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Application of satellite imagery for vector-borne disease monitoring in sub-Saharan Africa: An overview

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Abstract

This work presents an overview of the application of satellite imagery or remote sensing (RS) data for vector-borne disease (VBD) monitoring in sub-Saharan Africa. We discussed the different vector-borne disease conditions that are prevalent and endemic in parts of sub-Saharan Africa and how satellite imagery (RS data) can be used in monitoring these conditions. Key disease conditions considered include malaria, human African trypanosomiasis, leishmaniasis, lymphatic filariasis, loa loa filariasis, rift valley fever, dengue, yellow fever, and rickettsioses. Furthermore, we explored some of the current ways remote sensing data and geographical information systems (GIS) are being applied to monitoring these diseases. We discuss the efficacy of using strong spatial modelling techniques combined with RS data to enhance our comprehension of the role that environmental conditions play in influencing VBD vectors and transmission alongside the utilization of GIS/RS technologies for vector-borne illness surveillance, prevention, and control. Finally, we discussed how drone technology and new remote sensing platforms can provide improved monitoring and the impact of such improvements from a population health standpoint.

Keywords: Remote Sensing; Vector-Borne Diseases; Public Health; Disease Ecology; Climate Change

1. Introduction

The World Health Organization (WHO) reports that over one million people die each year from vector-borne diseases (VBDs) like leishmaniasis, Lyme disease, dengue, and malaria (Obradovic *et al.*, 2020). Several vector-borne diseases are not preventable through vaccines and necessitate a multifaceted approach involving vector management, prompt case identification, medicine, and community health education initiatives (Herdiana *et al.*, 2018). Surveillance systems and treatments should consider several social, economic, and environmental factors that influence the spread of vector-borne diseases. International trade, globalization, migration, climate change, and population movement significantly influence global disease trends. Several Vector-Borne Diseases (VBDs) are indigenous to sub-Saharan Africa and continue to pose a significant challenge in the area, highlighting their particular significance in that region.

Advancements in Geographic Information Systems (GIS) and Remote Sensing (RS) technology have enabled the production of digital map data using earth-observing satellite sensors and analysis of geographical and temporal settings, as noted by Ouma (2016). Tropical vector-borne diseases are highly influenced by climatic and

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environmental factors due to the vulnerability of intermediate hosts, free-living stages, and vectors. Prior studies have mostly concentrated on utilizing GIS/RS technology along with spatial and space-time.

modeling methods in the field of VBDs (Eisen and Eisen, 2011). The potential use of these technologies and methods for preventing, monitoring, and controlling tropical vector-borne diseases is an important subject that has not received adequate attention, especially in sub-Saharan Africa (Fournet *et al.*, 2018). Future VBD research should focus on adjusting mapping and modeling techniques for circumstances with limited resources and high illness prevalence (Ratmanov *et al.*, 2013). The current study intends to comprehensively analyze the utility of remote sensing data for detecting vector-borne illnesses in sub-Saharan Africa.

2. Literature Search

The study utilized five scientific databases and a systematic search strategy to identify research articles on the application of remote sensing data for monitoring vector-borne diseases in sub-Saharan Africa (PubMed, Google Scholar, Scopus, IEEE, and Science Direct) (Chibi *et al.*, 2023). Furthermore, there were books, dissertations, master's theses, and conference proceedings. The search terms "sub-Saharan Africa" and the keywords "vector-borne disease," remote sensing, prevention, diagnosis, and management" were inputted into the search engine. Sub-Saharan Africa, which includes countries such as Benin, Burkina Faso, Cape Verde, Cote d'Ivoire, The Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Niger, Nigeria, Senegal, Sierra Leone, and Togo, harbors a diverse range of vector-borne diseases (VBDs) and the organisms that transmit them. The inclusion criteria for references related to remote sensing (RS) and geographic information systems (GIS) applications in studying vector-borne diseases (VBDs) in sub-Saharan Africa were relaxed according to Longbottom (2022). An exhaustive list of abstracts was acquired and scrutinized for the present study; any publications meeting the inclusion criteria were thoroughly investigated. The review encompassed all publications published until 2023.

3. Results and discussion

3.1. Distribution of vector-borne disease in sub-Saharan Africa

3.1.1. Human African trypanosomiasis

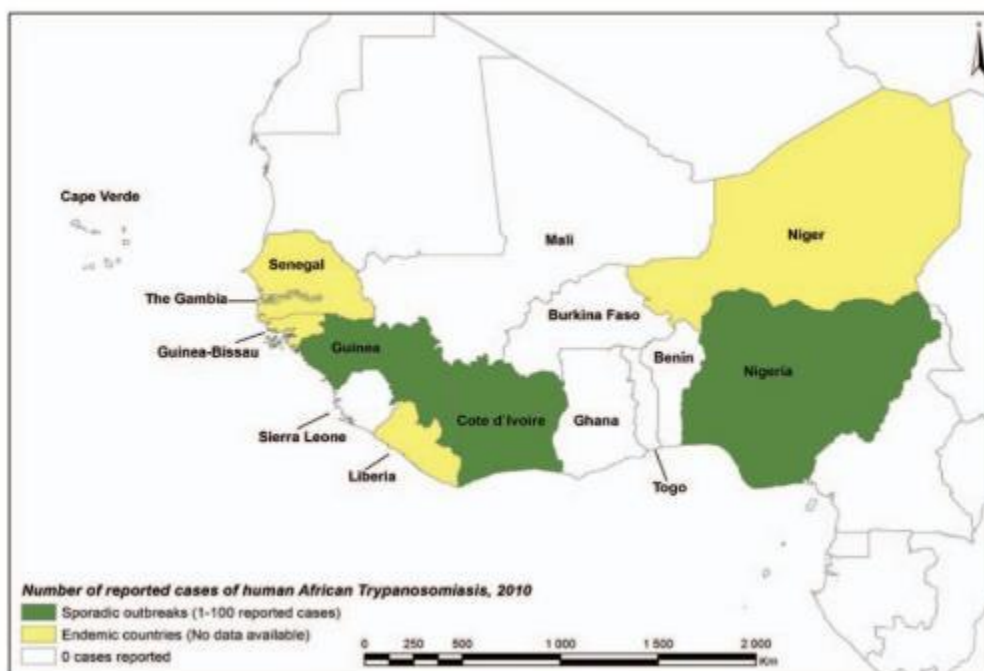


Figure 1 The WHO data, acquired from <http://www.who.int>, shows the geographic distribution of human African trypanosomiasis (*Trypanosoma brucei gambiense*) in sub-Saharan African nations in 2010.

Trypanosoma brucei gambiense protozoa cause Human African Trypanosomiasis (HAT), also known as sleeping sickness, and are transmitted by tsetse flies (*Glossina spp.*) (Azeem *et al.*, 2023). *T. b. gambiense* primarily resides in humans in sub-Saharan Africa. While pigs and some wild animal species have been recognized as reservoirs, animals often have little role (Hamill *et al.*, 2013). HAT is prevalent in several nations in sub-Saharan Africa, including Guinea, Cote d'Ivoire, and Nigeria. Disease mapping and sleeping sickness control have long been closely connected. The prominent initiative focused on disease prevention, research, and advocacy is the Atlas of Health and Technology (Bardosh *et al.*, 2017).

3.1.2. Leishmaniasis

Leishmaniasis is a group of vector-borne infections caused by more than 20 species of the protozoan genus *Leishmania*, which can lead to deadly systemic sickness or localized skin ulcers. Leishmaniasis is considered one of the "most neglected illnesses" due to limited resources for diagnosis, treatment, and prevention. It is intimately associated with poverty, as sandflies carrying the phlebotomine virus attack humans (*Phlebotomus spp.*). Leishmaniasis can be classified as either zoonotic (using at least one mammalian reservoir) or anthroponotic (using humans as the only reservoir engaged in transmission and the source of vector infection) based on the mechanism of transmission (Montaner-Angoiti & Llobat, 2023). Leishmaniasis is widespread in sub-Saharan Africa, with 11 out of 15 nations in the region reporting incidences of the cutaneous form of the illness. A recent study in Senegal investigated the seroprevalence of antibodies against *L. infantum*, the causative agent of visceral leishmaniasis, in the human population (Ngouateu and Dondji, 2022). A large-scale study using GIS/RS technology is now required to investigate the distribution of *L. infantum* in sub-Saharan Africa and find a potential vector.

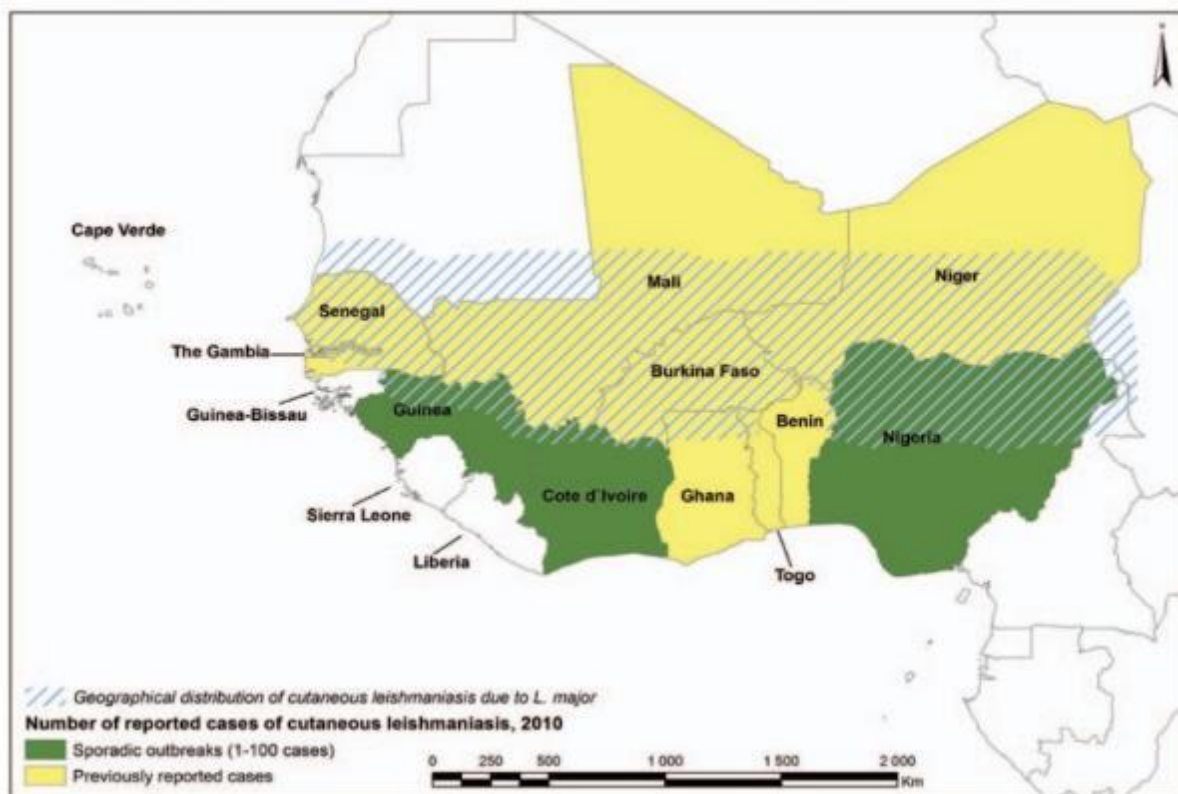


Figure 2 Geographic distribution of *Cutaneous leishmaniasis* in sub-Saharan African countries in 2010 (data from the WHO, retrieved from <http://www.who.int>).

3.2. Dengue and yellow fever

Dengue sickness is caused by a tropical pathogenic virus. The dengue virus mostly spreads through the mosquito *Ae. Aegypti* and humans are the main reservoirs for this virus (Dehghani and Kassiri, 2021; Mudele *et al.*, 2020). While dengue is prevalent in tropical and subtropical regions, its prevalence in Africa remains unknown (da Silva *et al.*, 2022). In sub-Saharan Africa, the major way the dengue virus is spread is through sylvatic circulation, with lower primates serving as the primary reservoir (Raulino, 2021). The dengue virus is widespread in West Africa, with

evidence of its presence detected in 11 countries in the region (Figure 3). Yellow fever (YF) is an acute viral hemorrhagic disease transmitted by infected *Aedes* spp. mosquitoes in West Africa (Adam and Jassoy, 2021). Untreated yellow fever results in a mortality rate of up to 50% for individuals with severe symptoms, and there is currently no cure available (Kuno, 2024). The YF virus impacts multiple vertebrate species and is found in urban and rural settings (Silva *et al.*, 2020). Mosquitoes are the principal vectors and monkeys are the predominant hosts in the sylvatic cycle. The virus is transmitted between humans and mosquitoes in the urban cycle, mostly by *Ae. aegypti* mosquitoes (Agboli *et al.*, 2021). The virus in Africa can spread through an intermediary cycle with *Aedes* spp. mosquitoes in savannah tree holes and coming into contact with humans or nonhuman primates (Milton *et al.*, 2020). Mosquitoes can also undergo vertical transmission, which may play a vital role in maintaining the sylvatic cycle (Alencar *et al.*, 2021). All countries in sub-Saharan Africa, except for the Sahara Desert regions of Mali and Niger, have widespread occurrences of yellow fever.

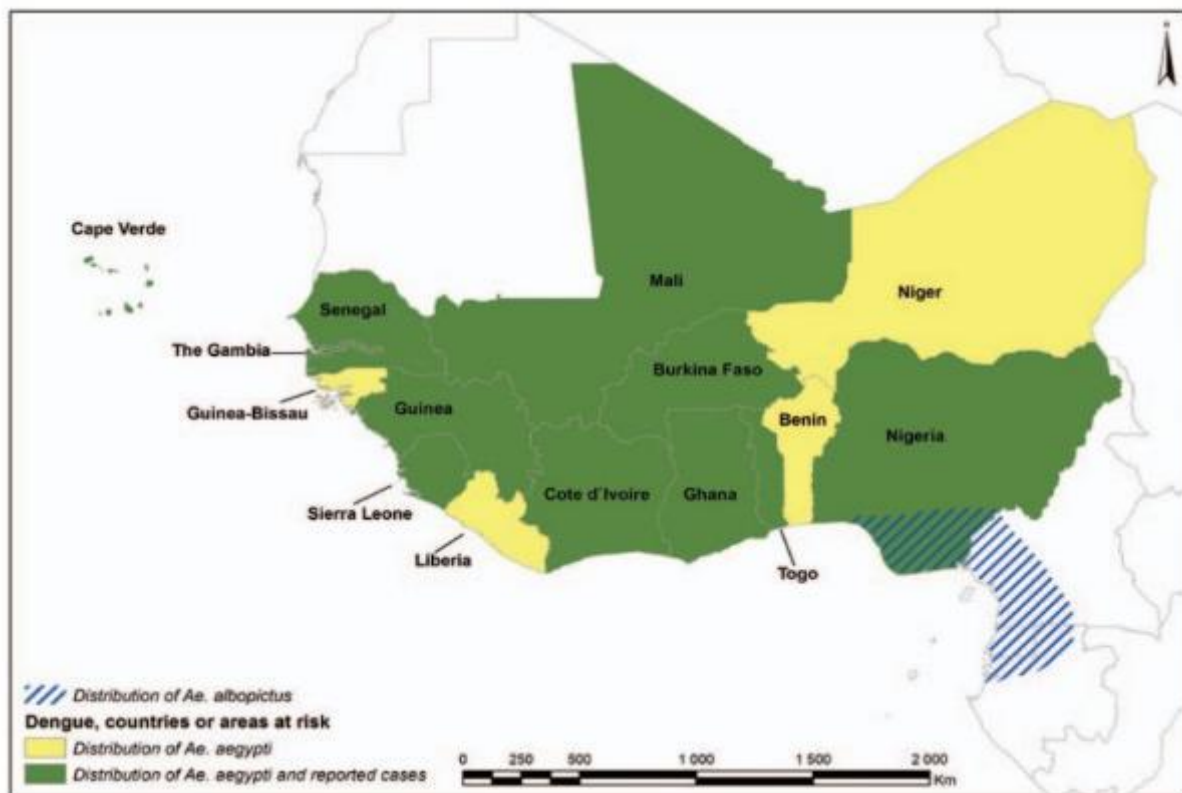


Figure 3 Geographic distribution of dengue in Sub-Saharan African countries in 2011 (data from the WHO, retrieved from <http://www.who.int>).

3.3. Malaria

Most articles about vector-borne diseases in sub-Saharan Africa primarily focus on malaria. People can get malaria, an infectious disease, from female *Anopheles* mosquitoes that are infected with the *Plasmodium* parasite (Mwema, 2021). Malaria poses a significant public health threat, with more than 200 million infections and perhaps up to 1 million deaths each year (Oladipo *et al.*, 2022). People with symptomatic and asymptomatic malaria in endemic regions act as reservoirs for the virus. Every West African country has a native population of malaria, although the disease's impact differs based on the nation's efforts to address it. In Africa, many efforts have been made to collect and organize the entomological, parasitological, and epidemiological data that are currently accessible. Nevertheless, there remains significant uncertainty regarding the yearly incidence of malaria cases and their geographical distribution (Feufack-Donfack *et al.*, 2023). The Mapping Malaria Risk in Africa (MARA/ARMA) project was established to develop comprehensive malaria risk maps covering the whole continent.

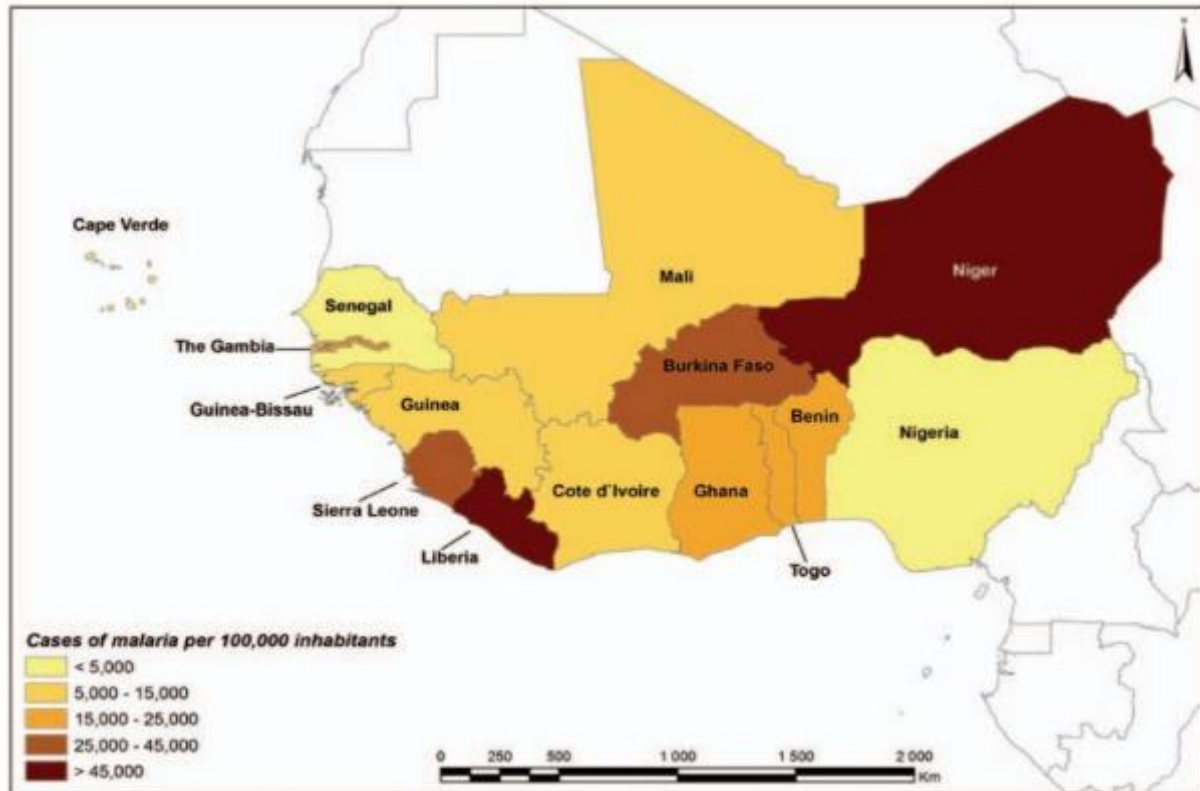


Figure 4 Malaria cases per 100,000 people in West African countries in 2010 or the most recent year for which data was available (source: <http://www.who.int>).

3.4. Filariasis

Wuchereria bancrofti, an endemic parasite causing lymphatic filariasis (LF), is transmitted by vectors and is a parasitic infectious disease prevalent in tropical areas, especially in sub-Saharan Africa (Wanji *et al.*, 2019). *Anopheles gambiae sensu lato* is a mosquito species native to West Africa responsible for transmitting malaria caused by *Plasmodium falciparum* and lymphatic filariasis. In Africa, humans are the only reservoir hosts for the LF parasite (Ratmanov *et al.*, 2013). *Onchocerca volvulus*, a filarial parasitic nematode, causes the parasitic disease onchocerciasis, also referred to as "river blindness" (Brattig *et al.*, 2021). It is transmitted through the bites of infected Simulium (black fly) vectors, which thrive in rivers and streams with fast-flowing water. The African Programme for Onchocerciasis Control (APOC) oversees the management of the illness in sub-Saharan Africa (Geissler *et al.*, 2020). The filarial parasite *Loa loa* is responsible for causing *Loa loa* filariasis, also referred to as loiasis. The sickness is exclusive to equatorial rainforests in Central and West Africa, as stated by Kelly-Hope *et al.* (2018). Chrysops flies are the vectors of *L. loa*. Humans are the primary reservoir for *L. loa*. Several West Sub-Saharan African countries have widespread occurrences of LF, loiasis, and onchocerciasis (Ajendra *et al.*, 2022).

3.5. Rift Valley fever

Rift Valley fever (RVF) is an arthropod-borne virus that primarily causes high mortality rates and widespread miscarriages in domestic animals, but it can also infect humans. Rats and camels are the primary natural reservoirs of the RVF virus, with most infected animals belonging to these species (Oluwayelu *et al.*, 2018). *Aedes* and *Culex* mosquitoes are the main vectors of the virus. People can acquire the RVF virus via sick animals or through transmission by mosquitoes (Sarwar, 2016). A large Rift Valley Fever outbreak occurred in southern Mauritania and northern Senegal in 1987. All nations in West Africa are susceptible to Rift Valley Fever (RVF) (Lancelot *et al.*, 2019).

3.6. Crimean-Congo haemorrhagic fever

Tick-borne viruses are responsible for causing Crimean-Congo haemorrhagic fever. The virus is a significant cause of illness globally, particularly in West Africa (Mourya *et al.*, 2014). *Hyalomma* genus's ixodid ticks, which act as its main arthropod carrier, are distributed similarly. Humans primarily contract the infection by nosocomial transmission, contact with infected livestock, and tick bites (Perveen *et al.*, 2021). Although serological examinations of

cattle in West Africa have shown the enzootic circulation of the Crimean-Congo haemorrhagic fever virus, only a small number of human cases have been recorded (Bente *et al.*, 2013).

3.7. Rickettsioses

Tickborne rickettsioses are a common cause of systemic fever sickness among travellers from wealthy nations, ranking second only to malaria. Their prevalence in native communities, especially in West Africa, is not well understood. *Rickettsia felis* is widespread in Senegal, with a prevalence of 4.4 per cent. *Rhipicephalus evertsi* ticks are responsible for transmitting Mediterranean spotted fever, a disease that was documented in Senegal (Parola *et al.*, 2013). Extensive entomological studies have been carried out on ticks to examine the presence of Rickettsia species, together with serological research on the prevalence of rickettsioses (Parola *et al.*, 2013). Although efforts have been made to map the geographic distribution of rickettsioses in Africa, geostatistical analysis has not been conducted. Instead, infected sites or counties with reported cases have been represented as points (Ratmanov *et al.*, 2013). Therefore, West African borrelial and rickettsial vector-borne illnesses have not received the appropriate level of attention.

Views on the use of remote sensing and geographic information systems in the research of vector-borne illnesses.

GIS facilitates the comparison of disease trends with environmental data, whereas remote sensing technologies can forecast variables such as temperature, humidity, and vegetation by utilizing high-resolution satellite data. Satellite remote sensing (RSS) has shown promising results in assessing the danger of several vector-borne diseases (VBDs) in different spatial dimensions in recent years (Oerke, 2020). Satellite-based images are characterized by their spectral, temporal, and geographical resolution. Some limited attempts to utilize RS in epidemiology have not shown to be as effective as expected, according to Dlamini *et al.* (2019). GIS/RS technologies are undoubtedly a valuable information source for epidemiologists. It is crucial to carefully consider all the advantages and disadvantages of GIS/RS technology and to refrain from overestimating them (Dargie, 2008). Restricted attempts have been made to apply RS in epidemiology, however, the procedures have not proven to be as beneficial as expected. Moreover, while VBD treatments might obscure the link between sickness and the environment, it is important to acknowledge and deal with them. No association was discovered between remotely sensed data and the risk of malaria in recent investigations of malaria indicators in Zambia and Angola.

The traditional modelling method seeks connections between multivariate environmental data and patterns of vector presence or absence to map vectors and vector-borne diseases (Cuervo *et al.*, 2023). Basic statistical models can be helpful in linking a limited number of environmental variables collected from satellite data (Schuenemeyer and Drew, 2011). Simple statistical models are often used to establish linear correlations between environmental variables and presence/absence data, even though these associations are likely to be complex and non-linear. The next step is to create sophisticated process-based models incorporating vector biology to predict diseases and their probability (Peters *et al.*, 2020).

Regression models have been widely utilized in landscape epidemiology. The type of regression model (logistic, Poisson, linear, etc.) is determined by the nature of the outcome variable to be predicted (binary, count, continuous, etc.) (Mudele *et al.*, 2021b; Mudele *et al.*, 2021c). In addition, other studies have shown that classical machine learning and modern neural network approaches can also be used for early warning systems to inform planning and intervention (Mudele *et al.*, 2020, Mudele *et al.*, 2021a). Covariates such as environmental factors recorded at sampled sites are included in such analyses (Dasgupta *et al.*, 2011). The model is used to interpret illness patterns based on covariates or predict outcomes in places without outcome data using covariate values from those locations.

Aside from regression modelling, spatial epidemiology utilizes several techniques including discriminant analysis, generalized additive and linear models, Bayesian estimation techniques, geographical clustering, and others (Dhewantara *et al.*, 2019). Conventional models require data on both the existence and non-existence of the condition. Alternatively, when absence data is lacking, various "presence-only" models might be used. One presence-only machine learning approach for ecological niche modelling is Maxent, which is based on maximum entropy. Covariate independence is not required for implementing this method, which is effective with very small sample sizes. Moreover, in Africa, where there is a lack of complete surveillance data from all regions, these advantages can be crucial (Townsend Peterson *et al.*, 2007).

There are two primary ways of spatial modelling: extrapolation using relationships between vector or VBD data and environmental or socioeconomic predictor variables, and interpolation based on spatial dependence in vector or VBD data (Eisen and Eisen, 2011). When there is a lack of reliable monitoring data, using the latter method can

be an efficient way to understand the degrees of threat. Model extrapolation is restricted to areas that have similar biological and climatic characteristics as the region where the model was developed (Murray and Cohen, 2017).

Efforts to control diseases in sub-Saharan Africa have mostly focused on malaria, TB, and AIDS (Kealey, 2010). NTDs encompass additional sources of fever and sickness. The 21st century offers a chance to comprehensively document and study the epidemiology of diseases in sub-Saharan Africa (Junior *et al.*, 2021).

The unknown origins of fever in West Africa have not been thoroughly researched. Malaria is commonly associated with most fevers. NTDs are identified as the primary source of fever among both indigenous populations and tourists, as per a recent study by Maze *et al.* (2018). *Borrelia crocidurae*-related tick-borne relapsing fever has been found again, and there have been reports of rickettsiae, such as *Rickettsia felis*. Fresh infections from the Rickettsiae family were discovered in the vicinity (Mediannikov *et al.*, 2014).

There is a lack of research on the geographical distribution of disease-carrying ticks in sub-Saharan Africa. Conversely, the study of Ixodes ticks in North America has significantly improved due to the utilization of GIS/RS technologies (Ledwaba *et al.*, 2022). Geospatial modelling has demonstrated that GIS/RS-based environmental factors such as elevation, slope, vegetation, soil type, temperature, and moisture can predict high concentrations of *I. pacificus* and *I. scapularis*, the main tick vectors of Lyme disease in North America (Kazemi Garajeh *et al.*, 2023). Studies on *R. felis* infection in sub-Saharan Africa could use the same research methods.

Epidemiologists now commonly use innovative GIS/RS methods to study various vector-borne diseases. Vector habitats are identified and described by analysing the relationship between vector density and environmental factors obtained from satellites, including temperature, humidity, elevation, vegetation, rainfall, surface water, land use, land cover type, and soil moisture (Fornace *et al.*, 2021). Epidemiologists can now explore new spatial analysis techniques using RS data, GIS, and statistical software on desktop computers, which are cost-effective and practicable (Arifin *et al.*, 2016).

Maps showing the seasonal risk of VBDs will be needed to monitor the impact of changing vector ecology. Risk maps that integrate GIS/RS, advanced analytical tools, and a landscape ecology approach can be highly beneficial for developing research subjects, identifying surveillance requirements, and guiding fieldwork and control efforts (Huang *et al.*, 2012).

This approach, based on ecological analysis, requires gathering all available epidemiological data and supporting it with field research. The most efficient GIS/RS applications for studying Vector-Borne Diseases in sub-Saharan Africa are either large-scale research using data from published scientific literature or small-scale studies using data from community-based monitoring. Collaboration within the epidemiology community may improve research on VBD in West Africa. The main goal of using GIS/RS technologies in studying vector-borne diseases VBD is to reduce the disease impact by generating data that promotes the adoption of preventive measures by individuals and helps public health agencies allocate their limited resources effectively for prevention, surveillance, and control (Lock-Wah-Hoon *et al.*, 2020). There is significant potential for enhancing vector-borne infectious disease surveillance, prevention, and control in sub-Saharan Africa through the utilization of GIS/RS technologies.

3.8. Utilizing drones and newly acquired remotely sensed data for disease mapping.

Drones developed for private and civilian use have made some remote sensing capabilities accessible for scientific applications (Pajares, 2015). Unmanned aerial vehicles (UAVs) or basic drones are being used to swiftly assess various humanitarian situations from above. Drone data, which comprises high-resolution photographs at local scales, can be challenging to store and process due to its size (Daud *et al.*, 2022). Managing drone data will require an upgraded processing and storage capacity due to a single drone flight collecting over 70 terabytes of data. Drone data will certainly be classified as big data and will require storage optimization methods such as simplifying irrelevant information (Giordan *et al.*, 2020). Many firms that use drones now manage large amounts of data by only gathering and keeping what they need. Drones provide precise geographical and temporal data, crucial for understanding the connections between environmental factors and disease spread (Daud *et al.*, 2020). Drones are intended to enhance current remote sensing technologies by offering a new level of usefulness and localized mapping applications to established methods (Mathews *et al.*, 2023). An exploratory study was undertaken to examine the mapping of microorganisms in the atmosphere and the transmission of microbial traffic, such as the flu, within the same species. The study utilized a hypothetical model fed with data from drones (Tidey *et al.*, 2023).

This study considers drones for their real-time operation and their capability to attain high spatial and temporal resolutions at local scales, which is beneficial for epidemiological purposes (Fornace *et al.*, 2014). Drones are being studied for their ability to capture real-time data at lower costs and could be beneficial for mapping disease outbreaks during emergencies. Drones provide precise and detailed data that is essential for identifying the environmental elements that impact infectious diseases. Drones provide real-time data, enabling the mapping of changes as they occur. Drones are becoming increasingly prevalent due to ongoing studies into their capabilities and the discovery of new applications.

3.9. Final Remarks

Studies have explored the advantages of using remote sensing, GIS, and statistics in disease mapping and epidemiology, with a predominant focus on sub-Saharan Africa. It is essential for end users and non-experts to have the capability to access, retrieve, and evaluate satellite data for the efficient utilization of remote sensing technology. Preparatory stages before integrating such data into models as covariates also influence how successfully non-specialists accept and use them. RS data is valuable in disease mapping and epidemiology for developing near real-time monitoring spatial models that can predict temporal and spatial patterns of vector-borne diseases and transmission risk accurately.

Factors at different landscape and geographic scales influence the dynamics of vector-borne diseases in a particular location. For instance, the interaction between parasites, hosts, and vectors leads to the transmission of malaria. Integrating GIS spatial analysis techniques with remote sensing data of varying resolutions can enhance and guide vector surveillance and control efforts at local, regional, and continental scales. The results of a few of the research mentioned above have been utilized to support and demonstrate how remote sensing and GIS technology can give epidemiologists a fresh viewpoint when it comes to identifying the environmental causes of the diseases in question.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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