In the follows, we examinate a tomato species data from Holt eta al. The data consist of week count Yp of the number of infected plants over a time intervals of seven days aproximatly. To link the data to the SLI-SI dynamics, we specify the following Negative Binomial observation model:

Yp~NegBin(\lambda\_t,phi)

\lambda\_t = \int^{t}\_{0} b \*L\_p (s) ds.

We aim to estimate beta\_p, r\_1, r\_2, b, beta\_v, theta, and the vector population. To do this, we postulate the following priors

beta\_p ~ Normal(0.05,0.03)

r\_1 ~ Inv-Gamma(2.005,0.01005)

r\_2 ~ Inv-Gamma(2.005,0.01005)

b ~ Inv-Gamma(3.125,0.159375)

beta\_v ~ Normal(0.003,0.003)

C ~ Uniform(50,100)

theta ~ Normal(0.4, 0.05)

We fit the SLI-SI model using Stan’s NUTs algorithm using 5 chains, each with 100 500 iteratioons of which the first 500 are warm-up to automatically tune the sampler, and then a sample is saved every fif- tieth samples, leading to a total of 10,000 posterior samples.

We examine the convergence of the parameters by inspecting the trace plots of all chains indicating that there is no lack of convergence for both models and by checking the Rˆ convergence statistic reported by Stan. If the chains have not yet converged to a common distribution the Rˆ statistic will be greater than one (Gelman et al., 2013; Stan Development Team, 2018).

Considering the nature of B. Tabacci, we consider the following initial condition. First, we introduce 1 000 plant at begin of harvest season. We proposed 65 infected latent plant and one infectiuos plant. In papers [][], they deduce a proportion of vectors per plants of 50 to 100 vectors. We use this information to estimate the total vector population, and take a initial vector population as 60 000 susceptibles vectors and 1000 infected vectors, the remain of vector we introduce in the Dv compartment.

The parameters that we estimate are beta\_p, r\_1, r\_2, b, beta\_v, theta, and C, using the default Holt parameter value as mean of the priors.

In our model beta\_p, beta\_v represents the infection rates. We postulated for theses parameters normal distributions priors since .....

The replanting rates r\_1, r\_2 are proposed as inverse gamma distribution, because we analyze the time of incubation/infection of the disease in the plants of the crop, and we replant these latents/infected plants.

Similarly, we proposed a inverse gamma for the incubation time period of the disease.

For last, the propotion of vectors that arrivals susceptibles or infected, theta, we postulated a normal distribution prior since it is impposible know the exactly proportion of susceptible vectors or infected.