

# Jewell Approach

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The overall goal is to use active surveillance to target high-risk households, which is thought to be more efficient than random targeting. However, it is unclear whether this would be more efficient than treating houses around an infected house. Below I have summarized the approach along with questions that remain.

## 1. Data needed

- Covariate data
  - location
- Observed data
  - detection of bugs at time points ( $N(t)_i$ )
  - spray time of houses ( $R(t)_i$ )
- Unobserved data
  - infection times of notified houses ( $I(t)_i$ )
  - infected houses that are not yet detected

\*we also have known uninfected: In their model, S is unobserved but in ours it is partially observed

Houses are either

- Susceptible (S): not infected (partially observed)
- Infected (I): infected (unobserved)
- Notified (N): known infected (observed)
- Recovered (R): known treated (observed)

Transmission rate between infected  $i$  and susceptible  $j$  and observed (notified)  $i$  and susceptible  $j$ :

$$\beta_{ij} = \begin{cases} \text{hop rate } \lambda * (1 - \phi) & \text{if } \rho_{ij} < C \\ \text{jump rate } \lambda * \phi & \text{if } \rho_{ij} > C \end{cases}$$

where  $\lambda$  is the number of dispersal events per house, and  $\phi$  is the proportion of jumps. For now, we assume  $C = 30$  meters. We can use estimates from the synthetic likelihood approach:  $\phi = 0.188$  and  $\lambda = 0.0102$  (invasions per occupied house per week).

where  $\rho_{ij}$  is the distance between houses  $i$  and  $j$  in meters.

They include time-dependent infectivity function  $h(\cdot)$  describing how the infectivity increases as the length of infection increases. Let  $K_i(t)$  be the number of bugs observed in the  $i$ th house at time  $t$ . I think it makes sense to think of  $h(\frac{K_i(t)}{\max(K_i(t))})$ , with the outcoming ranging from 0 to 1 (fractions of max infectivity of 1).

There are several models used to estimate population growth rates:

- Ricker model:

$$N_{t+1} = N_t * \exp(r(1 - \frac{N_t}{k}))$$

where  $r$  is the intrinsic growth rate and  $k$  is the carrying capacity.

- Hassell model:

$$N_{t+1} = \frac{a * N_t}{(1 + b * N_t)^c}$$

- Beverton-Holt model:

$$N_{t+1} = \frac{a * N_t}{1 + b * N_t}$$

This is the same as the Hassell model with  $c = 1$ .

Thus, total infection pressure becomes

$$\tau_j = \beta_0 + \sum_{I_i < I_j < R_i} \beta_{ij} \cdot h(I_j - I_i)$$

## 2. Likelihood

Rate of notification conditional on an infection is  $F_D(d) = ???$

$f_D$  is the distribution of  $D_i = N_i - I_i$ .

In homogenous mixing Markov model,  $f_d \sim \exp(\lambda)$ .  $F_D(d) = \int_d^\infty f_D(y)dy$  (as far as my understanding – this should be the cdf but seems to be 1- cdf). Jewell uses a variation of the exponential distribution. In our case, this is some function of the number of bugs and time of notification.

$$f(D_i) = f(\# \text{ bugs observed at } N_i)$$

$$\begin{aligned} f(\mathbf{I}, \theta | \mathbf{N}, \mathbf{R}) &= \prod_{j=1, j \neq k}^{[\mathbf{I}]} (\tau_j(I_j^-)) \exp\left(-\int_{I_k}^{T_{obs}} \left(\sum_{j=1, j \neq k}^{[\mathbf{S}(\mathbf{T}_{obs})]} \tau_j(t)\right) dt\right) \\ &\times \prod_{j=1}^m f_D(N_j - I_j) \times \prod_{j=m+1}^{[\mathbf{I}]} (1 - F_D(T_j - I_j)) \times \text{prior} \end{aligned}$$

where

$$T_j = \begin{cases} T_{obs} & \text{if } j \text{ is currently presumed susceptible but is unknowingly infected} \\ C_j & \text{if } j \text{ is sprayed before infestation status is known} \end{cases}$$

$k$  = initial infection (the likelihood is conditional on index case). We don't know the index case, so how do we handle? Either epicenter regression or use 2010 data as index cases. I haven't seen a situation with multiple first cases, so not sure if second option would work.

What about prior? The Jewell paper uses Gamma prior for  $\theta$ . Synthetic likelihood results for informative prior?

We are interested in  $R_i$ . Define  $R_i$  as the expected number of further premises a premises  $i$  would infect were it the index infection in a hypothetical infection where all other houses started as susceptibles, conditional on all parameters.

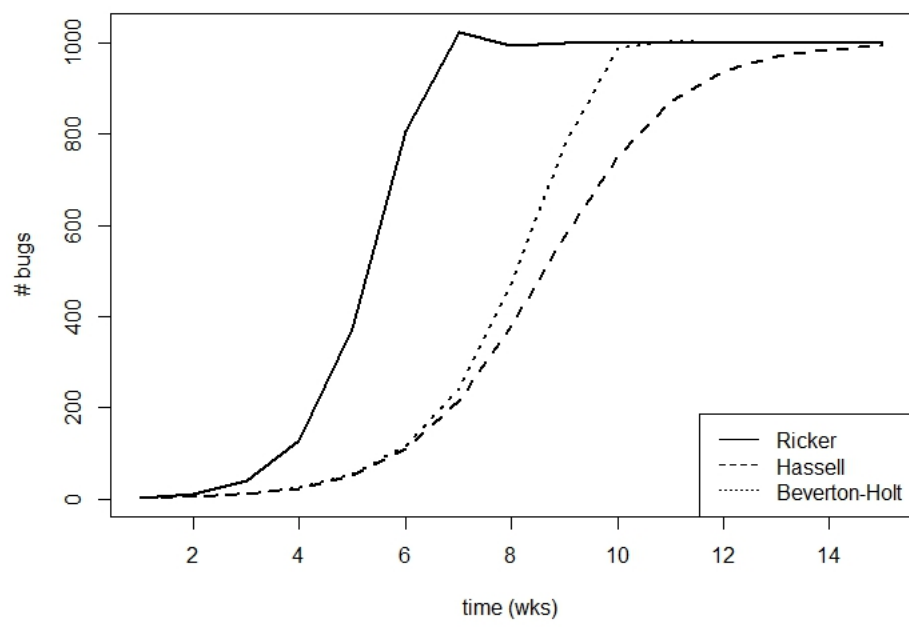


Figure 1: Models when  $k = 1$  and  $r = 1.23$  (estimated from Rabinovich, 1972)