HIV with contact tracing: a case study in approximate Bayesian computation

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The SIR Model

Our study is restricted to the sexually transmitted epidemic of HIV in cuba.

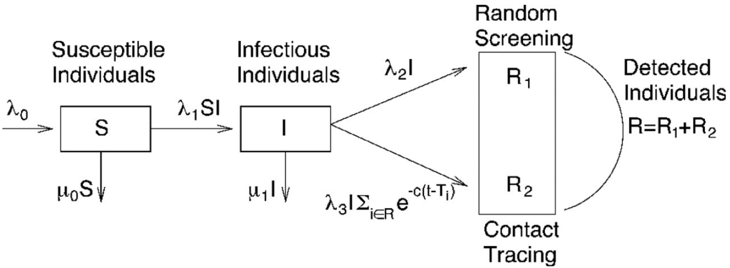


Figure : Schematic description of the SIR model with contact tracing

Parameter of interest: λ_1,λ_2 and λ_3.

Why Not MCMC

Marcov Chain Monte Carlo Method is not always good with SIR models

- Computationally prohibitive for high-dimensional missing observations (Cauchemez and Ferguson,2008; Chis Ster and others, 2009)
- Fine-tuning of the proposal distribution is required for efficient algorithms (Gilks and Roberts, 1996)

What If We Use MCMC

Observed data: removal time: $\Gamma_1 = 0, \Gamma_2, \cdots, \Gamma_n$, $\Gamma_i \in [0, T]$
Missing data: infectious time: $I_1, I_2, \cdots, I_m$,$I_1 < 0$
Prior:
$\lambda_1 \sim Gamma(a_1, v_1)$
$\lambda_2 \sim Gamma(a_2, v_2)$,
$y \sim \theta exp(\theta y) I(y < 0)$, y is the density of I_1

Metropolis Hasting Algorithm with Gibbs sampling

Sampling posteriors

- $f(\Gamma, I|\lambda_1, \lambda_2, I_1) = \prod_{i=1}^{n} \lambda_2 Y_{\Gamma_j^-} \prod_{j=2}^{m} \lambda_1 X_{I_j^-} Y_{I_j^-} exp\{-\int_{I_1}^{T} (\lambda_1 X_t Y_t + \lambda_2 Y_t) dt\}$
- $\pi(\lambda_1|\Gamma, I, I_1, \lambda_2) \sim \Gamma(a_1 + \int_{I_1}^{T} X_t Y_t dt, m - 1 + v_1)$
- $\pi(\lambda_2|\Gamma, I, I_1, \lambda_1) \sim \Gamma(a_2 + \int_{I_1}^{T} Y_t dt, n + v_2)$

M-H step inside

abbreviate $f(\Gamma, I|\lambda_1, \lambda_2, I_1)$ by $f(I)$

- Moving an infection time: $\frac{f(I-\{s\}+\{t\})}{f(I)} \wedge 1$, t is sampled uniformly on(I_1, T)
- Removing an infection time: $\frac{f(I-\{s\})m}{f(I)(T-I_1)} \wedge 1$
- Adding a new infection time: $\frac{f(I+\{t\})(T-I_1)}{f(I)(m+1)} \wedge 1$

Approximate Bayesian Computation

Two Approximation are at the core of ABC

- Replacing observations with summary statistics: Use posterior $p(\theta|S(x) = S_{obs})$ instead of $p(\theta|x)$

  In a fully observed SIR model, Summary statistics are R_t^1 and R_t^2, where $R_t^1 + R_t^2 = R_t$, $t \in [0, T]$. R_t^1 and R_t^2 are sufficient statistics.
- Simulation-based approximations of the posterior. (More will be described on the partially observed model.)

The Algorithm

1. Generating N random draws$(\theta_i, s_i), i = 1, \cdots, N$. The parameter θ_i is generated from the prior distribution π, and the vector of summary statistics s_i is calculated for the ith data set that is simulated from the generative model with parameter θ_i.

2. Associate to the ith simulation, the weight $W_i = K_\delta(s_i - s_{0bs})$, where δ is a tolerance threshold and K_δ a (possibly multivariate)smoothing kernel.

3. The distribution $\sum_{i=1}^N W_i \delta_{\theta_i} / \sum_{i=1}^N W_i$, in which δ_θ denotes the Dirac mass at θ, approximates the target distribution.

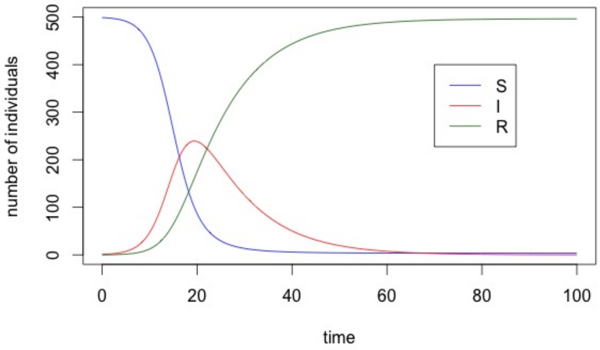
$\lambda_j, j = 1, 2, 3$, is estimated by $\hat{\lambda}_j = \sum_{i=1}^N \lambda_{j,i} W_i / \sum_{i=1}^N W_i$.

How to simulate summary statistics using stochastic SIR models

Main difficulty: the rate of detection changes with time.
Assumption: λ_0, μ_0 are such that the size of the population of S remains constant. Q: How come?

1. $S = S_0, I = I_0, R = 0$ Current time: Γ
2. Assume k events has already be simulated, now come to (k+1)th event simulate $\epsilon \sim exp(C_k)$, where $C_k = \lambda_1 S_{t_k} I_{t_k} + (\mu_1 + \lambda_2) I_{t_k} + \lambda 3 I_{t_k} R_{t_k}$, $\Gamma' = \Gamma + \epsilon$
3. Stop if $\Gamma' > T$
otherwise, simulate $U \sim unif(0, C_k)$

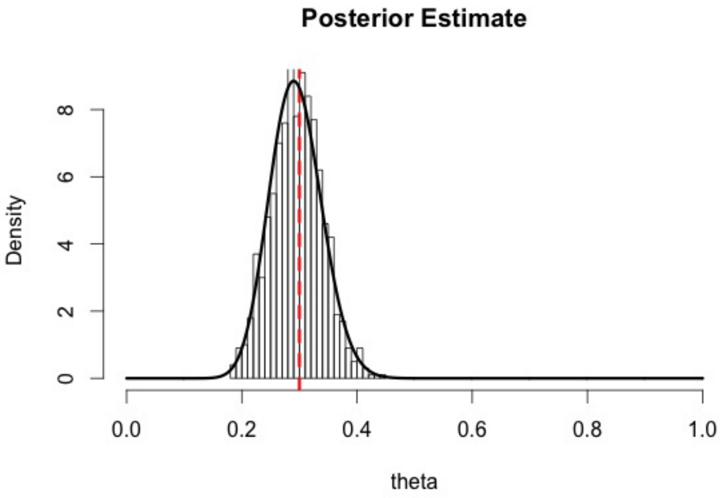
Example: Simulation from deterministic SIR model



What to do if we obtain the simulated summary statistics

ABC - rejection-sampling algorithm.
ABC - smoothing kernel

Example



Challenges

Things I will do next:

- applying abc method to with the second approximation.
- applying abc method to the real data: Cuban database.

The End

Thank you all for the attention!