Service 1989).

Larval mosquito populations were sampled fortnightly throughout the period of rice crop development in 1985 (Wood *et al.* 1991 a). An airborne MSS collected data simultaneously in bands designed to simulate the Landsat Thematic Mapper (TM). A normalized difference vegetation index (NDVI) was then calculated for individual fields on each of the sampling dates and the differences in spectral signal between rice fields producing high and low numbers of Anopheline larvae were followed throughout the growing season. The NDVI was considered an important variable since Rejmankova *et al.* (1988) had previously demonstrated percentage rice crop cover to be positively correlated with mosquito larval production. The results showed that higher values of NDVI in the early growing season (June) were associated with high mosquito producing rice fields, but that the spectral separation (between high and low mosquito producing fields) diminished to a minimum in mid July, when percentage rice crop cover exceeded 100 per cent. A discriminant analysis which incorporated information from Landsat-TM equivalent channels 1, 2, 3, 4 and 7, was able to distinguish between high and low mosquito producing fields with an overall accuracy of 75 per cent. The uneven distribution of high mosquito producing fields was also shown to be related to patterns of surrounding land-use, with 70 per cent of the high mosquito producing fields being within 1·5 km of livestock pasture (i.e., potential hosts). A more detailed survey in 1987 repeated the above work and included data on the distance to livestock in a geographical information system (GIS) (Wood *et al.* 1991 b). An identical discriminant analysis combined with cattle distance data resolved high and low producing fields with an accuracy of 90 per cent, with errors of omission (not identifying high producing fields) and commission (identifying as a high producing field one which is not) of 10 and 40 per cent respectively (Wood *et al.* 1992 b).

The second phase of the project investigated the population dynamics of *Anopheles albimanus* and *Anopheles pseudopunctipennis* in the tropical wetlands of Chiapas, Mexico, where malaria is endemic (Roberts *et al.* 1991). Pope *et al.* (1994) used two Landsat-TM scenes of the area, one from the dry and one from the wet season, to provide an unsupervised classification of the region. The resulting clusters were assigned to land-cover types on the basis of colour-infrared aerial photographs and field inspection of 30 test sites. These sites were independently sampled for mosquito density and information was collected on environmental variables affecting water and vegetation characteristics (Rejmankova *et al.* 1991). The sites were then grouped into 16 habitat types using a cluster analysis and correlations were performed between the habitat types and land-cover units (Rejmankova *et al.* 1992). The land-cover units were subsequently ranked as having high, medium or low mosquito production potential on the basis of these correlations. Incorporating this information

into a GIS, sites of high mosquito production around the towns of La Victoria and Efrain Gutierrez were found to occupy only 9 per cent of the designated control area, allowing the potential for substantial streamlining of control campaign effort and resources.

A separate study demonstrated how such information could be used effectively by identifying particular villages at high risk within the control area (Beck *et al.* 1994). Dry and wet season Landsat-TM scenes were again subjected to an unsupervised classification. A stepwise discriminant analysis and linear regression were then used to establish the relationship between vector abundance and landscape element proportions. In both cases transitional swamp and unmanaged pasture habitats were identified as most important, and in combination it was possible to distinguish between villages with high and low vector abundance to an overall accuracy of 90 per cent. In addition, the authors noted that such an analysis could be extrapolated spatially, albeit with a diminished accuracy, to the whole of the Chiapas coastal region where malaria is a significant health problem.

Rejmankova *et al.* (1995) have also shown that the density of adult *Anopheles albimanus* mosquitoes around villages in Belize could be reliably predicted using multi-spectral Satellite Pour l'Observation de la Terre (SPOT) High Resolution Visible (HRV) data. Productive larval habitats were first identified as marshes containing relatively few emergent aquatic plants and a high coverage of cyano-bacterial mats. An unsupervised Bayesian maximum likelihood classification was then applied to a single SPOT scene covering a test site occupying northern Belize. The classes generated were subsequently assigned to individual 'landscape elements' based on field observations. Human settlements were identified with ancillary map data and located more precisely on subsequent field visits with a global positioning system (GPS). These settlements were divided into two groups according to their distance from the larval habitat class. Group 1 was composed of settlements closer than 500 m and group 2 of settlements further than 1500 m. Based on independent measurements, a landing rate of greater than 0·5 mosquitoes per human per minute (during the hours of maximum mosquito activity from 6:30 p.m. to 8:00 p.m.) was used as a threshold for high adult mosquito density (Rodriguez *et al.* 1996). Group 1 was predicted as having adult mosquito densities higher than this threshold and group 2 lower. These predictions were tested by collecting mosquitoes landing on humans during the hours of peak activity within each of the settlements. The resulting predictions were 100 per cent accurate for group 2 and 89 per cent accurate for group 1.

Roberts *et al.* (1996) investigated the utility of multi-spectral SPOT-HRV data in predicting the distribution of the malaria vector *Anopheles pseudopunctipennis* in central Belize. Previous investigations had shown that altitude and the presence of filamentous algae in sun-exposed pools to be critical determinants for the presence of *An. pseudopunctipennis* larvae (Rejmankova *et al.* 1993). Using the SPOT and cartographic data 49 sites were chosen and predicted to have a high or low probability for *An. pseudopunctipennis* presence. The criteria used in site selection were the distance of the houses from waterways, their altitude above such waterways, as well as the amount of forest between the houses and the waterway. The SPOT data provided more contemporary information than the cartographic data and hence allowed map errors to be corrected. It also showed information on important aspects of environmental suitability which could not be attained from the maps, such as the size of a waterway or the degree to which it was open from sunlight. Collections of

mosquitoes were then made in a sample of these sites to test the predictions. Four of the eight sites that were predicted as high probability locations for presence of *An. pseudopunctipennis* were positive and all low probability sites (0 of 12) were negative. The absence of *An. pseudopunctipennis* at four high probability locations was thought to be due to field population densities of the species being below the threshold of the sampling effort.

4.3. *Application of low spatial resolution imagery*

Work in relation to mosquito vectors has not been restricted to high spatial resolution imagery. Global area coverage (GAC) NDVI data from the National Oceanic and Atmospheric Administration's (NOAA) Advanced Very High Resolution Radiometer (AVHRR) have been applied to the problem of Rift Valley fever (RVF) epidemics in Africa (Linthicum *et al.* 1987, 1990). Rift Valley fever is a viral disease transmitted by various species of *Culex* mosquitoes to domestic animals and closely associated human populations (Wilson 1994). The work on a regional scale showed that high NDVI values in Kenya were good indicators of seasonally flooded linear depressions, known as dambos. These habitats were highly suitable for mosquito breeding and hence closely associated with RVF epidemics. On the basis of this initial work an RVF virus epidemic was correctly predicted in central Kenya following exceptionally high NDVIs throughout 1988 and 1989 (Bailey and Linthicum 1989).

The work progressed to incorporate higher spatial resolution Landsat-TM and multi-spectral SPOT-HRV imagery to locate individual areas of high RVF risk determined by the NDVI (Linthicum *et al.* 1991). Operational application of the technique, however, was hindered because investigators were not able to discriminate flooded from dry dambos. Data from an airborne Synthetic Aperture Radar (SAR) were therefore incorporated to detect dambo flooding status (Pope *et al.* 1992). A significant advantage of using SAR was that data collection was independent of cloud coverage, especially important during the East African rains. The study also demonstrated that the spatial resolution of current satellite-borne SARs was not sufficient to reveal many of the smaller dambos in the region.

Linthicum *et al.* (1994) also investigated an unusually severe and extensive outbreak of RVF in the West African Senegal river basin in 1987. The RVF outbreak was particularly unusual in that it occurred during a period of only moderate rainfall. Analysis of multi-spectral SPOT-HRV scenes for the period of the epidemic revealed extensive flooding in Mauritania to have peaked in October 1987, as a result of the construction of the Diama and Manatelli dams on the river Senegal. This coincided exactly with the period of maximum RVF disease activity in the area. Furthermore, maximum values of Local Area Coverage (LAC) NDVIs were associated with increased rice production (and hence productive mosquito larva habitats) around the newly flooded regions in Daro and Rosso, the foci of RVF outbreaks. Unfortunately, no statistics were presented in the study.

Thomson *et al.* (1995 b, 1996) also investigated the potential of coarse spatial resolution GAC and Local Area Coverage (LAC) NOAA-AVHRR data, as well as Cold Cloud Duration (CCD) data from the Food and Agriculture Organisation's (FAO) African Real Time Environmental Monitoring using Imaging Satellites (ARTEMIS) programme to predict malaria epidemics in the Gambia. They concluded, however, that although there were clear relationships between satellite sensor data and environmental variables associated with malaria transmission, it was diffi-

cult to predict how these would affect adult mosquito abundance and behaviour. For instance, along the River Gambia a decrease in rainfall may at times increase available Anopheline breeding sites by increasing the number of suitable pools in the alluvial soils at the river margin. They also noted that relationships between malaria incidence and environmental variables were complicated by sociological factors, because in areas where Anopheline abundance was greatest and hence biting most frequent, people were more likely to protect themselves with insecticide-impregnated bed nets (Thomson *et al.* 1995 a).

4.4. *Future potential*

A wide range of remotely sensed imagery has been utilized with respect to mosquito-borne diseases and the work has progressed significantly from habitat characterizations at high spatial resolution to work that has inferred habitat quality (and hence disease risk) for both larval and adult forms from the village to regional scale. These studies indicate the substantial potential for risk monitoring, so that it might be possible to initiate mosquito control efforts prior to disease outbreaks. Furthermore, despite the perceived expense several of the studies have demonstrated that remote sensing techniques can be cost effective components of mosquito control campaigns (i.e., Wagner *et al.* 1979) which augurs well for their future operational application.

5. Leishmaniasis

5.1. *Disease and vector biology*

Approximately 20 species and subspecies of the protozoal parasite genus *Leishmania* cause leishmaniasis in humans (Chang and Bray 1985). The disease complex can result in symptoms ranging from skin ulcers that heal without treatment caused, for example, by cutaneous infection with *Leishmania major*, to extensive and permanent tissue destruction (often around the mouth and nose), due to mucocutaneous infection by species such as *Leishmania braziliensis* in a small number of cases. The most serious of the diseases, visceral leishmaniasis, or kala-azar, is caused by *Leishmania donovani*, a life-threatening parasite which invades and destroys immune system cells often associated with the liver and spleen (Peters and Killick-Kendrick 1987). Untreated visceral leishmaniasis usually results in death and it is estimated that 350 million people are at risk worldwide, with approximately 12 million people infected at any one time (WHO 1990).

Humans become infected with leishmaniasis through the bites of female sandflies containing the *Leishmania* parasite (family Psychodidae, see figure 1(*b*)). Most types of *Leishmania* infect small mammals, which can also act as reservoirs of the human disease (Lane 1987). Sandflies usually inhabit arid environments and are active only at night; during the day they seek cool and humid microclimates such as crevices in walls or animal burrows (Theodor 1936). The larval habitat is poorly known and is thought from laboratory observations to be in soil with a high organic matter content, on which the larvae feed.

5.2. *Application of low spatial resolution imagery*

Cross *et al.* (1996) used a combination of weather data and AVHRR-GAC data to predict the geographic and seasonal distribution of *Phlebotomus papatasi* in southwest Asia. The impetus for the work was to understand the dynamics of leishmaniasis in the Middle East because it historically, and remains to the present day, a major

but temporally and geographically variable source of morbidity in troop deployment to the region. A computer model was developed using the occurrence of *P. papatasi* (as determined by a literature search of all reported incidences in the region since 1930) as a dependent variable and the mean synoptic weather data (duration not reported) as independent variables. The predictions were therefore only valid for the 114 meteorological stations on which the analysis was based. Mean monthly NDVI data from the NOAA-AVHRR calculated for the period 1982–1994 were then determined for each weather station. The results of the frequency of NDVI levels versus the probability of vector occurrence was then used to established NDVI limits for vector presence (0·00–0·06). A probable distribution map for the species was subsequently generated by assigning vector presence or absence to pixels over the entire Middle East, for all months of the year, based on their mean NDVI values. This significantly expanded on information available in the literature and has provided useful information on the spatial and temporal distribution of *P. papatasi* in the region.

5.3. *Future potential*

Despite the relatively poor knowledge of the ecology of the sandfly vector (particularly in its larval stages) the above study has shown that insight can be gained by investigating remotely sensed variables that may correlate with intermediate host distributions and hence disease risk. Furthermore, information gathered in this way can be immediately useful for epidemiological management and may also provide clues to help direct studies of the ecology of the species concerned.

6. Onchocerciasis

6.1. *Diseases and vector biology*

Onchocerciasis is a disease causing considerable morbidity due to the response of the human immune system to invasion of the eye and skin (resulting in river blindness and onchodermatitis respectively) and the lymphatic system by several distinct strains of the nematode worm *Onchocerca volvulus* (WHO 1987). Each strain is transmitted between humans by one of several species of haematophagous female blackflies (flies of the family Simuliidae, see figure 1 (*c*)). Most blackflies have a life cycle in which the larvae filter-feed in fast-flowing, well-oxygenated freshwater streams and rivers. The disease occurs in 34 countries with 18 million people infected with the worm of which 267 000 have been blinded (WHO 1995).

6.2. *Remote sensing application*

Baker and Abdelnur (1986 a) used Landsat–Return Beam Vidicon (RBV) imagery and aerial photography to determine the course of rivers for control of *Simulium damnosum* s.l. in the Bahr el Ghazal region of south-western Sudan. The satellite imagery was necessary because the only available maps of the region were too poor in detail and accuracy to be of use. The information on river and stream distributions were used in combination with details of the local road network and habitations to strategically position monitoring sites. The criteria used to locate the traps were that they should be situated close to villages, accessed easily throughout the rainy season and spaced so as to monitor as large a part of the river as possible. The 11 chosen sites were then used to monitor biting and disease transmission rates for a 2-year period. Controls were instigated in the third year of the study by treating stretches of the river with insecticide to kill the larvae. The 2-year pre-control phase of the

study allowed the effects of intervention to be quantified. It was found that control efforts resulted in a 70 per cent reduction in the number of bites experienced by the local population and a reduction of 80 per cent in the transmission of onchocerciasis (Baker and Abdelnur 1986 b).

Landsat-TM data have been used to map land-cover within the nine countries of the West African Onchocerciasis Control Program (OCP) to help governments plan development potential for land on which onchocerciasis had been controlled (WHO 1985). Furthermore, Servat *et al.* (1990) describe how satellites were used to transmit water discharge data from a network of measuring instruments in remote rivers and streams throughout the OCP catchment area. This allowed a more reliable estimate of the amount of insecticide needed to control local blackfly populations, so increasing the efficacy of the control campaign and reducing running costs.

6.3. *Future potential*

Adult blackflies disperse up to 500 km from larval breeding sites and it seems likely that dispersal patterns are determined by wind fields, and fly survival by local climatic conditions, both of which may be monitored remotely (Baker *et al.* 1990). In general, however, the spatial distribution of infection reflects the distribution of riverine breeding sites (Crosskey 1990). The potential to map these types of riparian habitats from space is high using SPOT-HRV and Landsat-TM imagery, but the ability to determine habitat suitability is thought to be low because of the temporally dynamic nature of the specific flow conditions required for the larvae (C. Back, personal communication 1995). There are no examples of remote sensing techniques having been applied directly to adult blackfly surveillance. Furthermore, now that Ivermectin provides effective chemotherapy future large-area vector control campaigns seem unlikely (Gillies and Awadzie 1991, Davies 1994). Resurgence often occurs, however, where drug delivery and/or community uptake of chemotherapy is poor. The greatest role for remote sensing therefore, might be in combination with GIS to establish buffer zones around potential breeding sites to target very localized control and help manage land-use in these areas with prior knowledge of disease transmission potential.

7. Trypanosomiasis

7.1. *Disease and vector biology*

Tsetse flies (*Glossina* spp., see figure 1(*d*)) are an entirely African family of haematophagous flies, the *Glossinidae*, in which both sexes can transmit protozoan trypanosome parasites between vertebrate hosts while feeding (Ford 1971). They are unusual in being larviparous, with each female giving birth to a single full-grown larva once every 7–10 days. The larva then rapidly burrows into the soil, pupates, and the adult emerges approximately one month later. Thus tsetse birth rates and mortality rates are extremely low compared to other disease vectors (Rogers 1988).

Fifty million people in Africa are presently at risk from contracting human trypanosomiasis or sleeping sickness (Kuzoe 1993) which, when left untreated, proves fatal due to the invasion of the central nervous system by the trypanosomes. Tsetse flies are also vectors for trypanosome species which infect cattle, causing animal trypanosomiasis or 'nagana' (Hoare 1972). The occurrence of animal trypanosomiasis excludes livestock from an area of approximately 10 million km² and is therefore a major constraint on livestock productivity in Africa (Murray and Gray 1984).

7.2. *Application of high spatial resolution imagery*

The NASA-HAO was again among the first to look at the potential of remote sensing for the identification of tsetse fly habitats (Giddings 1976). Near-infrared data from Landsat-2 MSS were used to map land-cover at a test site in Tanzania. Although such mapping was considered feasible, no conclusions were drawn on how this might help in tsetse control.

Kitron *et al.* (1996) analysed tsetse fly catches from sets of biconical traps set in the Lambwe Valley of Western Kenya during 1988–1990. They found that a multiple regression using the seven wavelength bands of the Landsat-TM was able to explain 87 per cent of the variance in fly catch density. The Landsat-TM band 7 that is associated with soil-water content was found to be consistently highly correlated, reflecting the importance of soil moisture in tsetse survival (Rogers and Randolph 1986). The data were also used to calculate the NDVI, but this did not improve the relationship over that with the original bands. The spatial autocorrelation in the data was assessed using Moran's (*I*) statistic and found to explain a significant part of the association between the fly density and the spectral data. Kitron *et al.* (1996) stressed that these spatial factors should be further investigated and on the basis of this work stated:

> 'the incorporation of remotely sensed imagery into a GIS with ground data on fly density and environmental conditions can be used to predict favourable fly habitats in inaccessible sites, and to determine number and location of fly suppression traps in a local control programme'.

7.3. *Application of low spatial resolution imagery*

Rogers and Randolph (1991, 1994) explored the utility of GAC-NDVI data derived from the NOAA-AVHRR in a study of tsetse fly ecology and distribution in West Africa, since they considered the NDVI to integrate a variety of environmental factors of importance to tsetse survival. They found an inverse relationship between monthly NDVI and fly mortality rate in the Yankari game reserve in Nigeria and significant nonlinear relationships between tsetse fly abundance and NDVI in the northern part of Côte d'Ivoire. Later, they focused on a 700 km transect running north–south through Côte d'Ivoire and Burkina Faso. This area is of particular epidemiological interest since sleeping sickness is found only in the central region of the transect, despite the local vector (*Glossina palpalis*) occurring throughout.

The solution of this conundrum lay in the length of a particular vein in the tsetse's wing. This vein length is an indicator of overall fly size, which is determined by the environmental conditions experienced by the maternal fly while she is gestating the larva (approximately one month before the new adult fly emerges from its puparia). Mean vein lengths for flies caught at eight equidistant sample sites along the north–south transect were related to the NDVI of the previous month for each site. During the wet season, the NDVIs across the transect were all high and fly size was uniformly large. In the dry season, however, fly size was strongly correlated with NDVI, with flies in the drier north significantly smaller than those in the wetter south. Mortality increases with decreasing fly size in tsetse and similar size differences have been shown to be related to a significant increase in *Glossina palpalis* mortality in Kenya (Dransfield *et al.* 1989). These data were interpreted as indicating a geographical gradient in the degree of man–fly contact and thus trypanosome transmission potential. In the south, low mortality rates resulted in high densities of flies,

but the flies were not nutritionally stressed (even seasonally) and so did not often resort to biting man, who is not a favoured host. Conversely, in the north fly populations suffered too high a mortality to pose a serious health risk. Only in the central areas was there an intermediate density of sufficiently stressed flies, resulting in a regional and seasonal focus of disease transmission.

Further work illustrated correlations between the monthly incidence of trypanosomiasis and mean monthly NDVIs (Rogers 1991). Positive correlations were shown in settlements surrounding the Olambwe Valley game reserve in Kenya and negative correlations in Kigulu County on the shores of Lake Victoria in Uganda. The differences were attributed to the contrasting ecology of the respective tsetse vector species. In Uganda the vector *Glossina fuscipes* coexists with man throughout the year. The flies prefer other mammal hosts and only bite humans frequently when they require more blood-meals in the dry season. Transmission therefore increases as vegetation cover and photosynthetic activity (and hence the NDVI) decrease in the dry season, leading to a negative correlation. In contrast, the local vector *Glossina pallidipes* in Kenya spends most of its time in dense scrub thickets in the centre of the game reserve, but spreads out from the thicket, and comes into contact with humans that inhabit the reserve margins, when humid conditions allow fly dispersal in the rainy season. Transmission therefore increases as the NDVI increases in the wet season, resulting in a positive correlation. These initial studies showed that both tsetse distribution and abundance, and disease incidence and prevalence could be related to the NDVI at low spatial resolutions, although the interpretation of the variable correlations required a knowledge of local conditions and fly biology from ground studies.

Rogers and Williams (1993) describe the application of NOAA-AVHRR GAC-NDVI data and synoptic meteorological temperature data to the problem of predicting the distribution of *Glossina morsitans* in Zimbabwe, Kenya and Tanzania. Temperature data (a critical climatic variable in determining the survival of tsetse (Bursell 1959)) were included in the analysis by interpolating data from meteorological stations to grid squares covering the whole of Zimbabwe. When these data were combined with NDVI variables in a linear discriminant analysis the historical distribution of *Glossina morsitans* in Zimbabwe, as described in Ford and Katondo (1977), were predicted with an accuracy of over 80 per cent. Historical distributions were used because the authors considered them to reflect the original fly habitat more closely than present-day distributions. This is because current geographical ranges have been extensively modified by the elimination of game, the rinderpest panzootic at the end of the last century (that killed over 85 per cent of domestic stock) and the activities of tsetse control campaigns in the present (Ford 1971).

The utility of these statistical approaches was shown in two studies that investigated how tsetse distributions might be modified with global climate change (Rogers and Randolph 1993, Rogers 1995). Rogers and Randolph (1993) looked again at the distributions of *Glossina morsitans* in Zimbabwe, Kenya and Tanzania. Using elevation, NDVI and synoptic temperature data they were able to predict the distribution to an overall accuracy of 82 per cent. The mean temperature difference between areas suitable and unsuitable for tsetse was shown to be only 0–1° C and hence the distributions were very sensitive to temperature changes. The scenario of increasing the average temperature by 1° C throughout the region resulted in the predicted range of *Glossina morsitans* expanding into the presently unfavourable and livestock-productive highland areas of Zimbabwe.

Rogers (1995) continued this theme and contrasted the distribution changes predicted for *Glossina morsitans* and *Glossina pallidipes* in Kenya and Tanzania using a similar elevation, NDVI and synoptic meteorological temperature dataset. The distribution of *Glossina morsitans* was again found to expand, given scenarios of $1°–3°$ C warming, but the range of *Glossina pallidipes* contracted substantially. The sensitivity of such analyses was illustrated by taking elevation out as a predictor variable, causing the range of *Glossina pallidipes* to expand. Given such uncertainty, the author suggested that studies should focus on understanding the reasons for present and past distributions before extrapolating through time.
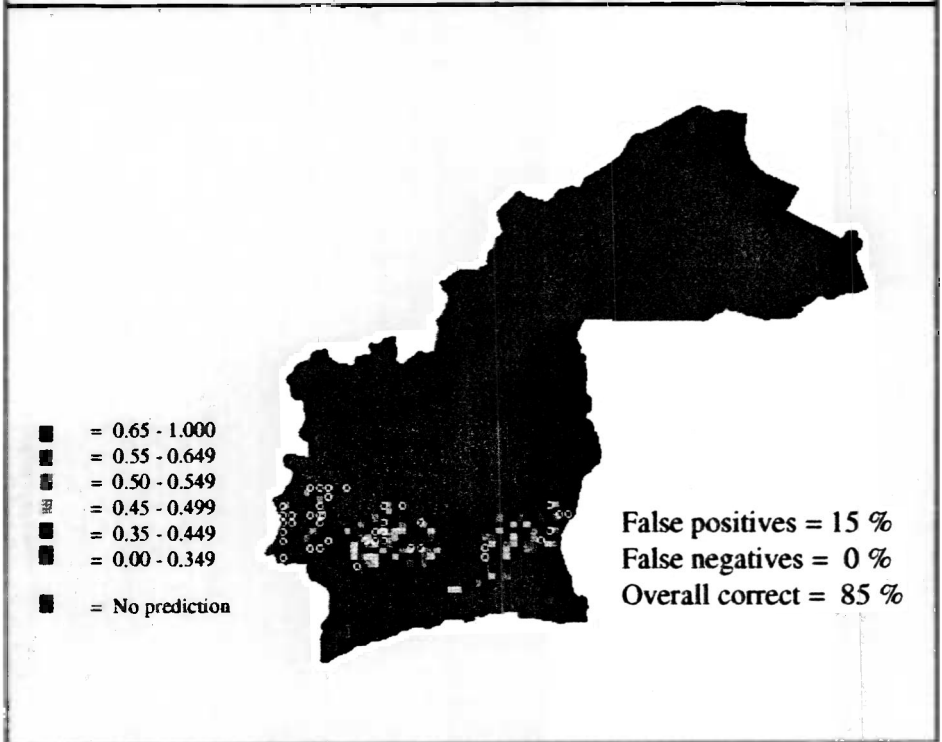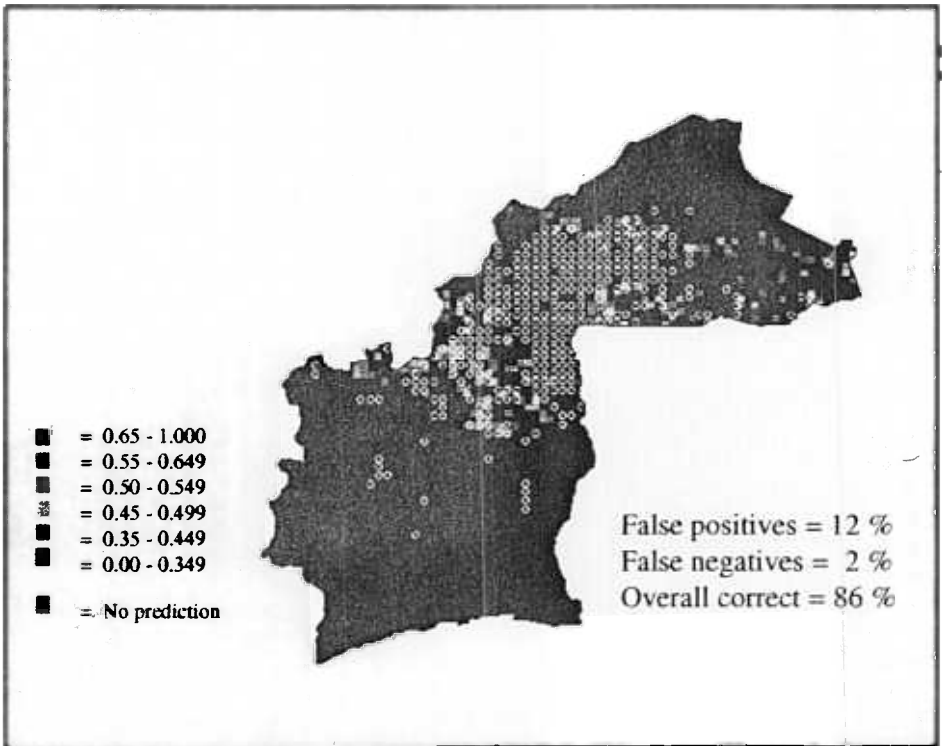
Rogers and Williams (1994) describe the application of temporal Fourier analysis to monthly GAC-NDVI data for the period 1987–1989 with a view to characterizing and hence classifying vegetation type. The temporal Fourier analysis achieved significant dimension reduction of the satellite sensor dataset while generating biologically meaningful predictor variables. The products generated by the analysis included the mean signal value, the amplitude of the signal variation and the timing of the peak signal for the duration of the data time-series, all of which reflect significant aspects of vegetation seasonality or phenology. They demonstrated that both ecological features and ecological processes could be characterized by temporal Fourier analysis, yielding outputs that are easier to interpret than those produced by the more traditional principal components analysis approach.

The critical importance of temperature in tsetse fly life histories (Rogers 1979, Rogers and Randolph 1986) promoted the investigation of the potential for extracting pan-African surrogates of land surface temperature from the thermal channels of the NOAA-AVHRR. The channel 4 brightness temperature was found to be the most accurate of the AVHRR thermal channels at the broad spatial scale and through a range of habitats (Hay 1993). Daily temperature data were not freely available to the general epidemiological community at the time so corrections for signal attenuation by atmospheric water and variation in land surface emissivity could not be attempted.

Rogers *et al.* (1996) applied a temporal Fourier analysis to a time-series of monthly GAC-NDVI (1981–1992), monthly maximum NOAA-AVHRR channel 4 brightness temperature data (1987–1992) and CCD data derived from the Meteosat satellite (1988–1992). This combination of imagery gave seasonal information on vegetation, temperature and rainfall so that the environmental niche of the tsetse fly was considered to have been more comprehensively described. These data were then used in combination with a 0·083° spatial resolution Digital Elevation Model (DEM) for Africa to predict contemporary tsetse distributions in the Côte d'Ivoire and Burkina Faso.

The resulting predicted distributions of two ecologically contrasting tsetse species are reproduced in figures 2(*a*) and 2(*b*). The maps were based on the results of discriminant analysis of the Fourier processed satellite variables and DEM data described above, from which the 10 variables that gave the greatest separation between presence and absence sites in multivariate space (as measured by the Mahalanobis distance) were selected. The classification of each point on the map was then defined by its closeness in multivariate space to the 'clouds' of pixels representing fly absence or presence, determined by posterior probabilities.

Glossina tachinoides (figure 2(*a*)), a member of the *palpalis* species group of tsetse, is adapted to riverine environments and is implicated in human sleeping sickness transmission. As the map details, the species occurs throughout southern Burkina

Legend (top map):
= 0.65 - 1.000
= 0.55 - 0.649
= 0.50 - 0.549
= 0.45 - 0.499
= 0.35 - 0.449
= 0.00 - 0.349

= No prediction

False positives = 12 %
False negatives = 2 %
Overall correct = 86 %

Legend (bottom map):
= 0.65 - 1.000
= 0.55 - 0.649
= 0.50 - 0.549
= 0.45 - 0.499
= 0.35 - 0.449
= 0.00 - 0.349

= No prediction

False positives = 15 %
False negatives = 0 %
Overall correct = 85 %

Faso and into northern Côte d'Ivoire and can therefore tolerate a range of environmental conditions. In contrast *Glossina nigrofusca* (Figure 2(b)) is a member of the ancestral *fusca* tsetse species group which is adapted to the forest environment and of little epidemiological importance. Its distribution is restricted to a discrete band in the southern half of Côte d'Ivoire indicating more limited ecological tolerances. The overall percentage of correct predictions of presence and absence was approximately 85 per cent in each case. False negative prediction (the prediction of absence when in fact flies are present) was very low 1–2 per cent with the number of false positive predictions (the prediction of fly presence when they are absent) an order of magnitude higher.

The presence or absence of the eight tsetse species was predicted with accuracies ranging from 67 per cent to 100 per cent (average = 82·3 per cent). A further dataset for the abundance of five of tsetse species across the northern part of Côte d'Ivoire was analysed and fly abundance categories predicted with accuracies from 30 per cent to 100 per cent (average = 73·0 per cent). In this investigation the thermal data appeared to be the most useful of the predictor variables, followed by vegetation and rainfall indices. The trend was for false positive predictions (average = 12 per cent) to be higher than the false negative predictions (average 3 per cent) which was seen to have significant implications for operational use. False negative predictions were considered of primary importance since they indicated fly inhabited areas 'missed' by the analysis and potentially by subsequent control campaigns using such data. Tsetse populations could therefore quickly re-establish from these untreated locations. False positive predictions were considered less important but of interest since they indicated areas of potentially favourable habitat. These studies showed that Fourier processed satellite surrogates were able to cope with the range of environmental factors and biological adaptation demonstrated by these contrasting species of tsetse.

Robinson *et al.* (1997 a, 1997 b) used GAC-NDVI data from the NOAA-AVHRR and interpolated elevation and climate surfaces to investigate the habitats of *G. m. morsitans, G. m. centralis* and *G. pallidipes* in part of southern Africa. Data reduction was achieved by using averages, maxima, minima and estimates of variation in the time series. They first analysed the tsetse distributions with respect to single environmental variables (Robinson *et al.* 1997 a) which had the advantage that it required no assumption to be made about the distribution of the data but the disadvantage that it could miss important interactions between variables. They extended this analysis to include multivariate methods (Robinson *et al.* 1997 b) and found classical linear discriminant analysis to be limited in its predictive power because of its

Figure 2. (a) and (b). The distribution of *Glossina tachinoides* (a) and *Glossina nigrofusca* (b) in Côte d'Ivoire and Burkina Faso. The map is based on a linear discriminant analysis of the Fourier processed satellite variables and DEM data described in Rogers *et al.* (1996). The classification of each point is defined by its closeness in multivariate space (measured by the Mahalanobis distance) to the 'clouds' of pixels representing fly absence or presence. A probability of finding the species of fly in a given pixel was then assigned on the basis of these distances. Accuracy is determined by the overall percentage of correct predictions, the percentage of false positives (the prediction of fly presence when they are absent) and the percentage of false negatives (the prediction of absence when in fact flies are present). 'No prediction' indicates a pixel with variable values more extreme than any of the training set pixels. North is to the top of the page.

assumption of common co-variances in the data. Maximum likelihood classification was not subject to this constraint, and produced a better prediction when *a priori* probabilities of presence and absence were used. The predictions were refined when the habitat was subdivided, prior to classification, on the grounds of a bimodality detected on the third component axis of a principal component analysis. The results of the predictions were good, particularly for *G. m. centralis* and *G. m. morsitans*, which gave overall correct predictions of 92·8 per cent and 85·1 per cent, with a Kappa index of agreement between the prediction and the training data of 0·73 and 0·64 respectively. For *G. pallidipes*, 91·7 per cent of predictions were correct but the value of Kappa was only 0·55; these investigations revealed very clear differences between the habitats of the two subspecies *G. m. centralis* and *G. m. morsitans*; a distinction that has often been disputed by taxonomists.

7.4. *Future potential*

The correlations discovered in the work on tsetse are all the more remarkable when it is considered that tsetse are relatively independent of particular environmental resources such as water, which is often associated with characteristic vegetation types (cf. dracunculiasis, onchocerciasis, malaria and schistosomiasis). As in other vector studies, however, the approach to describing tsetse and disease distribution and abundance is essentially a statistical one. The next step will involve relating the environmental variable surrogates in the satellite sensor data stream to the demographic rates of birth and death of tsetse populations, so that process-based models for this group of vectors may be constructed. This approach is both biologically more realistic and more capable of predicting the impacts of environmental changes on vectors and diseases, explaining why, and not simply where, tsetse and trypanosomiasis occur.

8. Tick-borne disease

8.1. *Diseases and vector biology*

The biology of ticks is quite different from that of insects. Ticks of the family Ixodidae (see figure 1 (*e*)) take a blood-meal only once per life-cycle stage, as a larva, nymph and adult (Sonenshine 1991). To act as vectors, therefore, ticks must transmit the pathogen between stages within the same generation (trans-stadially), and sometimes from female to the larvae of the next generation via the eggs (trans-ovarially). Between meals ticks drop from their hosts into the vegetation where they undergo long periods of development, lasting between one and twelve months depending on ambient temperature. The survival and development rates of ticks, and therefore the transmission dynamics of the tick-borne pathogens, are thus directly determined by environmental conditions (Sonenshine 1993 a).

Ticks are second only to mosquitoes in the number and diversity of viral, bacterial and protozoan pathogens they transmit to humans and their livestock (Sonenshine 1993 b). For example, the three genera *Rhipicephalus*, *Hyalomma* and *Amblyomma* are vectors for protozoan parasites of the genus *Theileria*, the most important being *Theileria parva* the causative agent of east coast fever (ECF) in cattle. This disease has a major economic impact in Africa through the reduction in cattle numbers and productivity, with associated costs in human welfare (Mukhebi 1992). In temperature regions, ticks of the *Ixodes ricinus* complex are the major vectors for the bacterial spirochete *Borrelia burgdorferi*, responsible for Lyme borreliosis (Lyme disease) in humans throughout Asia, Europe and North America (Burgdorfer *et al.* 1982).

8.2. Application of high spatial resolution imagery

Amblyomma variegatum was accidentally introduced to the Caribbean on cattle imported from Africa where it is a vector for heartwater, a fatal tick-transmitted disease caused by the protozoan *Cowdria ruminantium*. Hugh-Jones and O'Neil (1986) were among the first to investigate the potential for Landsat-1 MSS imagery to identify tick habitats, specifically for *Amblyomma variegatum* in St Lucia. The major regions of tick infestation were located in arid, rough grazing habitat in the north of the island, characteristically dominated by the mesquite *Prosopis juliflora*. The Landsat-MSS images revealed that this habitat was expanding as a result of poor grazing management, thus explaining the increasing incidence of heartwater in the region.

Hugh-Jones (1991 b) extended this pilot study using Landsat-TM imagery to try to infer habitat quality for *Amblyomma variegatum* in Guadeloupe. Tick density was measured in 103 cattle herds, and associated environmental variables were recorded along transects across the surrounding grazing habitat. A discriminant analysis of these variables, which included plant composition, grazing cover, soil type and depth, slope and rainfall, distinguished four main tick habitats. These were lightly infested dry meadows, moderately infested foothills, heavily infested dry scrub and rocky grasslands. These four habitats could be discriminated remotely and were resolved by an unsupervised classification of a 1986 Landsat-TM scene of Grand Terre, Guadeloupe (Hugh-Jones *et al* 1988). Subsequently, a 'moisture index' (MI) based on the NDVI and the response of Landsat-TM band 7 to the water content of vegetation $((4-7)(4+7))$ and the Perpendicular Vegetation Index (PVI) (Richardson and Weigand 1977) were derived for each pixel (Hugh-Jones *et al* 1992). A 5×5 pixel array was then centred upon each visible farm and a cluster analysis performed on the tick density in each of the farms against the variance in the raw waveband data, the MI and PVI. It was found that herds in grazing areas with a high variance in the band values (indicating heterogeneous vegetation) had more ticks than areas with low variances (i.e., homogeneous vegetation). Furthermore, within the heterogeneous areas those with higher PVI and MI values (i.e., more vegetation and moisture respectively) had higher tick densities.

Daniel and Kolar (1990) investigated the possibility of forecasting the occurrence of *Ixodes ricinus* from Landsat-5 MSS data. They worked on a scene centred on Poteply, a popular recreational area south-west of Prague and an historic focus of tick-borne encephalitis. Long-term field studies in the area enabled the selection of pixels for a supervised maximum likelihood classification (incorporating bands 2, 3 and 4) separating the scene into coniferous, leaved and mixed forest classes, as well as water basins, glades and housing developments. Though no statistics were presented the authors state that the leaved and mixed vegetation classes were characteristic of high tick density areas, especially where the spatial heterogeneity of such classes was high, indicating the presence of ecotones considered particularly favourable for *Ixodes ricinus*. This work has resulted in the production of 'risk maps' for *I. ricinus* and tick borne encephalitis in parts of the Czech Republic.

8.3. Application of low spatial resolution imagery

Predicting the distribution and abundance of the brown ear tick, *Rhipicephalus appendiculatus*, has been the focus of much recent research as it is the principle vector of ECF in Africa. The most widely used models have been based on the Program CLIMEX which calculates the climatic suitability of geographical regions

for arthropod species using a temperature dependent growth index, moderated by four user-defined stress indices (hot, cold, dry and wet) (Sutherst and Maywald 1985). Driven by a synoptic meteorological dataset the resulting predictions for the pan-African distribution of *Rhipicephalus appendiculatus* have been compared visually with the observed distribution of ticks (Lessard *et al.* 1990, Perry *et al.* 1990). Further visual comparison with mean maximum GAC-NDVI values for 1987 provided a 'remarkable visual correlation' between the known distribution of *Rhipicephalus appendiculatus* and NDVI values greater than 0·15 (Perry *et al.* 1991). Again no statistics were presented in these studies, but using both the NDVI values and CLIMEX the authors predicted that suitable habitat for *Rhipicephalus appendiculatus* existed in western and central Ethiopia and therefore that the region was at risk from ECF in the future (Norval *et al.* 1991). Given that CLIMEX also predicted suitability of much of the Zaire basin and many parts of West Africa, areas from which *R. appendiculatus* has never been recorded, the accuracy of the predictions from this model and the underlying methodology are open to question. The CLIMEX model has also been used recently to predict an expansion in the range of the mosquito *Anopheles farauti sensu stricto* (s.s.) vector for malaria in northern Australia, given a climate change scenario of a 1·5°C average increase in temperature and a 10 per cent increase in summer rainfall (Bryan *et al.* 1996). Again no statistics were presented on the accuracy of predicting present day distributions using CLIMEX.

Randolph (1993, 1994) took an explicitly biological approach to understanding the abiotic constraints on the distribution of *Rhipicephalus appendiculatus*. Correlations between the seasonally variable abundance of this tick in southern Africa and simultaneously monitored meteorological data and a more recently pro- cessed GAC-NDVI dataset for the region (1987–1989) indicated that the major abiotic constraint is moisture availability to the desiccation-vulnerable egg and larval stages. This was confirmed when the author derived seasonal interstadial mortality indices from published datasets in both equatorial and southern Africa, and showed strong correlations between mortality at the female-to-larval stage and factors deter- mining moisture availability. The critical climatic factor, however, that determines moisture availability to ticks varies geographically; in equatorial regions, rainfall and consequent soil moisture was most important, while in the temperate regions low daily minimum temperatures providing high condensation appear to allow good survival in the dry season. Indeed, in certain southern sites conditions that are too wet result in high mortality, perhaps because of fungal infections of the eggs (Randolph 1997). The influence of these variable conditions presumably underlies the observed correlations between tick mortality rates and the NDVI at the time of larval emergence; the correlation was negative in equatorial Africa, where high rainfall and thus high NDVI is favourable to tick survival, but positive in Zimbabwe where high minimum temperatures and related high NDVI are unfavourable.

8.4. *Future potential*

Satellite sensor data are therefore potentially very useful in modelling tick popula- tions, augmenting or even replacing climatic data where these are unavailable on a sufficiently fine temporal or spatial scale and presenting a significant advance on previous techniques. Temporal Fourier processing of AVHRR data appears to offer a unique insight into seasonal events that are important in tick population dynamics.

9. Schistosomiasis

9.1. *Disease and non-vector intermediate host biology*

Schistosomiasis, or bilharzia, is caused by four species of trematode flatworms (flukes) that belong to the genus *Schistosoma* (Basch 1991). The juvenile stages (or cerariae) penetrate human skin around hair follicles or wounds when they come into contact with mud or water containing the parasite. The schistisomula then migrate through the blood stream via the heart and lungs to the liver, before moving to their final site in the blood vessels around the gut or bladder where they mature into adults and mate. The resulting eggs contain protease enzymes that enable digestion and subsequent penetration of the bladder or bowel walls facilitating their passing in the urine or stools of infected individuals. If expelled into water they develop into free-swimming miracidia. These miracidia will in turn locate and penetrate aquatic snails (*Bulinus* spp. and *Biomphalaria* spp.) and semi-aquatic snails (*Oncomelania* spp., see figure 1 (*f*)) where they pass the juvenile stage of their life cycle before emerging into the surrounding water. The snails are referred to as intermediate hosts and not vectors because they do not transfer infection directly to other organisms via contamination or inoculation.

Schistosomiasis affects approximately 200 million people throughout the tropics, and although it has a relatively low mortality rate in global terms (less than 200 000 people per year), morbidity is high due to the severe and debilitating illness associated with the immune response to the presence of schistosome eggs in tissues (WHO 1990).

9.2. *Application of high spatial resolution imagery*

A sophisticated, early study to predict areas endemic for schistosomiasis using a combination of weather variables and Landsat-3 MSS data was performed by Cross *et al.* (1984). This was to enable estimation of the potential disease casualty rates arising from schistosomiasis during military operations in the Philippines. Initially, data from 157 weather stations were interpolated to provide mean monthly temperature and precipitation data at any given site throughout the islands. A discriminant analysis was then used to predict the probability of disease occurrence based on 324 survey observations of disease prevalence. A 1973 Landsat-MSS scene covering the islands of Leyte and Samar was then chosen, because unusually for the region, it contained less than 10 per cent cloud cover. The mean and variance in bands 4, 5, 6 and 7 were calculated for the 52 disease survey sites within the scene and regressed against the previously calculated probabilities of disease occurrence. A disease distribution map was then produced using the statistical correlation between the probabilities of occurrence and the Landsat-MSS waveband variables. The accuracy levels attained were not reported.

Chen and Hu (1991) used Landsat and NOAA sensor data (types and dates unspecified) to identify 'geo-ecological zones' associated with *Oncomelania* habitats in China, although no details of accuracy were presented. Micro-ecological environments favourable to *Oncomelania* were then divided into areas affected by flooding, by extremes of the dry season and by human agricultural production since management procedures and priorities in the regions would vary accordingly. Regional databases providing information on the spatial and temporal dynamics of schistosomiasis were stated to be under construction in order to assist Chinese health departments in disease control and disaster relief efforts.

The trematode fluke species *Fasciola hepatica* is a parasite of cattle and other large mammals in many regions of the world. In Louisiana and the Gulf of Mexico

the amphibious snail, *Fossaria bulimoides*, is the intermediate host. Zukowski *et al.* (1991, 1993) demonstrated that the risk to individual farms and surrounding rangelands could be related to the extent of the preferred habitat of *F. bulimoides*, relict beach habitat or chenier soils in association with heavy marsh. This work was significantly improved by incorporating updated land cover and slope information from Landsat-4 MSS (Malone *et al.* 1992, Malone and Zukowski 1992).

9.3. *Application of low spatial resolution imagery*
Based on this experience Malone *et al.* (1994, 1997) describe how NOAA-AVHRR LAC channel 4 brightness temperature data were used to determine the relative risk of schistosomiasis due to *Schistosoma mansoni* and the invertebrate intermediate snail host for *Biomphalaria* spp. in the Nile delta. The difference between day and night temperature was thought to reflect hydrological factors that affect the relative suitability of canals and drains as habitats for snail intermediate hosts. Wetter and hence more suitable habitats were thought to have lower day–night temperature differences due to the thermal inertia of water. Lower temperature differences were then demonstrated to be significantly correlated with the wetter hydrologic regimes suitable for the snail hosts of schistosomiasis in this region. Details of operational application were not outlined.

9.4. *Future potential*
While the potential of remote sensing techniques has been demonstrated with respect to schistosomiasis control and its use strongly advocated (Malone 1995), there has been no documentation of attempts to apply the techniques in existing control operations.

10. Dracunculiasis
10.1. *Disease and non-vector intermediate host biology*
Dracunculiasis or Guinea worm disease is caused by the nematode worm *Dracunculus medinensis* (Whitfield 1993). Infection begins by drinking water contaminated with microscopic crustaceans (such as the copepod genus *Cyclops*, see figure 1 (*g*)) infected with *Dracunculus medinensis* larvae. The larvae are released as the copepods are digested and then burrow through the gut wall and migrate to the subcutaneous tissues where they mate. The mated female worms (which can reach a metre in length) then migrate towards the ankles and feet where they induce a fluid-filled blister on the hosts' skin, approximately 8–10 months after infection. When the blister bursts *Dracunculus medinensis* larvae are released on each occasion that the lesion is immersed in water for the following month. This is usually frequent as people often relieve the burning pain caused by infection by cooling the wound in water. Dracunculiasis is not often fatal but is painful and debilitating, often crippling people for periods of up to two months. This has been shown to have considerable adverse affects on agricultural productivity (Belcher *et al.* 1975). The disease is endemic to 18 African and 2 Asian countries and is thought to affect between 1–3 million people annually, the majority of whom are in West Africa.

10.2. *Application of high spatial resolution imagery*
There is no medical treatment for dracunculiasis but the disease can be virtually eliminated with the provision of safe water. For eradication to remain effective over large areas, intensive health education and community mobilization are required.

Clarke *et al.* (1991) describe how the United Nations Children's Fund (UNICEF) used Landsat-TM data to identify small and remote settlements in dracunculiasis endemic areas of Benin to form the basis of a management system for dracunculiasis control. The authors found that the: 'combination of remote sensing and GIS technologies offered the epidemiologist a new and important means by which to effectively implement solutions to public health management problems'. Moreover, they were also aware that once initiated such a database could be of considerable use to the control efforts for other diseases. This work has continued and the GIS database elaborated and maintained to enable analysis of the spatial patterns of dracunculiasis in Benin, and to evaluate the effectiveness of various intervention policies designed to combat the spread of the disease (Tempalski 1994).

Ahearn and De Rooy (1996) set out to test the hypothesis that optimization of water and sanitation interventions in areas with high dracunculiasis had a measurable socio-economic impact (as assessed by the area of land cultivated) using a temporal analysis of Landsat-TM data. The study was centred on the Kwara state in Nigeria where dracunculiasis is prevalent throughout, but UNICEF control efforts have been targeted in particular areas. Post-harvest scenes were collected immediately before eradication efforts commenced in the 1985 growing season and after the remedial effects of intervention should have been evident in 1991. It was expected that as the area of land cultivated increased the NDVI would decrease during the time of harvest as more land would be left exposed. A measurable decrease in the NDVI was recorded and the potential to monitor the impact of control campaigns noted.

10.3. *Future potential*

There would seem to be little potential to expand the use of remote sensing in dracunculiasis control beyond the regional planning aid shown above, since control of the disease comes about through the education of local communities, who are easily located on high spatial resolution imagery, rather than any direct control of the intermediate host.

11. Conclusions on future application and co-operation

Data from satellite remote sensing have shown potential to assist in the understanding and control of several of the most significant and widespread of diseases affecting humans, and show significant but varying potential for application to others. From this overview it can be seen that the degree of sophistication with which remote sensing has been applied to epidemiological problems has been highly variable, generally reflecting the time for which remote sensing has been adopted by a specific group of the disease vector control community.

Considerable advancement from the primary problem of habitat distribution mapping, to the incorporation of aspects of vector ecology has occurred where there has been sufficient time, funding and a multidisciplinary approach in investigations. A general criticism of much of the early studies, however, is the general lack of reporting statistics in dissemination of work.

The perception that remote sensing is not appropriate in technologically developing regions persists and is manifest in the form of frequent objections to the cost of image processing equipment, expertise and ground truth (Bos 1990, Arambulo and Astudillo 1991, Barinaga 1993, Kleiner 1995). These problems are real concerns but are diminishing as: (1) computer processing and data storage facilities become relatively cheaper, (2) recent changes in the philosophy of satellite image dissemination have resulted in

data becoming more widely and freely available (Mulcahy and Clarke 1994, Justice *et al.* 1995), and increasingly accessible (e.g. James and Kalluri 1994) and (3) the history of successful application of remote sensing techniques in epidemiology expands.

The application of remote sensing has also been shown to be cost effective in mosquito control campaigns (Fleetwood *et al.* 1981, Welch *et al.* 1989 a) and to provide baseline datasets which can be subsequently expanded and find application far beyond the motivation for their original assembly (Clarke *et al.* 1991). This is of critical importance in the evaluation of vector control strategies where resources are often acutely limited (Mills 1994).

Our understanding of the spatial and temporal distribution of invertebrate intermediate hosts and the diseases they transmit has been enhanced by understanding the statistical associations between the ecological variables and processes observed remotely and invertebrate intermediate host biology. This understanding will only develop, however, when processed-based models using remote sensing data as real-time inputs to equations describing the survivorship of intermediate host species are generated. In epidemiology we are fortunate that a rudimentary understanding of the underlying invertebrate intermediate host biology is often available because the diseases transmitted have long been a threat to man and hence a focus of research. Further close investigation of specific test sites will be required if the information to drive these models is to be generated. It is a priority to understand these interactions, however, since they will enable 'best guesses' to be made of the impact of global climate change on disease distributions (Rogers and Packer 1993, Patz *et al.* 1996).

The most detailed epidemiological understanding will therefore come about through relating dynamic demographic processes (such as mortality rates) to satellite data, rather than using satellite imagery for purely static mapping exercises. The desire for such a detailed mechanistic or biological understanding must be tempered, however, by the pragmatism of funding agencies and those in the developing tropics who are more concerned with a statistically accurate, operational control system than knowing precisely the causative relationships between an invertebrate intermediate host and its habitat.

Remote sensing of ecological processes is not a replacement for fieldwork. It provides a complementary approach, which can extend our understanding of epidemiological processes in space and time in a way that has hitherto not been logistically feasible (Rogers and Williams 1993). In addition, remote sensing highlights the need for even more comprehensive surveying to obtain ground data that enables a more rigorous basis for its spatial extrapolation and to provide the inputs to processed-based models. This is especially true when the ecology of the diseases and their intermediate hosts, as well as human behaviour patterns that affect transmission vary substantially both spatially and temporally, significantly complicating our understanding. Concurrent advances in GIS will help in data management and co-ordination of control programs although this aspect is not considered fully in the present review.

The range of satellite sensors for Earth observation have a variety of resolutions (spectral, spatial and temporal) that have been variously utilized with respect to disease control and management. The future will see a further increase in the range of data available as well as its speed of dissemination (Hay 1997) and thus present new challenges and opportunities for synergism between the epidemiological and remote sensing communities.

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