Study Group Meeting

Intelligent Systems for Vector-Borne Disease

Delmenhorst, 06 – 07 July 2023

Organizer:

Prof. Dr. Peter Haddawy

HWK Alumnus / Mahidol University, Bangkok, Thailand

Program

Thursday, July 6, 2023 – Day 1

9:30 – 10:40   **Welcome, Overview, Introductions**
Peter Haddawy

Session I: Mosquito Monitoring

- *Patchara Sriwichai*
Sylvatic and domestic mosquito vectors in Thailand

- *Myat Su Yin*
An update on MosquitoSong sensors

10:40 – 11:00   *COFFEE BREAK*

11:00 – 11:30   **Session I (cont'd)**

- *Steffen Knoblauch*
Key drivers for inner-urban dengue occurrence

11:30 – 13:00   **Session II: Pandemic Preparedness I**

Introduction to the session
Peter Haddawy

- *Anuwat Wiratsudakul*
Let's explore the global genetic database of
coronaviruses with deep learning techniques:
Any next COVID-19 out there?

- *Saranath Lawpoolsri*
Mosquito-borne zoonotic diseases

- *Dominique Bicout*
Observational surveillance: Case of work-related
health problems

13:00 – 14:00   *LUNCH & PHOTO*

| 14:00 – 15:30 | **Session III: Pandemic Preparedness II – Modeling** |

- *Chaitawat Sa-ngamuang*
  A toolbox for analyzing human mobility aspects of disease transmission

- *Julian Heidecke*
  Process-based models of West Nile virus dynamics: Understanding seasonal patterns and the impact of climate change

- *Edmund Yamba (online)*
  The invasion of Anopheles stephensi in Ghana: Climate suitability for its thrivability and expansion range

| 15:30 – 16:00 | *COFFEE BREAK* |

| 16:00 – 17:00 | **Session IV: Pandemic Preparedness III** |

- *Kingsley Badu*
  Vector-borne disease surveillance for pandemic preparedness

- *Gloria Chechet*
  Assessing genetic diversity of dengue virus serotypes in Aedes mosquitoes: A step toward pandemic preparedness in Nigeria

| 17:00 – 18:30 | **Breakout Session I** |

Breakout (1 hr)

Reporting (30 min)

| 18:30 | *DINNER* |

Friday, July 7, 2023 – Day 2

9:30 – 10:40   **Introduction to day 2**
                Peter Haddawy

                Session V: Dengue
                - *Dumrong Mairiang*
                  Considerations for prognostic models in the
                  management of dengue patients in Thailand

                - *Peter Haddawy*
                  A Bayesian approach to prognostic prediction of DHF
                  with partial information

10:40 – 11:00   *COFFEE BREAK*

11:00 – 12:30   **Session VI: Dengue & Trypanosomes**

                - *Thomas Barkowsky*
                  Overview of dengue apps

                - *Lokachet Tanasugarn*
                  Dengue control methods: A Scoping Review

                - *Ibrahim Mahamat*
                  Trypanosome species and their vectors in southern
                  Chad. What is known so far?

12:30 – 13:30   *LUNCH*

13:30 – 15:00   **Breakout Session II**

                Breakout (1 hr)

                Reporting (30 min)

15:00 – 17:00   **Poster & Demo Session**

                COFFEE SERVED

17:00 – 18:00   **Discussion & Wrap-up**

18:00   *DINNER*

Abstracts

Patchara Sriwichai

Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Thailand

Title: Sylvatic and domestic mosquito vectors in Thailand

Abstract: The human-monkey interface in Thailand has become one of the arbovirus transmission hotspots where people are more prone to sylvatic and domestic mosquito vectors. Our studies aimed to investigate the mosquito density and Arbovirus infectivity rate of mosquito vectors among 4 zones from monkey habitat to human coexisting villages (Zone 1-4) in Prachuap Khiri Khan Province, Thailand. Total 11,274 mosquitoes from 11 species were captured during the peak of Dengue transmission in wet season which most found the Culicine group; Culex quinquefasciatus (81.33%), Aedes aegypti (18.39%), and Aedes albopictus (0.04%). Percent infection rates of Dengue virus (DENV) and Chikungunya virus (CHIKV) in Ae. aegypti were 0.96% and 13.53% respectively. Positive DENV samples were obtained from mountain and fringe zones while positive CHIKV samples were collected among all areas except urban zones. Interestingly, positive DENV and CHIKV were detected from the mosquitoes emerging from larva in the fringe zones, representing the possibility of vertical transmission of the CHIKV in the area. This study showed the potential of arbovirus transmission in the co-human and monkey habitat area, shading potential of virus borne transmission by Ae. aegypti. The additional vector control program should be concerned.

Myat Su Yin

Mahidol-Bremen Medical Informatics Research Unit, Faculty of ICT, Mahidol University, Thailand

Title: An update on MosquitoSong sensors

Abstract: Accurate and comprehensive data on mosquito populations are crucial for effective disease prevention and control. Traditional methods of monitoring mosquito populations are labor-intensive and not suitable for large-scale monitoring. To address these limitations, our research focuses on utilizing mosquito wingbeats for population surveys and control efforts. However, the current data collection and annotation process is time-consuming and resource-intensive, and laboratory-collected datasets lack biodiversity information. In response, our team has developed an IoT sensor that automatically classifies mosquito species and determines their sex based on wingbeat audio signals. To streamline data acquisition, we propose an IoT platform that integrates with the Biogents BG-Counter 2 smart mosquito trap and incorporates a cost-effective acoustic sensing device. Initial assessments indicate successful integration, seamless data transmission, and satisfactory audio quality for wingbeat classification. This solution offers an efficient and field-based approach for gathering wingbeat data from a diverse range of mosquito species.

Steffen Knoblauch

GIScience Research Group, Heidelberg University, Heidelberg, Germany

Interdisciplinary Centre of Scientific Computing (IWR), Heidelberg University, Heidelberg, Germany

Title: Key drivers for inner-urban dengue occurrence

Abstract: The spatiotemporal occurrence of dengue fever in cities is often unexplained. However, knowledge about the driving factors of urban outbreaks are essential to conduct effective vector control. Mosquito distribution maps, taking into account limited mosquito flight ranges, and modelling inner urban human movement patterns could be one chance to support future interventions. Current research approaches on these topics will be highlighted during this talk.

Anuwat Wiratsudakul

Department of Clinical Sciences and Public Health, Faculty of Veterinary Science, Mahidol University, Thailand

Title: Let's explore the global genetic database of coronaviruses with deep learning techniques: Any next COVID-19 out there?

Abstract: The genetic diversity of coronaviruses allows these pathogens to infect various animal species, including humans. Take SARS-CoV-2 (the coronavirus that causes COVID-19) as an example; the virus can infect humans, tigers, cats, ferrets, minks, and other animal species. It is likely that some other coronaviruses may jump across species and cause similar catastrophic pandemics in the future. We thus propose a deep-learning technique to identify and prioritize animal coronaviruses that may spill over to human populations. We also propose to identify the relevant host species and parts of genetic materials that facilitate coronaviruses to infect humans. Our study is composed of four consecutive steps: (1) Preparing the coronavirus databases, (2) Labeling data for deep learning identification, (3) Designing a deep learning system, and (4) Analyzing the genetic data with various deep learning techniques such as Convolutional Neural Network (CNN), Recurrent Neural Network (RNN), and LSTM (Long Short-Term Memory) architectures. With these techniques, we can prioritize the coronaviruses that should be closely watched and targeted for early detection. This leads to the mitigation of future outbreaks through the prevention and control measures implemented in a timely fashion.

Dominique Bicout

Univ. Grenoble Alpes, CNRS, UMR 5525, VetAgro Sup, Grenoble INP, TIMC, 38000 Grenoble, France

Title: Observational surveillance: Case of work-related health problems

Abstract: Surveillance of both diseases and associated exposures is a major issue of public health, in particular for identifying and preventing new threats for health. Indeed, environmental exposure – health associations remain poorly understood and sometimes not elucidated due to the lack of exploitation of data and global view of population exposures including critical periods of exposure or during exposed occupations. In the occupational health context, the French national occupational disease surveillance and prevention network (RNV3P) have constructed a growing database that records every year since 2001 all Occupational Health Problems (OHPs)

diagnosed by a network of physician specialists. The nation-wide network aims to provide and develop an expertise on the disease–(multi)-exposure relationships, and uses the RNV3P database for developing the surveillance of OHPs and for the detection of emerging associations between diseases and (occupational) environmental exposures.

To improve our understanding and capability of analyzing occupational environment – health associations, we employed the Observational Surveillance method, based on the Occupational Exposome approach, for an optimal exploitation of the RNV3P database. The method involves structuring the data in terms of an occupational exposome, i.e., a relational network of significant occupational exposures associated with OHPs. It allows the identification of significant associations (disease related exposures and/or sectors) and the study of the spectrosome, i.e., the dynamical and structured spectrum of exposures associated to OHPs. Such observational surveillance can be implemented routinely for a or an ensemble of OHPs (e.g., identified and targeted OHP groups) for analyzing and tracking trend changes or detecting emergent events in occupational exposures – pathology associations and relationships.

As an illustration of how the observational surveillance can be conducted, we have considered the case of Non-Hodgkin Lymphomas (NHLs), a cancer whose incidence has been increasing since 1970s and whose risk factors are not yet well known.

Chaitawat Sa-ngamuang
Mahidol-Bremen Medical Informatics Research Unit, Faculty of ICT, Mahidol University, Thailand

Title: A toolbox for analyzing human mobility aspects of disease transmission

Abstract: Human mobility is one of the crucial components in the transmission of infectious diseases. However, understanding the role of human mobility in disease transmission is complicated due to its complexity in spatial and temporal aspects, and the uncertain interaction between humans and environments in different areas. Investigating such complexities requires a combination of different tools, which is labor-intensive and requires time to learn all the tools. Therefore, there is a need for integrated software that combines the needed analysis capabilities to speed the analysis process and create rapid feedback loops that facilitate data exploration and modeling.

In this talk, we present an integrated web-based application that provides the necessary functionalities to visualize and analyze the relationship between human mobility and infectious disease transmission. The system provides the visualization of human mobility based on time and demographics. Our system will also support estimating the individual risk of exposure based on such interaction between mobility and spatiotemporal risk. Lastly, the system will provide an agent-based simulation using models learned from mobility data. The simulation will allow a user to explore various control strategies.

The demonstration of the software will be performed by studying the effect of human mobility on malaria transmission in an area along the Thai-Myanmar border. The demonstration will be carried out using mobility data that was gathered over a period of one year using a smartphone application installed on the phones of study participants.

Julian Heidecke
Interdisciplinary Center for Scientific Computing and Heidelberg Institute of Global Health, Heidelberg University, Heidelberg, Germany

Title: Process-based models of West Nile virus dynamics: Understanding seasonal patterns and the impact of climate change

Abstract: West Nile virus (WNV) is a mosquito-transmitted pathogen that can cause severe disease with central nervous system involvement in birds, humans, and other mammals. The virus circulates mainly between wild birds and mosquitoes of the genus Culex, while humans act as dead-end hosts as they do not produce sufficient viraemia to transmit the pathogen back to mosquitoes. In recent decades WNV has emerged as a serious health risk in Europe due to increasingly widespread and intense circulation. Climate change impacts WNV transmission via multiple pathways. Amongst them increasing temperature impacts suitability for WNV mosquitoes and transmission facilitating its spread to new areas. This talk will discuss the role of process-based models in understanding the complex interactions that result in WNV transmission. The incorporation of environmental drivers in models will be introduced as well as their value in understanding seasonal patterns and the potential impacts of climate change.

Gloria Chechet
Department of Biochemistry, Africa Centre for Excellence in Neglected Tropical Diseases and Forensic Biotechnology, Ahmadu Bello University, Zaria. Nigeria

Title: Assessing genetic diversity of dengue virus serotypes in Aedes mosquitoes: A step toward pandemic preparedness in Nigeria

Abstract: Pandemic preparedness is a critical global health priority, particularly in regions prone to emerging infectious diseases. Dengue fever, caused by the dengue virus, has emerged as a significant public health concern in Nigeria. Understanding the genetic diversity of dengue virus serotypes circulating among Aedes mosquitoes is crucial for effective preparedness and response. We have assessed the genetic diversity of dengue virus serotypes in selected regions of northeastern Nigeria. Aedes mosquito samples were collected and screened for dengue virus using molecular techniques. Serotype-specific PCR assays were employed to identify the circulating serotypes, and genetic diversity was assessed through sequencing and phylogenetic analysis. Our findings revealed the presence of multiple dengue serotypes, including DENV-1, DENV-2, and DENV-4 in Aedes albopictus. DENV-4 serotype being reported for the first time in Nigeria. This information is invaluable for pandemic preparedness, as it provides insights into the serotype diversity and potential for severe disease outcomes underscoring the need for comprehensive surveillance and response systems. The identification of circulating serotypes will enable accurate diagnostic capabilities, facilitate appropriate clinical management, inform targeted vector control strategies, and aid in the development of effective vaccines. By incorporating serotype-specific considerations into pandemic preparedness plans, Nigeria can enhance its capacity to prevent and control dengue outbreaks, mitigating the impact on public health and strengthening overall preparedness efforts in the region.

Dumrong Mairiang

Faculty of Medicine Siriraj Hospital, Mahidol University and National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Pathumthani, Thailand

Title: Considerations for prognostic models in the management of dengue patients in Thailand

Abstract: Dengue hemorrhagic fever (DHF) could be predicted with high accuracies (AUC of ROC 90%) using machine learning models. The models may assist medical personnel in managing dengue patients. However, models must be implemented carefully in clinical practice. There are various medical facilities with varying capacities for treating dengue patients. First, a primary care unit (PCU) can provide rudimentary care, but laboratory capabilities are not available. Second, a general hospital's satellite primary care unit (PCU plus) and outpatient department (OPD) can provide rudimentary care and laboratory services. An inpatient department (IPD) of a general hospital can collect all necessary longitudinal clinical and laboratory data. In addition, not all required features for predictive models may be available simultaneously. Usable prognostic models should be able to deal with incomplete data and provide predictions that can be updated as new data become available. In this talk, the user requirements for a prognostic tool from experienced dengue clinicians in Thailand will be discussed.

Peter Haddawy

Mahidol-Bremen Medical Informatics Research Unit, Faculty of ICT, Mahidol University, Thailand

Title: A Bayesian approach to prognostic prediction of DHF with partial information

Abstract: Dengue virus infection is a major global health problem. While dengue fever rarely results in serious complications, the more severe illness dengue hemorrhagic fever (DHF) has a significant mortality rate due to the associated plasma leakage. Proper care thus requires identifying patients with DHF among those with suspected dengue so that they can be provided with adequate and prompt fluid replacement. In this work, we use 18 years of pediatric patient data collected prospectively from two hospitals in Thailand to develop Bayesian network models to predict DHF among patients with suspected dengue. The use of Bayesian networks is driven by the need to provide rolling predictions at any point in time during the progression of the disease, even before some information, such as lab tests, may be available. Because they compute posterior probability distributions given avaialble evidence, Bayesian networks are ideally suited to this requirement. We evaluate the models with complete information and in some common partial information scenarios. The produced models are able to predict DHF with high accuracy (ranging from and AUC of 0.8 given one day of patient information and 0.9 given three days) and perform in the needed flexible manner with partial information on any given day.

Thomas Barkowsky

Bremen Spatial Cognition Center, University of Bremen, Germany

Title: Overview of dengue apps

Abstract: In collaboration with our partners at Mahidol University we develop mobile apps and web-based systems to support the diagnosis of dengue, for monitoring dengue inpatients in critical states of the disease, as well as for dengue vector control following dengue outbreaks.

Focusing mainly on the latter, I will present our web-based system for managing dengue index cases, for organizing control tasks performed by public health care staff working in local facilities in the infection area as well as in the field, and for monitoring the progress of the actions taken. A mobile app integrated with this system is used for data collection and for reporting about the measures taken at the suspected infection sites. The system is currently pilot tested in one province in Thailand. It may, however, also be employed in other regions affected by dengue, and it could be extended to also help combat further vector-borne disease

Lokachet Tanasugarn

Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Thailand

Title: Dengue control methods: A scoping review

Abstract: The continuously increasing number of cases and expanding geographical range has posed dengue as one of the most important vector-borne diseases worldwide. Several methods have been implemented aiming at controlling the spread of dengue. The objective of this review is to provide a comprehensive summary of published literature related to dengue vector control methods in the past ten years.

We systematically searched for studies that aimed at evaluating dengue control methods on PubMed, EMBASE, and SCOPUS. The search results were limited to original research studies reported either in English or Thai during 2013 to 2023. Additionally, we carried out add-on searches in parallel fashion through online Thai citation index centre, Thai University online catalogue, and related conference abstracts. Two reviewers work independently to screen abstracts and full text articles. We extracted and presented important components of the included study. We further categorized the control methods by country to explore the trend of studied intervention by regions.

From 6,465 identified records, we included 120 studies in the final analysis. Most recent studies incorporated more than one control method reflecting the interdisciplinary approach to dengue control. Notably, studies from Thai national databases appeared to emphasize on community engagement and participation more than international counterparts.

The results of this study illustrate the variety of methods to control dengue. In response to the evolving threat of dengue, the scientific community needs to come up with more effective and culturally appropriate dengue control strategies to ensure suppression of this ever-looming threat of arboviral diseases.

Ibrahim Mahamat

Dept. of Public Health, Faculty of Human Health Sciences, University of N'Djaména

Title: Trypanosome species and their vectors in southern Chad. What is known so far?

Abstract: African trypanosomes are parasites mainly transmitted by tsetse flies. They cause trypanosomiasis in humans and animals. In Chad, trypanosomosis are endemic. This study investigates the genetic diversity and distribution of trypanosomes and their vectors in Mandoul, an isolated area where a vector control campaign is ongoing, and Maro and Lake Iro, areas where the control had not started.

Human and cattle blood samples and biological and mechanical vectors were collected. Trypanosomal DNA was detected using PCR targeting internal transcribed spacer 1 and glycosomal glyceraldehyde-3 phosphate dehydrogenase, followed by amplicon sequencing.

Trypanosoma brucei gambiense, the human pathogenic specie and T. congolense the animal pathogenic were identified in humans in Maro. In cattle, tsetse and tabanids, T. brucei, T. congolense, T. vivax, T. simiae, T. theileri, T. godfreyi and T. simiae were detected. Besides, DNA from an unknown Trypanosoma sp.-129-H was identified in a man with a history of a cured trypanosomiasis infection and persisting symptoms. Furthermore, evidence for additional unknown trypanosomes was obtained in tsetse. The vector identification showed the presence of the Glossina fuscipes group in all three study areas. Besides, G. tachinoides and G. morsitans submorsitans were found in Maro and Lake Iro. Tabanus formosiensis, T. amaenus, and T. autumnalis were the 3 evident mechanical vectors identified in the areas.

Vector control activities in Mandoul reduced the tsetse population and thus the pathogenic parasites. Nevertheless, T. theileri, T. vivax, and T. simiae are frequent in cattle suggesting transmission by mechanical vectors. In contrast, in Maro and Lake Iro, transhumance to/from the Central African Republic and no vector control may have led to the high observed diversity. Active trypanosomiasis infections stress the need to enforce monitoring and control campaigns. Additionally, the various species in humans and cattle indicate the necessity to investigate the infectivity of the unknown trypanosomes regarding their zoonotic potential.