Research Assessment Exercise 2020
Impact Case Study

University: Hong Kong Baptist University
Unit of Assessment (UoA): 13 Computer Studies/Science (Incl. Information Technology)

Title of case study: A Computational Approach to Malaria Elimination with Chinese Center for Disease Control and Prevention (China CDC)

(1) Summary of the impact (indicative maximum 100 words)

Interdisciplinary researchers at HKBU have developed novel risk assessment methods for the optimal allocation of anti-malaria surveillance and intervention resources. These methods have resulted in significant changes to the overarching guidelines and field practices for front-line malaria surveillance and control of the China CDC. These guidelines have become essential and integral to strategic actions for China to achieve malaria elimination and prevent re-establishment of transmission. As a result, Tengchong, once a city in China with the highest rate of prevalence of malaria, has become the first China-Myanmar border city certified malaria free — four years ahead of its target date. The World Health Organisation (WHO) and the Health Poverty Action (HPA) have recognised the importance of the HKBU methods to systematically control malaria and planned a wider deployment for the eradication of malaria globally. Bhutan, Cambodia, and Sri Lanka also have initiated the collaboration with HKBU to adopt the developed methods in their malaria control programmes and eradication plans to help mitigate malaria transmission and outbreaks.

(2) Underpinning research (indicative maximum 500 words)

It is an acknowledged fact that malaria is one of the most endemic and life-threatening global health concerns. The WHO reported in 2019 that nearly half of the world's population remains at risk from this potentially fatal disease. Prof. Jiming Liu at HKBU has identified the key issue in eliminating malaria with very limited anti-malaria resources: how to assess malaria transmission risks in different geographical regions, such that the resources for malaria epidemic control and prevention are directed to local populations in the greatest need to achieve the ultimate goal of halting the spread of this life-threatening disease. Addressing the above issue is a very challenging task as:

a) Malaria transmission is not directly observable and difficult to infer because it is a complex dynamic process determined by various factors originating from disease pathogens and parasites, vector species, human populations, and the environment;
b) In countries or regions nearing qualifying malaria elimination, a high proportion of cases are imported cases found among hard-to-trace migrants or dispersed mobile populations in remote border areas; and
c) The limited local CDC surveillance resources make the comprehensive and timely detection of malaria cases an often difficult and time-consuming exercise.

Funded by numerous external research grants [G1-G5], Liu has strategically built an interdisciplinary research team of experts in machine learning, data analytics, and computational epidemiology, and tackled the above challenges employing a systematic approach, by using fundamentally new machine learning methods for risk assessment in data-starved situations.

To infer malaria transmission, Liu's team has proposed a new framework, modelling three sources of risk: i) intra-region transmission risk (based on factors like population, temperature, rainfall, and elevation); ii) inter-region transmission risk (inferred as population mobility between regions); and iii) imported risk (based on population, elevation, and the distance to border). The proposed Poisson-regression-based model maximises a posterior solution for risk assessment via the Alternating Direction Method of Multipliers (ADMM) [P1]. To investigate the influence of the vector to intra-region transmission risk, the team used factors based upon the region's vectorial capacity (VCAP) (estimated using temperature and rainfall), population, infected-mosquito-to-human probability, and infected-human-to-mosquito probability to infer the risk by means of novel recurrent neural networks (RNNs) [P2] and Markov chain Monte Carlo (MCMC) [P3].

Beyond the physiological properties of the pathogens and hosts, the social contact of the host population is also important towards understanding and predicting the prevalence of infectious diseases. Unlike existing work that modelled static social contact, Liu's team considered dynamic social contact and proposed an epidemic-model-based tensor deconvolution framework to represent the spatio-temporal patterns of social contact as factors of the tensors based on multiple data sources, including surveillance data, socio-demographic census data, and physiological data from medical reports [P4].

To model the imported cases, a key component in the malaria elimination phase, Liu's team has developed a new method to infer the cross-border mobility patterns, incorporating various factors including population, historical infection case numbers, and socio-economic indices. Combined with the estimated VCAP, a heterogeneous diffusion network was constructed, and a maximum likelihood method was proposed for estimating imported risks [P5].

To achieve accurate and timely detection of malaria cases with limited resources, Liu's team has developed a Group Sparse Bayesian Learning (GSBL) method to identify key locations for active surveillance [P6]. The model which was learned using historical infection case numbers in different locations infers appropriately the numbers of future infection cases, with only less than one third of the locations being selected as the sentinel/observational sites.

(3) References to the research (indicative maximum of six references)

[P1] **Zhang, Y.**, **Cheung, W.K.W.**, and **Liu, J.***, "A unified framework for epidemic prediction based on Poisson regression," in ***IEEE Transactions on Knowledge and Data Engineering***, 27(11):2878-2892, 2015.

[P2] **Shi, B.**, **Liu, J.***, Zhou, X.N., and Yang, G.J., "Inferring Plasmodium vivax transmission networks from tempo-spatial surveillance data," in ***PLoS Neglected Tropical Diseases***, 8(2):e2682, 2014.

[P3] **Shi, B.**, **Tan, Q.**, Zhou, X.N., and **Liu, J.***, "Mining geographic variations of Plasmodium vivax for active surveillance: A case study in China," in ***Malaria Journal***, 14:216, 2015.

[P4] **Yang, B., Pei, H., Chen, H., Liu, J.***, and Xia, S., "Characterizing and discovering spatiotemporal social contact patterns for healthcare," in ***IEEE Transactions on Pattern Analysis and Machine Intelligence***, 39(8):1532-1546, 2017.

[P5] **Yang, B.**, Guo, H., Yang, Y., **Shi, B.**, Zhou, X.N., and **Liu, J.***, "Modeling and mining spatiotemporal patterns of infection risk from heterogeneous data for active surveillance planning," in *Proceedings of the 28th AAAI Conference on Artificial Intelligence* ***(AAAI 2014)***, pp. 493-499, 2014.

[P6] **Pei, H.**, Yang, B., **Liu, J.***, and Dong, L., "Group sparse Bayesian learning for active surveillance on epidemic dynamics," in *Proceedings of the 32nd AAAI Conference on Artificial Intelligence* ***(AAAI 18)***, pp. 800-807, 2018.

Key Research Grants:

[G1] **Liu, J.** (PI), "A Computational Method of Inferring Disease Diffusion Networks and Its Empirical Validation in Epidemiologic Surveillance," RGC/HKBU211212, 2013-2015, HK$700,000.

[G2] **Liu, J.** (PI), "Uncovering Spatiotemporal Patterns of Disease Diffusion through Data-driven Phylogeographic Inference," RGC/HKBU12202415, 2015-2019, HK$496,028.

[G3] Wan, X. (PI), **Liu, J.** (Co-I), "Characterizing the Disease Diffusion in Networks and Its Empirical Application," RGC/HKBU12202114, 2015-2017, HK$500,000.

[G4] **Liu, J.** (PI), "Modeling and Inferring Latent Diffusion Networks for Active Surveillance and Prediction of Infectious Diseases," RGC/HKBU12201318, 2019-2021, HK$692,318.

[G5] **Liu, J.** (PI), "Overcoming Data Heterogeneity, Dependency, and Noise: A Novel Spatio-Temporal Learning Framework," RGC/HKBU12201619, 2020-2022, HK$731,089.

(4) Details of the impact (indicative maximum 750 words)

With the novel machine learning methods for spatio-temporal risk assessment and prediction developed and demonstrated by Liu's team, the Department of Computer Science has strategically founded a Joint Research Laboratory with the most authoritative policymakers in China on malaria elimination, namely, the National Institute for Parasitic Diseases (NIPD) in the China CDC [S1]. The primary mission of this unique joint working platform is to enable HKBU researchers (Liu's team) to work directly with policymakers and practitioners (national, provincial, and city-level CDC's) as well as their counterparts in the regions. This effectively enables them to introduce and deploy changes in their respective policy guidelines and practices for the time-critical malaria elimination and post-elimination phases, in the following three focused geographical regions, which have the highest priority in achieving the targets of the *WHO Global Malaria Programme in Asia*, where complex transmission patterns, a high proportion of imported cases, and limited surveillance resources present serious challenges:

a) **The most malaria-endemic city in China – Tengchong:** Field implementation, adoption, and evidence-based practices by the NIPD and front-line practitioners in Tengchong;

b) **The key region for malaria elimination in China – the China-Myanmar border:** Field introduction of the developed technologies (for example, training of village doctors) on the China-Myanmar border for malaria case management; and

c) **The key region for global malaria elimination – Greater Mekong Subregion (GMS) and Southeast Asia (SEA):** Engaging policymakers at the national level in eight SEA/GMS countries and the WHO regional coordinators, to: i) define country-specific challenges in malaria control and surveillance; ii) identify priority (sub)regions for applying the HKBU technologies for their respective elimination and/or post-elimination campaigns; iii) onsite and offsite technical capacity building; and iv) formal adoption of the HKBU technologies into their national programmes/initiatives.

The work conducted by Liu's team to accelerate the pace of malaria elimination and eradication globally has several profound and far-reaching impacts and ramifications as evidenced below:

a) Elimination of malaria in Tengchong: Tengchong CDC has deployed the developed risk assessment methods, resulting in major improvements in timely surveillance and intervention.

Tengchong was the most malaria-endemic city in China during 2010-2012. It has 658,207 rural residents widely distributed across a large mountainous area of 5,845 square kilometers, and it shares its borders with Myanmar for 148 kilometers with over one million border crossings per year. However, surveillance resources are extremely limited and are comprised of only four local CDC staff members who possess the necessary know-how.

Tengchong CDC has used the methods developed by Liu's team to: i) identify high-risk locations; ii) skillfully allocate anti-malaria resources; and iii) develop a surveillance strategy for deployment. As a result, Tengchong enjoys the distinction of becoming the first China-Myanmar border city certified as malaria free (i.e., with zero indigenous cases) in 2016. This milestone was achieved four years ahead of China's malaria elimination target of 2020 [S2, S3]. Moreover, the number of malaria infection cases (including the imported cases) in Tengchong was reduced by 95% from 2010 to 2017, a 10.4% superior rate than the reduction observed in cities that did not adopt Liu's methods [S2].

b) Changes to China CDC's guidelines and practices: WHO has pointed out that addressing the risk of malaria carried by the cross-border population is crucial to eventually eliminating the disease and also maintaining the progress achieved in China. To proactively prevent the re-introduction of imported malaria cases, China CDC has built upon the success of malaria elimination in Tengchong, by endorsing and adopting Liu's methods into the guidelines for active malaria surveillance and anti-malaria resource allocation for all the cities and counties in the China-Myanmar border region [S4]. The practices have thus far achieved encouraging results in 2019: the seven towns selected out of eighteen towns in Tengchong managed to cover 77.8% of the imported cases during April to June, the peak months of case importation [S5, S6]. Mang and Zhenkang, two other China-Myanmar border cities, have similarly commenced using the practices since May 2019 [S7]. Moreover, the local CDC staff and village doctors use the mobile APP developed by Liu's team to facilitate their malaria case management.

c) Ongoing deployment in Bhutan, Cambodia, Sri Lanka, and Thailand: Greater Mekong Subregion (GMS) and Southeast Asia (SEA) are the focal points for global malaria elimination as the parasite resistance to artemisinin detected in these regions could completely reverse all the achievements of control and elimination efforts globally and lead to large-scale epidemics. With no new drug available, the only way to eliminate and stop the spread of artemisinin resistance to other parts of the world is to accelerate the pace towards malaria elimination and eventual eradication.

To transfer the developed methods for accelerating malaria elimination in the GMS and SEA countries, Liu's team has integrated them into an online AIM (AI-enabled Malaria control and prevention) tool [S8] and provided deployment planning, priority-specific situation analysis, context-aware technical training, and hands-on practice to the policymakers, public health officials, and practitioners from the WHO Malaria Mekong Elimination (MME) team, the Health Poverty Action (HPA), and the health authorities of eight GMS and SEA countries including Bhutan, Cambodia, India, Indonesia, Lao PDR, Sri Lanka, Thailand, and Vietnam. After rigorous evaluation, delegates from these countries have recognised the importance and effectiveness of the developed methods and tools in risk assessment and resource allocation [S8]. The health authorities of Bhutan, Cambodia, and Sri Lanka have officially planned to adopt and implement the HKBU-developed methods and tools to tackle respective country-specific challenges. The plans have covered almost all the epidemiological phases of malaria elimination [S9]. In phase-order, the plans are:

1) **Control phase:** The Technical Bureau of the National Malaria Center in Cambodia's Ministry of Health has decided to use AIM to establish an early warning system. This will predict the malarial vector capacity and assess the malaria transmission risk in various districts of Stung Treng, Ratanakiri, and Mondulkiri provinces. These areas continue to remain in the intensified control phase.
2) **Elimination phase:** The Royal Center for Disease Control in Bhutan has decided to adopt AIM to identify high-risk village groups in the three most malaria-endemic districts, Sarpang, Samtse, and Samdrup Jongkhar, for context-aware case surveillance in the elimination phase.
3) **Re-introduction Prevention phase:** The Anti Malaria Campaign of the Ministry of Health in Sri Lanka has decided to adopt AIM to assess the malarial re-establishment risks in Sri Lanka.

The WHO MME team and the HPA have also collaborated with Liu's team to apply the AIM technology to malaria risk assessment as well as early warning for all GMS countries [S10].

(5) Sources to corroborate the impact (indicative maximum of 10 references)

[S1] Strategic Collaboration Agreements between Computer Science Department of HKBU and NIPD of China CDC (Phase 1, Phase 2, and Phase 3)
[S2] Contribution to Malaria Elimination in Tengchong, the China's Most Malaria-endemic City
[S3] Certification of Tengchong's Achievement in Malaria Elimination in 2016
[S4] Adoption of HKBU's Methods in China's Implementation Programme for Active Malaria Surveillance in the China-Myanmar Border Region
[S5] Adoption of HKBU's Active Surveillance Strategy by Tengchong Bureau of Health
[S6] Effectiveness of HKBU's Active Surveillance Strategy in Tengchong
[S7] Adoption of HKBU's Active Surveillance Strategy by Mang CDC and Zhenkang CDC in the China-Myanmar Border Region
[S8] Engagements with GMS/SEA Countries, WHO MME, and HPA for Deployment Planning, Situation Analysis, and Context-aware Technology/Know-how Transfer
[S9] Adoption of HKBU's AIM Tool by Royal Centre for Disease Control, Ministry of Health, *Bhutan*; National Center for Parasitology, Entomology & Malaria Control, Ministry of Health, *Cambodia*; and Anti Malaria Campaign, Ministry of Health, *Sri Lanka*
[S10] Adoption of HKBU's AIM Tool by WHO and HPA for Malaria Control/Elimination in GMS