

## DEEP LEARNING APPLICATIONS FOR PREDICTING DENGUE FEVER OUTBREAK

**Sumiko Anno<sup>1</sup>, Takeshi Hara<sup>2</sup>, Hiroki Kai<sup>3</sup>, Yi Chang<sup>4</sup>, Ming-An Lee<sup>5</sup>, Kei Oyoshi<sup>6</sup>, Yosei Mizukami<sup>6</sup> and Takeo Tadono<sup>6</sup>**

<sup>1</sup>Shibaura Institute of Technology, Japan

<sup>2</sup>Gifu University, Japan

<sup>3</sup>Remote Sensing Technology Center of Japan, Japan

<sup>4</sup>National Cheng Kung University, Taiwan

<sup>5</sup>National Taiwan Ocean University, Taiwan

<sup>6</sup>Japan Aerospace Exploration Agency, Japan

The number of dengue fever patients has increased in Taiwan in recent years, and measures are urgently needed to prevent dengue fever outbreaks. The mechanisms underlying the outbreaks must be clarified in order to develop a predictive model and take appropriate precautions. Unfortunately, these mechanisms are complex, and the factors involved in the generation, propagation, and spread of dengue fever have yet to be fully elucidated. However, the outbreaks are known to be influenced by the interplay of factors that include rising temperatures, including rising sea surface temperatures (SSTs); increasing rainfall due to global warming; and rapid urbanization. These factors contribute to inadequate water and sewage treatment systems. Subsequently, water storage containers, as well as discarded automobile tires and other containers that fill with rainfall, allow mosquito breeding and vector dispersion. In addition, rising temperatures, rapid urbanization lead to human displacement and travel, contribute to the spread of dengue virus-infected mosquitoes. Here I present a conceptual framework that helps clarify how these factors contribute to dengue fever outbreaks in Taiwan. This framework uses satellite remote sensing data and deep learning, which is a machine learning technique, as well as our current, ongoing research findings.

### Recent Publications

1. Sumiko Anno (2016) *Gene-environment interaction analysis: methods in bioinformatics and computational biology*, Pan Stanford Publishing Pte. Ltd., ISBN 9789814669634.
2. Sumiko Anno, Keiji Imaoka, Takeo Tadono, Tamotsu Igarashi, Subramaniam Sivaganesh, Selvam Kannathasan, Vaithehi Kumaran, Sinnathamby Noble Surendran (2015) *Space-time clustering characteristics of dengue based*

on ecological, socio-economic, and demographic factors in northern Sri Lanka, *Geospatial Health*, 10(376):215-222.

3. Sumiko Anno, Keiji Imaoka, Takeo Tadono, Tamotsu Igarashi, Subramaniam Sivaganesh, Selvam Kannathasan, Vaithehi Kumaran, Sinnathamby Noble Surendran (2014) *Assessing the temporal and spatial dynamics of the dengue epidemic in Northern Sri Lanka using remote sensing data, GIS and statistical analysis*. *Journal of Geophysics & Remote Sensing* 3(4):1-5.
4. Sumiko Anno, Kazuhiko Ohshima, Takashi Abe, Takeo Tadono, Aya Yamamoto, Tamotsu Igarashi (2013) *Approaches to Detecting Gene-Environment Interactions in Human Variation Using Genetic Engineering, Remote Sensing and GIS*. *Journal of Earth Science and Engineering* 3(6):371-378.
5. Sumiko Anno, Kazuhiko Ohshima, and Takashi Abe (2010) *Approaches to understanding adaptations of skin color variation by detecting gene-environment interactions*. *Expert Review of Molecular Diagnostics* 10(8):987-991.

### Biography

Sumiko Anno is an Associate Professor of Shibaura Institute of Technology. Her research is interdisciplinary, ranging from Molecular Biology to the Earth Sciences, and uses Genetic Engineering, Remote Sensing, and Geographic Information System Technologies. She has received three research achievement awards in Japan and in other countries, including an award for the work that was published in 2016 as *"Gene-Environment Interaction Analysis: Methods in Bioinformatics and Computational Biology"*. She is currently interested in exploring the application of artificial intelligence to public health issues.

annou@sic.shibaura-it.ac.jp