Comparing Vector-host model and SIR type model for dengue transmission

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Dengue: a mosquito-borne viral disease of tropics and sub-tropics.

- Recognized in over 100 countries
- 50-100 million annual infections
- Carried by *Aedes aegypti* mosquitoes

The contour lines of the January and July isotherms indicate the potential geographical limits of the northern and southern hemispheres for year-round survival of *Adeas aegypti*, the principal mosquito vector of dengue viruses.

Objectives

Idea

- Various mathematical models are used to model dengue, some track mosquitoes explicitly while others capture it in transmission term.
- Little guidance exists for which type of model should be preferred.
- In particular, there has been no comparison of how well these models explain observed incidence.

Goals

- Exploring the impact of modeling assumptions on the dengue dynamics.
- Finding parameter estimates of dengue models.
- Explaining the dengue data from Thailand.
- Choosing a model which explains the Thailand data more parsimoniously.

Models and Approach

We considered simple dengue models with and without explicitly modeling mosquitoes, fit both models to DHF incidence data, and used model selection to compare the models.

- Two mathematical models of dengue transmission.
  - Vector–host model
  - SIR type model
- Used *Bayesian MCMC* to fit DHF data from Thailand to the two models.
- Uncertainty and sensitivity analysis on R_0 using *PRCC*.
- Used *AIC* to choose a model which fits data most parsimoniously.

Data

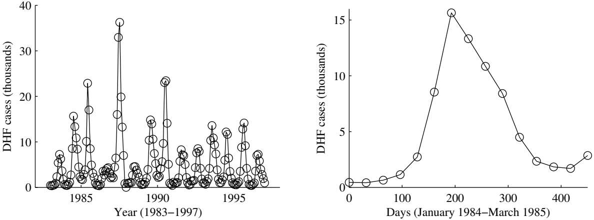


Figure: DHF cases in Thailand

- The Thailand Ministry of Public Health have been recording number of Dengue hemorrhagic fever (DHF) cases since 1972.
- We use data from one epidemic for estimation *(January 1984 to March 1985)*.

Models

- *Vector–host model*

$$\begin{aligned}
\frac{\mathrm{d}H_S}{\mathrm{d}t} &= B_H - mc\beta_H \frac{V_I}{V} H_S - \mu_H H_S,\\
\frac{\mathrm{d}H_I}{\mathrm{d}t} &= mc\beta_H \frac{V_I}{V} H_S - \gamma_H H_I - \mu_H H_I,\\
\frac{\mathrm{d}H_R}{\mathrm{d}t} &= \gamma_H H_I - \mu_H H_R,\\
\frac{\mathrm{d}V_S}{\mathrm{d}t} &= B_V - c\beta_V \frac{H_I}{H} V_S - \mu_V V_S,\\
\frac{\mathrm{d}V_I}{\mathrm{d}t} &= c\beta_V \frac{H_I}{H} V_S - \mu_V V_I,
\end{aligned}$$

- *SIR model*

$$\begin{aligned}
\frac{\mathrm{d}H_S}{\mathrm{d}t} &= B_H - \beta \frac{H_I}{H} H_S - \mu_H H_S,\\
\frac{\mathrm{d}H_I}{\mathrm{d}t} &= \beta \frac{H_I}{H} H_S - \gamma_H H_I - \mu_H H_I,\\
\frac{\mathrm{d}H_R}{\mathrm{d}t} &= \gamma_H H_I - \mu_H H_R,
\end{aligned}$$

Bayesian MCMC

- **Priors**
  - Uniform priors chosen for parameters with estimates available in literature.
  - Used Least-square fitting to obtain Initial guess estimates for parameters with no available estimates in literature.
- **Likelihood Function**

  Using the least-squares error between the cumulative DHF data D_i and the model prediction,

  $$E^2 = \sum_{i=1}^{15} \left(D_i - y_i(\theta) \right)^2,$$

  we assumed the errors were Gaussian, giving the likelihood function

  $$L(\theta) = \Pr(D \mid \theta) = \exp\left(-E^2 \right).$$

Metropolis Algorithm

- Metropolis Algorithm is an adaptation of a random walk that uses acceptance/rejection rule to converge to the target distribution.
  - At each step, we sample a proposal from a symmetric jumping distribution.
  - Calculate loglikelihood ratio (involves solving ODE's with proposal)
  - Jump is accepted if ratio is less than $\alpha \in U(0,1)$
- Update the covariance matrix of Jumping distribution after fixed number of iterations. (**Adaptive Metropolis Alg.**)
- Convergence
  - **Gelman Rubin Test** (compares the variances within each chain and variances between the chains)

Results

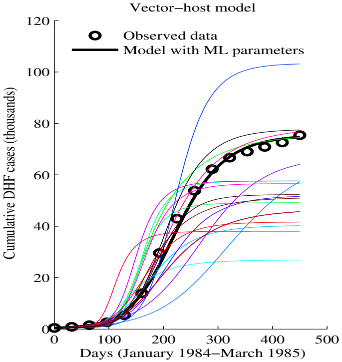


Figure: The cumulative DHF cases from the data, and from the models with the maximum–likelihood parameter estimates and 20 samples from the posterior parameter distribution.

Posterior

$\beta_{aH} = mc\beta_H$ and $\beta_{aV} = c\beta_V$

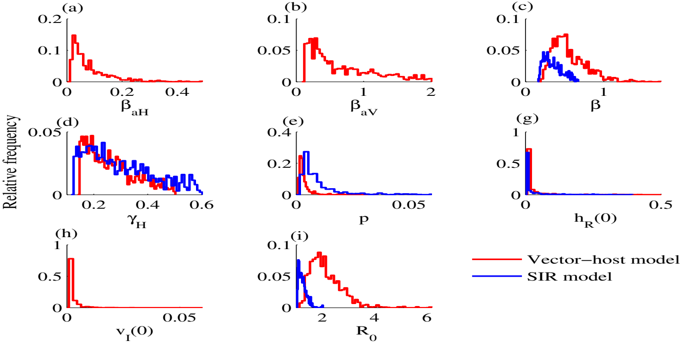
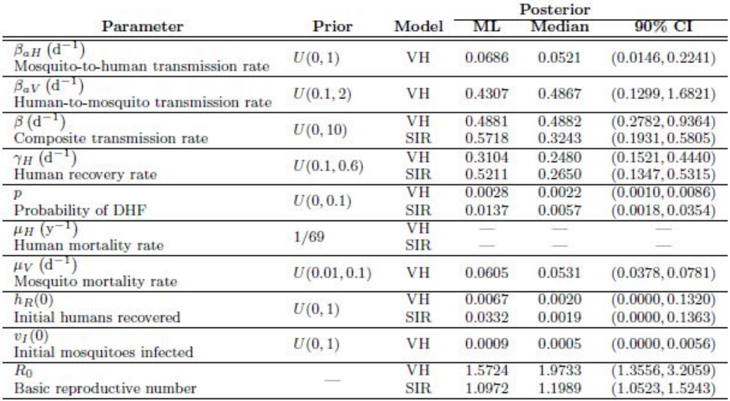


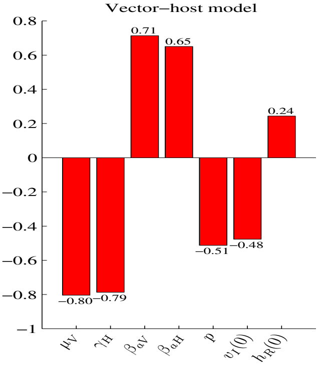
Figure: Posterior parameter densities for the vector–host and SIR models. (For the vector–host model, $\beta = \beta_{ah}\beta_{av}/\mu_v$.)

Posterior



Parameter	Prior	Model	Posterior ML	Posterior Median	Posterior 90% CI
β_{aH} (d^{-1}) Mosquito-to-human transmission rate	$U(0,1)$	VH	0.0686	0.0521	$(0.0146, 0.2241)$
β_{aV} (d^{-1}) Human-to-mosquito transmission rate	$U(0.1,2)$	VH	0.4307	0.4867	$(0.1299, 1.6821)$
β (d^{-1}) Composite transmission rate	$U(0,10)$	VH SIR	0.4881 0.5718	0.4882 0.3243	$(0.2782, 0.9364)$ $(0.1931, 0.5805)$
γ_H (d^{-1}) Human recovery rate	$U(0.1,0.6)$	VH SIR	0.3104 0.5211	0.2480 0.2650	$(0.1521, 0.4440)$ $(0.1347, 0.5315)$
p Probability of DHF	$U(0,0.1)$	VH SIR	0.0028 0.0137	0.0022 0.0057	$(0.0010, 0.0086)$ $(0.0018, 0.0354)$
μ_H (y^{-1}) Human mortality rate	1/69	VH SIR	— —	— —	— —
μ_V (d^{-1}) Mosquito mortality rate	$U(0.01,0.1)$	VH	0.0605	0.0531	$(0.0378, 0.0781)$
$h_R(0)$ Initial humans recovered	$U(0,1)$	VH SIR	0.0067 0.0332	0.0020 0.0019	$(0.0000, 0.1320)$ $(0.0000, 0.1363)$
$v_I(0)$ Initial mosquitoes infected	$U(0,1)$	VH	0.0009	0.0005	$(0.0000, 0.0056)$
R_0 Basic reproductive number	—	VH SIR	1.5724 1.0972	1.9733 1.1989	$(1.3556, 3.2059)$ $(1.0523, 1.5243)$

Sensitivity Analysis on R_0



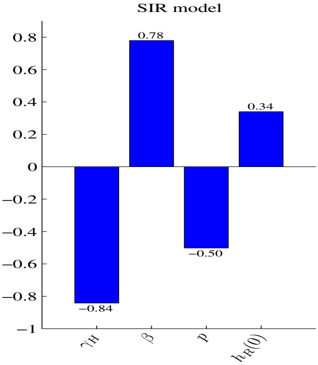


Figure: PRCCs for the effect of each parameter on R_0 for the vector–host and SIR models.

Model Selection

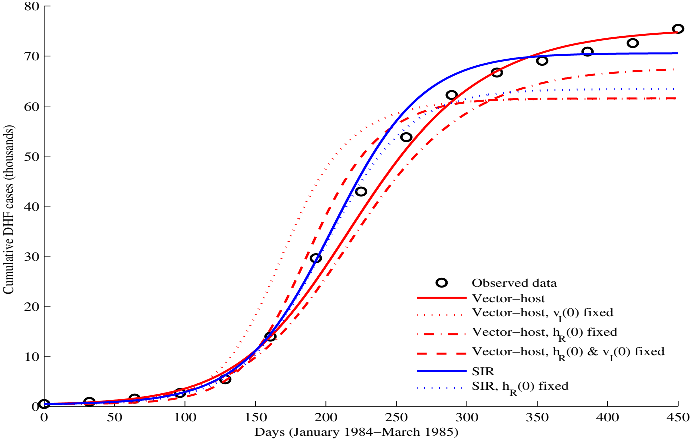
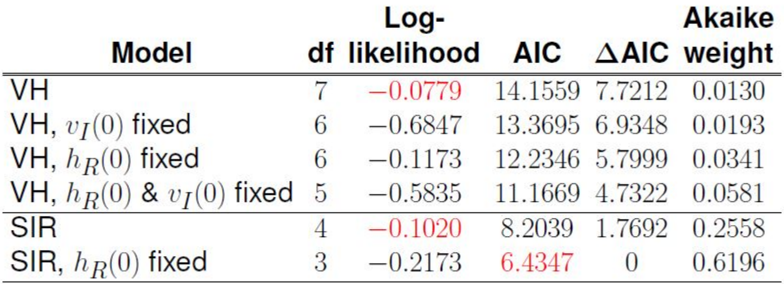


Figure: The maximum likelihood fits of models to the data.

Model Selection



Model	df	Log-likelihood	AIC	ΔAIC	Akaike weight
VH	7	-0.0779	14.1559	7.7212	0.0130
VH, $v_I(0)$ fixed	6	-0.6847	13.3695	6.9348	0.0193
VH, $h_R(0)$ fixed	6	-0.1173	12.2346	5.7999	0.0341
VH, $h_R(0)$ & $v_I(0)$ fixed	5	-0.5835	11.1669	4.7322	0.0581
SIR	4	-0.1020	8.2039	1.7692	0.2558
SIR, $h_R(0)$ fixed	3	-0.2173	6.4347	0	0.6196

- The SIR model with fixed $h_R(0)$ had the minimum AIC value, implying this model was the best among the models.
- The difference in AIC between the best model and the others (AIC) gave "considerably less support" for all the vector-host models and "substantial support" for both SIR models.
- There was only a 12 % probability that any of the vector–host models was best.

Conclusions

- Both the models fit the incidence data well.
- Parameter estimates were consistent with existing published values.
- PRCC values showed that all the parameters except initial conditions have significant influence on the magnitude of the basic reproduction number R_0.
- AIC model selection found the **SIR** model with fixed $h_R(0)$ to be **substantially better** than the **vector–host** model.
- Incorporating mosquito population explicitly in a dengue model may not be necessary to explain the incidence data from Thailand.

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Thanks......