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.

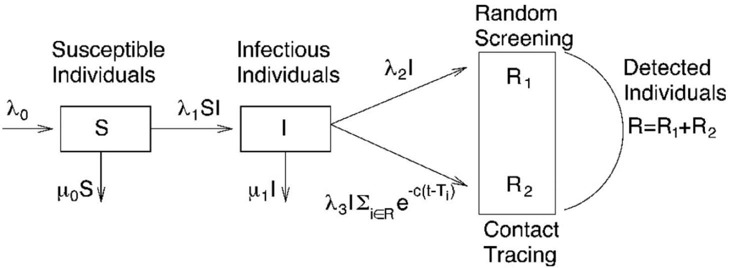


Figure : Schematic description of the SIR model with contact tracing

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)

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.

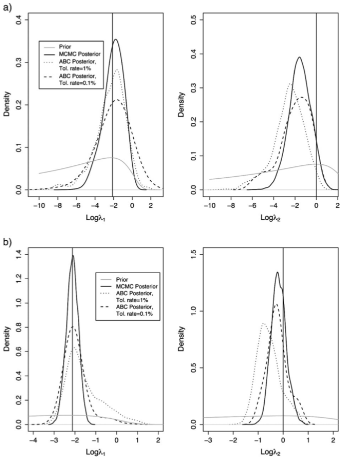
3. The distribution $\sum_{i=1}^N W_i \delta_{\theta_i} / \sum_{i=1}^N W_i$, in which δ_θ denotes the Dirac mass at θ, approximates the target distribution.

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

The Result From A Fully Observed Model

Part a: The data consists 3 detection time

Part b: The data consists 29 detection time



Approximate Bayesian Computation

When full observations are unavailable, summary statistics is composed of:

- R^1_T and R^2_T,
- $R^l_{j+1} - R^l_j$, $l = 1, 2$, for each year j.
- $I_{j+1} - I_j$, for $j = 0, \cdots, 5$.
- Mean time during which an individual is infected but has not been detected yet.

"Curse of dimensionality"

The Second Core Approximation

Correction Adjustment: $\theta_i^* = G_{s_{obs}}^{-1}(G_{s_i}(\theta_i))$, $i = 1, \cdots, N$.

Available methods for choosing G:

- Local linear regressions of Beaumont and others (LOCL)
- Nonlinear conditional heteroscedastic regressions of Blum and Francois (NCH)

Discussion

- ABC applications have been restricted to models with moderate number of parameters.
- Statisticians are more experienced with MCMC.
- No ABC with regression adjustment have been developed so far for infinite- dimensional summary statistics.

The End

Thank you all for listening!