Current Approaches to Modeling Vector-Borne Diseases Transmission: *A Study in the Tropics*

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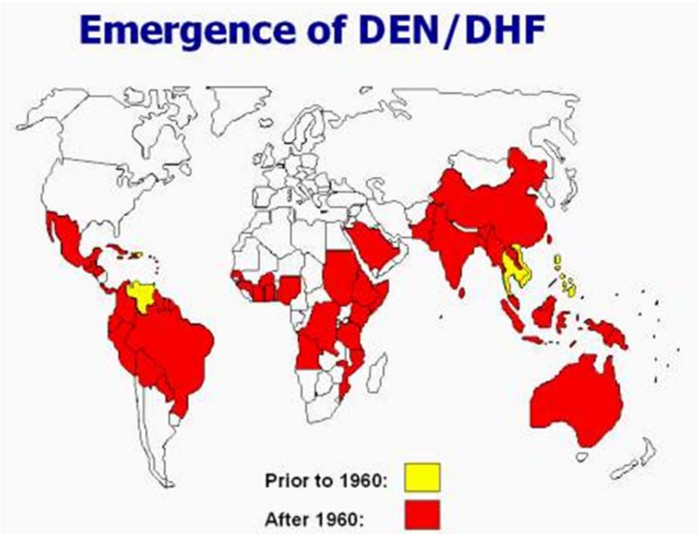
Overview

- Dengue in Indonesia
  - Time series regression (ARIMA)
- Malaria
  - Vector habitat classification (Korea)
  - Neural Networks (Thailand and Indonesia)
  - Agent-based simulation (Thailand)
  - Biological compartmental model

Dengue

- Endemic in more than 110 countries
  - Tropical, subtropical, urban, peri-urban areas
- Annually infects 50 – 100 million people worldwide
- 12,500 – 25,000 deaths annually
- Symptoms: fever, headache, muscle and joint pains, and characteristic skin rash (similar to measles)
- Primarily transmitted by *Aedes* mosquitoes
  - Live between 35°N - 35°S latitude, >1000m elevation
- Four serotypes exist
  - Infection from one serotype may give lifelong immunity to that serotype, but only short-term to others
  - Secondary infection increases the severity risk

Dengue Geographic Spread



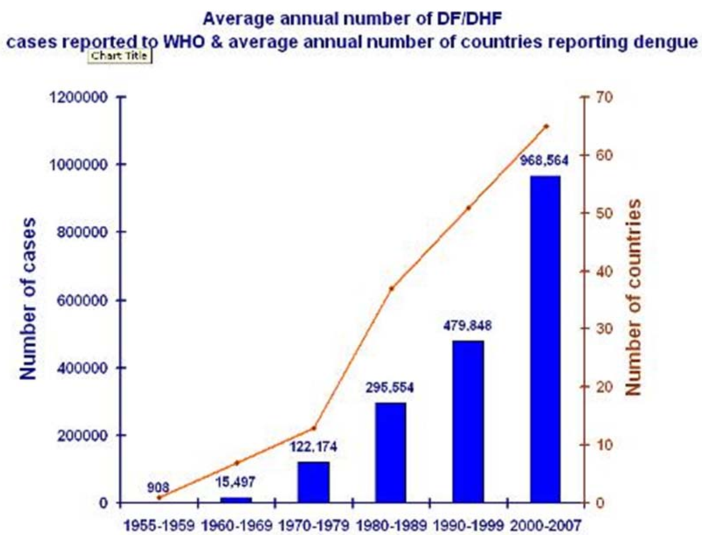
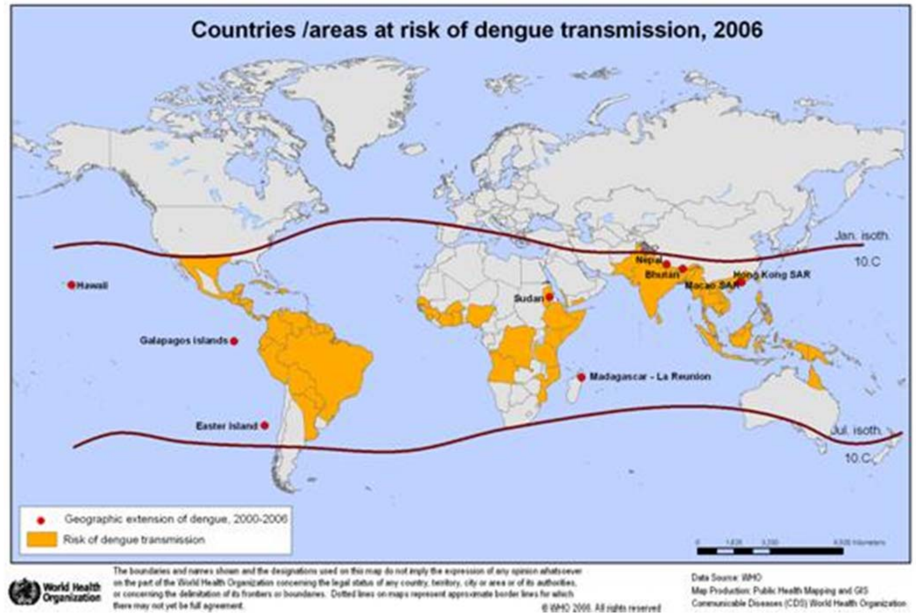
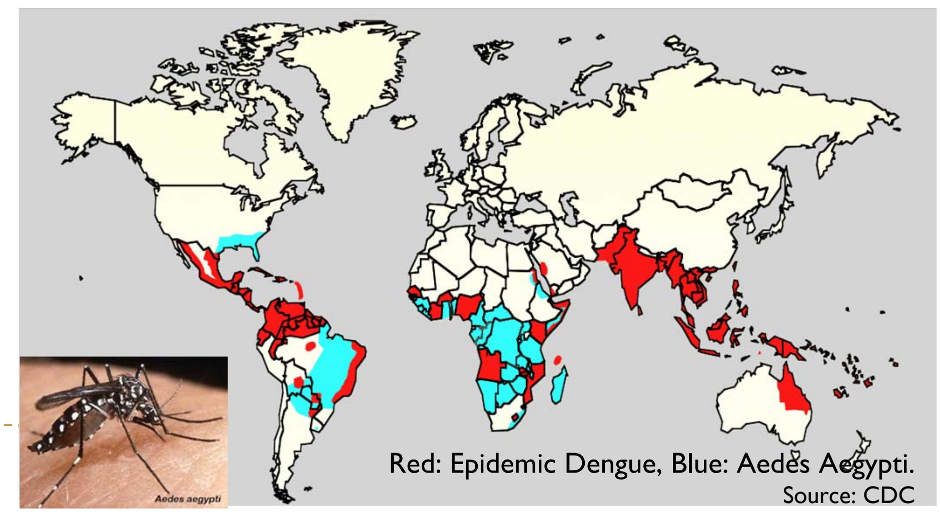


Image source: WHO – Global Alert and Response – Impact of Dengue

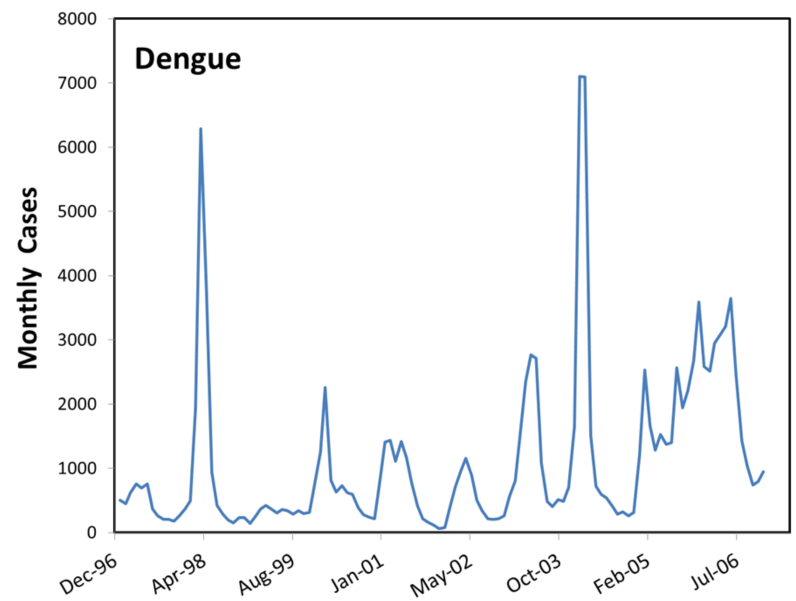




Red: Epidemic Dengue, Blue: Aedes Aegypti.
Source: CDC

Dengue In Indonesia

- First reported in 1968 in 2 provinces
- 10,000 – 25,000 inter-epidemic background cases annually
- Secondary infection is significant
- Dengue peak typically coincides with rainy season
- Population growth and unplanned urbanization may contribute to the increase in dengue cases
- Cost Indonesia ~$363 million annually
  - ~$40 million in medical expenses



Data source: Indonesia Ministry of Health

Dengue In Indonesia
ARIMA Analysis

- Auto-Regressive Integrated Moving Average
  - Class of time series regression technique
  - Developed by Box-Jenkins (1970)
- Data characterized by strong auto-correlation
  - Violates Ordinary Linear Regression Assumption
- Accounts seasonality
- Assume ***stationary*** series
  - Constant mean and variance across time
    - *Differencing*: Regular $z(t) = y(t) - y(t-1)$, Seasonal $z(t) = y(t) - y(t-s)$, where s is seasonality period
    - *Transformation*: logarithmic, square root

Dengue in Indonesia
ARIMA Analysis

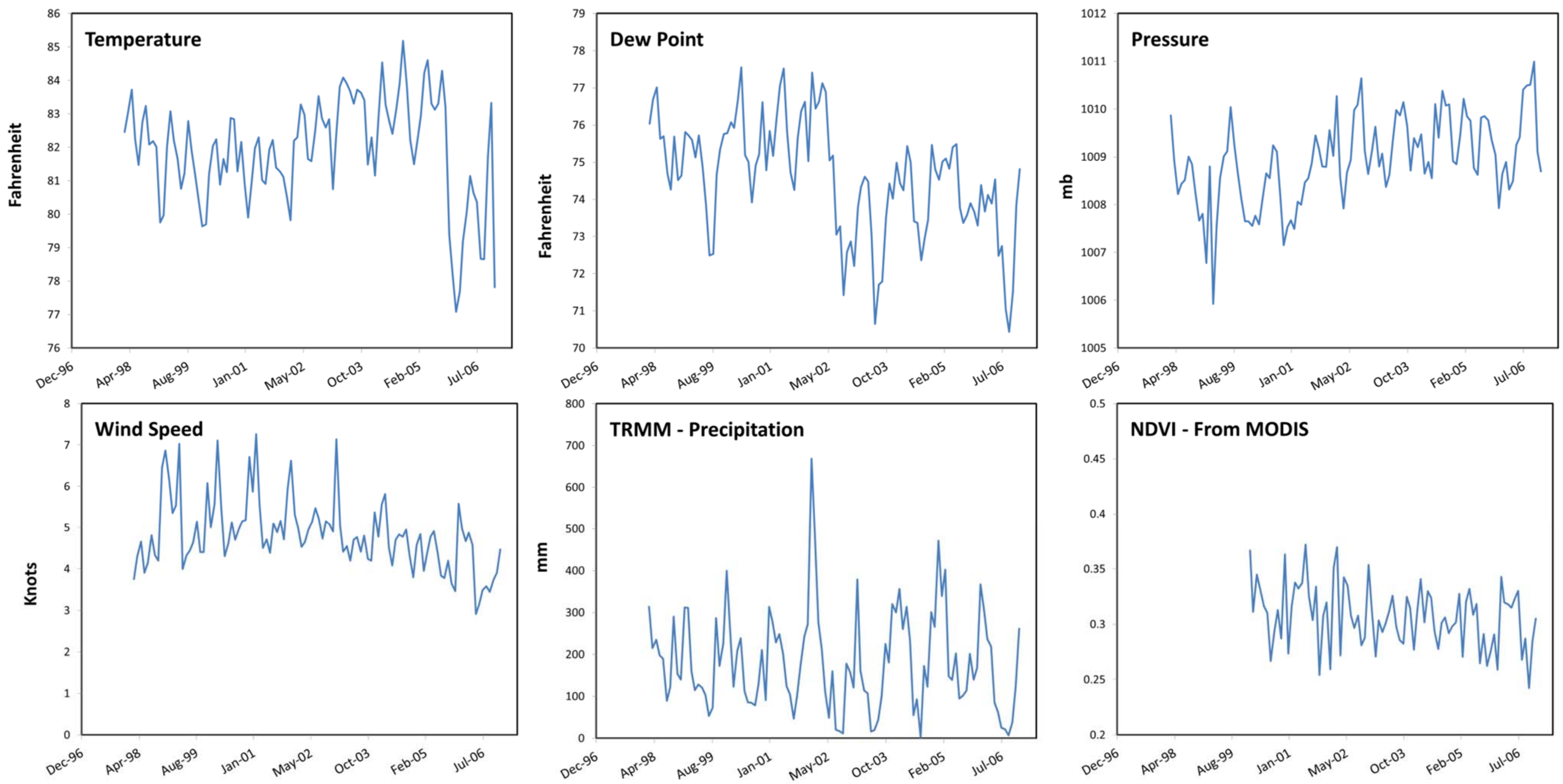
- General formulation: ARIMA(p,d,q)
  - p: autoregressive order
  - d: differencing order
  - q: moving average order (lagged error)
- *Let*
  - Y_t = response variable (dependent variable)
  - $Z_t = Z_t - Z_{t-1} - \ldots - Z_{t-d}$
- Then $Z_t + \phi_1 Z_{t-1} + \phi_2 Z_{t-2} + \ldots + \phi_p Z_{t-p} = \mu + \theta_1 \varepsilon_{t-1} + \theta_2 \varepsilon_{t-2} + \ldots + \theta_q \varepsilon_{t-q}$

$$Z_t + \sum_{i=1}^{p} \phi_i Z_{t-i} = \mu + \sum_{j=1}^{q} \phi_j \varepsilon_{t-j}$$

- Multivariate ARIMA
  - Covariate lag order determined through cross-correlation function

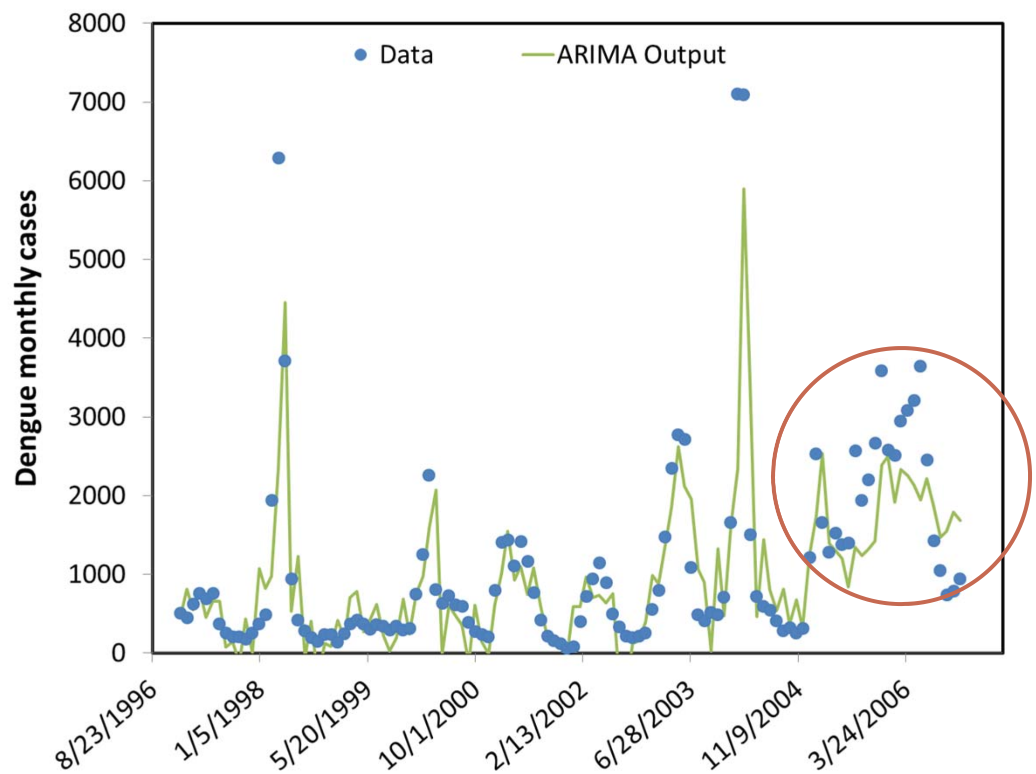
Dengue in Indonesia
ARIMA Analysis

- Environmental variables used



Dengue in Indonesia
ARIMA Analysis

- Best model output
- Environmental variable included as input: TRMM and Dew Point
- Peak timing can be modeled accurately up to year 2004
- Vector control effort by the local government started in early 2005



Malaria

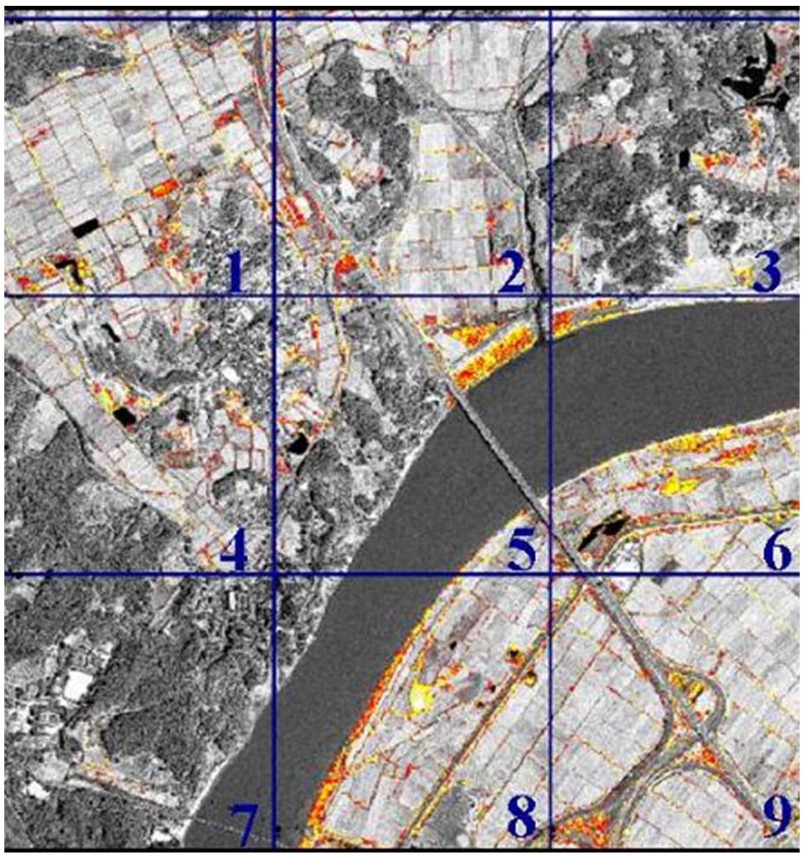
- 300 – 500 million cases per year worldwide
- 1-3 million deaths per year
  - ~ 1 death every 30 seconds
- 40% of the world's populations at risk
- 35 countries contribute to 98% of global malaria deaths
  - 30 in sub-Saharan Africa, 5 in Asia
- Highest risks
  - Children, pregnant women, anyone with depressed immunoresponse
- ACT is becoming less sensitive
- Climate change may cause outbreaks in previously unaffected regions

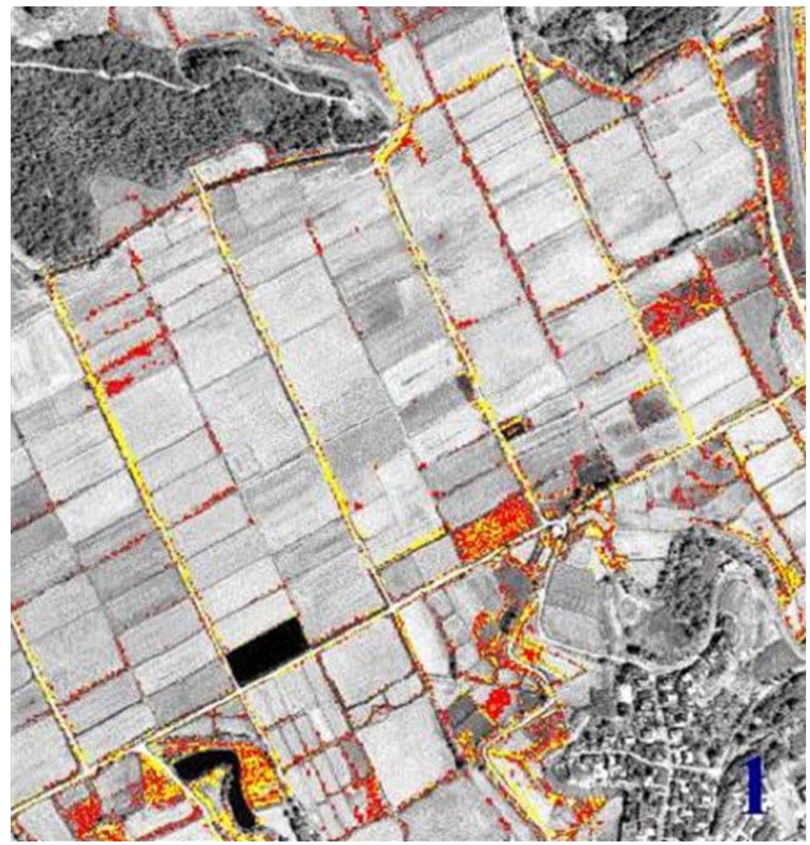
Malaria in Korea

- Malaria caused by *P.vivax*
  - Eradicated from Korea ~30 yrs ago
  - Re-emerge in North and South Korea in 1993
- Study area
  - US Army's Camp Greaves in South Korea (N. Kyunggi Province)
  - 43 sample sites, predominant habitats:
    - Rice fields (26 sites) and ditches (13 sites)
  - Predominant species: *Anopheles Sinensis*
- Study objective
  - Identify potential *Anopheles Sinensis* larval habitat (irrigation and drainage ditches) so as to aid vector control effort

Malaria in Korea
Larval Habitat Identification

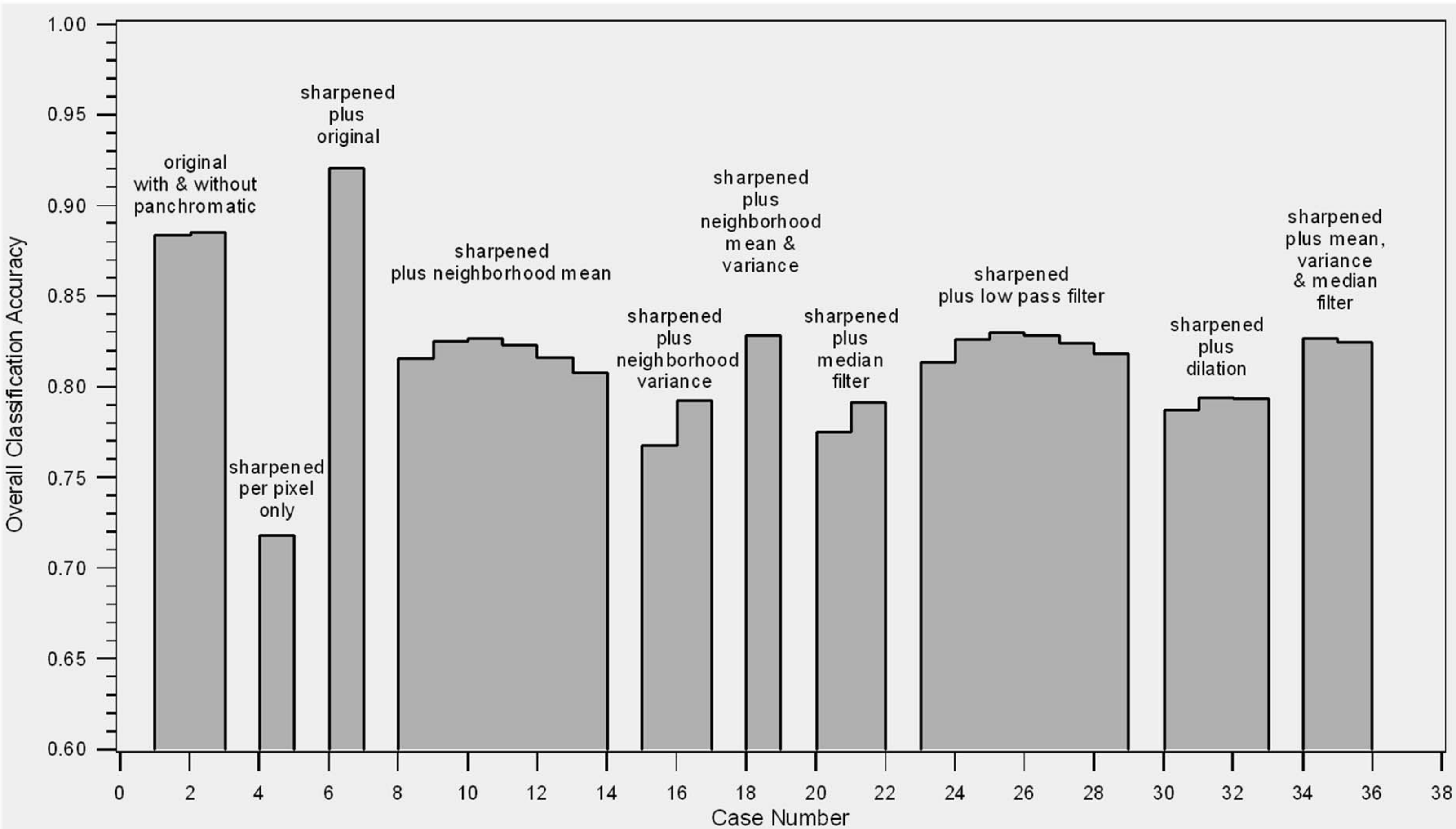
- Classification using pan-sharpened 1-m resolution IKONOS data on a 3.2 x 3.2 km test site





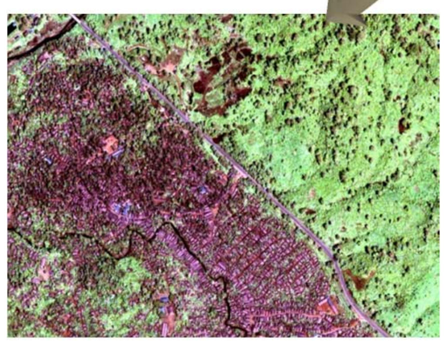
Malaria in Korea
Larval Habitat Identification

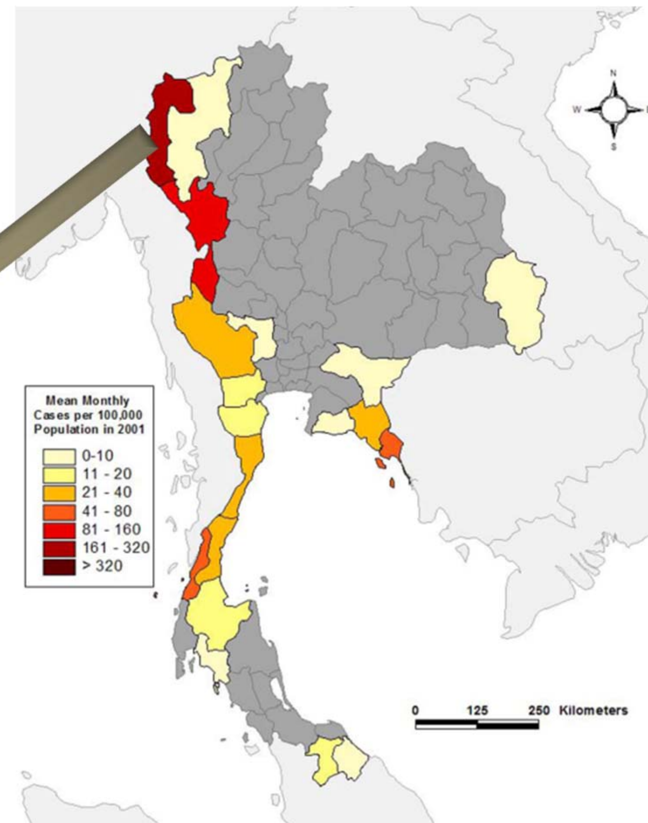
- Classification accuracy



Malaria in Thailand

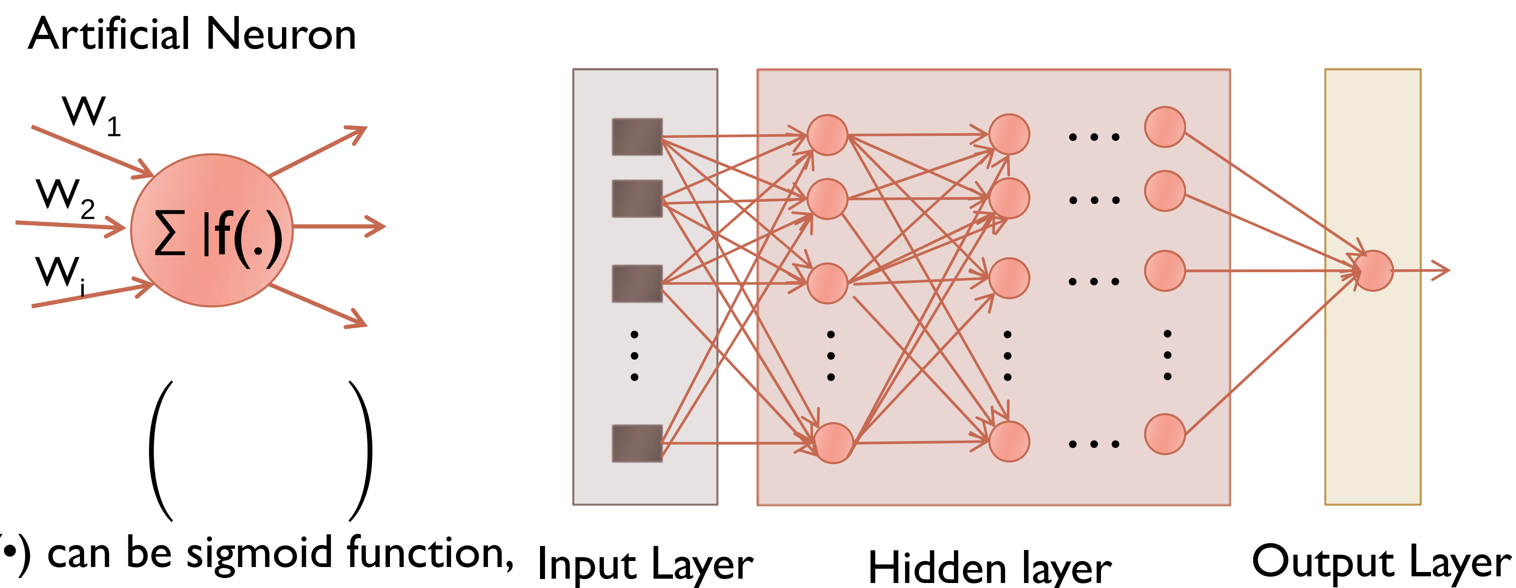
- Leading cause of morbidity and mortality in Thailand
- ~50% of population live in malarious area
- Most endemic provinces are bordering Myanmar & Cambodia
  - Significant immigrant population
  - Mae La Camp
    - Largest refugee camp
    - >30,000 population





Malaria in Thailand
Neural Network Analysis

- Objective: to predict malaria cases in endemic provinces using environmental parameters
- Neural Network
  - Artificial-intelligence method that mimic the functioning of brain



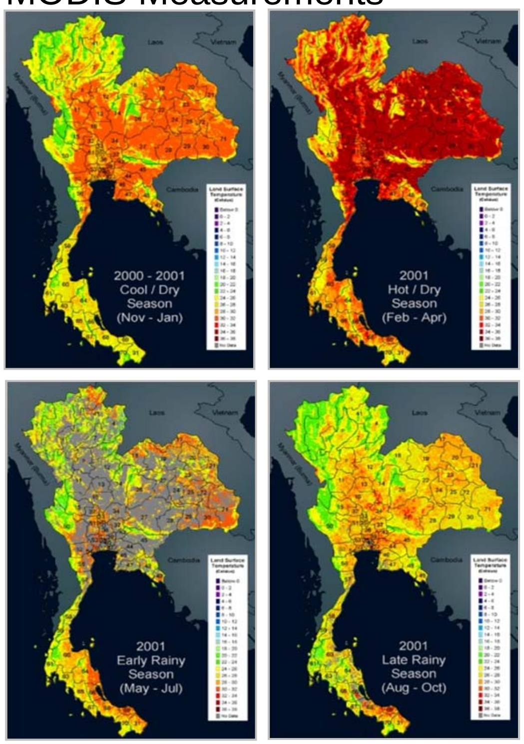
f(•) can be sigmoid function, radial basis function, etc

  - Network was trained using backpropagation

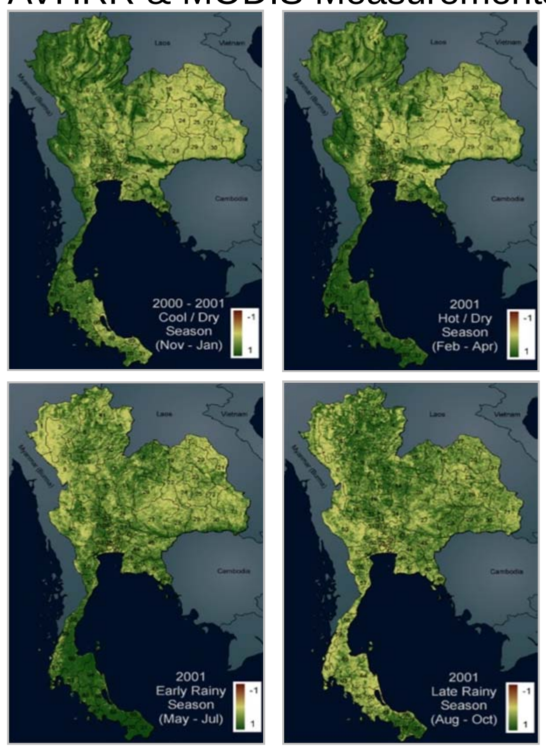
Malaria in Thailand
Neural Network Analysis

- Satellite-observed meteorological & Environmental Parameters for 4 Thailand seasons

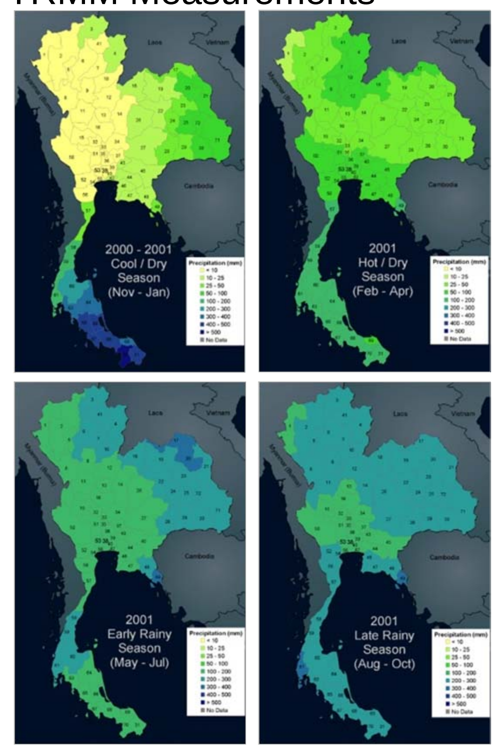
Surface Temperature
MODIS Measurements



Vegetation Index
AVHRR & MODIS Measurements



Rainfall
TRMM Measurements

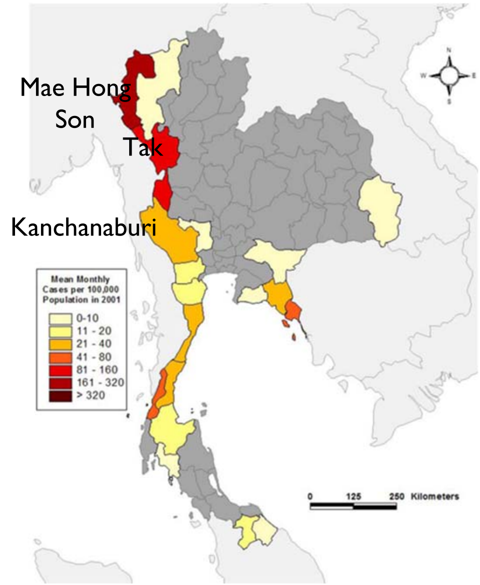


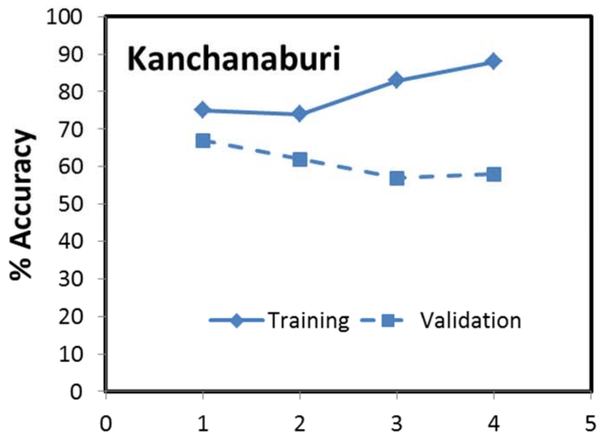
Malaria in Thailand
Neural Network Analysis

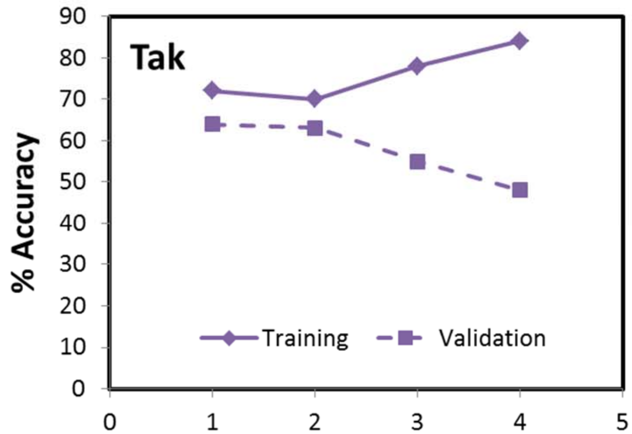
- Training and validation accuracy

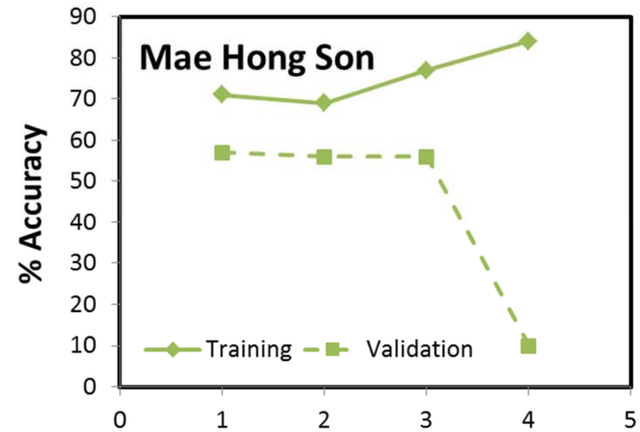
	Input	Hidden Layer	Hidden Node
Model 1	t, T, P, P (lag 1), H, V	1	1
Model 2	t, P, P (lag 1), H, V	1	1
Model 3	t, T, P, P (lag 1), H, V	1	2
Model 4	t, T, P, P (lag 1), H, V	1	3

t = time, T = temperature, P = precipitation, H = humidity, V = NDVI

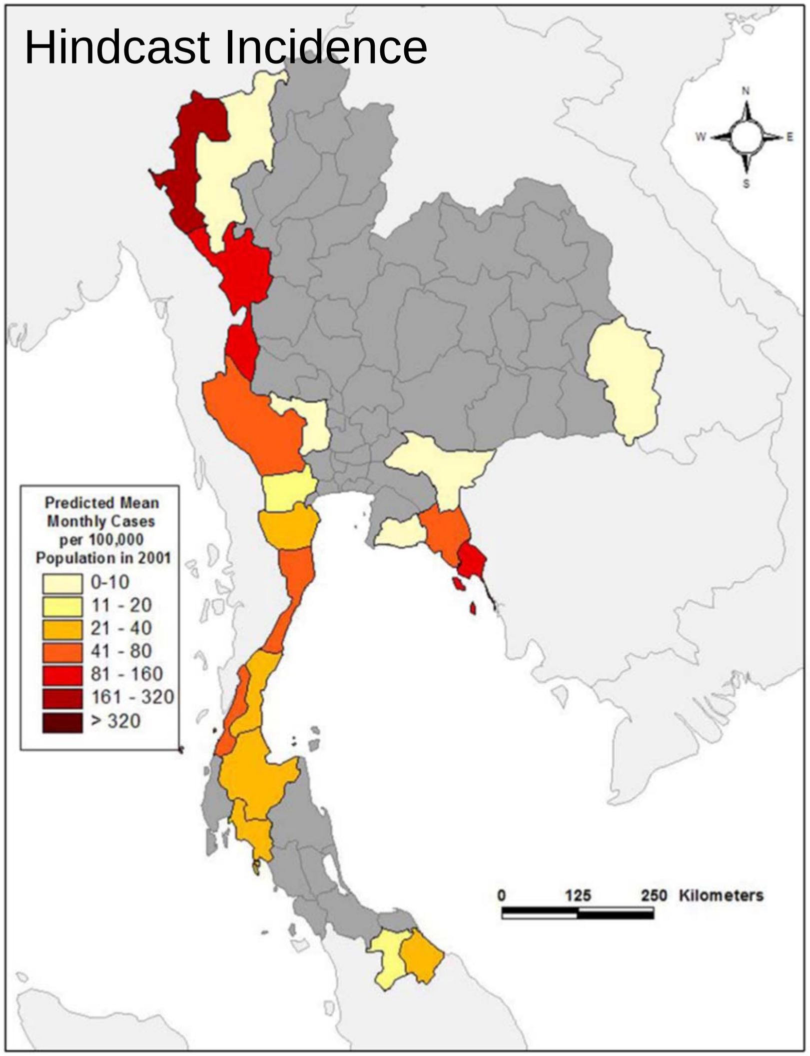


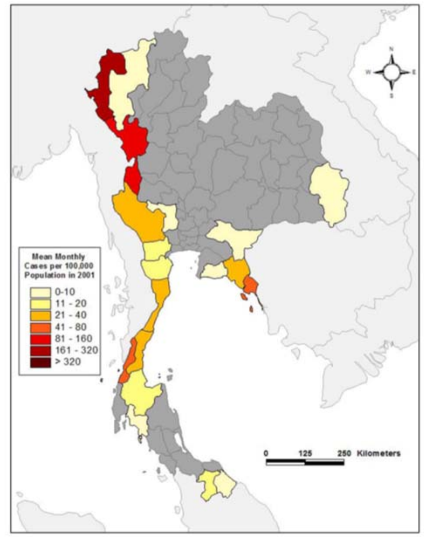




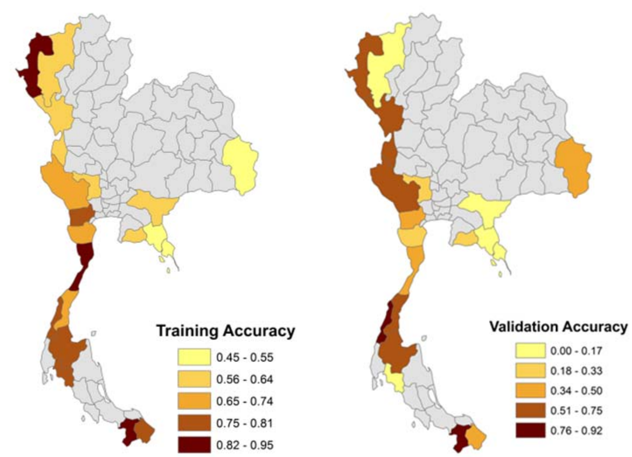


Malaria in Thailand
Neural Network Analysis



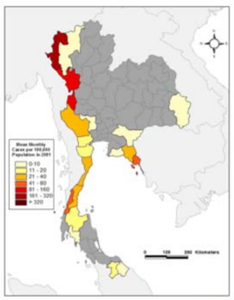


Actual Malaria Incidence



Malaria in Thailand
Agent-Based Simulation

- Kong Mo Tha (KMT) village, Kanchanaburi
- In Collaboration with AFRIMS and WRAIR
- Malaria surveillance study (1999 – 2004)
  - Blood films from ~450 people per month
  - Larval and adult mosquito collection



A. sawadwongpori, A. maculatus

A. barbirostris, A. campestris

A. dirus

A. minimus, A. maculatus

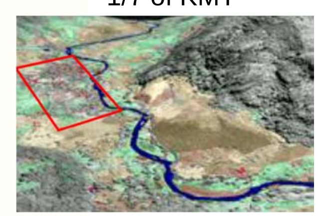
Malaria in Thailand
Agent-Based Simulation

- A small hamlet example

23 houses
2 cattle sheds
24 clusters of larval habitats

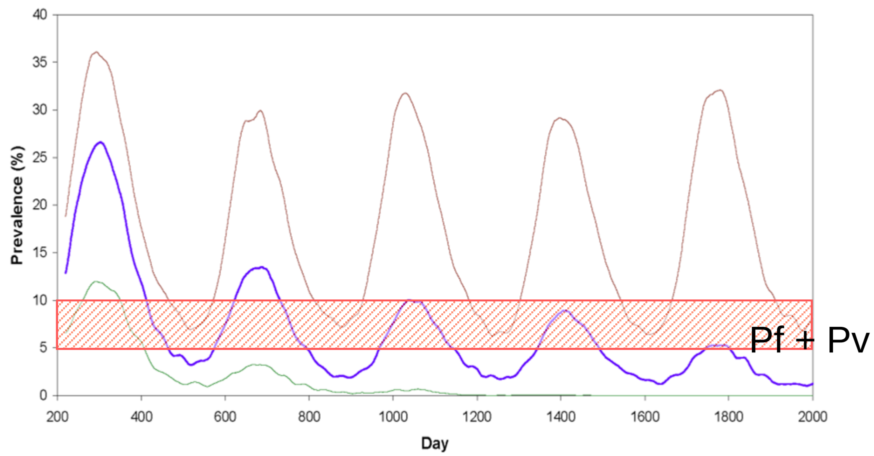
69 adults
23 children
8 cows

1/7 of KMT

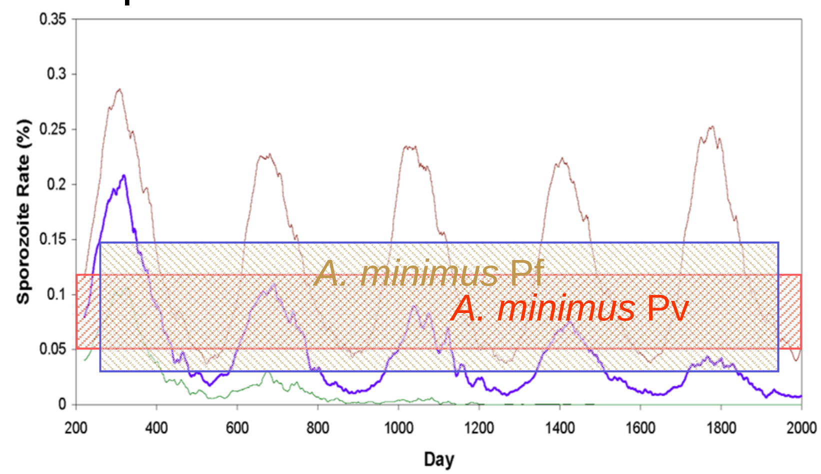


Malaria in Thailand
Agent-Based Simulation

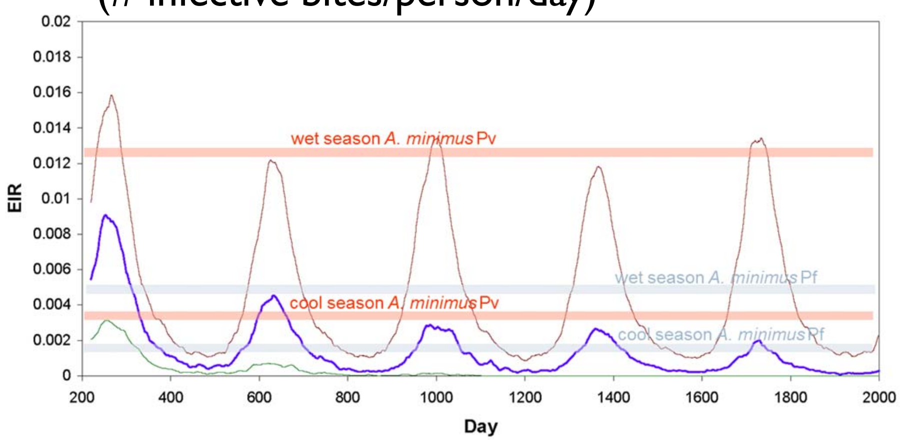
- Prevalence



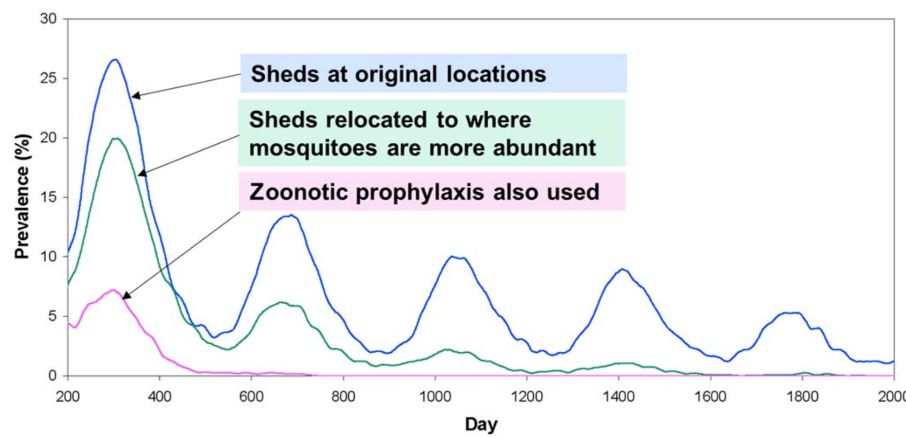
- Sporozoite Rate



- Entomological Inoculation Rate
(# infective bites/person/day)

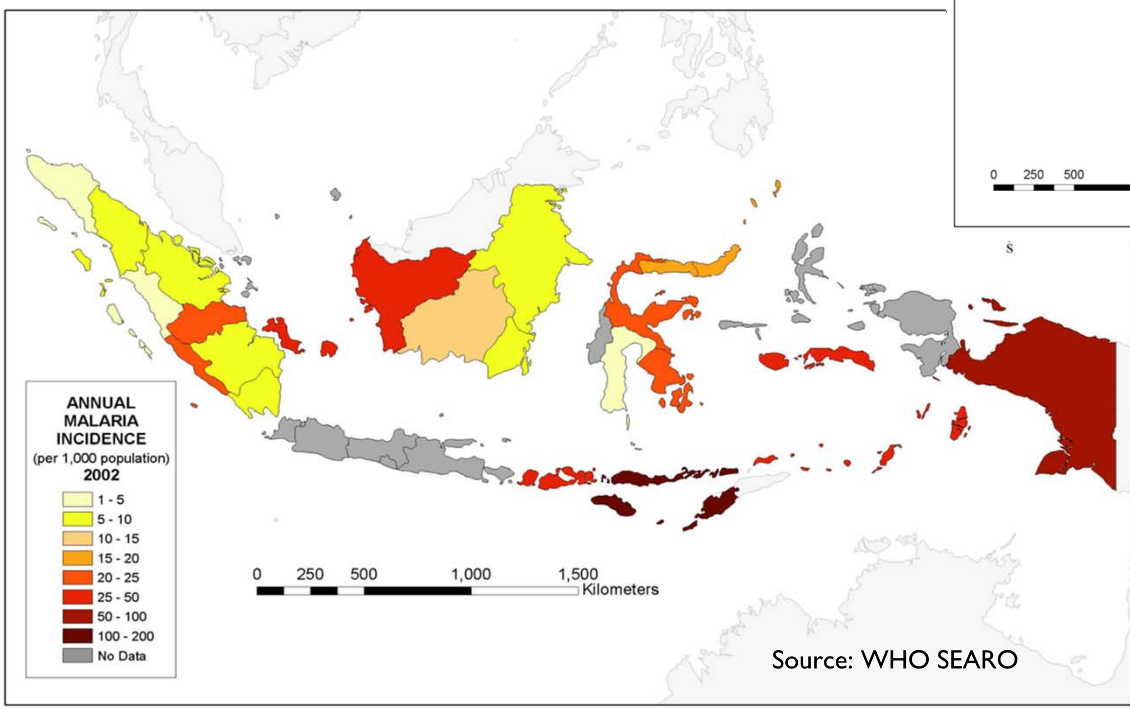


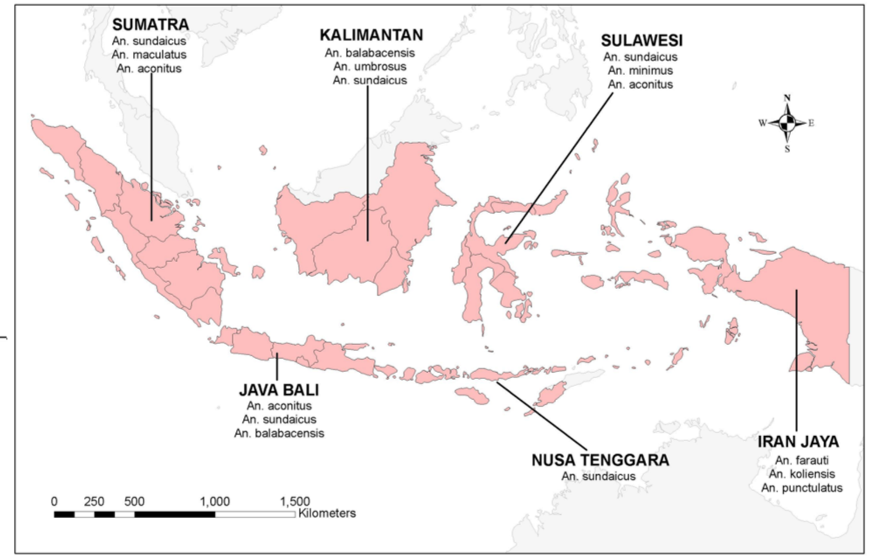
- Scenario analysis



Malaria in Indonesia

- 40% of Indonesian population live in malaria area
- ~ 500 reported deaths each year
- Most cases are outside of the main island

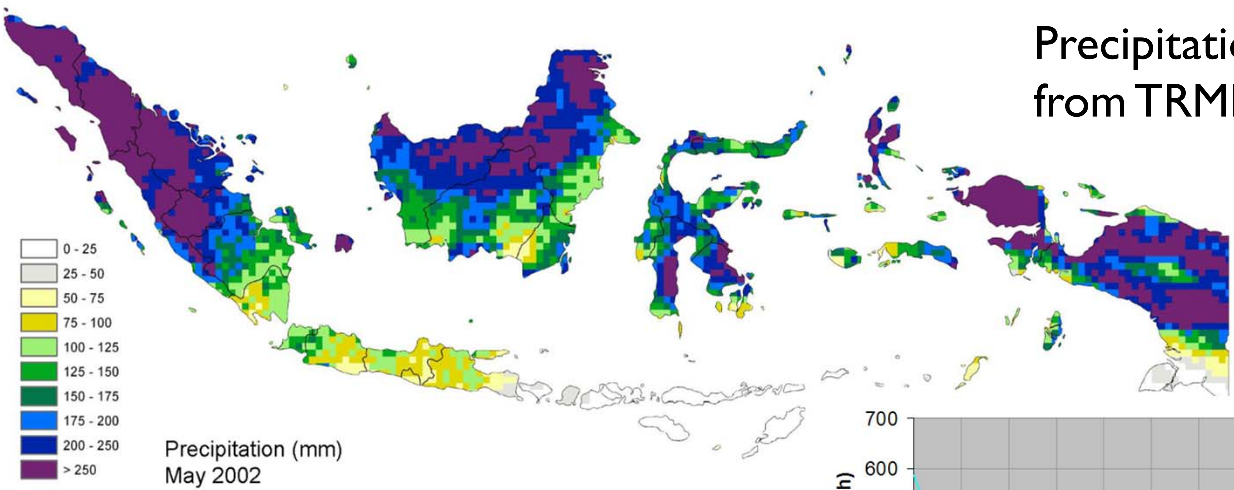




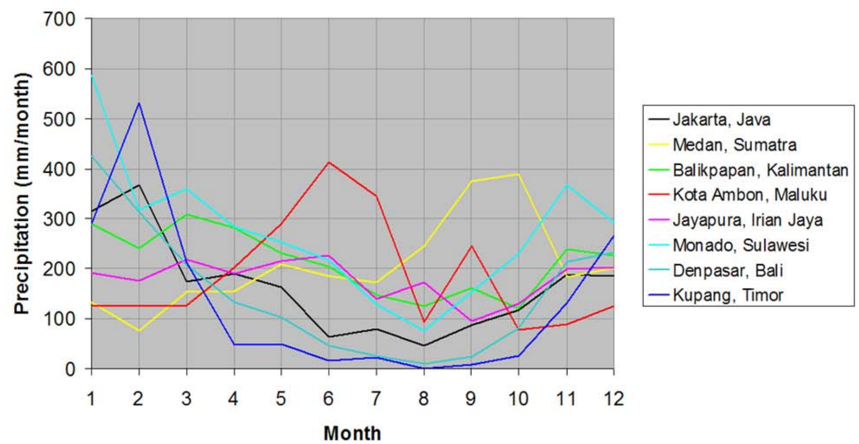
- Major malaria species distribution in Indonesia

Malaria in Indonesia
Neural Network Analysis

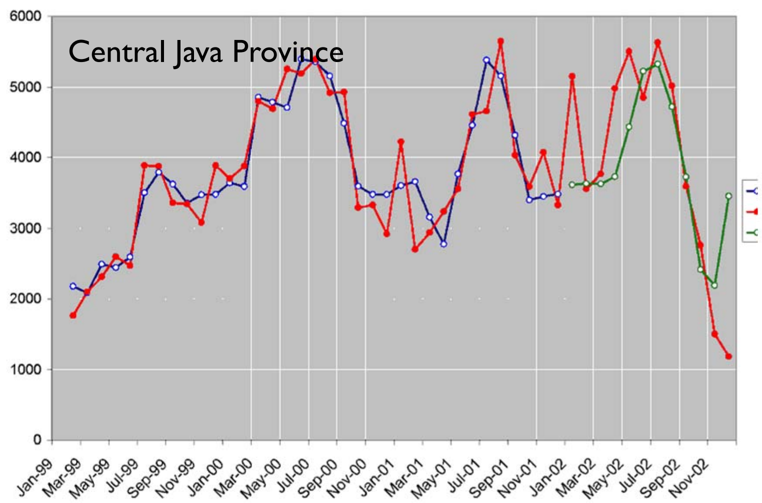
- Rainfall pattern – which drives malaria transmission – varies considerably between provinces

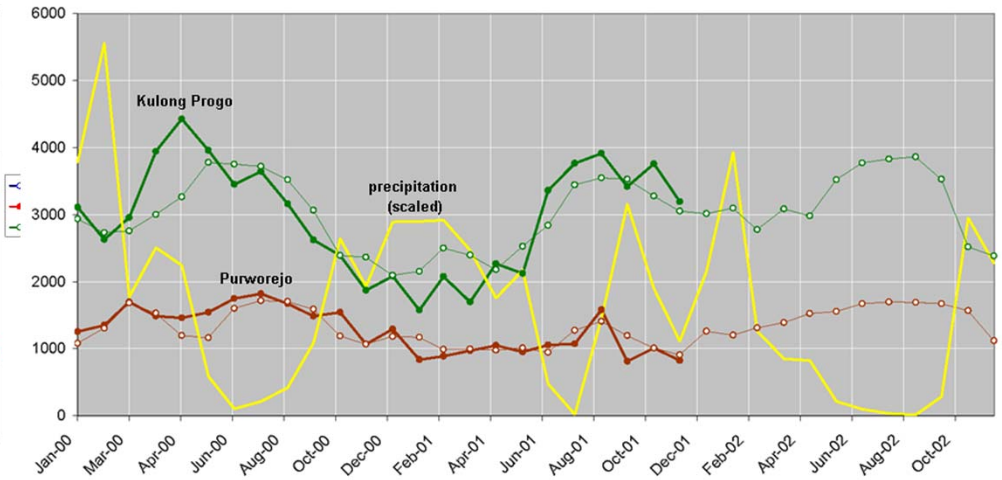


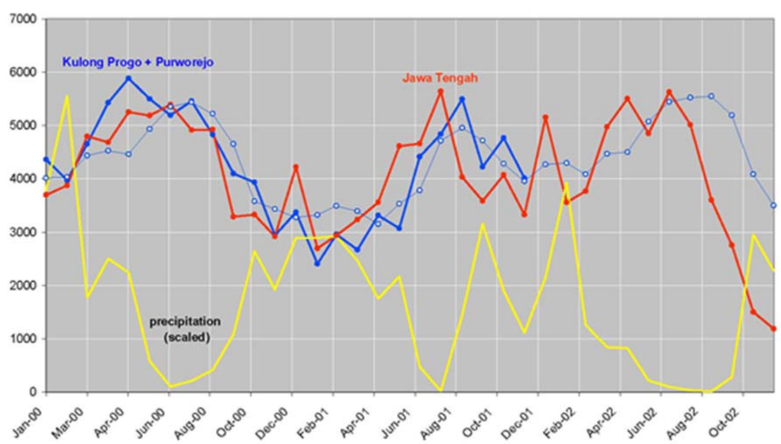
Precipitation from TRMM

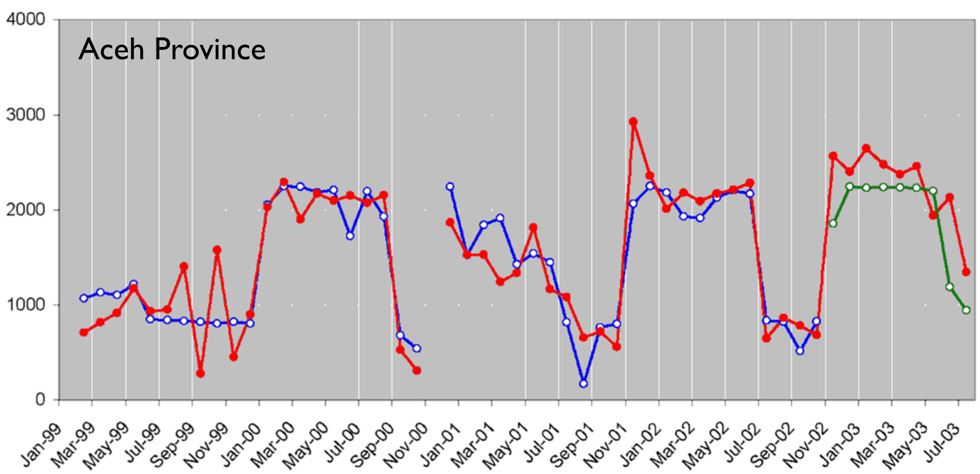


Malaria in Indonesia
Neural Network Analysis

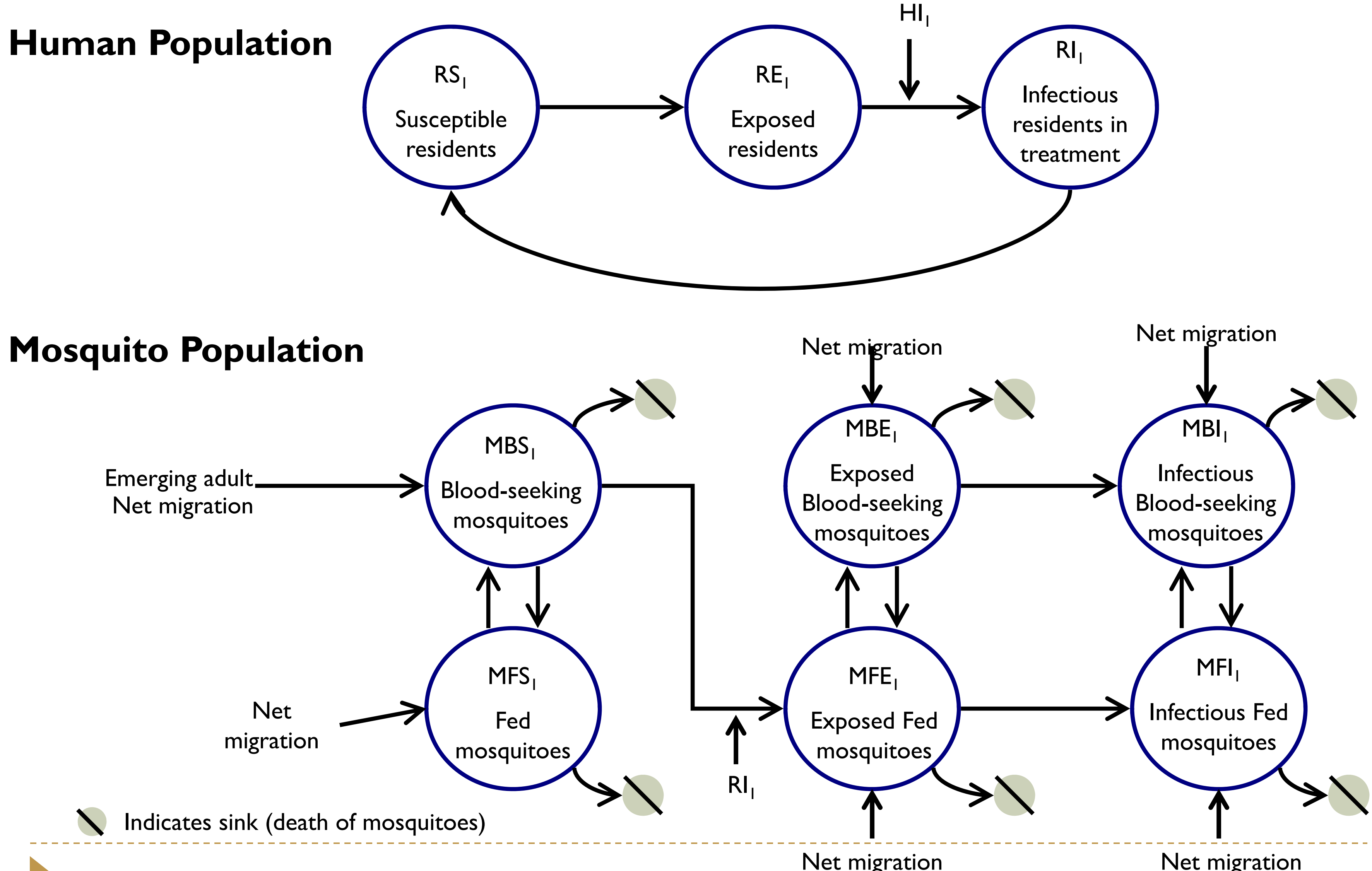


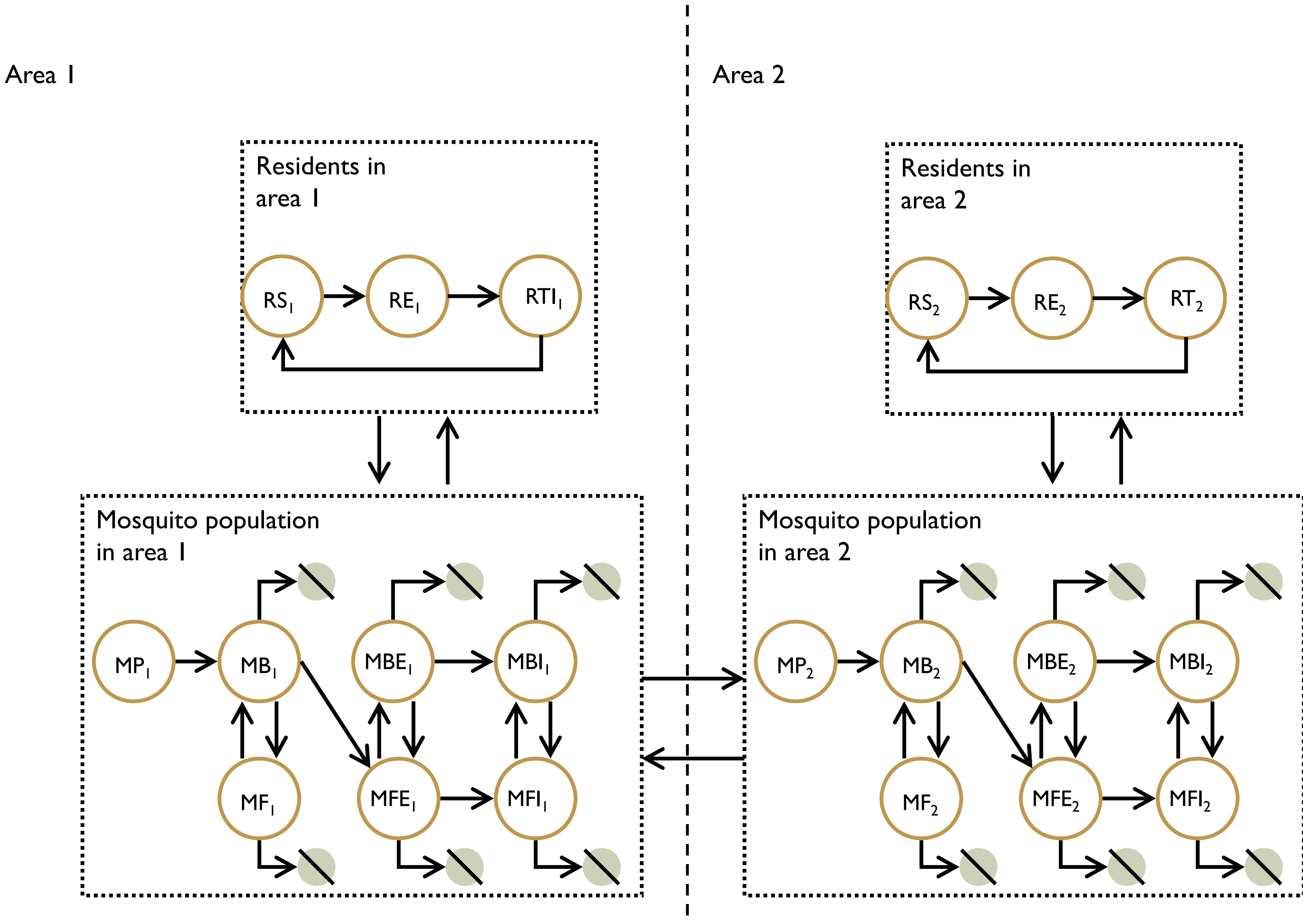






Biological Compartmental Model





Area 1
Area 2
Residents in
area 1
RS1
RE1
RTI1
Residents in
area 2
RS2
RE2
RT2
Mosquito population
in area 1
MP1
MB1
MBE1
MBI1
MF1
MFE1
MFI1
Mosquito population
in area 2
MP2
MB2
MBE2
MBI2
MF2
MFE2
MFI2

Biological Compartmental Model

- Toy model: 3-site, 24 ODEs
- For each site, *k* (*k*=*1,2,3*), mosquito density can be described as:

$$\frac{d}{dt}bs_k = \varepsilon_k \, f(\mathrm{L}) + \sum_{j \neq k} (\phi_{j,k}\, bs_i - \phi_{k,j}\, bs_k) + \sigma\, os_k - \alpha\, bs_k - \theta bs_k$$

$$\frac{d}{dt}os_k = \alpha\, bs_k\, (1 - \beta_{M,k}\, ri_k) + \sum_{j \neq k} (\phi_{j,k}\, os_i - \phi_{k,j}\, os_k) - \sigma\, os_k - \theta\, os_k$$

$$\frac{d}{dt}be_k = \sum_{j \neq k} (\phi_{j,k}\, be_i - \phi_{k,j}\, be_k) + \sigma\, oe_k - \alpha\, be_k - \theta\, be_k - \lambda_M\, be_k$$

$$\frac{d}{dt}oe_k = \alpha\, be_k + \alpha\, \beta_{M,k}\, bs_k\, ri_k + \sum_{j \neq k} (\phi_{j,k}\, oe_i - \phi_{k,j}\, oe_k) - \sigma\, oe_k - \theta\, be_k - \lambda_M\, oe_k$$

$$\frac{d}{dt}bi_k = \sum_{j \neq k} (\phi_{j,k}\, bi_i - \phi_{k,j}\, bi_k) + \sigma\, oi_k - \alpha\, bi_k - \theta\, bi_k + \lambda_M\, be_k$$

$$\frac{d}{dt}oi_k = \alpha\, bi_k + \sum_{j \neq k} (\phi_{j,k}\, oi_i - \phi_{k,j}\, oi_k) - \sigma\, oi_k - \theta\, bi_k - \lambda_M\, oi_k$$

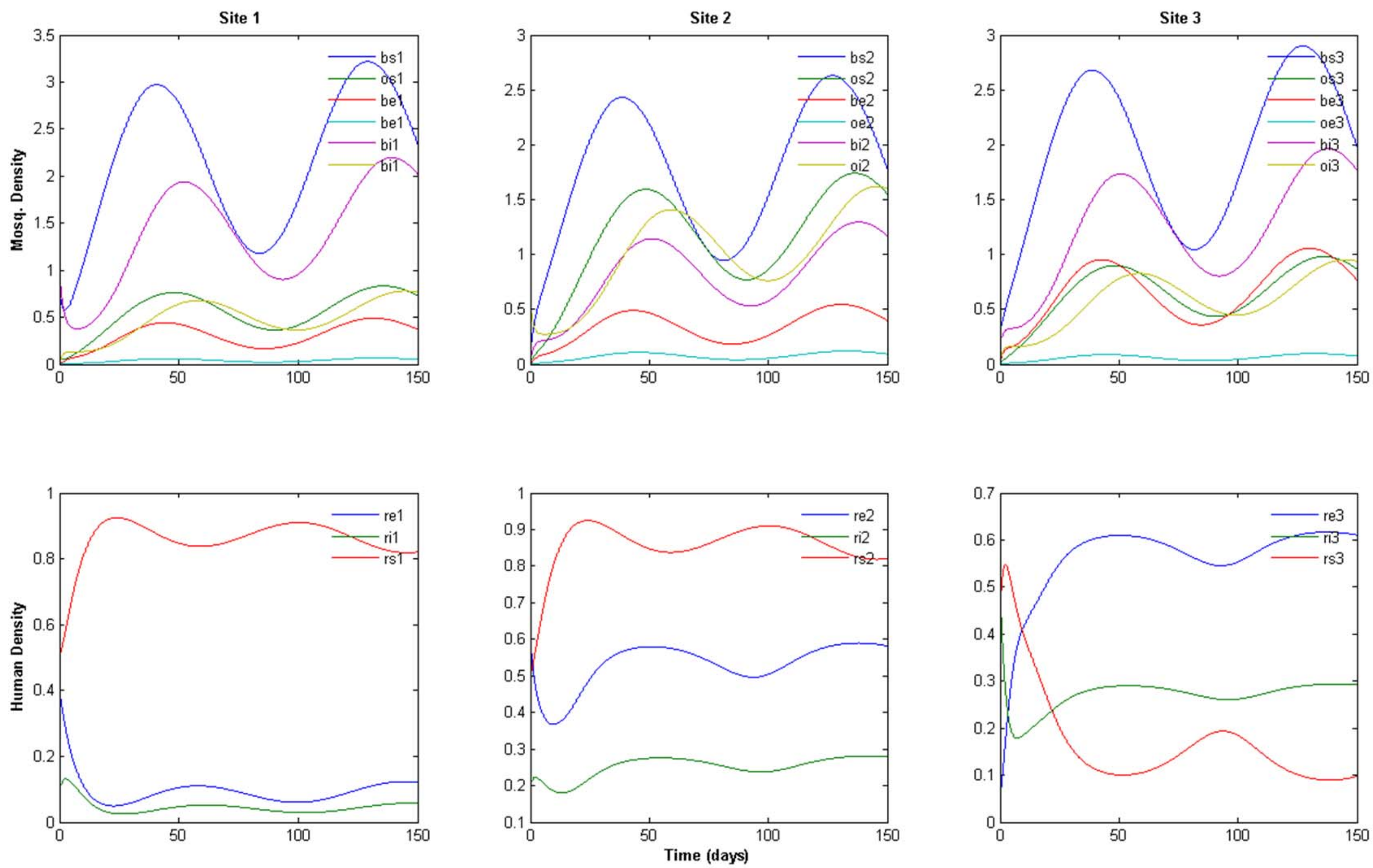
Where *f*(L) is a sinusoidal function representing temperature and rainfall variability

- Human/resident density can be described as:

$$\frac{d}{dt}re_k = \alpha\, \beta_{H,k}\, bi_k\, rs_k - \lambda_H\, re_k \qquad \frac{d}{dt}ri_k = \lambda_H\, re_k - \tau\, ri_k \qquad 1 = re_k + ri_k + rs_k$$

Biological Compartmental Model

- Preliminary result



THANK YOU