

Infectious Disease Surveillance IT Platform

Concept Paper



Version 1.0 September 7, 2021

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Issue History

Issue Number	Review and Approval	Description of Version	Date
1.0	Lim Teck Sin	Original	May 28, 2008

Distribution List

Copy Number	Recipient
1	Project Filing - KOOPrime
2	Duke University
3	Novartis Institute of Tropical Diseases

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SECTION 1.0 EXECUTIVE SUMMARY

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SECTION 2.0 INTRODUCTION

The **DengueInfo Web Portal (DengueInfo)** was conceived and setup in Sep 2005 via a research collaboration between Novartis Institute of Tropical Diseases and Genome Institute of Singapore to serve as repository for the dengue virus genomic and clinical information. In 2007, the collaborative effort was taken to a new height by KOOPrime which provided a robust and scalable platform. The portal was subsequently launched globally on 7th Nov 2007 at the congress of the Asia Pacific Society for Medical Virology held in New Delhi.

2.1 What Is DENGUEINFO?

DengueInfo facilitates basic research in key aspects of dengue biology and advance anti-viral and vaccine research by integrating the growing number of dengue virus genome sequences with relevant literature and curated epidemiological information

The portal is now one of the flagship resources for the global dengue community, providing standardized and quality information, with hundred of thousands of hits on the portal yearly.

An important set of contents that users from various countries tap on is the dengue genome sequences obtained from viruses isolated in Singapore via the Early Dengue (EDEN) a longitudinal prospective study initiated by members of the Singapore Dengue Consortium. Collaborations with researchers from other countries in the region through have further increased the number full sequenced viruses. The EDEN sequences are particularly valuable, given that they are already mapped with anonymised clinical data. The vision of the DengueInfo is that the database will be further enriched by users around the

3.1 GIS frontend and generic 'geographical' database

While DengueInfo has demonstrated its value in the archival and sharing of data, it needs a powerful front-end to present data in a geographical manner, given that this will be important in the understanding of how infectious diseases are communicated among the pathogens, vectors and human subjects. Secondly, while DengueInfo collects both clinical and genomic data, there is a gap in the availability of generic 'geographical' and 'social' parameters.

Initial work has been done by Nanyang Polytechnic (NYP) to correlate the data on dengue incidence in Singapore with various physical geographic features of the island.

NYP harvests geographical data with respect to HDB estates, population distribution, and vegetation from various internet based sources. The data are curated manually, for example by using Google Earth as a guide. While the information are presently limited to Singapore, layers of such data are already developed for popular "GIS" software tools like Google Map and Microsoft Virtual Earth.

An objective will be to integrate such geographical features and visualization frontend so that novel and important correlations can be rapidly and timely discovered between such geographical data and those existing in DengueInfo.

3.2 Laboratory integration for rapid alert of outbreaks

There is a strong drive in recent months by Singapore to adopt the Health Level 7 (HL7), a standard specified to facilitate the transfer / exchange of data residing on disparate computer systems in health care settings. Given this initiative, there is opportunity for DengueInfo to integrate directly with various hospital / commercial laboratories via HL7 so that test results can be readily extracted from instruments, mapped with anonymised patient data extracted from hospital in-house Electronic Medical Record systems and warehoused in DengueInfo for surveillance purpose.

KOOPrime recently completed such a laboratory data extraction and integration work using HL7 for a Hepatitis B clinical cohort system deployed at National University Hospital and Centre for Molecular Medicine.

The reliability of data will be enhanced via such an approach, because

- errors that may occur via manual submission of clinical data are reduced
- laboratory test results are used for studies instead of clinical observations that maybe subjective in nature

The response time for DengueInfo to alert potential outbreaks will be shortened, because

- the data processing process is now shortened with the bypass of human intervention
- the aggregation of data across multiple laboratories will bring up patterns much faster

Such laboratory based data, together with pathogen and vector data can be visually presented as layers on the GIS systems adopted (section 3.1).

In addition, diagnostic rules can also be coded on clinical decision support system (e.g. an expert system deployed by KOOPrime for a project on Temporal Mandibular Diseases) so that alerts can be triggered automatically once certain drugs / chemicals / test kits consumption patterns or thresholds are exceeded.

3.3 Medical Ontologies

Suitable medical ontologies system (e.g. from Apelon, HealthLanguage) are to be identified and adopted to standardize the clinical terminologies use across the various data collection sites in hospitals and laboratories.

It is only when terminologies (e.g. naming and coding of diseases, organisms, etc.) are standardized that data can be exchanged readily between the various key healthcare organizations in Singapore.

3.4 Algorithm for 'Ring Fencing' of hotspots

A novel 'Digital Ring Fence' (DRiF) strategy was developed by an advisor of KOOPrime (Prof KC Lun) to corral the spread of infection by isolating and monitoring individuals that have come into contact with infected individuals / pathogens / vectors.

This approach involves the mathematical investigation of the spread and control of infectious diseases, with DRiF providing overall risk of infection from its epicenter. By applying the DRiF strategy, areas of population concentrations can be readily identified to direct outbreak containment efforts.

An objective will be to map the DRiF on GoogleMap as another visual layer so that DengueInfo will be able to guide the rapid execution of intervention protocols against outbreaks.