We are IntechOpen,
the world's leading publisher of
Open Access books
Built by scientists, for scientists

6,900
Open access books available

186,000
International authors and editors

200M
Downloads

154
Countries delivered to

Our authors are among the

TOP 1%
most cited scientists

12.2%
Contributors from top 500 universities

WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com

The Geospatial Approach on Eco-Epidemiological Studies of Leishmaniasis

João Carlos Araujo Carreira,

Mônica de Avelar Figueiredo Mafra Magalhães and

Alba Valéria Machado da Silva

Additional information is available at the end of the chapter

http://dx.doi.org/10.5772/57210

1. Introduction

1.1. Leishmaniasis

Leishmaniasis is a vector-borne disease transmitted by numerous sand fly species caused by obligate intracellular parasitic protozoa of the genus Leishmania. It can infect besides the man, a wide range of sylvatic and domestic mammal hosts producing either tegumentar or visceral lesions.

The life of *Leishmania* get going, when phlebotomine sand flies, mostly *Lutzomyia* in the New Word and *Phlebotomus* in the Old Wold, become infected during the blood meal, by ingesting infected mononuclear phagocytic cells. The amastigotes in the gut of sand flies, differentiates into promastigotes and multiply. In the *Viannia* subgenus the parasites develop in the hindgut of the vectors while in the *Leishmania* subgenus, the growth occurs in the midgut. In the insect's gut several promastigotes differentiate into metacyclic forms and migrate to the proboscis.

The parasites are transmitted by the bite of infected female of phlebotomine sand flies during the blood meal when the insects inject from their proboscis, the metacyclic promastigotes. Those forms are capable to survive inside the phagolysosomes of macrophages and other types of mononuclear phagocytic cells. Once inside of the cells, promastigotes differentiate into amastigotes, a stage that is associated mammal tissues. The amastigotes multiply by simple division and continue to infect other mononuclear phagocytic cells (Figure 1).

INTECH
open science | open minds
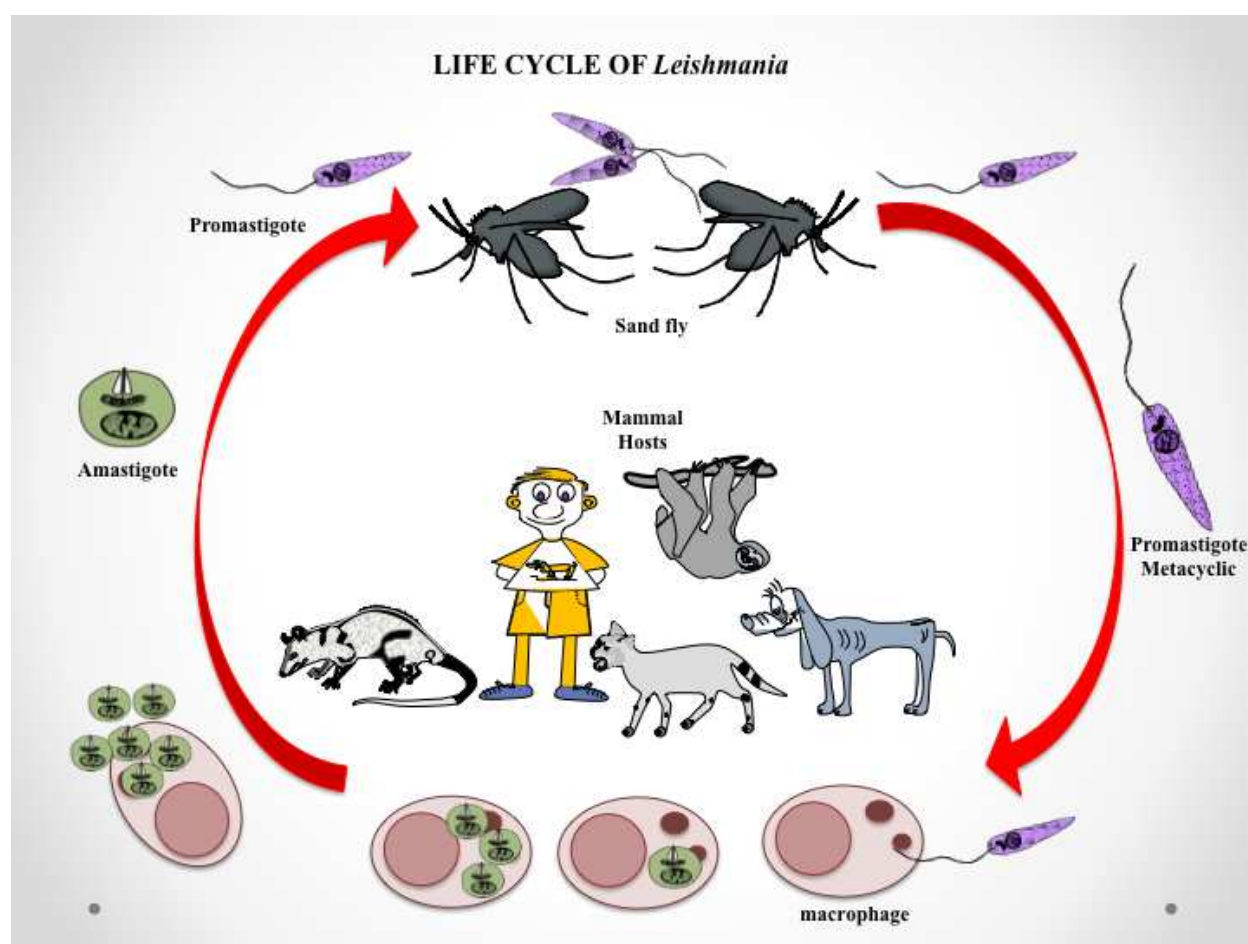
Figure 1. Life cycle of *Leishmania.*

Depending on the parasite and host species in addition to numerous factors related to the hosts' genetic background, the progress of the infection might be influenced, determining if the patient will become symptomatic or sick, eventually resulting in cutaneous or visceral leishmaniasis.

The geographical distribution of leishmaniasis includes 88 countries and almost 350 million of peoples live in these areas where the disease has been considered one of the most severe problem of public health. The majority of the countries affected are in the tropics and sub-tropics, consequently leishmaniasis covers a wide range from rain forests in Central and South America to deserts in West Asia [1,2] (Table 1 and 2).

Depending on the eco-epidemiological conditions, the leishmaniasis can present sylvatic or domestic transmission cycles (Figure 2). Among the most important factors composing those conditions, we could mention the environmental characteristics (biotic and abiotic factors) as well as the parasite, vector and host species involved.

The sylvatic cycles are quite ancient; they have been molded for millions of years before the emergence of man, through co evolutionary relationships among the parasite, vectors and

SPECIES	CLINICAL FORMS	REGION	VECTOR	HOST
Leishmania major	Cutaneous	Asia, Africa	*Phlebotomus papatasi*	Human, rodents
Leishmania tropica	Cutaneous	Europe, Asia, Africa	*P.sergenti*	Human, dogs, rock-hyraxes
Leishmania aethiopica	Cutaneous, mucocutaneous	Africa	*P. longipes, P. pedifer*	Human, hyracoids
Leishmania infantum	Visceral	Europe, Asia, Africa	*P. perniciosus, P. ariasi*	Human, dogs, sylvatic canids
Leishmania donovani	Visceral, PKDL	Asia, Africa	*P. argentipes, P. orientalis*	Human
Leishmania siamensis	Visceral	Europe, Asia, and North America	?	Human, horse, cows

Table 1. The main species of *Leishmania* from the Old World: with the correspondent clinical forms, regions of occurrence, vectors and mammal hosts. (? - Not known).

SPECIES	CLINICAL FORMS	REGION	VECTOR	HOST
L (V) braziliensis	Cutaneous, mucocutaneous	South and Central America	*Nyssomyia intermedia, N. whitmani, Migonemyia migonei*	Human, terrestrial rodents, marsupials, equines, dogs, cats
L (V) peruviana	Cutaneous	South America	*Lutzomyia peruensis, L. verrucarum*	Human, dogs, rodents* opossums*
L (V) guyanensis	Cutaneous	South America	*L. umbratilis*	Human, sloth, anteater, rodents, opossums
L (V) panamensis	Cutaneous	South and Central America	*L. panamensis, L. trapidoi*	Human, sloth, arboreal animals, monkeys, rodents, hunting dogs
L (L) mexicana	Cutaneous, diffuse cutaneous	South, Central and North America	*L. olmeca*	Human, forest rodents
L (L) amazonensis	Cutaneous, diffuse cutaneous	South America	*L. flaviscutellata, L. panamensis*	Human, forest rodents, marsupials, fox
L (L) pifanoi	Cutaneous, diffuse cutaneous	South America (Venezuela)	*L. flaviscutellata* *	Human, Rodents?
L (L) venezuelensis	Cutaneous	South America (Venezuela)	*L. olmeca* *	Human, domestic cats, rodents?
L (L) infantum	Visceral	South, Central and North America	*L. longipalpis, L. cruzi, L. evansi*	Human, sylvatic canids and felids, opossums, dogs

Table 2. The main species of *Leishmania* from the New World: with the correspondent clinical forms, regions of occurrence, vectors and mammal hosts. (*- Putative).

mammal hosts. Mammal reservoirs and insect vectors have been continuously maintaining the parasites in equilibrium without human involvement.

In our time sylvatic cycles are restricted to wild places where disease outbreaks can eventually occur when people make incursions or settlements in those areas.

Concerning to domestic cycle an intra-domiciliary type (figure 2) of transmission is characteristic and the principal components for the disease establishment and maintenance, are the occurrence of vectors with the capacity of domiciliary human landing/biting, besides humans and domestic animals as mammal hosts [2].
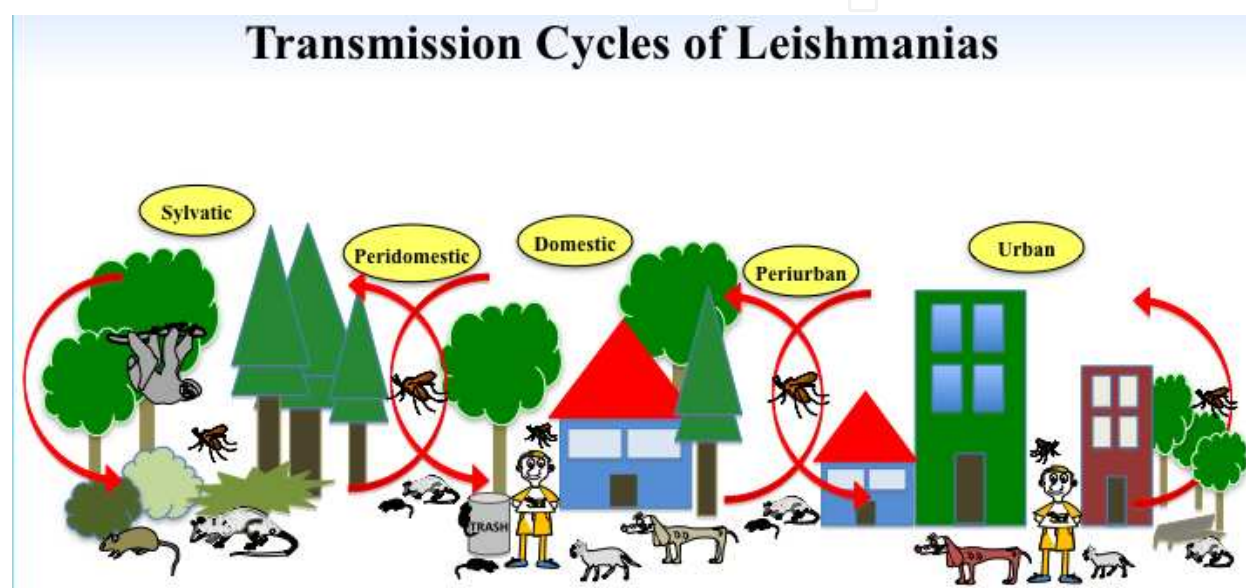
Figure 2. Schematic drawing: eco-epidemiological picture of transmission cycles of Leishmanias.

The earliest steps for the origin of domestic cycles of leishmaniasis probably started around 12.000 years ago, when the ancient human populations began to practice sedentary agriculture and also have introduced domestic animals and livestock causing drastic alterations on the natural habitats.

As a result of such environmental modifications, a large avoidance of the sylvatic animals occurred from the surroundings of human habitations; that together with the insertion of new potential mammal hosts gave rise to a progressive adaptation process in some populations of sylvatic vectors toward a domiciliary behavior. Then little by little certain sand flies populations adopted some introduced species as their new feeding sources [2-4].

In our time, after thousands of years of interaction with domestic mammals as hosts, some vectors hosts species that originally were totally sylvatic, have evolved to exist even in great urban areas, permitting the transmission of the parasite and its maintenance practically restricted to the participation of domestic and/or synanthropic hosts, sand fly and the man [5-7].

So, actually the eco-epidemiological picture of leishmaniasis could be represented as a complex puzzle where each piece is formed by the interaction of a parasite species with their correlated hosts and vectors, in a determined habitat. Nevertheless, it should not be considered as a static process because the occurrence of other parasite species, besides the action of the temporal component they can play a very important role, by influencing the whole process making it possible the occurrence of a variety of transmission patterns that sometimes may result in disease.

Considering the several difficulties to elaborate Leismaniasis control plans, probably the most significant is the high complexity of eco-epidemiological features of the disease. They are greatly influenced by the wide distribution of the parasites, the existence of a large variety of vector species in addition to the pressure of local environmental factors affecting the populations of human hosts, vectors and reservoirs [3-4,8].

The leishmaniasis control measures in use, including spraying to eliminate the adult forms of the vector, diagnosis and treatment of human patients and elimination of seropositive dogs, have failed in preventing new epidemics [9,10].

Therefore, a spatial and temporal approach to analyze endemic foci of the disease could be very a useful method to understand the dynamic of transmission [11,12].

1.2. Methods

Geographic information systems (GIS) and remote sensing (RS) are important tools that comprise computational systems, which permit to map and analyze environmental factors related to the spatial and temporal distribution environmental components that affect the distribution of diseases [12]. The availability of climatic, geological and phytographic digital data and the accessibility of GIS software also have permitted the implementation of several epidemiological studies in relation to ecological factors and disease prediction, as well as have been providing evidences that its use is indispensable before the elaboration of control plans [5, 11,12].

As examples of GIS software we could mention: ArcGis, TerraView, TerraHidro, Gvsig, etc.

The Remote Sensing is also an important data resource for presentation of vegetation, land cover and land use as well as the categorization of the habitats and population density of insect vectors, parasite and reservoir hosts [12,13].

An important feature available in GIS methodology consists of Kernel's method. It is considered a new class of pattern analysis algorithms also utilized in GIS, which can operate on a wide-ranging types of data and relationships. Correlation, factor, cluster and discriminant analysis are just some of the types of pattern analysis tasks that can be performed on data as diverse as sequences, text, images, graphs and of course vectors. The method provides also a natural way to merge and integrate different types of data [5,14].

Kernel density estimators belong to a class of estimators called *non-parametric* density estimators. In comparison to parametric estimators where the estimator has a fixed functional form (structure) and the parameters of this function are the only information we need to store, Non-

parametric estimators have no fixed structure and depend upon all the data points to reach an estimate [15].

Differently from conventional histograms where it is necessary to sub-divide the whole data in equal intervals and also to determine the end point of each interval, producing a not smooth representation. On the kernel method those problems can be minimized by the production of a kind of smooth histogram [15] (Figure 3).
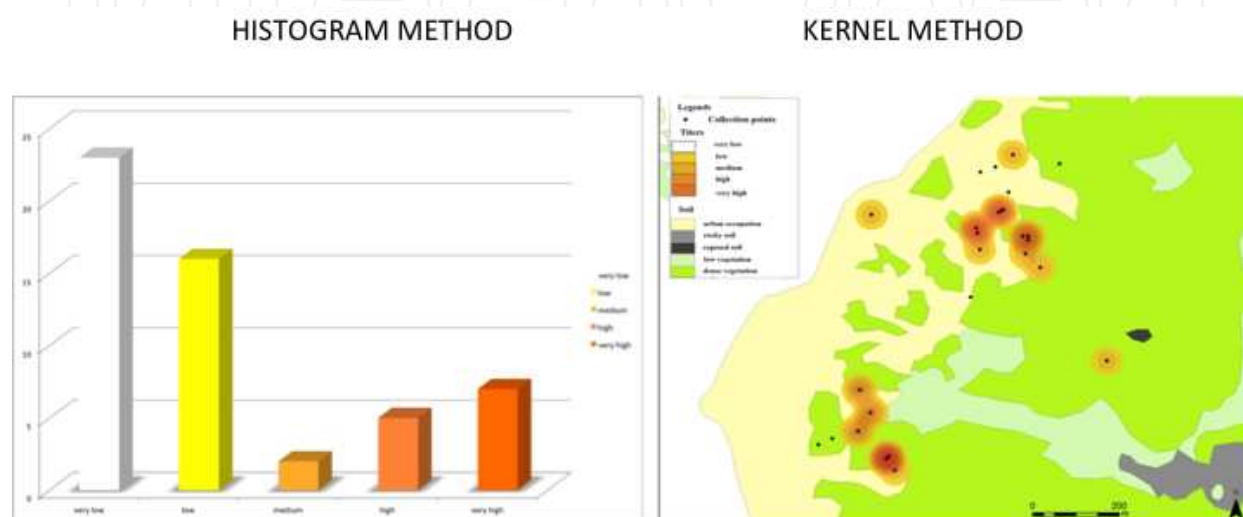

Figure 3. Depiction of doghouses geo-referenced and canine leishmaniasis cases in function of serological titers, represented by histograms and Kernel method (ArcGis).

Other attributes of GIS methodology very useful to the study epidemiology of leishmaniasis is the possibility to create digital maps after performing cluster analysis on the populations of vectors and mammal hosts, including the man; and also to represent circumscribed areas in the same maps, indicating potential regions of vector flight or putative hosts' home ranges [11,14,16] (Figure 4 and 5).

Clustering is a method also applied in GIS, and comprises a common technique for statistical data analysis used in many fields, including machine learning, data mining, pattern recognition image analysis and bioinformatics.

So, the use of new technologies based on eco-epidemiological indicators is essential on the identification of circumstances that impair the spread and maintenance of the disease and certainly could be used to set priorities for implementing disease control measures, thus reducing operational costs and increasing their effectiveness.

In conclusion, the notorious difficulty in controlling the transmission of leishmaniasis, a disease caused by a parasitic protozoa described at 1903 and that still persists currently showing a re-emerging pattern in some places, indicates that such parasites have been developing a great number of evolutionary advantages and despite all the efforts of scientists an effective control was not achieved yet. It is important to remember that those organisms
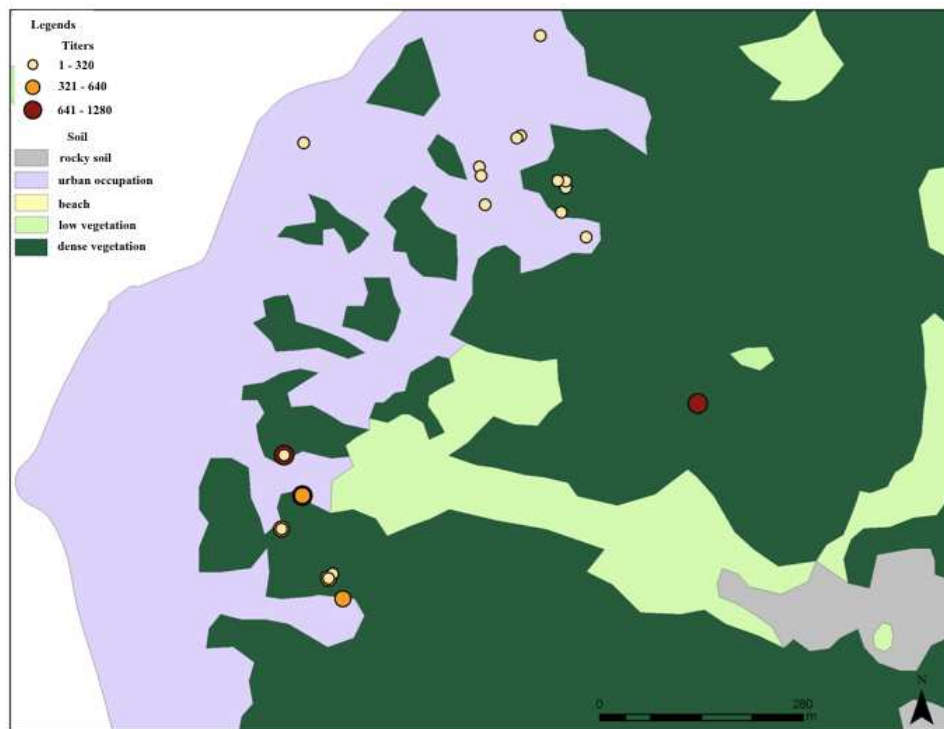
Figure 4. Vegetation, land cover and land use patterns and general distribution of canine leishmaniasis cases, with the respective serological titers, from an endemic focus in Brazil (ArcGis).
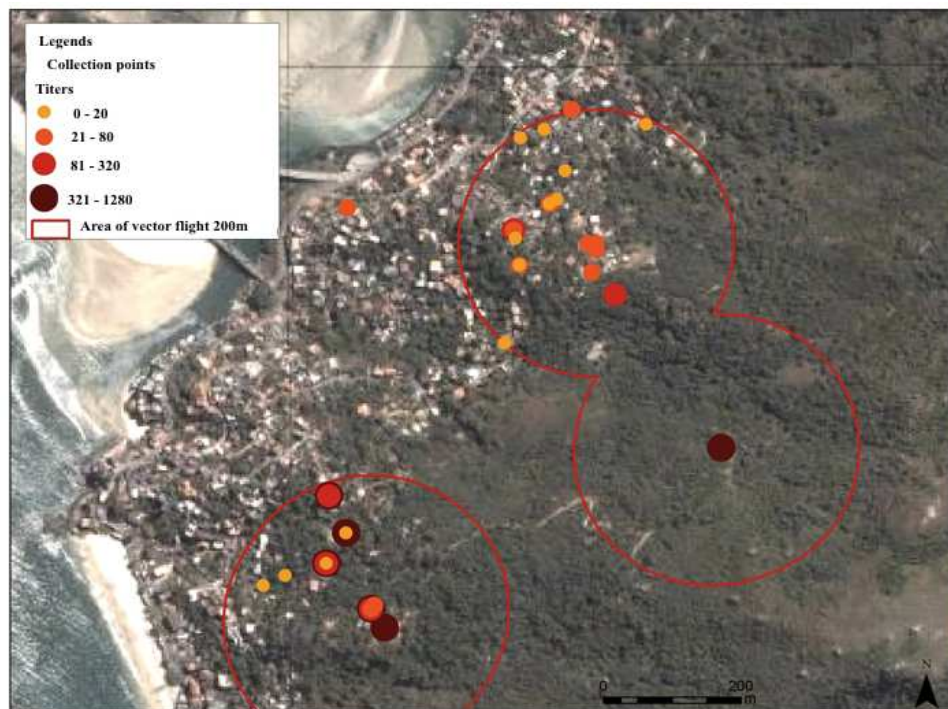
Figure 5. Visual interpretation of an aerial mosaic of photographs from an endemic focus in Brazil, showing the area of influence of the vector flight and the general distribution of canine *Leishmania* infections in addition to the serological titers (source: website of the Pereira Passos Institute http://www.armazemdedados.rio.rj.gov.br/).

have been dwelling on earth for millions of years before of us and it certainly represents that they have skills we not elucidated yet.

2. Overview

The first studies on leishmaniasis utilizing the geoprocessing technology were carried out in the 90s. After that, several groups from different parts of the world have studied important epidemiological aspects of this disease through the integration of results obtained from serological techniques, biological characteristics and population analysis of vectors and hosts with environmental factors such as: elevation, temperature parameters, mean monthly precipitation, relative humidity, land surface temperature parameters (including amplitude), normalized-difference vegetation index NDVI and land cover.

In the following section we presented a chronological review including the more relevant papers, originated from studies achieved in the Old World and New World, using the above-mentioned approach.

3. Leishmaniasis in the Old World

Elnaiem 1998 [17] in Sudan, investigating the importance of the effect of environmental data (obtained from digital records collected by satellites), such as: rainfall, minimum and maximum temperatures, soil class, vegetation and land-surface-temperature indices, on a population of *Phlebotomus orientalis*, observed a significant association of this sand fly with the presence of the tree species *Acacia seyal* and *Balanites aegyptiaca* and with the black cotton (vertisolic) soils of eastern Sudan. The authors also showed that positive sites were found to have significantly higher annual mean maximum and minimum daily temperatures and the annual mean maximum normalized-difference vegetation index (NDVI) value was also found to be significantly higher in these in comparison with those places where no *P. orientalis* were found.

Bern et al 2005 [18] studied the spatial patterns and risk factors for anthroponotic visceral leishmaniasis in Bangladesh. Integrating the GIS approach with data related to history, active case detection, and serologic screening, from residents had kala-azar, they observed that the risk was highest for persons 3–45 years of age, and no significant difference by sex. Considering the age-adjusted multivariable models, 3 factors were identified: proximity to a previous kala-azar patient, bed net use in summer and cattle per 1,000 m2. The authors observed no difference by income, education, or occupation; land ownership or other assets; housing materials and condition; or keeping goats or chickens inside bedrooms. The results confirmed a strong clustering occurrence and suggested that insecticide-treated nets could be effective in preventing kala-azar.

In this study, the households were mapped by a GPS and the data were processed into ArcGis. Through the GIS data, distances were determined from the household to the closest kala-azar

cases in the previous year. Kernel density estimation was used to estimate cattle per 1,000 m^2 in order to calculate the effect of cows, oxen or calves on the kala-azar risk for nearby residents.

Ryan et al 2006 [19], studying visceral leishmaniasis in Kenya, used *Leishmania*-specific antibodies to estimate the seroprevalence and GIS and spatial clustering techniques to study the presence of spatial clusters in two villages. In only one of the villages, significant associations among seropositivity and house construction, age, and proximity to domestic animal enclosures were found. In the same place, a significant spatial cluster of VL was found and the spatial distribution of cases in the two villages was different with respect to risk factors, such as presence of domestic animals. The authors suggested that disease control efforts could be focused on elimination of sand fly habitat, placement of domestic animal enclosures, and targeted use of insecticides.

Sudhakar et al., 2006 [20] in a study carried out in India, analyzed in Silicon graphic image processing system, using ERDAS software, some data obtained from a remote sensing satellite.

The GIS functions were applied to quantify the remotely sensed landscape proportions of 5 km^2 buffer in determined places of high occurrence of sand flies in endemic and nonendemic areas. Through the combination of remote sensing (RS) and geographical information system (GIS) they developed landscape predictors of sand fly abundance an indicator of human vector contact and as a measure of risk prone areas.

It was indicated, that the environmental factors such as type and density of settlements, proximity to these with that of water bodies, marshy areas with succulent weed cover and also crops of high succulent in nature like sugarcane, bananas coupled with local prevailing conditions had definitely interactive influencing effect of vector density and also incidents of vector borne diseases.

Rossi et al 2007 [21] in Southern Italy, applied GIS and SR to analyze the distribution of the *Leishmania infantum-Phlebotomus perniciosus* parasite-vector system in relation to environmental features of two opposite sides (coastal and Apennine) of an area of intense transmission of human and canine leishmaniasis.

The cumulative density, a term determined by the authors as the number of specimens/m2 of sticky trap/two nights, of this vector species was related as significantly more abundant in the coastal side. The authors suggested that the predominance of green vegetated environments in the coastal side, in contrast with the predominance of urban environment in the Apennine side, could be responsible for the different *P. perniciosus* densities between the areas.

Ready 2010 [22] reported that climate change could affect leishmaniasis distribution, by the effect of temperature on parasite development in insect vector, or because of the effect of environmental variation on the range and seasonal abundances of the sand fly species.

He also suggested that bio-climate zones and their vegetation indicators vary regionally, and continuing climate change could alter the patterns of land cover and land use. Thus, the GIS-based spatial modeling of the Emerging Diseases in a changing European Environment was providing analysis of alterations in climate and land cover and their effects on sand flies.

Bhunia et al 2010 [23] in India, through satellite imagery complemented with a GIS database, estimated parameters such as altitude, temperature, humidity, rainfall and the normalized difference vegetation index (NDVI) for correlation with the distribution of Kala-azar. They observed that the highest prevalence was below 150 m of altitude with very few cases located above the 300 m level and a low NDVI value ranges correlated with a high occurrence of the disease. They also showed, that most of the cases occurred in non-vegetative areas or low density vegetation zones highlighting that the low density vegetation zones were significant for the *P. argentipes* vector distribution in the disturbed areas.

Khanal et al 2010 [24] in Nepal, merged results from a serological test made in humans and domestic animals with GIS technology to evaluate the exposure to *L. donovani* on two populations in a recent focus of visceral leishmaniasis (VL). They used a Poisson regression model to evaluate the risk of infection in humans associated with seropositive animals in the proximities of the household. It was also demonstrated that seropositive animals and humans were spatially clustered and the presence of positive goats, past VL cases and the proximity to a forest island increased the risk of occurrence of seropositivity in humans. The authors also suggested that goats might play some role in the distribution of *L. donovani*, in the VL focus studied.

Bhattarai et al 2010 [25] also in Nepal, with the purpose of determining possible reasons for persistence of VL during inter-epidemic periods, they mapped cases *Leishmania* infections among apparently healthy persons and animals in an area of active VL transmission. The results of a bivariate K-function analysis showed the occurrence of spatial clustering of *Leishmania* spp.–positive persons and domestic animals, addition the investigation through classification tree, determined that the proximity of *Leishmania* spp.–positive goats ranked as the first risk factor for *Leishmania* infection among persons.

Salahi-Moghaddam et al 2010 [26] in Iran performed a serological study on a population of dogs from an endemic area.

No significant correlation between topographic conditions and the prevalence of positive cases was observed after regression analysis. Nevertheless, positive correlations were found in relation to the amount of rainfall, between infected dogs with high titers (≥1/640) and the number of days with temperatures below 0 °C during one year. The same correlation was observed when they were considered past meteorological records, conversely the humidity showed an inversely correlated with the *Leishmania* infections.

The authors suggested that in mapped areas the prevailing low temperatures could represent an important factor influencing the distribution of leishmaniasis.

More recently, Bhunia et al 2013 [27] in India, assumed that the utilization of GIS and RS technologies on the control of VL dates back to the late 2000s and those control programs have mostly focused on mapping prevalence and association of *Phlebotomus argentipes* habitats, predicting transmission risk in relation to ecological transformation.

Besides, the authors proposed that the multiplicity of satellite and sensors technics offer relevant data to assembly spatial, spectral and temporal scales. They also argued about the

advantages of remotely sensed imagery technology in studies in sand fly ecology and vector-borne diseases, by the generation of a proper household breeding documentation at higher spatial resolution.

4. Leishmaniasis in the New World

One of the first works, carried out in the New World that have exploited SR- satellite imagery technology on an epidemiological survey with American Cutaneous Leishmaniasis, was presented by Miranda et al 1996 [28] in Brazil. In that study, the data were plotted on a TM-LANDSAT image a color composition of bands 3, 4 and 5 (see supplementary information on table 3,4 and 5) that were considered useful to identify the relevant vegetation (shrubs and trees) within the boundaries of the studied areas and in their neighborhood about 250 meters from the perimeter of each area. It was suggested, the use of means qualified as presenting a larger view of a geographical area, composed the advantages of remote satellite sensing to study this endemic foci.

Lima et al 2002 [29] also in Brazil, studied the geographical distribution of notified human TL cases and correlated with the occurrence of the remaining vegetation and water streams, through satellite monitoring (LANDSAT level 4).

They observed that the geographical distribution of cases displayed a higher concentration in the northern and western regions of the studied area and a close relationship between TL and modified native forest areas, gallery forest areas or the remnants of both.

Landsat 4-5 Thematic Mapper (TM) and Landsat 7 Enhanced Thematic Mapper Plus (ETM+)		
Band	**Wavelength**	**Attributes**
Band 1 - blue	0.45-0.52	Bathymetric mapping, differentiating soil from vegetation and deciduous from coniferous vegetation
Band 2 - green	0.52-0.60	Highlights peak vegetation, useful for assessing plant vigor
Band 3 - red	0.63-0.69	Distinguish vegetation slopes
Band 4 - Near Infrared	0.77-0.90	Accentuates biomass content and coastlines
Band 5 - Short-wave Infrared	1.55-1.75	Categorizes wetness matter of soil and vegetation; permeates thin clouds
Band 6 - Thermal Infrared	10.40-12.50	Thermal mapping and predictable soil wetness
Band 7 - Short-wave Infrared	2.09-2.35	Hydrothermally transformed rocks related to mineral deposits
Band 8 - Panchromatic (Landsat 7 only)	.52-.90	15 meter resolution, sharper image definition

Table 3. Parameters utilized on Landsat 4-5 Thematic Mapper (TM) and Landsat 7 Enhanced Thematic Mapper Plus (ETM+) methodologies (based on the data obtained from the website http://landsat.usgs.gov).

Landsat 8 Operational Land Imager (OLI) and Thermal Infrared Sensor (TIRS)		
Band	**Wavelength**	**Attributes**
Band 1 – coastal aerosol	0.43-0.45	coastal and aerosol analyzes
Band 2 – blue	0.45-0.51	Bathymetric mapping, characterizing soil from vegetation and deciduous from coniferous vegetation
Band 3 - green	0.53-0.59	Highlights peak vegetation, which is functional for plant vigor assessing
Band 4 - red	0.64-0.67	Distinguishes vegetation slopes
Band 5 - Near Infrared (NIR)	085.-0.88	Highlights biomass and coastlines
Band 6 - Short-wave Infrared (SWIR) 1	1.57-1.65	Distinguishes wetness content of soil and vegetation; infiltrates thin clouds
Band 7 - Short-wave Infrared (SWIR) 2	2.11-2.29	Enriched wetness content of soil and vegetation and thin cloud infiltration
Band 8 - Panchromatic	.50-.68	15 meter resolution, intense image definition
Band 9 – Cirrus	1.36 -1.38	Increased detection of cirrus cloud pollution
Band 10 – TIRS 1	10.60 – 11.19	100 meter resolution, thermal mapping and predictable soil wetness
Band 11 – TIRS 2	11.5-12.51	100 meter resolution, enhanced thermal mapping and predictable soil wetness

Table 4. Parameters utilized on Landsat 8 Operational Land Imager (OLI) and Thermal Infrared Sensor (TIRS) methodologies (based on the data obtained from the website http://landsat.usgs.gov).

Landsat Multi Spectral Scanner (MSS)			
Landsat MSS 1, 2,3 Spectral Bands	**Landsat MSS 4,5 Spectral Bands**	**Wavelength**	**Attributes**
Band 4 - green	**Band 1 - green**	0.5-0.6	Sediment-laden water, delimits areas of shallow water
Band 5 - red	**Band 2 - red**	0.6-0.7	Cultural features
Band 6 - Near Infrared	**Band 3 - Near Infrared**	0.7-0.8	Vegetation boundary between land and water, and natural features of landscape
Band 7 - Near Infrared	**Band 4 - Near Infrared**	0.8-1.1	Infiltrates atmospheric cloud over best, highlights vegetation, boundary between land and water, and natural features of landscape

Table 5. Parameters utilized on Landsat Multi Spectral Scanner (MSS) method (based on the data obtained from the website http://landsat.usgs.gov).

Peterson et al 2004 [30] investigates the potential of ecological niche modeling techniques for interpolating into unsampled areas in order to understand the geographic distributions of vector species. They used multiple subsamples from accessible distributional points to analyze the question of how much sampling is needed to assemble a suitable distributional interpretation for vector species.

The Genetic algorithm for rule-set prediction (GARP) was utilized for modeling the ecological niches. The authors inferred that GARP associates ecological characteristics of known occurrence points to those randomly sampled from the rest of the study region, pursuing the development of a series of decision rules that can best summarize those factors related with the presence of species.

They also demonstrated that moderate sampling densities at sample sizes that possibly could characterize many epidemiological studies, including the distributions of vector or reservoir were sufficient to produce excellent briefs of the geographic distributions of species permits development of geographic predictions for poorly known species to promote the knowledge about geographic aspects of disease systems.

Carneiro et al 2004 [31] in Brazil, used geo-technologies including satellite images, as normalized difference vegetation index (NDVI), in the collection and analysis of epidemiological data from an LV endemic area. It was observed that, the power of specific variable such as: demographic density, age, occurrence of sand flies, contaminated dogs, and human living in specific area, as well as the practical value of using NDVI values to identify risk areas.

Salomón et al 2006 [32] in Argentine, utilized the RS to study the spatial distribution of Phlebotominae associated with a focus of tegumentary leishmaniasis. Satellite images were used to estimate the influence of the maximal and minimal flow of a river present on the area of study, on the transmission of the disease. The probable correlation with the gallery forest was also rated.

The images were obtained from LANDSAT 5 TM and 7 ETM, they were georreferenced using satellite ephemeris and the nearest-neighbor method. The Band 5 was also used to discriminate areas covered by the river, and the neighboring the land uncovered of vegetation trough visual identification.

The authors concluded that the fishing spots were significantly overflowed during the transmission peak because the spatial restricted flood could concentrate vectors, reservoirs, and humans in high places.

They also suggested through both spatial distribution of vectors and remote sensing data the higher transmission risk in the area it is still related with the gallery forest, despite of the urban influence.

Margonari et al 2006 [5] in Brazil, applied the GIS methodology integrated with demographic, socio-economic and environmental data to study some aspects of the epidemiology of a visceral leishmaniasis focus.

It was observed that among biogeographic parameters such as: altitude, area of vegetation influence, hydrographic, and areas of poverty, only altitude showed to influence emergence

of leishmaniasis because most canine and human cases of leishmaniasis cases were localized between 780 and 880 m above the sea level and at these same altitudes, a large number of phlebotomine sand flies were collected.

Nieto et al 2006 [33] also in Brazil, used models developed within a GIS employing Genetic Algorithm Rule-Set Prediction (GARP) and the growing degree day (GDD)-water budget (WB) concept to predict the distribution and potential risk of visceral leishmaniasis (VL).

It was described a high and moderate prevalence sites for VL were significantly related to areas of high and moderate risk prediction. Indeed the area expected by the GARP model, hinged on the number of pixels that overlapped among eleven annual model years and the quantity of potential generations per year that could be completed by the *Lu. longipalpis-L. chagasi* system by GDD-WB analysis.

In both the GARP and the GDD-WB prediction models suggested that the highest VL risk was characterized by a semi-arid and hot climate (Caatinga), but the risk in the interior forest and the Cerrado was lower and the coastal forest was predicted as a low-risk area due to the unsuitable conditions for the vector and VL transmission.

Neto et al 2009 [34] in Brazil, applied GIS and SR to examine factors associated with the incidence of urban VL. They observed that the annual incidence rates were related to socioeconomic and demographic indicators as well as the vegetation index.

The highest incidence occurred in the peripheral areas of the city and areas with high population growth and abundant vegetation. On the other hand the percentage of households with piped water was inversely associated with the disease incidence.

The authors conclude that spatial distribution of the disease in the area was heterogeneous, and the incidence was associated with the peripheral neighborhoods fullest vegetation cover, considered subject to anthropic action.

Shimabukuro et al 2010 [35] in Brazil, utilized GIS and SR to study the geographical distribution of American cutaneous leishmaniasis and its phlebotomine vectors and generate risk maps. They observed that generally, the sand fly vector species evaluated have presented unique and heterogeneous distributions, although often overlapped. Numerous sand fly species were highly localized, while the others were much more largely spread.

The authors emphasized the complexity and geographical pattern of ACL transmission in the region.

Valderrama-Ardila et al 2010 [36] in Colombia, evaluate through spatial analysis, the environmental risk factors for CL. The applicant predictor variables were land use, elevation, and climatic (mean temperature and precipitation).

They observed that incidence of the disease was higher in townships with mean temperatures in the middle of the county's range. The frequency was independently associated with forest or shrubs and lower population density. The coverage of forest or shrub have not presented main changes over time.

The results confirmed the effect of weather and land use in leishmaniasis transmission.

Silva et al 2011 [14] in Brazil, studied a dog population from an endemic focus of LV. Through GIS and SR and applying kernel density estimator with Gaussian function and smooth kernel of 100 m radius, they observed local variations related to infection the incidence and distribution of serological titers, i.e. high titers were noted close to areas with preserved vegetation, while low titers were more frequent in areas where people kept chickens.

The authors conclude that the environment plays an important role in generating relatively protected areas within larger endemic regions, but it could also contribute to the creation of hotspots with clusters of comparatively high serological titers indicating a high level of transmission compared with neighboring areas.

Cluster analysis of the serological titers in dogs in the study area showed a non-random distribution, demonstrating that the patterns of transmission of canine VL can undergo local alterations, producing hotspots where the risk of infection was very high compared to neighboring areas.

It was suggested the possibility to predict the specific places of high-risk VL transmission within an endemic area through the mapping of canine serological titers.

Almeida et al 2011 [37] in Brazil, used spatial analysis to identify regions at highest risk of VL in an urban area. They showed from kernel ratios results, that peripheral census tracts were the most heavily affected. The spatial analysis showed that local clusters of high incidence of VL could change their locations depending on the time, suggesting that the pattern of VL is not static, and the disease may occasionally spread to other areas.

The authors also observed a spatial correlation between VL rates and all socioeconomic and demographic indicators evaluated, such as: 1) illiteracy rate; 2) children less than five years of age as a percentage of the total population; 3) mean income of heads-of-households; 4) percentage of permanent private households connected to the water supply; 5) percentage of households with regular garbage collection; and 6) percentage of permanent private households connected to the sewage system.

Foley et al 2012 [38], created a very useful tool that comprises a new map service within VectorMap (www.vectormap.org). Using the words of the authors, "It allows free public online access to global sand fly, tick and mosquito collection records and habitat suitability models, given the short home range of sand flies, combining remote sensing and collection point data, offering a powerful insight into the environmental determinants of sand fly distribution.

Sand fly Map uses Microsoft Silverlight and ESRI's ArcGIS Server 10 software platform to present disease vector data and relevant remote sensing layers in an online geographical information system format. Users can view the locations of past vector collections and the results of models that predict the geographic extent of individual species. Collection records are searchable and downloadable, and Excel collection forms with drop down lists, and Excel charts to country, are available for data contributors to map and quality control their data.

Sand fly Map makes accessible, and adds value to, the results of past sand fly collecting efforts. It is detailed the workflow for entering occurrence data from the literature to Sand fly Map, using an example for sand flies from South America.

The proper use of a global positioning system (GPS) device and a detailed text description of the locality are encouraged to minimize this uncertainty [39]. The calculation of spatial uncertainty, for example for Martins et al [40], allows data to be matched to appropriate resolution remote sensing data, for modeling or other spatial analyses".

Saraiva et al 2012 [41] in Brazil, utilizing GIS methodology associated with serological tests, studied a VL focus. They described the occurrence of serologically positive dogs was spread out throughout all geographical area. The places of concentration of serologically positive dogs appeared both in risk areas and outside them.

Overlaying the map of the human and canines cases with factors traditionally related to VL as vegetation, hydrography, and areas of poverty, it was not possible identify a spatial correlation between them, which demonstrates that in urban areas there are still unknown parameters.

Souza et al 2012 [42] in Brazil, carried out a space-time analysis of AVL cases in humans. They conclude by the time series analysis, a positive tendency over the period analyzed, completing that the disease was clustered in the Southwest side of area of study, suggesting it could require special attention with regard to control and prevention measures.

Finally, González et al 2013 [43] in Colombia, have surveyed the spatial distribution of two vector species of *L. infantum*, after predicting its future dispersal into climate change situations to establish the potential dissemination of the disease. They used ecological niche models through the Maxent software and 13 Worldclim bioclimatic coverages. Through predictions for the pessimistic CSIRO A2 scenario, was calculated the higher increase in temperature in function of non-emission reduction, and by the optimistic Hadley B2 Scenario, was predicted the minimum increase in temperature.

Concerning the climate change projections, they observed an overall reduction in the spatial distribution of the two vector species, progressing a shift in the vertical distribution for one species and restricting the other to certain regions at the sea level.

The authors predicted an outcome for VL vectors in Colombia and suggested that Changes in spatial distribution patterns could be affecting local abundances due to climatic pressures on vector populations thus reducing the incidence of human cases.

4. Conclusion

In conclusion, the employment of a geospatial approach to interpret eco-epidemiological phenomena related to vector borne diseases have been used for some groups in significant studies. The possibilities of use of that very effective tool, considering the advances on computational knowledge and the possibilities of accessing information at a global level, make this technology indispensable to make a broad analysis objecting the optimizing of planning control campaigns.

Author details

João Carlos Araujo Carreira[1*], Mônica de Avelar Figueiredo Mafra Magalhães[2] and
Alba Valéria Machado da Silva[3]

*Address all correspondence to: carreira@ioc.fiocruz.br; jcacarreira@gmail.com

1 Núcleo IOC- Jacarepaguá/Fundação Oswaldo Cruz, Rio de Janeiro, Brazil

2 Laboratório de Geoprocessamento, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil

3 Laboratório de Bioquímica de Proteínas e Peptídeos, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil

References

[1] TDR for research on diseases of poverty. http://www.who.int/tdr/research/ntd/leishmaniasis (accessed 04/03/2013).

[2] Lainson R, Rangel E. *Lutzomyia longipalpis* and the ecoepidemiology of American visceral leishmaniasis, with particular reference to Brazil – A review. Memórias do Instituto Oswaldo Cruz 2005; 100: 811-827.

[3] Ashford RW. The Leishmaniasis as emerging and reemerging zoonoses. International Journal for Parasitology 2000; 30: 1269-1281.

[4] Maia-Elkhoury ANS, Alves WA, Sousa-Gomes ML, Sena JM, Luna EA. Visceral leishmaniasis in Brazil: trends and challenges. Cad Saúde Pública 2008; 24: 2941-2947.

[5] Margonari C, Freitas CR, Ribeiro RC, Moura ACM, Timbó M, Gripp AH, Pessanha JE, Dias ES. Epidemiology of visceral leishmaniasis through spatial analysis, in Belo Horizonte municipality, state of Minas Gerais, Brazil. Memórias do Instituto Oswaldo Cruz 2006; 101: 31-38.

[6] Silva, AVM, Paula AA, Pereira DP, Brazil RP, Carreira JCA. Canine Leishmaniasis in Brazil: Serological Follow-Up of a Dog Population in an Endemic Area of American Visceral Leishmaniasis. Journal Parasitology Research 2009; 2009: 1-6.

[7] Carreira JCA, Silva AVM, Pereira DP, Brazil RP. Natural infection of *Didelphis aurita* (Mammalia: Marsupialia) with *Leishmania infantum* in Brazil. Parasites & Vectors 2012; 5:111 - 116.

[8] Cabrera MAA, De Paula AA, Camacho LAB, Marzochi CA, Aguiar GM, Xavier SC, Da Silva AVM, Jansen AM. Canine Visceral Leishmaniasis in Barra de Guaratiba, Rio de Janeiro, Brazil: assessment of some risk factors. Revista do Instituto de Medicina Tropical de São Paulo 2003; 45: 79-83.

[9] Ministério da Saúde. Brasil: Editora MS. Manual de Vigilância e Controle da Leishmaniose Visceral; 2003.

[10] Palatnik-de-Souza CB, Dos Santos WR, França-Silva JC, Da Costa RT, Reis AB, Palatnik M, Mayrink W, Genaro O. Impact of canine control on the epidemiology of canine and human visceral leishmaniasis in Brazil. American Journal of Tropical Medicine and Hygiene 2001; 65: 510-517.

[11] Bavia ME, Carneiro DDMT, Costa Gurgel H, Madureira Filho C, Rodrigues Barbosa MG. Remote Sensing and Geographic Information Systems and risk of American Visceral Leishmaniasis in Bahia, Brazil. Parassitologia 2005; 47: 165-169.

[12] Beck LR, Lobitz BM, Wood BL. Remote sensing and human health: new sensors and new opportunities. Emerging Infectious Diseases 2000; 6: 217-226.

[13] Zhou XN, Lv S, Yang GJ, Kristensen TK, Bergquist R, Utzinger J, Malone JB. Spatial epidemiology in zoonotic parasitic diseases: insights gainedat the 1st International Symposium on Geospatial Health in Lijiang, China, 2007. Parasites & Vectors 2009; 2:10-26.

[14] Silva AVM, Magalhães MAFM, Brazil RP, Carreira JCA. Ecological study and risk mapping of leishmaniasis in an endemic area of Brazil based on a geographical information systems approach. Geospatial Health 2011; 6 (1) 33-40.

[15] Shawe-Taylor J, Cristianini N. Kernel Methods for Pattern Analysis. Cambridge University Press; 2004.

[16] Elnaiem DA, Schorscher J, Bendall A, Obsomer V, Osman ME, Mekkawi AM, Connor SJ, Ashford RW, Thomson CM. Risk mapping of visceral leishmaniasis: the role of local variation in rainfall and altitude on the presence and incidence of kala-azar in Eastern Sudan. American Journal of Tropical Medicine and Hygiene 2003; 68: 10-17.

[17] Elnaiem DA, Connor SJ, Thomson MC, Hassan MM, Hassan HK, Aboud MA, Ashford RW. Environmental determinants of the distribution of *Phlebotomus orientalis* in Sudan. Annals of Tropical Medicine and Parasitology 1998; 92(8) 877-887.

[18] Bern C, Hightower AW, Chowdhury R, Ali M, Amann J, Wagatsuma Y, Haque R, Kurkjian K, Vaz LE, Begum M, Akter T, Cetre-Sossah CB, Ahluwalia IB, Dotson E, Secor WE, Breiman RF, Maguire JH. Risk Factors for Kala-Azar in Bangladesh. Emerging Infectious Diseases 2005; 11 (5) 655- 662.

[19] Ryan JR, Mbui J, Rashid JR, Wasunna MK, Kirigi G, Magiri C, Kinoti D, Ngumbi PM, Martin SK, Odera SO, Hochberg LP, Bautista CT, Chan AS. Spatial clustering and epidemiological aspects of Visceral Leishmaniasis in two endemic villages, Baringo District, Kenya. American Journal of Tropical Medicine and Hygiene 2006; 74(2) 308-317.

[20] Sudhakar S, Srinivas T, Palit A, Kar SK, Battacharya SK. Mapping of risk prone areas of kala-azar (Visceral leishmaniasis) in parts of Bihar state, India: an RS and GIS approach. Journal of Vector Borne Diseases 2006; 43: 115-122.

[21] Rossi E, Rinaldi L, Musella V, Veneziano V, Carbone S, Gradoni L, Cringoli G, Maroli. Mapping the main Leishmania phlebotomine vector in the endemic focus of the Mt. Vesuvius in southern Italy. Geospatial Health 2007; 2: 191-198.

[22] Ready PD. Leishmaniasis emergence in Europe. EuroSurveillance 2010; 15(10) 1-11.

[23] Bhunia GS, Kesari S, Jeyaram A, Kumar V, Das P. Influence of topography on the endemicity of Kala-azar: a study based on remote sensing and geographical information system. Geospatial Health 2010; 4(2) 155-165.

[24] Khanal B, Picado A, Bhattarai NR, Auwera GVD, Das ML, Ostyn B, Davies CR, Boelaert M, Dujardin JC, Rijal S. Spatial analysis of *Leishmania donovani* exposure in humans and domestic animals in a recent kala azar focus in Nepal. Parasitology 2010; 137: 1597-1603.

[25] Bhattarai NR, Auwera GV, Rijal S, Picado A, Speybroeck N, Khanal B, Doncker S, Das ML, Ostyn B, Davies C, Coosemans M, Berkvens D, Boelaert M, Dujardin JC. Domestic animals and Epidemiology of Visceral Leishmaniasis, Nepal. Emerging Infectious Diseases 2010; 16(2) 231- 237.

[26] Salahi-Moghaddam A, Mohebali M, Moshfae A, Habibi M, Zarei Z. Ecological study and risk mapping of visceral leishmaniasis in an endemic area of Iran based on a geographical information systems approach. Geospatial Health 2010; 5(1) 71-77.

[27] Bhunia GS, Kesari S, Chatteerjee N, Kumar V, Das P. The Burden of Visceral Leishmaniasis in India: Challenges in Using Remote Sensing and GIS to Understand and Control. Infectious Diseases 2013; 2013: 1-14.

[28] Miranda C, Massa JL, Marques CCA. Analysis of the occurrence of American Cutaneous Leishmaniasis in Brazil by remote sensing satellite imagery. Revista de Saúde Pública 1996; 30 (5) 433-437.

[29] Lima AP, Minelli L, Teodoro U, Comunello E. Tegumentary leishmaniasis distribution by satellite remote sensing imagery, in Paraná State, Brazil. Anais Brasileiros de Dermatologia 2002; 77(7) 681-692.

[30] Peterson AT, Pereira RS, Neves VFC. Using epidemiological survey data to infer geographic distributions of leishmaniasis vector species. Revista da Sociedade Brasileira de Medicina Tropical 2004; 37: 10-14.

[31] Carneiro DDMT, Bavia ME, Rocha WJSF, Lobão JSB, Oliveira CMFJB, Silva CEP, Barbosa MGR, Rios RB. Identificação de áreas de risco para Leishmaniose Visceral Americana, através de estudos epidemiológicos e sensoriamento remote orbital, em Feira de Santana, Bahia, Brasil (2000-2002). Revista Baiana de Saúde Pública 2004; 28(1) 19-32.

[32] Salomón OD, Orellano PW, Lamfri M, Scavuzzo M, Dri L, Farace MI, Quintana DO. Phlebotominae spatial distribution asssociated with a focus of tegumentary leishmaniasis in Las Lomitas, Formosa, Argentina, 2002. Memórias do Instituto Oswaldo Cruz 2006; 101(3) 295-299.

[33] Nieto P, Malone JB, Bavia ME. Ecological niche modeling for visceral leishmaniasis in the state of Bahia, Brazil, using genetic algorithm for rule-set prediction and growing degree day-water budget analysis. Geospatial Health 2006; 1:115-126.

[34] Neto JC, Werneck GL, Costa CHN. Factors associated with the incidence of urban visceral leishmaniasis: an ecological study in Teresina, Piauí State, Brazil. Cadernos de Saúde Pública 2009; 25(7) 1543-1551.

[35] Shimabukuro PHF, Silva TRR, Fonseca FOR, Baton LA, Galati EAB. Geographical distribution of American cutaneous leishmaniasis and its phlebotomine vectors (Diptera: Psychodidae) in the state of São Paulo, Brazil. Parasites & Vectors 2010; 3:121-133.

[36] Valderrama-Ardila C, Alexander N, Ferro C, Cadena H, Marin D, Holford TR, Munstermann LE, Ocampo CB. Environmental Risk Factors for the Incidence of American Cutaneous Leishmaniasis in a Sub-Andean Zone of Colombia (Chaparral, Tolima). American Journal of Tropical Medicine and Hygiene 2010; 82(2) 243-250.

[37] Almeida AS, Medronho RA, Werneck GL. Identification of Risk Areas for Visceral Leishmaniasis in Teresina, Piaui State, Brazil. American Journal of Tropical Medicine and Hygiene 2011; 84(5) 681-687.

[38] Foley DH, Wilkerson RC, Dornak LL, Pecor DB, Nyari AS, Rueda LM, Long LS, Richardson JH. Sand flyMap: leveraging spatial data on sand fly vector distribution for disease risk assessments. Geospatial Health 2012; 6(3) S25-S30.

[39] Foley DH, Wilkerson RC, Rueda LM. Importance of the "what", "when", and "where" of mosquito collection events. Journal of Medical Entomology 2009; 46: 717-722.

[40] Martins AV, Williams P, Falcao AL. American sand flies (Diptera: Psychodidae, Phlebotominae). Academia Brasileira de Ciencias, Rio de Janeiro; 1978.

[41] Saraiva L, Leite CG, Carvalho LOA, Filho JDA, Menezes FC, Fiuza VOP. Information System and Geographic Information System Tools in the Data Analyses of the Control Program for Visceral Leishmaniases from 2006 to 2010 in the Sanitary District of Venda Nova, Belo Horizonte, Minas Gerais, Brazil. Journal Tropical Medicine 2012; 2012: 1-10.

[42] Souza VAF, Cortez LRPB, Dias RA, Amaku M, Neto JSF, Kuroda RBS, Ferreira F. Space-time cluster analysis of American visceral leishmaniasis in Bauru, São Paulo State, Brazil. Cadernos de Saúde Pública 2012; 28(10) 1949-1964.

[43] González C, Paz A, Ferro C. Predicted altitudinal shifts and reduced spatial distribution of *Leishmania infantum* vector species under climate change scenarios in Colombia. Acta Tropica 2013; In Press.