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# GnosisGIS 2019

International Society for Geospatial Health



## Programme

**13<sup>th</sup> International Symposium on Geospatial Health**

Liverpool, United Kingdom  
September 16, 2019

### Venue

Liverpool Medical Institution  
Conference Centre  
114 Mount Pleasant  
Liverpool

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## Symposium Organizers

Laura Rinaldi, Jennifer McCarroll

## Scientific Committee

Laura Rinaldi, Robert Bergquist, Anna-Sofie Stensgaard

## Venue

Liverpool Medical Institution  
Conference Centre  
114 Mount Pleasant  
Liverpool L3 5SR T: (0151) 709 9125 x2

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# GnosisGIS

## International Society of Geospatial Health

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PROGRAMME AT A GLANCE

Sunday, September 15, 2019	
1:00 – 5:00 pm	Spatial Statistics Workshop, Liverpool Medical Institution, Conference Centre, Wolfson Room (Separate Registration)
7:00 – 9:00 pm	Welcome Reception, Liverpool Medical Institution Conference Centre, Council Room

Monday, September 16, 2019	
8:00 am	Registration and Coffee
8:30 am	Opening & Welcome
9:00 am	Session I
10:25 am	Coffee Break
11:00 am	Session II
12:15 pm	Lunch
2:00 pm	Session III
4:00 pm	General Assembly Meeting

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PROGRAMME

Monday, September 16, 2019	
8:30 am	Registration and Coffee
9:00 am	Opening & Welcome – Laura Rinaldi
<b>Session I</b>	<b>TITLE: Geospatial Health and Health Care</b> <b>Chairpersons: Robert Bergquist and Anne-Sofie Stensgaard</b>
9:30 am	<b>KEYNOTE: Towards a body of knowledge of Geospatial Health</b> Sherif Amer
9:50 am	<b>KEYNOTE: Malaria transmission modeling in the China-Myanmar border areas</b> XN Zhou
10:05 am	<b>A spatiotemporal change point detection for detecting outbreaks at small areas of emerging childhood infectious diseases</b> Phuong N. Truong
10:20 am	<b>Geospatial analysis of climatic parameters to improve risk-monitoring system of childhood illness in Bangladesh</b> T.A. Robin
10:35 am	Coffee Break
<b>Session II</b>	<b>TITLE: Towards NextGen tools</b> <b>Chairpersons: Sherif Amer and Fedor Korennoy</b>
11:00 am	<b>KEYNOTE: The changing landscape of schistosomiasis: new tools for detection and prediction in times of warming and elimination</b> Anna-Sofie Stensgaard
11:20 am	<b>KEYNOTE: Geospatial surveillance systems for vector-borne diseases</b> R Bergquist
11:40 am	<b>KEYNOTE: GEOHealth: a surveillance and response system resource for visceral leishmaniasis in Brazil</b> John B. Malone
12:00 pm	<b>Modelling of re-emerging of <i>Plasmodium vivax</i> malaria in Moscow (Russia) during 1999-2009</b> Natalia Shartova
12:15 pm	Lunch
<b>Session III</b>	<b>TITLE: Mapping and modelling pathogens and vectors</b> <b>Chairpersons: Laura Rinaldi and John Malone</b>
2:00 pm	<b>KEYNOTE: Global epidemiology of strongyloidiasis: filling the knowledge gap</b> Donal Bisanzio
2:20 pm	<b>Mapping changes in the spatio-temporal distribution of lumpy skin disease virus</b> Fedor Korennoy
2:35 pm	<b>Towards making spatial risk maps for helminth parasites in ruminants dynamic: a case study in Italy</b> Alizée Hendrickx
2:50 pm	<b>Documenting <i>Biomphalaria pfeifferi</i> along Lake Malawi, Mangochi District shorelines</b> Mohammad H. Alharbi
3:05 pm	<b>KEYNOTE VIA SKYPE: NASA's NextGen Remote Sensing instruments have arrived: data products for the thermodynamic paradigm for studying disease vectors</b> Jeffrey C. Luvall
3:25 pm	Spatial Statistics Workshop Student Presentations
4:00 pm	General Assembly Meeting
5:00 pm	End of GnosisGIS Symposium 2019

# ABSTRACTS



**Session I**  
**Geospatial Health and Health Care**

## Towards a Body of Knowledge of Geospatial health

Ellen-Wien Augustijn<sup>1</sup> and **Sherif Amer**<sup>1</sup>

<sup>1</sup>*Faculty of Geo-Information Science and Earth Observation, University of Twente, The Netherlands*

We present a flexible and incremental development pathway for establishing a collaborative and interdisciplinary Body of Knowledge of Geospatial health under the auspices of GnosisGIS. Our rationale is that we see Geospatial and Public Health sciences both as well-established scientific fields but an interdisciplinary Geo-health domain which is maturing only relatively slowly. A survey, as part of a MOOC on Geo-health in 2017, indicated that nearly all participating scientists and professionals described themselves as a Geo-IT or a Public Health specialist. This implies that the linkages that connect both scientific domains require further development and strengthening. One way of working towards this is the development of specific Geo-health curricula. Such curricula can potentially range from short courses (introductory, advanced) to full-fledged accredited educational programs, but can also be as modest as bringing together people/parties with relevant expertise.

Our point of departure is to connect to already existing sources rather than developing new Geo-health curricula from scratch. We propose to make use of an existing ontology (a set of concepts and their interrelationships) for Geo-Science such as the 'Living Textbook' developed by the Faculty of Geographic Information Science and/or the web-based Geographic Information Science and Technology Body of Knowledge developed by the American Association of Geographers. For the Public Health domain, a similar hierarchical breakdown into sub-knowledge areas, and topics might exist or can be devised with relative ease. Then, for each topic, we identify and connect to the relevant Geoscience study materials available in e.g. the Living Textbook. This approach will make it possible to develop alternative tailored Geo-health curricula in an incremental and structured manner. Obviously, this will require a step by step approach, ideally supported by external funding, but the idea is to realize this by building upon the collective Geo-health knowledge embedded in, and the active participation of, the GnosisGIS society.

## **Risk Evaluation, Surveillance and Forecast of Vector-Borne Tropical Diseases by Earth Observation Data Mining**

**Xiao-Nong Zhou**

*National Institute of Parasitic Disease, China CDC*

Among those diseases threatening human health and well-being, many epidemic and infectious diseases are closely related to natural environment due to the presence, breeding and evolution of their pathogens or reservoir hosts, especially vector-borne diseases (e.g. malaria and schistosomiasis, etc.) which rely heavily on their vectors. Therefore, monitoring the diseases' vector is an important way to prevent and control the vector-borne diseases. Because of complex spatial distribution and dispersion of typical diseases and their vectors, it is difficult to acquire relevant environmental factor data by traditional in-situ measurements. Remote sensing technology provides the capability of obtaining temporal-spatial variations of ground environmental factors. Taking into account of different type of massive data are involved, it is essential to bring together scientists from multiple disciplines along with domain experts to foster a substantial collaboration.

This study aims to apply advanced remote sensing and computing technologies into monitoring and early warning of vector-borne diseases, e.g. schistosomiasis and malaria. First is to reveal environmental factors which have significant influences on the breeding of epidemic disease and its vectors. Then the project will make full use of the advantage of European and Chinese earth observation resources and the partners capability to develop parameter inversion, feature extraction and pattern analysis methods that will be used to characterise environmental features and habitats that are mostly suitable for the growth and dispersion of vector-borne disease and dynamic monitoring. Furthermore, temporal-spatial models of the distribution of vector-borne diseases will be developed by data mining techniques. Finally, the driving mechanism and data assimilation methods of land surface process model will be explored in order to implement identification and early warning of vector-borne disease transmission areas.

The research results can be used to assess environmental characteristics around the sites of major infrastructure and facilities, and provide the suggestion on site selection and implementation of infrastructures. The synthetic feature extraction techniques developed for multi-source multi-level remote sensing data can also be applied to other service fields, sustainably making contribution to knowledge within the communities.

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## A spatiotemporal change point detection for detecting outbreaks at small areas of emerging childhood infectious diseases

Phuong N. Truong

*Department of Earth Observation Science, ITC Faculty, University of Twente, The Netherlands*

**Keywords:** spatiotemporal change point detection, outbreak, spatiotemporal disease incidences, emerging infectious diseases, children

**Background:** One of the most important issues in geographical epidemiology of infectious diseases is to identify epidemics from mapping excess health risk in space and time. This demands a statistical model that can delineate the spatial-temporal extents of the elevated excess risk. However, the application of the existing spatiotemporal conditional autoregressive (CAR) model for estimation of the excess risk produces considerable smoothing effects. The objective of this study is to develop a new efficient detection method for detecting the outbreaks of emerging infectious diseases in children population at small areas in space and time.

**Methods:** We propose a new partial partition spatiotemporal Bayesian CAR model to detect both the spatial and temporal abrupt changes in disease risk. The model is based upon random partition analysis of the areal georeferenced autocorrelated time series using spatially stochastic conditional autoregressive priors. The constant cohesion values in the random partial partition model are extended to a spatiotemporal cohesion function. The model's parameters are inferred as a Binomial distribution using Markov Chain Monte Carlo algorithm. We apply the new model to detect spatiotemporal outbreaks of childhood hand-foot-mouth disease in Vietnamese districts in 2012-2017.

**Results:** The results from applying the developed model to the case study of childhood hand-foot-mouth disease show abrupt changes in the disease relative risk between urban and rural districts in 2012. Spatial and temporal spillover effect can be considered in detecting those abrupt changes. The model produced a better fit as to mean square error of the relative risk (0.1).

**Conclusions:** The proposed model is improved in term of the ability to distinguish the spatiotemporal abrupt changes from the spatiotemporal trend. The new model enables the detection of HFMD epidemics in Vietnamese districts attributed to rapid temporal and geographical social-economic changes in Viet Nam in the last years.

## Geospatial analysis of climatic parameters to improve risk-monitoring system of childhood illness in Bangladesh

T A Robin<sup>1</sup>, Md. Arshad Hussain<sup>1</sup>, Imteaz Ibne Mannan<sup>2</sup>, Ishtiaq Mannan<sup>1</sup>, Uzma Syed<sup>2</sup>

<sup>1</sup>Save the Children, Bangladesh; <sup>2</sup>Formerly Save the Children, Bangladesh

### Background

Although pneumonia, respiratory disease and diarrhoea are leading causes of deaths of children under 5 in Bangladesh, surveillance systems have not been effective in predicting geographic disparities in disease outbreak. Climate indicators, such as rainfall, temperature and flooding are known contributors to health threats but these are not part of the decision support system. The assessment attempts to determine the relationship between disease occurrence and climatic conditions to improve predictive capacity.

### Methodology

Based on information of Bangladesh Meteorological Department from 1970 to 2014, the assessment evaluated climate indicators (temperature, rainfall, humidity) in three different seasonal clusters (pre-monsoon (January-April), monsoon (May-August), post-monsoon (September-December)) by sub-district. In addition, hotspot regions of three major diseases of children under age five have been identified in three distinct seasons based on DHIS2 information.

### Results

The assessment observed season wise variations in the hotspots of disease outbreaks. The area of hotspots increased for diarrhoea and pneumonia disease during the pre-monsoon season. The results of *t*-test indicated significant changes in ARI disease during pre-monsoon to monsoon ( $P=0.0006$ , CI=95%) and pre to post-monsoon season ( $P=0.0009$ , CI=95%). Situation of pneumonia changed from monsoon to post-monsoon season ( $P=0.032$ , CI=95%).

The analysis demonstrated association between disease events and climatic parameters. The regression analysis presented relationship between diarrhea diseases and temperature ( $P=0.035$ , CI=95%) and, between Pneumonia disease and humidity ( $P=0.002$ , CI=95%) during monsoon season. In pre-monsoon season, rainfall ( $P=0.0008$ , CI=95%) and humidity ( $P=0.0001$ , CI=95%) displayed relationship with diarrhea disease and total rainfall ( $P=0.032$ , CI=95%) with Pneumonia. Total rainfall ( $P=0.007$ , CI=95%), and humidity ( $P=0.028$ , CI=95%) showed association with diarrhea disease in post-monsoon season.

### Conclusion

The geospatial analysis of seasonal variations identified complex relationship with disease events and climatic parameters. Thus, national newborn and child health program of the government should monitor seasonal changes of disease incidence to prepare for response mechanisms.

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**Session II**  
**Towards NextGen tools**

## The changing landscape of schistosomiasis: new tools for detection and prediction in times of warming and elimination

**Anna-Sofie Stensgaard<sup>1</sup>**, Mita Eva Sengupta<sup>1</sup>

<sup>1</sup> *Center for Macroecology, Evolution and Climate, GLOBE Institute, University of Copenhagen*

Schistosomiasis is a water-based, infectious disease with high morbidity and significant economic burdens affecting >250 million people globally. On-going global changes is affecting both parasite and intermediate host snails, and in combination with recently up-scaled control as the goal is set for elimination, this is rapidly changing the disease endemic landscape. In sub-Saharan Africa, for example, the landscape is becoming ever more heterogeneous as different species of *Schistosoma* respond differently to both climatic changes and ongoing preventive chemotherapy. In order to proceed toward the end goal of schistosomiasis elimination, new sensitive tools to monitor progress toward environmental transmission interruption in "old" areas, as well as newly emerging areas outside the normal range, are thus needed. One promising tool for sensitive detection, large-scale monitoring and environmental surveillance, particularly in low-transmission settings, is environmental DNA (eDNA) based on water samples. This method could for instance be used to closely monitor areas declared free of transmission, but where infection might reside undetected by conventional methods - or where schistosomiasis is moving into new, unexpected territories outside the currently known range. Combined with solid knowledge of the parasite-snail species different responses to climate change, this could greatly improve our ability to develop 'real-time' and future risk maps of schistosomiasis transmission and to respond appropriately to these changing disease dynamics as we move forward toward 2020 targets and beyond.

## Geospatial surveillance systems for vector-borne diseases

**Robert Bergquist**

The epidemiology of the wide variety of viral and parasitic diseases that rely on vectors for their transmission are not only connected to climate factors but also the attributes, such as land use, land cover, soil data, altitude/aspect/slope, etc. play a role. Vector-borne diseases are thus restricted to specific niches, while our capability to delimit their distributions depends on by the accuracies of the tools available for the assessment of these variables. Depending on the specifications of the satellite/sensor system used, Earth-observing satellites provide data at specific spatial, spectral and temporal resolutions, while the ready-made WorldClim dataset can be used as an unchanging source of average monthly climate data over 1970-2000 for each km<sup>2</sup> of the global land areas except Antarctica. The launch of the Soil Moisture Active Passive (SMAP) satellite in January 2015 and the ECOSTRESS instrument onboard the International Space Station (ISS) since July 2018 both broaden the scope of readings by allowing improved structural and functional classification of global ecosystems. This information together with the availability of 31-cm panchromatic, ground resolution from commercial satellites, contribute to seamless mapping and modelling of diseases not only at the country or community scales, but also at the village level. This communication presents some currently available instruments for the collection of remotely sensed data related to vector-borne infections.

## GEOHealth: A surveillance and response system resource for visceral leishmaniasis in Brazil

Moara Rodgers<sup>1</sup>, Elivelton Fonseca<sup>4</sup>, Píxia del Mar Nieto<sup>1</sup>, **JC McCarroll**<sup>1</sup>, Mara Bavia<sup>3</sup>, Raul Guimaraes<sup>4</sup>, Rebecca Christofferson<sup>1</sup>, Jeffrey Luvall<sup>2</sup>, \*John B Malone<sup>1</sup>

<sup>1</sup> Louisiana State University, Baton Rouge, LA, USA; <sup>2</sup>NASA Marshall Space Flight Center, Huntsville AL, USA; <sup>3</sup>Federal University of Bahia, Salvador, Brazil; <sup>4</sup>Sao Paulo State University, Presidente Prudente, Brazil

**Aim:** Generate and compare potential distribution models for visceral leishmaniasis and its vector, the sand fly *Lutzomyia longipalpis*, using Worldclim 2.0 data (30-year long term climate normal, 1 km) and monthly soil moisture data (SMAP L4, 10km) for Bahia state and Sao Paulo state in Brazil.

**Methods:** Principal component analysis (PCA) was performed to reduce the dimension and collinearity of the dataset. Initial models were run in Maxent and the jackknife procedure was used to identify variables contribution to model performance so the most meaningful components would be used to generate potential distribution maps. A total of 8 components were identified in the PCA.

**Results:** Potential distribution models for visceral leishmaniasis and its vector, the sand fly *Lutzomyia longipalpis*, were generated using Worldclim 2.0 data and monthly soil moisture data for Bahia state and Sao Paulo state. Similar eco-epidemiological patterns of VL and vector distribution were observed by both models. Results indicate direct earth observing satellite measurement of soil moisture by SMAP can be used in lieu of models calculated from standard thermal and precipitation climate station data to assess VL disease risk and to guide control interventions.

**Conclusion:** Direct earth observing satellite measurement of soil moisture by SMAP can be used in lieu of models calculated from standard climate station data to assess VL disease risk and to guide control interventions.

## Modelling of re-emerging of *Plasmodium vivax* malaria in Moscow (Russia) during 1999-2009

Natalia Shartova<sup>1</sup>, Fedor Korennoy<sup>2</sup>, Varvara Mironova<sup>3</sup>, Mikhail Grischenko<sup>3</sup>, Mikhail Varentsov<sup>3</sup>

<sup>1</sup>Lomonosov Moscow State University, Faculty of Geography; <sup>2</sup>Federal Centre for Animal Health;

<sup>3</sup>Lomonosov Moscow State University, Faculty of Geography

Moscow region was seriously affected with 386 autochthonous malaria cases, including 90 within the city of Moscow alone during 1999-2008. Supposedly, the sources of infection were mostly labour migrants from Central Asian countries.

The aim of this study is to analyze the spatial distribution of malaria cases and to define the main factors of malaria transmission in a city located in temperate climate zone.

We used MaxEnt software for modelling distributions of malaria cases by applying a machine-learning technique called maximum entropy modeling. From a set of social and environmental covariates and georeferenced occurrence localities, the model expresses a probability distribution where each grid cell has a predicted suitability of conditions for malaria cases. We utilized the following environmental and social covariates as predictors: climate conditions, landscapes, maximum green vegetation fraction (MGVF), altitude, cottages construction density, road and railways density, distance to railways stations and cottages. The information about cottages was included because illegal labour migrants from Central Asian countries, where during that time malaria outbreak was occurred, were employed in the construction of cottages.

The modelling simulation was carried out using 10 replications. The results determined the average values and boundaries of the confidence interval of the distribution of territorial suitability for malaria cases. The greatest contribution to the model is made by the distance to cottage construction (47.5%), the type of landscape (16.3%), the railways density (13.9%), and MGVF (8%), which confirms that only the combination of environmental and social factors led to local transmission of malaria. The influence of climatic factors (average annual temperatures and precipitation) is less pronounced, which may be due to the relatively small variation of these parameters within the Moscow region. According to the model the most favorable conditions are typical for the territory of the city and the least – for the outskirts of the region.

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**Session III**

**Mapping and modelling pathogens  
and vectors**

## Global epidemiology of strongyloidiasis: filling the knowledge gap

**Donal Bisanzio**<sup>1</sup>, Dora Buonfrate<sup>2</sup>, Antonio Montresor<sup>3</sup>, Michael French<sup>1</sup>, Richard Reithinger<sup>1</sup>, Giovanni Giorli<sup>4</sup>, and Zeno Bisoffi<sup>2,5</sup>

<sup>1</sup>RTI International, Washington, DC, USA; <sup>2</sup>Centre for Tropical Diseases, IRCCS Sacro Cuore Don Calabria Hospital, Negrar, Verona, Italy; <sup>3</sup>Department of Control of Neglected Tropical Diseases, World Health Organization, Geneva, Switzerland; <sup>4</sup>Centre for Experimental Medicine & Rheumatology, William Harvey Research Institute, Barts & The London School of Medicine & Dentistry, Queen Mary University of London, London, UK; <sup>5</sup>Dipartimento di Diagnostica e Sanità pubblica, Università degli Studi di Verona, Italy

Strongyloidiasis is a common neglected tropical disease (NTD) in tropical and sub-tropical climatic zones. At the worldwide level, there is high uncertainty about strongyloidiasis burden. The range of estimated infected people varies from 30 to 370 million. This is an important knowledge gap which affects the planning of intervention to reduce the burden of strongyloidiasis in endemic countries. Similar to other soil-transmitted helminths, strongyloidiasis can be prevented and treated by preventive chemotherapy (PC) through mass drug administration (MDA). However, due to the limited knowledge on strongyloidiasis epidemiology no endemic country is conducting any infection or disease prevention and control efforts. Having an estimate of the global strongyloidiasis burden is crucial to plan prevention and control programming and reduce its toll on the global population.

This study aimed to estimate the global strongyloidiasis burden and calculate the population of school-age children needed to be covered with MDA in 2018. Epidemiological data on strongyloidiasis were gathered by literature review and merged with data on country characteristics obtained from public data sources. Prediction of strongyloidiasis prevalence for each country was performed using a spatio-temporal statistical modeling approach. The country prevalence obtained from the model was used to calculate the number of infected people and the fraction of school-age children to be covered by MDA.

We estimate the global prevalence of strongyloidiasis in 2018 to be 8.1% (95% CI: 4.2–12.4%), corresponding to 613.9 M (95% CI: 313.1–910.1 M) people infected; SEARO, AFRO, and WPRO regions accounted for 76.1% of the global infections. Moreover, we estimated that at least 238.8 M (95% CI: 134.1–317.4 M) school-age children live in areas where strongyloidiasis prevalence is over 5% and therefore need MDA.

The results of our study highlighted that global strongyloidiasis prevalence has been underestimated. Our results could be used to identify those countries in which strongyloidiasis prevalence is highest and MDA should be deployed for its prevention and control.

## Mapping changes in the spatiotemporal distribution of lumpy skin disease virus

G. Machado<sup>1\*</sup>, **F. Korennoy**<sup>2\*\*</sup>, J. Alvarez<sup>3</sup>, C. Picasso-Risso<sup>4</sup>, A. Perez<sup>4</sup>, K. VanderWaal<sup>4</sup>

<sup>1</sup>North Carolina State University, Raleigh, USA; <sup>2</sup>Federal Center for Animal Health, Vladimir, Russia; <sup>3</sup>Universidad Complutense, Madrid, Spain; <sup>4</sup>University of Minnesota, St Paul, USA.

Lumpy skin disease virus (LSDV) is an infectious disease of cattle transmitted by arthropod vectors which results in substantial economic losses due to impact on production efficiency and profitability, and represents an emerging threat to international trade of livestock products and live animals. Since 2015, the disease has spread into the Northern Hemisphere including Azerbaijan, Kazakhstan, the Russian Federation and the Balkans. The rapid expansion of LSDV in those regions represented the emergence of the virus in more temperate regions than those in which LSDV traditionally occurred. The goal of this study was to assess the risk for further LSDV spread through the a) analysis of environmental factors conducive for LSDV, and b) estimate of the underlying LSDV risk, using a combination of ecological niche modeling and fine spatiotemporally explicit Bayesian hierarchical model on LSDV outbreak occurrence data. We used ecological niche modeling to estimate the potential distribution of LSDV outbreaks for 2014-2016. That analysis resulted in a spatial representation of environmental limits where, if introduced, LSDV is expected to efficiently spread. The Bayesian space-time model incorporated both environmental factors and the changing spatiotemporal distribution of the disease to capture the dynamics of disease spread and predict areas in which there is an increased risk for LSDV occurrence. Variables related to the average temperature, precipitation, wind speed, as well as land cover and host densities were important drivers explaining the observed distribution of LSDV in both modeling approaches. Areas of elevated LSDV risks were identified mainly in Russia, Turkey, Serbia, and Bulgaria. Results suggest that, if current ecological and epidemiological conditions persist, further spread of LSDV in Eurasia may be expected. The results presented here advance our understanding of the ecological requirements of LSDV in temperate regions and may help in the design and implementation of prevention and surveillance strategies in the region.

**Keywords:** transboundary disease, disease mapping, Bayesian hierarchical model, Ecological niche modeling, spatial dynamics.

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## Towards making spatial risk maps for helminth parasites in ruminants dynamic: A case study in Italy

**Alizée Hendrickx**<sup>1</sup>, Maria Elena Morgoglione<sup>2</sup>, Laura Rinaldi<sup>2</sup>, Antonio Bosco<sup>2</sup>, Guy Hendrickx<sup>1</sup>, Cedric Marsboom<sup>1</sup>

<sup>1</sup>Avia-GIS, Zoersel, Belgium; <sup>2</sup>Department of Veterinary Medicine and Animal Production, University of Naples Federico II, CREMOPAR Campania Region, Naples, Italy

*Dicrocoelium dendriticum*, *Fasciola hepatica* and *Calicophoron daubneyi* are trematodes that occur in ruminant livestock. Although they have a different economic impact, in severe cases their occurrence can lead to loss of animals. Hence, modelling these parasites can help to improve management in higher risk regions. Until now static models are the golden standard. The aim of this master dissertation is to develop dynamic risk maps to evaluate the change of occurrence throughout the years. This is of particular interest because changes in weather conditions between years may be increased due to climate change, and dynamic models could visualize these changes on regional scales.

A dataset for the three parasites under study, covering Italy and ranging from 1999-2018, was provided by the Regional Center of Monitoring Parasitic Infections of Livestock (CReMoPAR, Campania region, Italy). Spatial patterns of the parasites' distribution were detected with a high infection risk in the southern part of Italy, mostly for *D. dendriticum*. The prevalence of the other parasites in Italy was lower. The most important predictor was temperature which is an important factor for the intermediate host and the free-living stages of the parasites. Other predictors, such as management and occurrence of the intermediate host(s), were not included and may further improve the predictive reliability of the models.

The georeferenced parasitological data were modelled using both machine learning (Random Forest) and statistical modelling techniques (Non-Linear Discriminant Analysis and General Linear Model). Defining the minimal sample size required for modelling individual years is important when making dynamic models. Though no individual year reached the sample size cut-off, the quality of the outputs obtained for the years with the highest number of observations is encouraging. Further research is needed to explore whether observed differences between years may be explained by regional differences in weather conditions.

## Documenting *Biomphalaria pfeifferi* along Lake Malawi, Mangochi District shorelines

**Mohammad H. Alharbi**, Charlotte Condemine, Josie Hesketh, E. James LaCourse, Peter Makaula, Sekeleghe A. Kayuni, J. Russell Stothard<sup>1\*</sup>

*Liverpool School of Tropical Medicine, Liverpool, UK*

Whilst the freshwater snail fauna of Lake Malawi is well-known to sustain local transmission of urogenital schistosomiasis, it was assumed, until recently, unable to sustain transmission of intestinal schistosomiasis. Upon malacological surveys conducted in November 2017, whilst *Bulinus* was commonly found, *Biomphalaria* was unexpectedly encountered in two sampling sites on the western shoreline of Mangochi District. Collected *Biomphalaria* snails were characterized by molecular DNA analysis of the mitochondrial cytochrome oxidase sub-unit 1 (COI) gene, inferring a genetic lineage of *Bi. pfeifferi* likely originating from nearby Zimbabwe. During a second malacological survey in May 2018, with additional sites surveyed, *Bi. pfeifferi* was found at 9 further locations, with its presence re-confirmed at a previously sampled location. One year later, a third malacological survey also confirmed *B. pfeifferi* on the western, and now eastern shorelines of Mangochi District. Collectively, these malacological surveys have confirmed the sustained presence of *B. pfeifferi* within Lake Malawi, adding to its list of endemic species. Our findings are of significant medical interest, since our recent parasitological surveys of school children have confirmed intestinal schistosomiasis. This raises concerns for local health authorities and tourists to this part of the lake for autochthonous transmission of intestinal schistosomiasis. Moreover our studies serve as excellent examples of how routine malacological surveillance can shed new light on the changing epidemiology of schistosomiasis in Lake Malawi.

## **NASA's NextGen Remote Sensing Instruments have arrived: Data Products for the Thermodynamic Paradigm for Studying Disease Vectors**

**Jeffrey C. Luvall**<sup>1</sup>, John B Malone<sup>2</sup>, Moara Rodgers<sup>2</sup>, PRIXIA del Mar Nieto<sup>2</sup>, Rebecca Christofferson<sup>2</sup>, JC McCarroll<sup>2</sup>, Elivelton Fonseca<sup>3</sup>, Raul Guimaraes<sup>3</sup>, Mara Bavia<sup>4</sup>

<sup>1</sup>NASA, Marshall Space Flight Center; <sup>2</sup>Louisiana State University, Baton Rouge, LA, USA; <sup>3</sup> Sao Paulo State University, Presidente Prudente, Brazil; <sup>4</sup> Federal University of Bahia, Salvador, Brazil

Remote sensing can be used to measure or evaluate or estimate both environment (state functions) and interface (process functions) defining vector habitats. The products of remote sensing can be integrated directly into the epidemiological equations to significantly enhance our understanding of disease vector's life cycles and habitats. The next generation of NASA's remote sensing instruments recently operational will provide a significant enhancement in our ability to study disease vector's life cycles and habitats. Three new instruments have become operational on the International Space Station (ISS) In June 2018, ECOSTRESS (The ECOSystem Spaceborne Thermal Radiometer Experiment on Space Station), a five channel, thermal IR instrument with 70 m resolution and approximately 4-5 day repeat cycle of day/night pairs along with DESIS a hyperspectral sensor system 235 channels (between 400 and 1000 nanometers), 30 m resolution, and data only being acquired on demand. In November 2018. GEDI (Global Ecosystem Dynamics Investigation). GEDI is a high-resolution laser ranging of Earth's forests and topography. These instruments set the stage for NASA's new global designated observables set of remote sensing measurements collecting hyperspectral and multispectral thermal data called SBG (Surface Biology Geology). The SBG is currently in the planning stage. The availability and use of level 1-4 data products generated from these ISS instruments will be discussed.