

RISK EVALUATION, SURVEILLANCE AND FORECAST OF VECTOR-BORNE TROPICAL DISEASES BY EARTH OBSERVATION DATA MINING

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List of Principal Investigators (PIs)

Topic Nr.	PIs	Title
32260_1	Prof. Alfredo Milani, Prof. Jiming Liu	Mosquito-borne diseases
32260_2	Prof. Juerg Utzinger, Prof. Lingli Tang	Snail-transmitted diseases
32260_3	Prof. Laura Rinaldi, Prof. Xiao-Nong Zhou	Tick-borne diseases

EXECUTIVE SUMMARY

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. schistosomiasis, malaria and dengue, 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. However, remote sensing experts may not exactly know what environmental factors are required to identify the incubators of vector-borne diseases. On the other hand, effective RS data processing and parameters retrieval techniques are also challenges for hygiene experts who are lack of experience of remote sensing applications. Taking into account of different type of massive data are involved, computing scientists with substantial intelligent data analysis expertise is crucial to successfully incorporate advance intelligent data analysis, such as data mining, pattern analysis. Consequently, any single of these disciplines is insufficient, it is essential to bring together scientists from computing science and remote sensing along with domain experts to foster a substantial collaboration. This proposed project aims to apply advanced remote sensing and computing technologies into monitoring and early warning of vector-borne diseases, e.g. schistosomiasis, malaria and dengue. 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. All the institution of the project can provide sufficient funding to run the whole project successfully. The outcomes of the project will help to decrease the scope and extent of vector-borne diseases, and improve prevention & control capabilities to vector-borne diseases. Additionally, the research results can be used to assess environmental characteristics around the sits 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.

ABSTRACT 32260_1: "Mosquito-borne diseases"

European Principal Investigator

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Chinese Principal Investigator

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Mosquito is one of most important vectors that can carry and transmit several vector-borne diseases which have caused significant human suffering, such as malaria and dengue, etc.. The capacity for mosquitoes' population transmitting diseases is closely related to natural environment due to the presence, breeding and evolution of their pathogens or reservoir hosts. Therefore, monitoring the mosquito population dynamics is an important way to prevent and control the mosquito-borne diseases. Due to the complexity in the life cycle of mosquito, it is difficult to acquire relevant environmental factor data by traditional in-situ measurements. Remote sensing (RS) technology provides the capability of obtaining a large scale of temporal-spatial variations of ground environmental factors. However, RS experts may not exactly know what environmental factors are required to identify the incubators or epidemic determinants of mosquito-borne diseases. On the other hand, effective RS data processing and parameters retrieval techniques are also challenges for epidemiological experts who are lack of experience of remote sensing applications. Taking into account of different types of massive data are involved, computing scientists with substantial intelligent data analysis expertise is crucial to successfully incorporate advance intelligent data analysis, such as data mining, pattern analysis. Consequently, any single of these disciplines is insufficient, it is essential to bring together scientists from computing science and remote sensing along with domain experts to foster a substantial collaboration.

This proposed project aims to apply advanced RS and computing technologies into monitoring and early warning of mosquito-borne diseases epidemics, e.g. malaria and dengue. First, the environmental factors which have significant influences on the breeding habitats of diseases and its vectors will be revealed based on existing literatures. Second, the project will make full use of the advantage of European and Chinese earth observation resources and the partners capability, so that parameter inversion, feature extraction and pattern analysis methods will be used to characterize environmental features and mosquito habitats that are mostly suitable for the growth and dispersion of mosquito-borne diseases and dynamic monitoring. Third, temporal-spatial models of the distribution of mosquito-borne diseases will be developed by data mining techniques. Fourth, the driving mechanism and RS data assimilation methods of land surface process model will be explored in order to establish the early warning system of mosquito-borne disease transmission in terms of scope and intensity. Finally, all of the institution in the project can provide sufficient funding to run the whole project successfully through free use of those data or modeling results. The major outcomes of the project will help to monitoring precisely the scope and intensity of mosquito-borne diseases, and improve the control capabilities to mosquito-borne diseases for the local disease control institutions. Additionally, the research results can be used to assess environmental characteristics around the sits 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.

ABSTRACT 32260_2: "Snail-transmitted diseases"

European Principal Investigator

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Chinese Principal Investigator

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Both schistosomiasis and fascioliasis, the snail-transmitted diseases, are the diseases of poverty, which affects almost 240 million and 2.4 million people worldwide, respectively. Infections are occurred when people expose themselves to infested water during routine agricultural, domestic, occupational and recreational activities or eating infested plant, which may encounter with the suitable habitats for the intermediate host snail of schistosomiasis and fascioliasis. Therefore, monitoring the ecological transformations of intermediate host snails is an important way to control the snail-borne diseases. Due to the complexity in the environment of vector habitats, it is difficult to acquire relevant environmental data by traditional front filed measurements. Geographic information system (GIS) and remote sensing (RS) technologies offer new opportunities for rapid assessment of schistosomiasis endemic areas, provision of reliable estimates of populations at risk, prediction of disease distributions in areas that lack baseline data and are difficult to access, and guidance of intervention strategies, so that scarce resources can be allocated in a cost-effective manner. This proposed project aims to apply advanced remote sensing and computing technologies in the control and prevention of schistosomiasis by monitoring and predicting the population of intermediate host snail. First, we will map the temporal-spatial distribution of schistosomiasis and fascioliasis at a large scale in term of the prevalence and transmission intensity data. Then, we will utilize the remote sensing image to identify and predict the suitable habitats for the intermediate host snail of schistosomiasis at a small scale. We will further develop computational models to characterize the relationships between the environmental factors and the infection dynamics, which can be helpful to predict the infection risk due to ecological transformations, particularly those induced by floods and water resource developments, and the potential impact of climate change. All of the institutions in the project can provide sufficient funding to run the whole project successfully. The outcomes of the project will help to further enhance the capability in infection risk mapping and disease prediction, and improve prevention & control capabilities to schistosomiasis. Additionally, the research results can provide the suggestion on site selection and implementation of intervention measures.

ABSTRACT 32260_3: "Tick-borne diseases"

European Principal Investigator

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Chinese Principal Investigator

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Tick-borne diseases are one of the most common classes of vector-transmitted infectious diseases and constitute a serious public health problem worldwide. The transmissions of these tick-borne diseases always correlate with various environmental connections and interactions between parasites and their host. The frequent emergence of human infections of tick-borne diseases always results from the environmental changes, which may cause the increased population size of parasites or their vectors as well as promote their geographic distributions. Therefore, it is essential to understand the processes of disease transmission by means of identifying the environmental and climatic determinants that affect the population density of disease vectors. Studies have shown that increase in the density of vectored ticks always parallel the increase in the incidence of human infections, such as babesiasis and theileiosis, through Ixodes scapularis ticks. Furthermore, the vector density accounts for environmental changes, including changes in climate, land-use, and other factors that may have recently provided the ecological conditions necessary for vectors' population growth. However, it is difficult to assessing the relevance of environmental factor data in a regional-scale. Remote sensing technology provides the capability of obtaining a large scale of temporal-spatial variations of ground environmental factors. Here we present a project aiming to apply advanced remote sensing (RS) technologies into collecting empirical data detailing the changes of environments and tick populations over the past decades. We use these temporally and spatially structured environmental data to build analytical models that identify the environmental factors correlated with the density of tick populations. We analyze tick density data in a geographic information systems (GIS) framework using samples collected throughout the dynamic phase of population expansion. Then the dynamic pattern of tick population growth and environmental variables that account for these patterns will be identified. In this way, a biogeographical framework will be established that can serve as the foundation to further explore the basic ecology and demographic history of this medically important vector species.