

# Emerging and vector-borne diseases: Role of high spatial resolution and hyperspectral images in analyses and forecasts

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**Abstract.** Many infectious diseases that are emerging or transmitted by arthropod vectors have a strong link to landscape features. Depending on the source of infection or ecology of the transmitting vector, micro-habitat characteristics at the spatial scale of square meters or less may be important. Recently, satellite images have been used to classify habitats in an attempt to understand associations with infectious diseases. Whether high spatial resolution and hyperspectral (HSRH) images can be useful in studies of such infectious diseases is addressed. The nature of questions that such studies address and the desired accuracy and precision of answers will determine the utility of HSRH data. Need for such data should be based on the goals of the effort. Examples of kinds of questions and applications are discussed. The research implications and public health applications may depend on available analytic tools as well as epidemiological observations.

**Key words:** Epidemiology, infectious diseases, remote sensing, GIS, environment

**JEL classification:** I1, I18

## 1 Introduction

The spatial and spectral resolutions of satellite image data are increasing, suggesting opportunities to apply such data to problems in which contact patterns, distances, or environmental factors are important. Various reports, including many in this issue, have suggested that higher resolution data, when combined with more powerful tools for data manipulation and analysis, should enhance efforts to identify time-space patterns that underlie the etiology and risk of many diseases. Most summaries have argued that certain environmental features important to exposure or transmission are not fully captured by lower resolution data, and that finer spatial resolution, as well as greater spectral range and detail, should enhance research and provide more useful results. Here we explore whether our understanding of certain infectious diseases will benefit from smaller pixel areas and finer

electromagnetic energy divisions. Specifically, we consider the opportunities and constraints presented by these new high spatial resolution and hyperspectral (HSRH) images when applied to studies of arthropod-transmitted and emerging infectious diseases. To avoid having “the tail wagging the dog,” it seems reasonable to first evaluate the likely benefits from the use such massive amounts of data. How will such analyses improve our understanding of the epidemiology, transmission patterns and risk factors for such diseases? As with most new technologies, utility depends upon intended goals. The application of these new data and tools to infectious disease research present both possibilities and problems.

### *1.1 Space, environment and disease*

Infectious or contagious diseases are fundamentally different than those that are non-infectious because a contagious process determines who becomes infected and sometimes ill. For this reason, the spatial patterns of infectious and susceptible people, as well as the nature and extent of their contacts, are basic determinants of exposure and disease risk. Although the proximal “cause” of an infectious disease is a specific pathogenic microbe (a species of bacteria, virus, protozoan, etc.), the spatial pattern of exposure is an important component of which and how many people become infected. In contrast, many non-contagious diseases result from a physical or chemical exposure (e.g. lead in soil, pesticides in water, radioactive isotopes, cholesterol in food, SO<sub>2</sub> in air), implying that the spatial pattern of contact with the environment is the primary characteristic of risk. People who share similar environments may have similar risks, but their proximity to each other influences common environmental exposures, not those involving *contagion*. This subtle difference is important in considering how finer resolution environmental data may be used to study disease risk.

Nevertheless, the environment may play a crucial role in transmission of *infectious* diseases by altering the likelihood of transmission. Although most human pathogenic microbes do not normally reside and replicate in the environment (exceptions include *Legionella* and *Clostridium*), they often depend on physical materials, arthropods or other animals for protection, nutrition or transmission. Diseases caused by microbes that are normally transmitted during blood-feeding by arthropods (e.g. mosquito-borne malaria, sandfly-borne leishmaniasis, blackfly-transmitted onchocerciasis) are termed “vector-borne.” Other infectious agents that are normally transmitted from one animal to another, with occasional transfer to people, give rise to “zoonotic” diseases (e.g. rabies, hantavirus pulmonary syndrome, anthrax). These two transmission-based and host-related patterns produce human diseases that have strong links to the environment. Other diseases are *both* vector-borne and zoonotic (e.g. tick-borne Lyme disease, mosquito-borne West Nile encephalitis, flea-borne plague), presenting an even greater possibility that finer spatial and environmental analyses might improve understanding. For these diseases, environmental features could influence pathogen survival, animal-host abundance, contact with humans, or vector feeding behavior, for example. Analysis of the nature and spatial patterns of

relevant environmental features should be useful in characterizing and reducing exposure risk.

### *1.2 “Emerging” diseases*

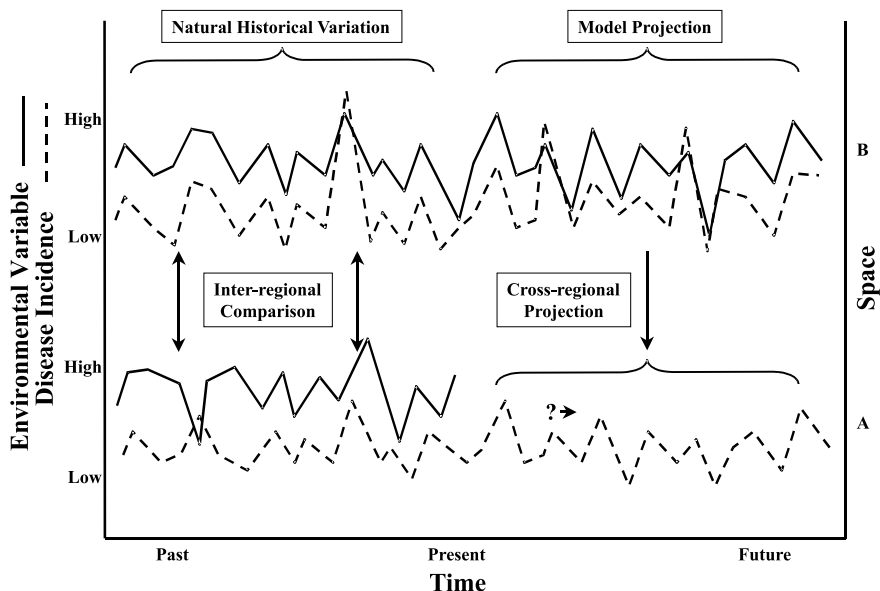
During the past decade, much attention has been focused on infectious diseases that have been termed “emerging,” “re-emerging” or “resurgent” (Lederberg et al. 1992; Centers for Disease Control and Prevention 1994). Definitions of what constitutes an emerging disease vary, but virtually all can be classified as

- (a) newly-recognized within the past few decades,
- (b) expanding distribution into new regions or habitats,
- (c) increasing incidence where currently found, or
- (d) increasing severity or resistance to treatment (Wilson 1994a).

Many diseases that are considered emerging share more than one of these characteristics. Environmental and spatial attributes are extremely important determinants of when and where emerging diseases appear (Wilson 2001). Thus, satellite-derived information on landuse/landcover, soil moisture, or water temperature, for example, could be important to understanding how new exposures occur, why emerging diseases are increasing, whether changing vector or animal host movement patterns are altering distributions, etc. Factors other than the time-space patterns of environmental change also are contributing to disease emergence (e.g. antibiotic use, food production practices, sexual behavior), yet environmental changes and human interaction with the environment are considered among the most important determinants.

### *1.3 Types of questions and approaches to investigation*

Research into environment and disease associations can be classified in various ways, but a simple typology involves comparisons of patterns over time, space or both (Fig. 1). Within one site, retrospective analysis of temporal changes (“natural historical variation”) has been used to determine whether fluctuations in environment correspond to those in disease incidence. Such studies are possible only if appropriate satellite image data are available for the period and location where disease surveillance had occurred. At any one point in time, associations among different locations (“inter-regional comparison”) can be used to evaluate whether similar environments in different places have similar disease profiles. Satellite image and epidemiological data from many places are needed for robust analysis. These two approaches aim to establish past or present environment-disease associations in either time or space, and therefore are hypothesis generating. One ultimate goal of such effort should be application of knowledge to predict where or when disease risk might be elevated. Hypothesized associations can be used to forecast how future changes in environment might affect transmission in one location (“model projections”) or how environmental patterns in a region may predict risk in other similar regions (“cross-regional projection”).



**Fig. 1.** Schematic illustration of the kinds of studies that compare environmental variables with disease incidence over time and space. Two locations are shown from the past, present, and future, with four general types of analysis that seek associations or make projections

The utility of remotely-sensed data in general, and of HSRH data in particular, partly depends on the type of study being undertaken. Studies aimed at the larger ecological community can help to characterize patterns, but may not help in understanding dynamics or mechanisms. Rather, investigations of one or a few populations are needed to comprehend dynamics, and of individuals to elucidate mechanisms. High spatial resolution and hyperspectral (HSRH) images should be more useful in studies at the levels of populations and individuals that are intended to better understand dynamics and mechanisms.

## 2 Spectral/spatial resolution and health applications

Recent advances in the quality and frequency of satellite images, combined with new methods and software for spatial analysis and geocomputing, have expanded opportunities in environmental monitoring and exposure assessment. The enhanced precision of HSRH images may lead to improved understanding of environment/human interactions that impact on infectious disease risk. However, the possibility that this enormous leap in resolution can be exploited has not yet been evaluated. Low spatial resolution images (obtained over large areas) have been used in studies of various kinds of diseases where environmental exposures are important. For example, remote sensing and spatial analysis have been shown useful in non-infectious diseases assessment involving pesticide exposure (Ward et al. 2000), air pollution (Todd 2000), marine contaminants (Gade and Alpers 1999), biogenic gasses (Diem and Comrie 2000) and mine sludge spills (Lopez-Pamo

et al. 1999). However, many more reports have been published that used lower spatial resolution images in studies of infectious diseases (reviewed by Beck et al. 2000). To begin evaluating how high resolution data and new analytic tools might enhance such research, we consider questions such as the following:

1. What are the relevant characteristics of transmission that remotely sensed data can capture and in what ways do they differ among diverse infectious diseases?
2. Are some diseases better suited to analysis using remotely-sensed environmental data and if so why?
3. How have less-detailed images been used previously to study infectious disease risk, and has their effectiveness been limited due to the relatively coarse spatial resolution?
4. Which of the critical environmental features can be better characterized using enhanced spectral and spatial resolution?
5. Are the tools for managing and analyzing these data available and easily applied, and if not then what needs to be improved?

### **3 Capturing important environmental features of transmission**

Appropriate contact between an infectious source of a microbe and a susceptible person is a necessary determinant of disease risk. The environment can mediate contact in many ways, but this depends on specific characteristics of transmission and types of microbes (Table 1). Directly-transmitted agents that normally infect only humans (causing anthroponoses such as AIDS or herpes) generally are less influenced by the environment, as they spend little or no time outside of the “environment” of their human host. Other anthroponoses, which are transmitted by vehicles (e.g. influenza, hookworm) or by vectors (e.g. malaria, dengue, onchocerciasis), and are more environmentally-sensitive to agent survival and transmission, involve life outside the human host, hence may be affected by vector abundance and behavior. Similarly, zoonoses that are either directly-transmitted or use a vehicle/vector are likely to be affected by environmental variables. The extent and nature of such influences, and the particular variables that are important, vary for each disease. Indeed, the role of the environment may change, even for the same disease, depending on ecological or social contexts.

Most emerging and/or vector-borne diseases are influenced by environmental characteristics that can be detected directly or indirectly from satellite images. A thorough review by Beck et al. (2000) identified at least 17 diseases for which satellite image data have been used to detect relevant environmental mapping opportunities. (See Beck et al. 2000 for details and citations.) Of these infectious diseases, all were either emerging ( $n = 12$ ), or vector-borne ( $n = 13$ ), or both. Furthermore, all but one of the non-vector borne diseases was a zoonosis (the exception being helminthiases, such as hookworm, where the larval stage of the parasite must spend time in soil before it can be transmitted to another human).

Satellite-derived information considered useful in understanding these diseases included patterns of vegetation (crop type, deforestation, rate of

**Table 1.** Examples of environmental effects on transmission of different types of microbes classified according to their mode of transmission and reservoir

Disease and transmission types	Cycle components	Examples of direct environmental determinants	Examples of indirect environmentally-based pathways
Anthroponoses – direct	Human → Human	Few (temperature?, humidity?)	Body fluids or excrement, aerosols, human behavior
Anthroponoses – indirect	Human → Vector/ Vehicle* → Human	Soil, water, vegetation, humidity, wind, food, temperature	Vector abundance and behavior, cropping patterns, sanitation, irrigation, urbanization, human behavior
Zoonoses – direct	Animal → Animal → Human	Vegetation, landcover, humidity, temperature	Animal reservoir abundance, human recreation and behavior, domestic animal husbandry, pet ownership patterns
Zoonoses – indirect	Animal → Vector/ Vehicle <sup>a</sup> → Human	Soil, water, vegetation, humidity, wind, food, temperature	Animal reservoir abundance, vector abundance, crop types, urbanization, wildlife habitat, housing type, human recreation and behavior, domestic animal husbandry, pet ownership patterns

<sup>a</sup> Examples of vectors include mosquitoes, ticks, sandflies, tsetse flies, etc.; vehicles might be water, food, air, vegetation, etc

green-up), habitat type (forest patches, ecotones), fresh water sources (permanent water, wetlands, flooding, soil moisture, canals), housing (human settlements, urban features), and ocean conditions (ocean color, sea surface temperature, sea surface height). Interestingly, there appears to be no simple associations among disease type, source of infection or transmission, and environmental features considered. For example, satellite image-derived features of vegetation (e.g. amount of forest, ecotone, or crops) were used to evaluate diseases as diverse as Chagas disease, hantavirus, leishmaniasis, Lyme disease, malaria, plague, Rift valley fever, schistosomiasis, trypanosomiasis and yellow fever. None of the microbes causing these diseases depend directly on vegetation for their survival or transmission. Despite enormous differences among this wide range of pathogens whose transmission cycles involved assorted animals and/or vectors, each was studied using characteristics of local vegetation. Similarly, water-related characteristics (e.g. extent of wetlands, flooding, presence of canals) obtained from satellite images also were used to study many of these same diseases, as well as cholera, filariasis, onchocerciasis and St. Louis encephalitis. Thus, there is no simple algorithm to define which remotely-sensed environmental characteristics will provide the most insight for any particular disease. Rather, the utility of satellite image data in general, and of HSRH data in particular,

depends on the specific information sought in the context of the transmission ecology and epidemiology of particular diseases and epidemiological conditions.

### 3.1 Important environmental characteristics of transmission

The study of some, but not all, infectious diseases is enhanced by remotely-sensed environmental data. For vector-borne diseases, most published reports have used such data to identify associations between spatial patterns of environmental features and vector abundance or disease incidence. These associations have been used to create “risk maps” of increased transmission probability (Kitron 2000). Most describe rather large areas of risk based on political boundaries (township, county, state) even though finer-scale satellite image data may have been used to characterize environmental features. This is particularly true for risk maps derived from epidemiological data that are spatially referenced to large areas, but also for those that extrapolate from vector or reservoir abundance data. Thus, the usefulness of HSRH data in describing environmental associations with disease risk partly depends on the spatial scale of the available disease-indicator data. Indeed, the extent to which fine scale environmental heterogeneity is important to evaluating transmission dynamics or mechanisms can not be determined without similar scale data on risk or incidence. Whether risk is uniform across such large areas depends on various transmission parameters.

### 3.2 Examples of vector-borne diseases

Diverse aspects of the environment influence vector abundance and behavior in a manner that is species-specific and at many different spatial scales. For example, *Anopheles* mosquitoes, which transmit the protozoa that cause human malaria, depend on water for egg-laying. The suitability or tolerance of water characteristics (turbidity, depth, exposure to sun, vegetation, nutrient content, movement, location, etc.) varies for each mosquito species. *Anopheles gambiae* and *A. funestus*, two important malaria vectors that coexist throughout much of eastern Africa, have specific micro-habitat requirements that differ in important ways. Larvae of *A. gambiae* are most abundant in small, temporary puddles with algae and little or no aquatic vegetation, whereas *A. funestus* larvae are associated with larger, semipermanent bodies of water containing aquatic vegetation and algae (Gimnig et al. 2001). The survival and blood-feeding of *Anopheles* adults, on the other hand, largely depends on nutrition as larvae, and availability of safe resting sites with high humidity and few predators (housing types, surrounding vegetation), characteristics that are different than those for larvae. Lindblade et al. (2000) demonstrated that micro-climatic factors (temperature, RH) at people’s houses influenced mosquito density, biting rates, sporozoite rates and entomological inoculation rates. Indeed, the average minimum temperature was significantly associated with the abundance of *Anopheles gambiae*. Coarse spatial resolution data from satellites would not be able to detect such differences. Overall, studies of these important micro-habitat associations might benefit from HSRH images, but

only if accompanied by data on a correspondingly finer spatial scale for vectors or cases.

In another study of malaria risk in relation to larval abundance of *A. vestitipennis* and *A. punctimacula* in Belize, Rejmankova et al. (1998) identified eight habitat types defined by dominant life forms and hydrology. Presence of both mosquito species overlapped in some habitats, but presence or absence was not always predicted accurately. Using SPOT multispectral satellite imagery, 10 land cover types were identified that corresponded to presence of one or the other species, but breeding sites in many locations were not identified. Whether greater spatial or spectral resolution data would have helped in this analysis is unclear, but the need for extensive entomological data, especially with environmental data of high precision, is evident.

Lyme disease, caused by *Borrelia burgdorferi* bacteria that are transmitted by ticks (*Ixodes* spp.), has very different environmental associations. In North America, most transmission occurs in the northeastern and north central U.S. Vector abundance depends on wildlife populations (e.g. white-tailed deer, small mammals) and has been associated with other abiotic habitat characteristics (temperature, humidity, soil type) (Wilson 1994b). However, all stages of this tick spend most of their lives on the ground or in vegetation (they do not fly or crawl more than a few meters). High spatial resolution environmental data might be used to identify micro-habitats suitable to tick survival, yet the ticks are so small that it is difficult to estimate their abundance except by averaging over larger areas (e.g. hectares). Hyperspectral data that might distinguish among vegetation types could be useful, but only if corresponding information on tick abundance and survival was available.

A study in Lyme disease-endemic suburban Westchester County, NY determined the seasonally-adjusted densities of *I. scapularis* nymphs and landscape composition at each of 337 residential properties (Dister et al. 1997). Relative measures of vegetation structure and moisture (wetness), as well as vegetation abundance (greenness) from a Landsat TM image were related to relative tick abundance. It was determined that "... high-risk properties were significantly greener and wetter than lower-risk properties." While this study was able to distinguish differences among communities and individual properties, there was insufficient spatial resolution to suggest specific locations or landcover type(s) within each residential property produced the most ticks. Thus, it is difficult to suggest how people might reduce personal risk.

Many more examples of different vector-borne diseases could be discussed to illustrate how the usefulness of HSRH images depends on the ecology and epidemiology of transmission, and the intended goals of the effort. While regional comparisons of indirect environmental indicators have produced temporal and spatial associations with disease risk, most such studies have characterized pattern, but not explained how it arose. Public health efforts often effectively reduce risk based on observed patterns, even without knowledge of mechanisms or dynamics (e.g. early years of AIDS, or centuries earlier the avoidance of swamps where there was "bad air" – "*mala aria*" in Italian). Many of the vector-borne diseases, however, have local, habitat-specific determinants of risk. Research aimed at understanding



mechanisms, and eventually reducing that risk should be able to benefit from widespread coverage of transmission-specific environmental variables that HSRH data offers. Once such associations are reasonably well established, HSRH data offer an even better tool for undertaking environmental surveillance that might lead to early warning of outbreaks or sites of elevated risk. Regardless, knowledge of transmission and intervention goals should be the horse that drives the cart that defines necessary data and analytic tools.

### *3.3 Examples of emerging diseases*

A more difficult challenge in the use of HSRH data is presented by emerging diseases, particularly those that are newly-recognized human infections. Disease emergence due to expanding distributions into new regions (see section 1.2 above) can be best anticipated or understood by cross-regional projection from other similar habitats. However, HSRH data may be unnecessary if it is known that the necessary reservoirs and/or vectors are present. (The recent introduction of West Nile virus into North America could have been considered possible without a finer understanding of the environment, as competent reservoirs and the primary vector mosquito, *Culex pipiens*, were known to be present). Similarly, it is difficult to see how such data will improve our predictive ability for diseases that emerge due to increasing severity or resistance to treatment. Factors such as hospital conditions, antibiotic use, or genetic changes in pathogens are not measurable by satellites.

Disease emergence attributed to suddenly increasing incidence in regions of existing transmission often results from environmental changes that alter exposure patterns. If knowledge of the epidemiological and ecological determinants of transmission already exists, satellite image data may be helpful in determining whether region-wide environmental changes have occurred. Should relevant variables or indicators be identified, HSRH data could be used to consider whether such changes might have altered transmission dynamics in important ways. In this context, changes in environmental variables associated with elevated risk could constitute another form of surveillance that might detect altered risk in a more timely manner. Again, more precise locations of exposures or cases would be needed to establish such associations with HSRH data. At present, however, we are unable to anticipate or accurately predict when and where most diseases are likely to emerge. Thus, HSRH data will be of limited value in enhancing such efforts until an underlying theory of transmission determinants is identified, and exposure risk incorporating environmental change has been hypothesized.

### *3.4 Variables likely to be important*

Studies to date have used variables from existing satellite technologies that were not designed to aid research on infectious disease ecology. Such data have been adapted to serve as proxies for relevant signals that might represent important risk indicators. Thus, the Normalized Difference

Vegetation Index (NDVI), or other environmental indices such as “greenness” or “wetness,” have been correlated with measures of transmission, disease or indices of risk, but at only at coarse spatial scales. Might HSRH data improve identification of more specific habitats of high risk, hence enhance prediction of cases in time or space? The answer may partly depend on finer *spatial* resolution of human exposure or cases. This, however, is made difficult by not knowing *where* some exposures occur (home, school, work, recreation), *when* risk is greatest (a function of incubation period), and *who* within a region is part of the area of evaluation (a function of their age, behavior, sex, etc.). Anticipating that the cart may precede the horse, the usefulness of HSRH data will depend strongly on the other data to be analyzed. Whether some environmental features can be better characterized using enhanced spectral and spatial resolution is a question that depends on the question.

#### 4 Conclusions

Even if the massive amounts of data implied in greater spectral and spatial resolution become available, does the capacity exist to efficiently analyze such data so that time-space questions of public health importance can be effectively addressed? Will understanding of local exposure and risk be improved over that from analyses using coarser spatial resolution data? HSRH imagery is new and not yet extensively used in environmental exposure assessment. The lack of application comes in part from a lack of analysis tools. In addition, there are more fundamental questions involving whether finer spatial scale and high-spectral resolutions are crucial to understanding risk of most globally-important vector-borne or emerging infectious diseases.

Exposures occur at many scales. Depending on the emerging or infectious disease of concern, climate (which is regional), weather, land-use patterns, agricultural practices, deforestation, water distribution (which are regional and local), as well as house planning and house construction (local) may all impact on risk of certain vector-borne or emerging diseases. This list is incomplete. The issue of how we address such complexity is critical. All scales are important in that they impact on each other, but it is important to understand how knowledge from each can be used to inform the others.

The spatial analytical methods and hardware/software opportunities to explore such massive data sets are just now being developed. Some methods will carry over with little modification from multispectral image processing (e.g. such as habitat classification, vegetation classification, signal processing, noise reduction and filtering). But most existing spatial analysis software will have to be modified to consider advanced spatial statistical methods and advanced modeling for HSRH data. The enormous size and spatial dependencies of such data sets create special problems in evaluation of exposure assessment and disease risk. For this reason, new tools are needed to manipulate spatially-enabled database management systems for very large data sets. The same is true of methods to study associated environmental exposures and their locations, and for documenting spatial heterogeneity, patches and patterns. For example, spectral libraries that can be rapidly

classified for exposure assessments are needed. Other analytic tools for assessing the statistical significance of these patterns, and for spatial modeling of exposures will enhance capacity. Yet once the obstacles are overcome, the potential for use of HSRH data in surveillance and early warning of outbreaks is enormous.

We are presented with an opportunity to revolutionize exposure assessment, including that involving environmental exposures influencing infectious diseases. Both the science and the technology are at complicated intersection involving spatial pattern analysis, geocomputing, and new HSRH sensing technology. Our ability to obtain relevant disease-associated information at a similar and relevant temporal and spatial scale is critical. Once such epidemiological data are gathered, the challenge must be addressed of combining them with relevant tools and knowledge from other disciplines such as spatial analysis, medical geography, infectious disease epidemiology, sociology, international relations and economics.

How can we best combine cutting-edge methods to enhance HSRH-based exposure assessment? For infectious diseases with transmission dynamics that are strongly affected by the environment, the answer must depend on the nature of that influence, the scale of environmental variability, and the question under consideration. Thus, the relevance and potential application of finer resolution data will vary with disease and environmental context. The potential of HSRH data must be evaluated in the context of the intellectual and practical demands of public health, and the statistical and technical capacity of people who obtain and process such data.

## References

- Beck LR, Lobitz BM, Wood BL (2000) Remote sensing and human health: new sensors and new opportunities. *Emerging Infectious Diseases* 6(3):217–27
- Centers for Disease Control and Prevention (1994) *Addressing Emerging Infectious Disease Threats: A Prevention Strategy for the United States*. Centers for Disease Control and Prevention, Atlanta, Georgia
- Diem JE, Comrie AC (2000) Integrating remote sensing and local vegetation information for a high-resolution biogenic emissions inventory—application to an urbanized, semiarid region. *Journal of the Air & Waste Management Association* 50(11):1968–79
- Dister SW, Fish D, Bros SM, Frank DH, Wood BL (1997) Landscape characterization of peridomestic risk for Lyme disease using satellite imagery. *American Journal of Tropical Medicine & Hygiene* 57(6):687–92
- Gade M, Alpers W (1999) Using ERS-2 SAR images for routine observation of marine pollution in European coastal waters. *Science of the Total Environment* 237–238:441–8
- Ginnig JE, Ombok M, Kamau L, Hawley WA (2001) Characteristics of larval Anopheline (Diptera: Culicidae) habitats in Western Kenya. *Journal of Medical Entomology* 38(2):282–288
- Kitron U (2000) Risk maps: transmission and burden of vector-borne diseases. *Parasitology Today* 16(8):324–5
- Lederberg J, Shope RE, Oaks SC (eds) (1992) *Emerging Infections, Microbial Threats to Health in the United States*. National Academy Press, Washington, DC
- Lindblade KA, Walker ED, Onapa AW, Katungu J, Wilson ML (2000) Land use change alters malaria transmission parameters by modifying temperature in a highland area of Uganda. *Tropical Medicine & International Health* 5(4):263–274

- Lopez-Pamo E, Baretino D, Anton-Pacheco C, Ortiz G, Arranz JC, Gumiel JC, Martinez-Pledel B, Aparicio M, Montouto O (1999) The extent of the Aznalcollar pyritic sludge spill and its effects on soils. *Science of the Total Environment* 242(1–3):57–88
- Rejmankova E, Pope KO, Roberts DR, Lege MG, Andre R, Greico J, Alonzo Y (1998) Characterization and detection of *Anopheles vestitipennis* and *Anopheles punctimacula* (Diptera: Culicidae) larval habitats in Belize with field survey and SPOT satellite imagery. *Journal of Vector Ecology* 23(1):74–88
- Todd LA (2000) Mapping the air in real-time to visualize the flow of gases and vapors: occupational and environmental applications. *Applied Occupational & Environmental Hygiene* 15(1):106–13
- Ward MH, Nuckols JR, Weigel SJ, Maxwell SK, Cantor KP, Miller RS (2000) Identifying populations potentially exposed to agricultural pesticides using remote sensing and a Geographic Information System. *Environmental Health Perspectives* 108(1):5–12
- Wilson ML (1994a) Developing paradigms to anticipate emerging diseases: transmission cycles and the search for pattern. *Ann NY Acad Sci* 740:418–422
- Wilson, ML (1994b) Population ecology of tick vectors: interaction, measurement and analysis. In Sonenshine DE, Mather TN (eds) *Ecological dynamics of tick-borne zoonoses*. Oxford, New York, pp 20–44
- Wilson ML (2001) Ecology and infectious disease. In: Aron JL, Patz J (eds) *Ecosystem Change and Public Health: A Global Perspective*. Johns Hopkins University Press, Baltimore, pp 283–324