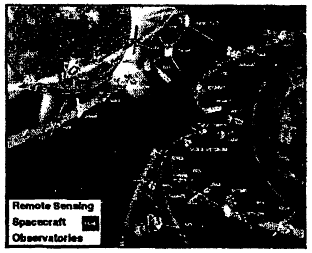
Simulation of Malaria Transmission among Households in a Thai Village using Remotely Sensed Parameters

Richard Kiang (richard.kiang@nasa.gov), Farida Adimi, NASA Goddard Space Flight Center, Greenbelt, MD 20771
Gabriela Zollner, Russell Coleman, Walter Reed Army Institute of Research, Silver Spring, MD 20910



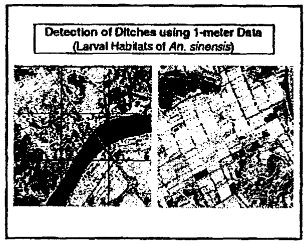
Malaria Modeling and Surveillance is a project in the NASA Applied Sciences Public Health Application Program. NASA satellite data, climate model output, ground measurements, and commercial satellites data are used for predicting malaria transmission risk. Thailand and Indonesia are our main application areas.

OBJECTIVES		BENEFITS
Detection of larval habitats *Textural-contextual classification*	→	Applying larval control as a preventive measure
Prediction of current and future endemicity *Neural network methods*	→	Strengthening and mobilizing public health support
Identification of key factors that sustain or promote transmissions *Agent-based discrete event simulation*	→	Cost-effectively curtailing malaria transmission

COLLABORATORS WHO SEARO, Thai MOPH, Indonesian MOH, Mahidol University, AFRIMS, NAMRU-2, WRAIR

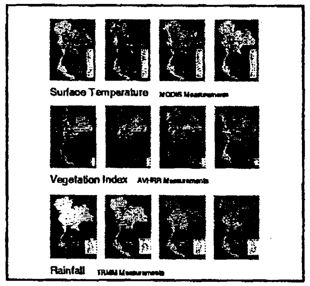
Our three objectives, the benefits, and the main techniques used are shown.

Remote sensing data, climate model output, and ground station measurements used in this project include those from TRMM, MODIS, ASTER, AVHRR, GMAO CGCM, SIESIP, GPCC and Ikonos.

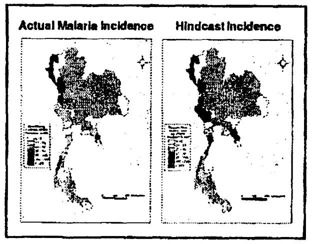

Detection of Ditches using 1-meter Data (Larval Habitats of *An. sinensis*)

An example for Objective 1:

Irrigation and drainage ditches are important larval habitats of *Anopheles sinensis*. Our textural-contextual classification techniques can accurately identify these potential larval habitats. This particular test site is in South Korea.



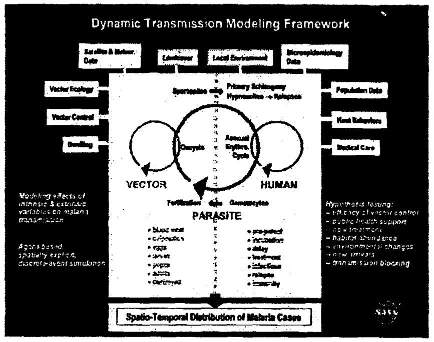
Our risk prediction model uses meteorological parameters derived from satellite and ground-based measurements. Surface temperature is from MODIS (Moderate Resolution Imaging Spectroradiometer), vegetation index is from AVHRR (Advanced Very High Resolution Radiometer) and MODIS, and precipitation is from TRMM (Tropical Rainfall Measuring Mission). Distributions of these parameters for the 4 Thailand seasons are shown.



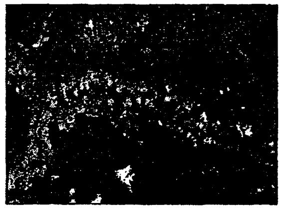
An example for Objective 2:

Neural network methods are used for forecasting or prediction, hindcasting is used to measure the performance. In this example, the left figure shows the actual average monthly incidence in 2001. And the right figure shows the hindcast one. The two are in good agreement.

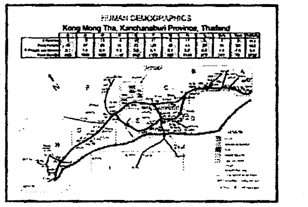
This poster mainly concerns Objective 3.



Our dynamic transmission model takes into account of the detailed interactions among the vector life cycle, sporogonic cycle, and human disease cycle, under the influence of intrinsic and extrinsic factors. Output of the model includes spatio-temporal distribution of malaria cases. Transmission hypotheses can be tested with this model and the key factors that promote or sustain transmission can be identified.



Malaria surveillance study was conducted over 5 years (Jun 99 – Jan 04) at Ban Kong Mong Tha, an AFRIMS intensive study site in western Thailand. Blood films from approximately 450 persons were collected each month. Microscopy and PCR were used to identify malaria species. The field data are used to validate our transmission model.



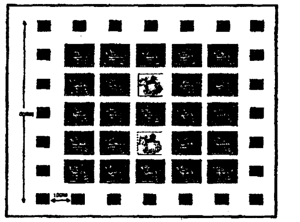
Kong Mong Tha was divided into 9 grids (from A to I). Attempt was made to incorporate an equal number of houses in each grid.

Demographic data were collected in each grid, including house type, no. inhabitants, age, sex.

At the end of the study there were 750 people in Kong Mong Tha, of which 700 were enrolled in our study.

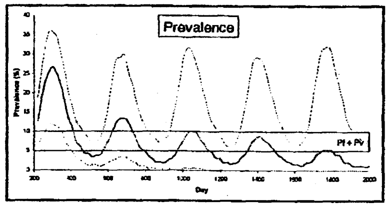
There was an average of 6 people per house, for the 120 houses in the village.

Major malaria vector species and their larval habitats in Kong Mong Tha. *A. minimus* is the most prevalent species, followed by *A. maculatus* and *A. barbirostris*. Among the anophelines collected from human landing catches, 50% were *A. minimus*, 20% were *A. maculatus*, 10% were *A. barbirostris*.

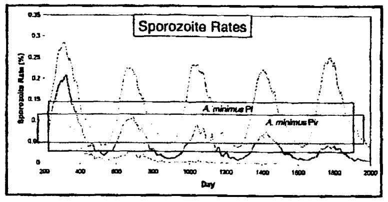


An example for modeling is given here – a hamlet with 23 houses and 2 cattle sheds, which are surrounded by 24 groups of larval breeding sites. Each household has 4 residents; and each resident has his or her own activity and immunity. This hypothetical hamlet is approximately 1/7 of a real test site. Although we can model the entire village, we still use this hamlet for quick hypothesis testing.

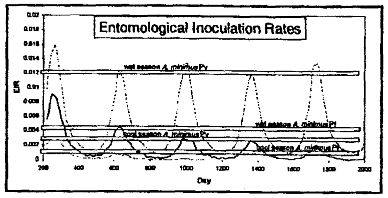
Comparison of Modeled Transmission Indicators With Field Measurements



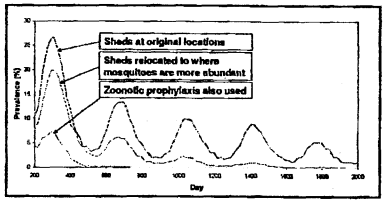
Modeled prevalence for 3 levels of mosquito populations. The blue time series is the nominal baseline. The shaded band shows the range of combined Pf and Pv prevalence based on blood films collected at the test site. We assume active case detection is always used.



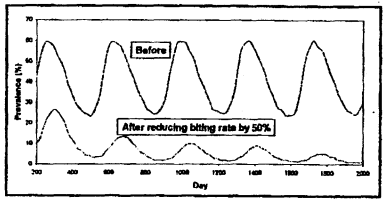
The modeled sporozoite rate is consistent with the measured rates for Pf and Pv. The measured rate, for *A. minimus*, is the binomial probability with at least one positive mosquito in a pool. Only the rates for *A. minimus* are shown.



Modeled EIR, expressed in the number of infective bites per person per day, is compared with the measured EIR in wet and cool seasons.



Well placed farm animal sheds and zoonotic prophylaxis may be a very cost effective way, relative to other vector control methods, for curtailing malaria transmission.



Bednets, personal protections and improved dwelling can significantly reduce malaria transmission.

SIMULATION OF MALARIA TRANSMISSION AMONG HOUSEHOLDS IN A THAILAND VILLAGE USING REMOTELY SENSED PARAMETERS

Richard K. Kiang [1] , Farida Adimi [1] , Gabriela E. Zollner [2] , Russell E. Coleman [2]
[1] NASA Goddard Space Flight Center, Greenbelt, MD, United States, [2] Walter Reed Army Institute of Research, Silver Spring, MD, United States

We have used discrete-event simulation to model the malaria transmission in a Thailand village with approximately 700 residents. Specifically, we model the detailed interactions among the vector life cycle, sporogonic cycle and human infection cycle under the explicit influences of selected extrinsic and intrinsic factors. Some of the meteorological and environmental parameters used in the simulation are derived from Tropical Rainfall Measuring Mission and the Ikonos satellite data. Parameters used in the simulations reflect the realistic condition of the village, including the locations and sizes of the households, ages and estimated immunity of the residents, presence of farm animals, and locations of larval habitats. Larval habitats include the actual locations where larvae were collected and the probable locations based on satellite data. The output of the simulation includes the individual infection status and the quantities normally observed in field studies, such as mosquito biting rates, sporozoite infection rates, gametocyte prevalence and incidence. Simulated transmission under homogeneous environmental condition was compared with that predicted by a SEIR model. Sensitivity of the output with respect to some extrinsic and intrinsic factors was investigated. Results were compared with mosquito vector and human malaria data acquired over 4.5 years (June 1999 – January 2004) in Kong Mong Tha, a remote village in Kanchanaburi Province, western Thailand. The simulation method is useful for testing transmission hypotheses, estimating the efficacy of insecticide applications, assessing the impacts of nonimmune immigrants, and predicting the effects of socioeconomic, environmental and climatic changes.