Estimating the Attack Ratio of Dengue Epidemics under Time-varying Force of Infection using Aggregated Notification Data

Flávio Codeço Coelho and Luiz Max Carvalho

Escola de Matemática Aplicada, Fundação Getúlio Vargas

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Summary

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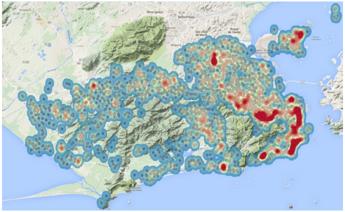
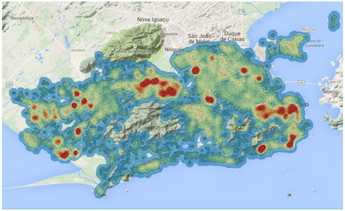
- Imunological structure of the population is also a key factor, but is mostly unknown.

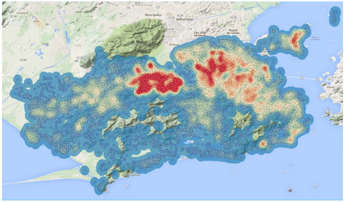
4 epidemics



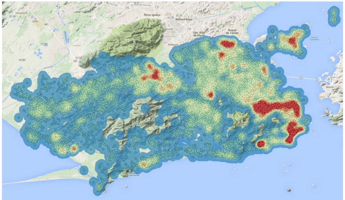
(a) 2010



(b) 2011



(c) 2012



(d) 2013

Effective Reproductive number(R_t)

The effective reproductive number can be easily estimated from the incidence time-series, Y_t:

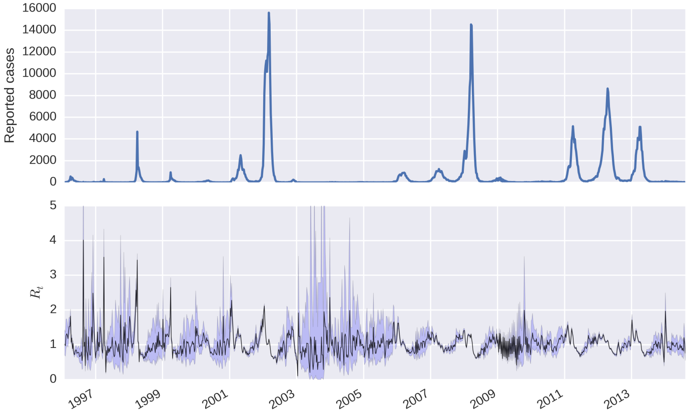
$$R_t = \left(\frac{Y_{t+1}}{Y_t} \right)^{1/n} \tag{1}$$

Where n is the ration between the length of reporting interval and the mean generation time of the disease.

Nishiura et. al. (2010)

R_t 's uncertainty

But what about the uncertainty about R_t ?
If we assume that the counts Y_t are Poisson distributed for all t, we can derive the probability distribution of R_t [1]



[1]Coelho, FC and Carvalho, LM (Submitted)

Environmental determinants

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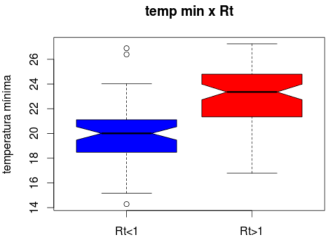
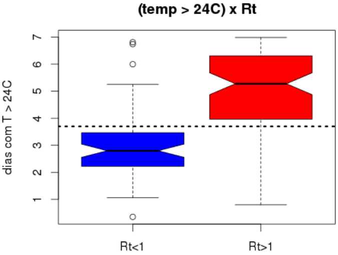
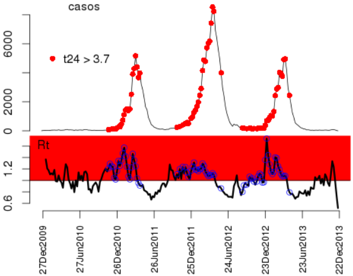
- Effects on mosquito reproduction are non-linear
- Delayed influence

R_t vs. Temperature







Single Strain SIR

Why not multi-strain? No Multi-strain data!!

$$\begin{aligned} \frac{dS}{dt} &= -\beta(t)SI \\ \frac{dI}{dt} &= \beta(t)SI - \tau I \\ \frac{dR}{dt} &= \tau I \end{aligned} \tag{2}$$

where $S(t) + I(t) + R(t) = 1 \; \forall \; t$.

Variable Force of Infection

From R_t , we can define a force of infection which varies with time:

$$\beta(t) = \frac{R_t \cdot \tau}{S} \tag{3}$$

But how do we get the value of S? we need to estimate S_0.

Estimating S_0

Bayesian framework:

- Define priors for S_0 in the range (0,1)

$$p(S_{0j}|\mathbf{Y_j}) \propto L(\mathbf{Y_j}|S_{0j}, R_t, m, \tau)\pi(S_{0j}) \tag{4}$$

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Estimating S_0

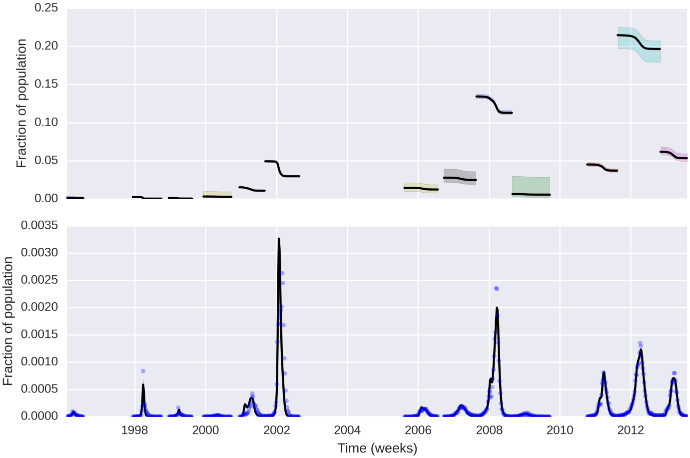
Bayesian framework:

- Define priors for S_0 in the range (0,1)
- Samples from prior, calculate $\beta(t)$ and run the model
- calculate Likelihood of data given current parameterization
- Determine posterior probability of parameterization

$$p(S_{0j}|\mathbf{Y_j}) \propto L(\mathbf{Y_j}|S_{0j}, R_t, m, \tau)\pi(S_{0j}) \tag{4}$$

Models vs Data

fiting the model to data (Rio de janeiro) to estimate S_0[2].



Posterior distribution for Susceptible (S) and infectious (I) individuous. Blue dots are data.

[2]Coelho FC et al., 2011

Attack Ratio

Once we have S_0, we can caculate the attack ratio:

$$A_j = \frac{\sum Y_j}{S_{0j}} \tag{5}$$

Attack ratio

Table : Median attack ratio and 95% credibility intervals calculated according to (5). Values are presented as percentage of total population. †: Year corresponds to the start of the epidemic, however the peak of cases may occur in the following year. ‡: Susceptible fraction. These results show considerable variation in AR between epidemics, consistent with the accquiring and loss of serotype-specific immunity.

Year†	median Attack Ratio	$S_0^{\ddagger}$
1996	0.39 (0.17-0.54)	0.00171(0.0012-0.0038)
1997	0.87 (0.74-0.87)	0.00273(0.0027-0.0032)
1998	0.5 (0.49-0.5)	0.00142(0.0014-0.0014)
1999	0.11 (0.037-0.2)	0.00345(0.0018-0.01)
2000	0.25 (0.24-0.27)	0.0155(0.015-0.016)
2001	0.48 (0.47-0.49)	0.0495(0.048-0.051)
2005	0.15 (0.1-0.21)	0.0147(0.01-0.021)
2006	0.11 (0.08-0.14)	0.0281(0.022-0.037)
2007	0.15 (0.15-0.15)	0.135(0.13-0.14)
2008	0.14 (0.031-0.31)	0.00672(0.003-0.024)
2010	0.18 (0.17-0.19)	0.0454(0.043-0.048)
2011	0.086 (0.082-0.094)	0.215(0.2-0.23)
2012	0.14 (0.13-0.15)	0.0621(0.058-0.068)

References

Nishiura H, Chowell G, Heesterbeek H, Wallinga J (2010) The ideal reporting interval for an epidemic to objectively interpret the epidemiological time course.
J R Soc Interface 7: 297–307.

Coelho FC, Codeço CT, Gomes MG (2011) A Bayesian framework for parameter estimation in dynamical models.
PLoS ONE 6: e19616.

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Arxiv. http://arxiv.org/abs/1502.01236