An SIS epidemic in a large population with individual variation

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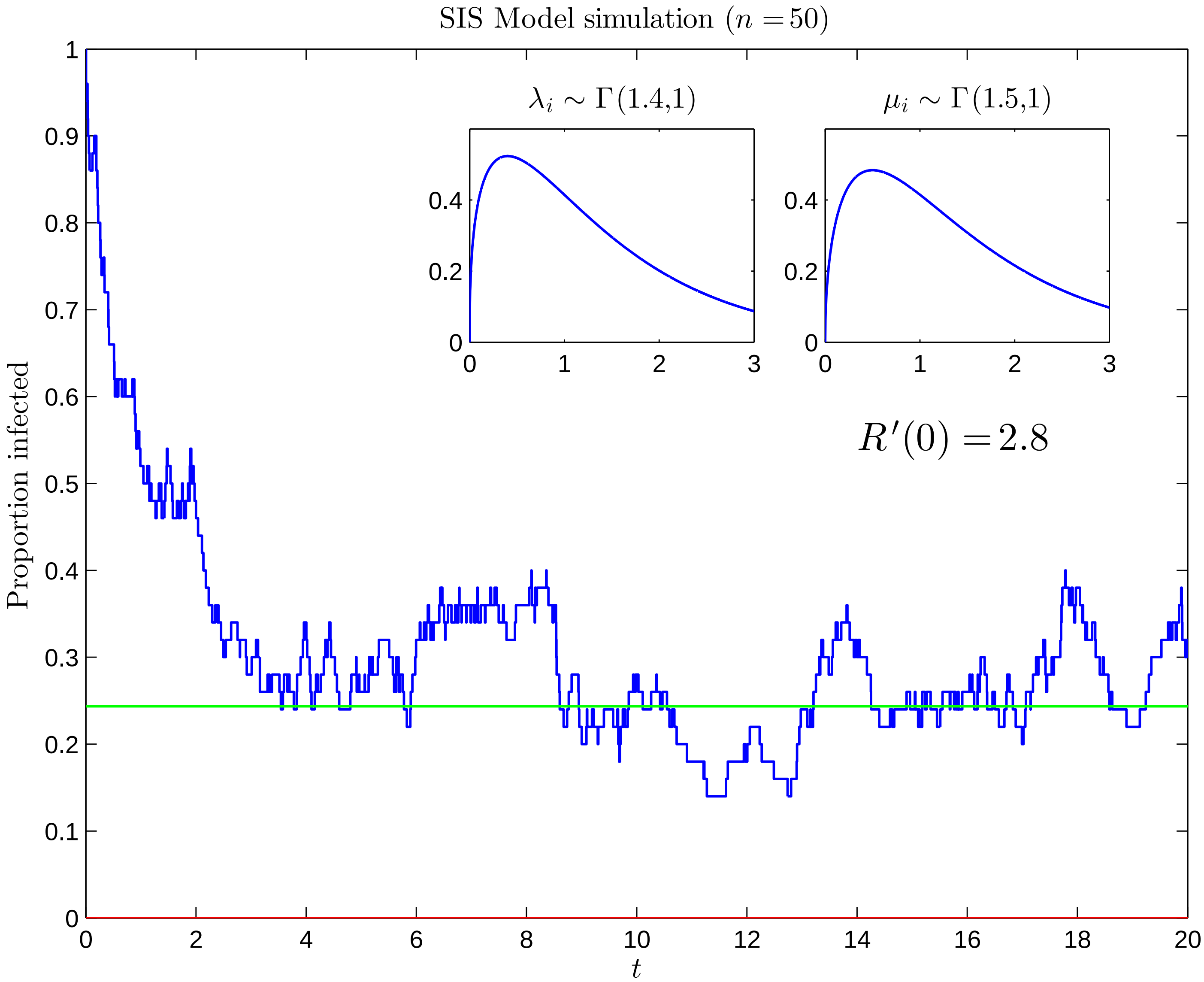
Main message



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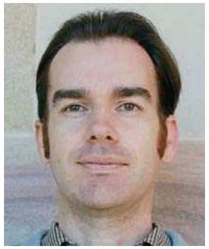


[MP1] McVinish, R. and Pollett, P.K. (2012) A central limit theorem for a discrete-time SIS model with individual variation. *Journal of Applied Probability* 49, 521–530.

[MP2] McVinish, R. and Pollett, P.K. (2013) The deterministic limit of a stochastic logistic model with individual variation. *Mathematical Biosciences* 241, 109–114.

The Stochastic SIS Model

The *SIS (Susceptible-Infectious-Susceptible) Model* was introduced [WD] to study infections, in a closed population of n individuals, that do not confer any long lasting immunity. If $Y(t)$ is the number of infectives at time t, then $(Y(t),\, t \geq 0)$ is a continuous-time Markov chain on $\{0, 1, \ldots, n\}$ with transitions

$Y \to Y+1$	at rate	$\frac{\lambda}{n} Y(n-Y)$	(infection)
$Y \to Y-1$	at rate	μY	(recovery)

[WD] Weiss, G.H. and Dishon, M. (1971) On the asymptotic behavior of the stochastic and deterministic models of an epidemic. *Mathematical Biosciences* 11, 261–265.

Behaviour for large n

The proportion of infectives $Y(t)/n$ obeys a *law of large numbers*.

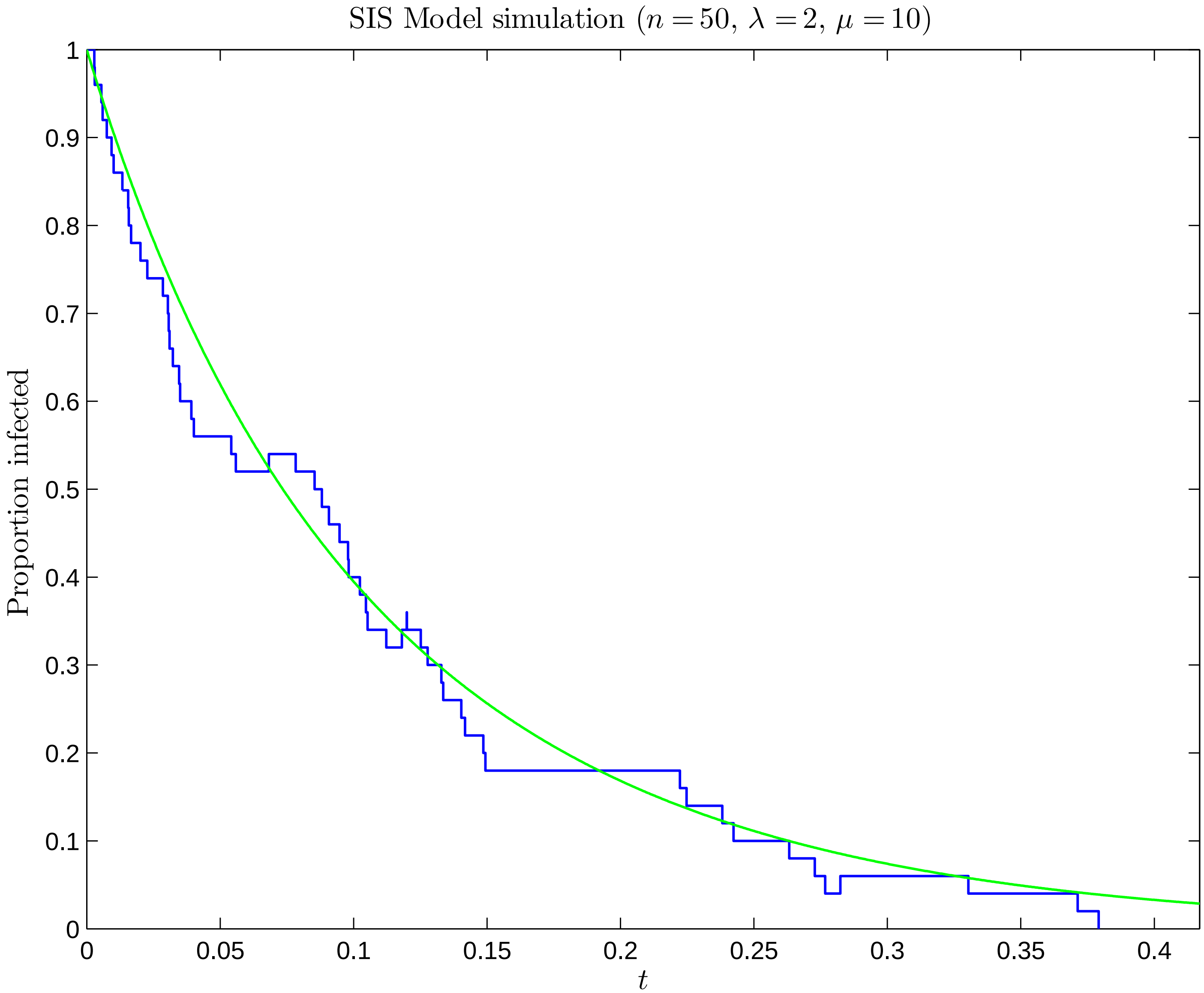
Theorem. If $Y(0)/n \to y_0$ as $n \to \infty$, then $(Y(t)/n)$ converges in probability uniformly over finite time intervals to the solution of the ODE

$$\dot{y} = \lambda y(1-y) - \mu y = \lambda y(1-\rho-y),$$

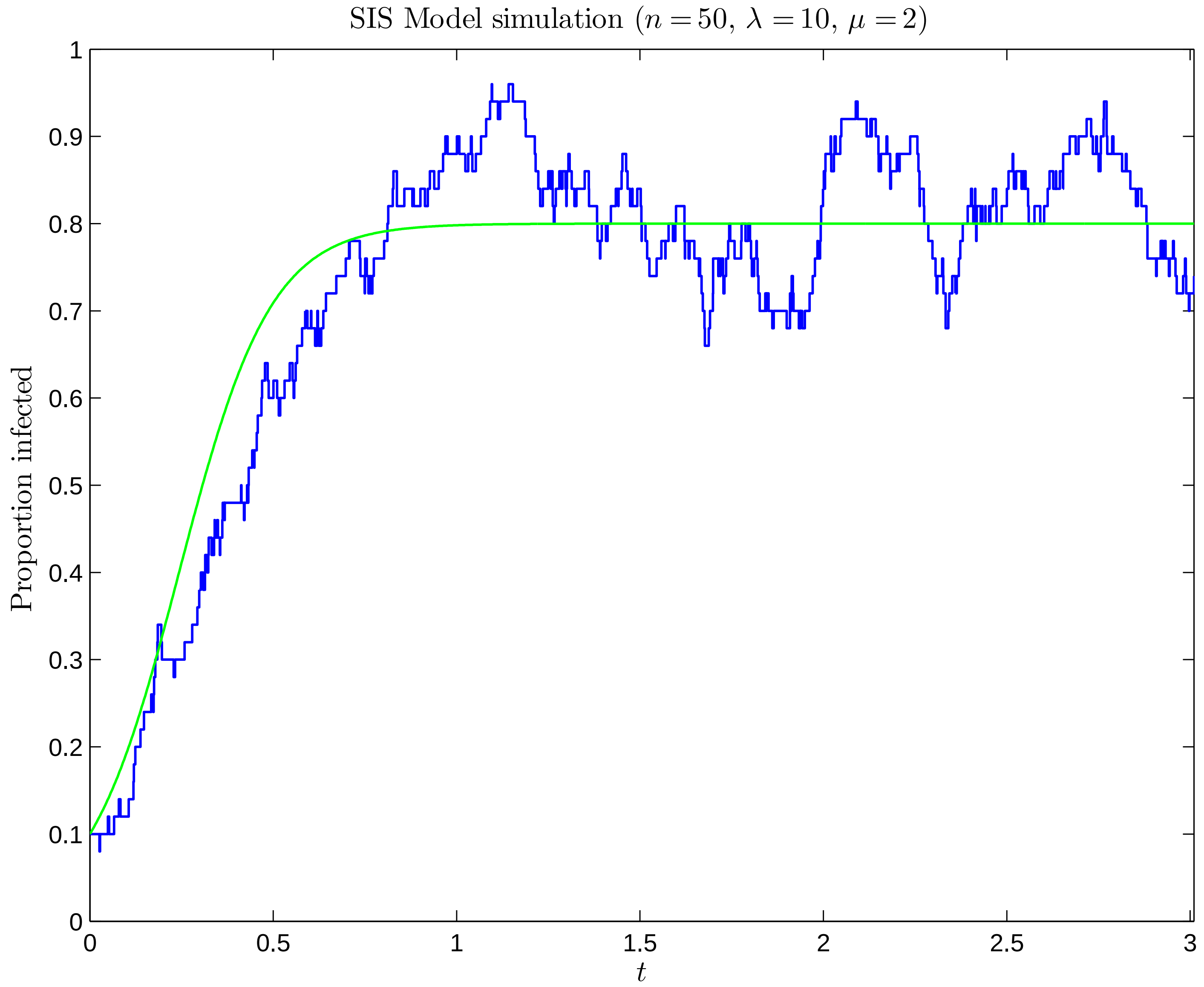
where $\rho = \mu/\lambda$, namely

$$y(t) = \frac{(1-\rho)y_0}{y_0 + (1-\rho-y_0)e^{-\lambda(1-\rho)t}}, \quad y(0) = y_0.$$

Infection dies out ($\lambda < \mu$)



Infection becomes endemic ($\lambda > \mu$)



Individual variation

Suppose now that the population is heterogeneous in that individuals have different characteristics: individual i $(i = 1, \dots, n)$ has

- an exponentially distributed recovery period with mean μ_i^{-1};
- a resistence level λ_i^{-1}; and,
- when infected, contributes κ_i to the infective potential of the population.

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- when infected, contributes κ_i to the infective potential of the population.

Let $X_i^{(n)}$ be 1 or 0 according to whether individual i is infected or not, and let $X^{(n)} = (X_1^{(n)}, \ldots, X_n^{(n)})$ be the state of the population.

The model

Suppose $(X^{(n)}(t),\ t \geq 0)$ is a continuous-time Markov chain on $\{0,1\}^n$ with transitions

$$(\ldots, 0, \ldots) \to (\ldots, 1, \ldots) \quad \text{at rate} \quad \lambda_i f\left(\frac{1}{n}\sum_{j=1}^{n} \kappa_j X_j^{(n)}\right)$$

$$(\ldots, 1, \ldots) \to (\ldots, 0, \ldots) \quad \text{at rate} \quad \mu_i.$$

$\uparrow$

Position i $(i = 1, \ldots, n)$

The function $f : \mathbb{R}_+ \to \mathbb{R}_+$ is Lipschitz continuous.

The model

For this talk take $\kappa_i = 1$ and $f(x) = x$, so that our Markov chain has transitions

$$\begin{aligned} (\ldots, 0, \ldots) &\to (\ldots, 1, \ldots) \quad \text{at rate} \quad \lambda_i \bar{X}^{(n)} \\ (\ldots, 1, \ldots) &\to (\ldots, 0, \ldots) \quad \text{at rate} \quad \mu_i, \end{aligned}$$

$\uparrow$

Position i $(i = 1, \ldots, n)$

where $\bar{X}^{(n)} = \frac{1}{n} \sum_{j=1}^{n} X_j^{(n)}$ (the *proportion* of the population that is infected).

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\begin{array}{lll}
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(\dots,1,\dots) \to (\dots,0,\dots) & \text{at rate} & \mu_i, \\
\quad\uparrow & & \\
\text{Position } i \ (i = 1,\dots,n) & &
\end{array}
$$

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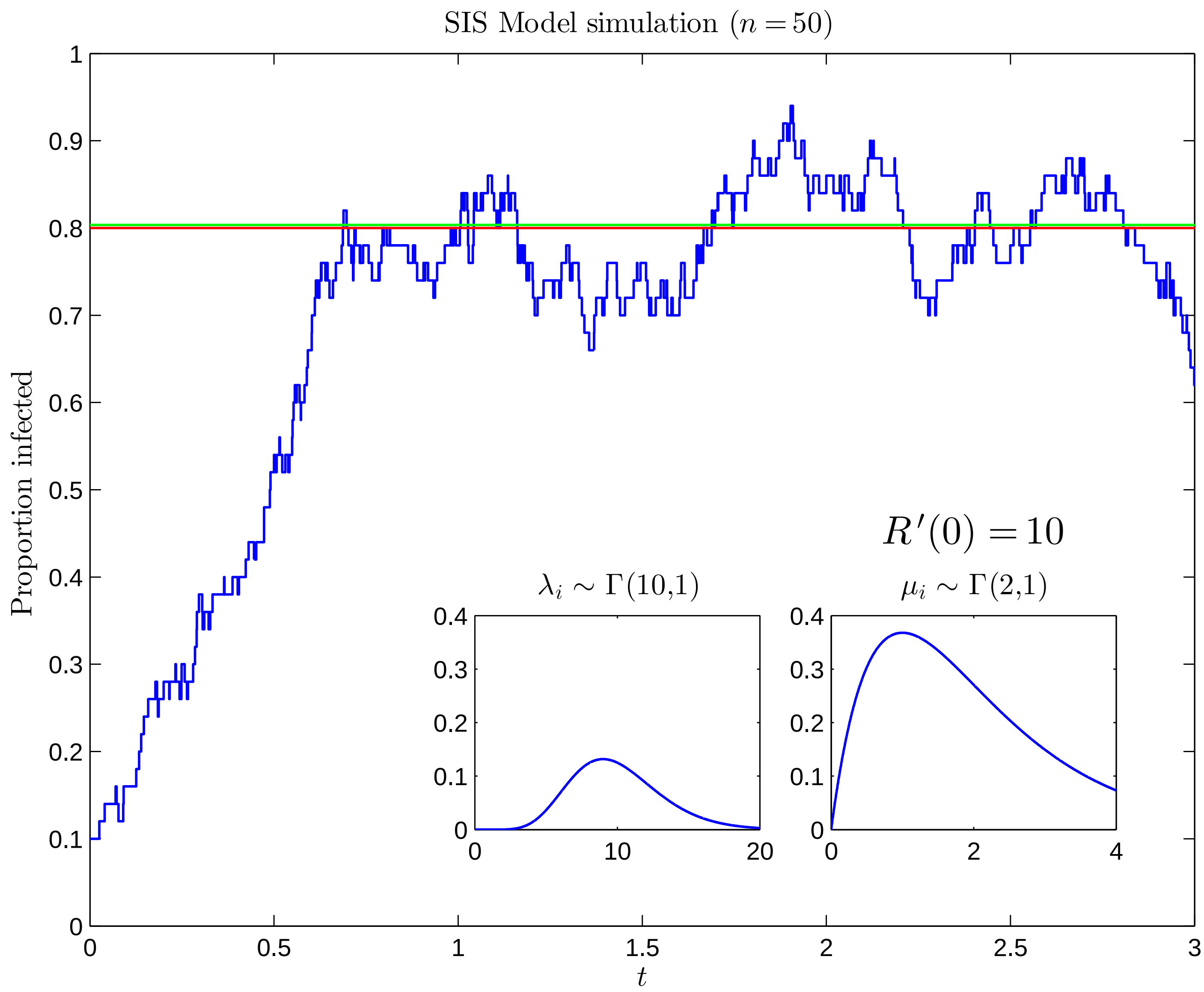
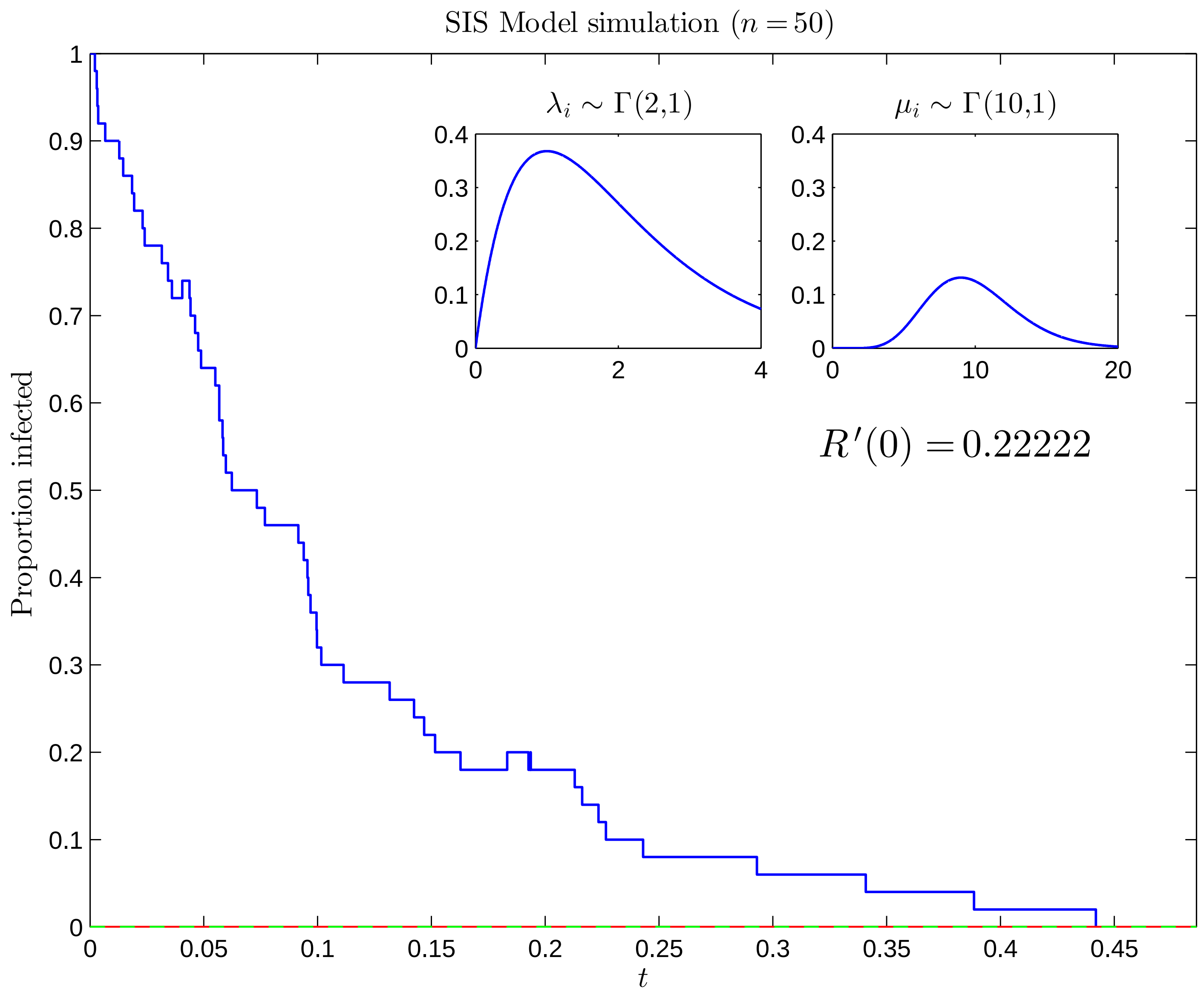
The plan: to get a handle on large n behaviour, and, then, to determine conditions for endemicity.

Endemicity

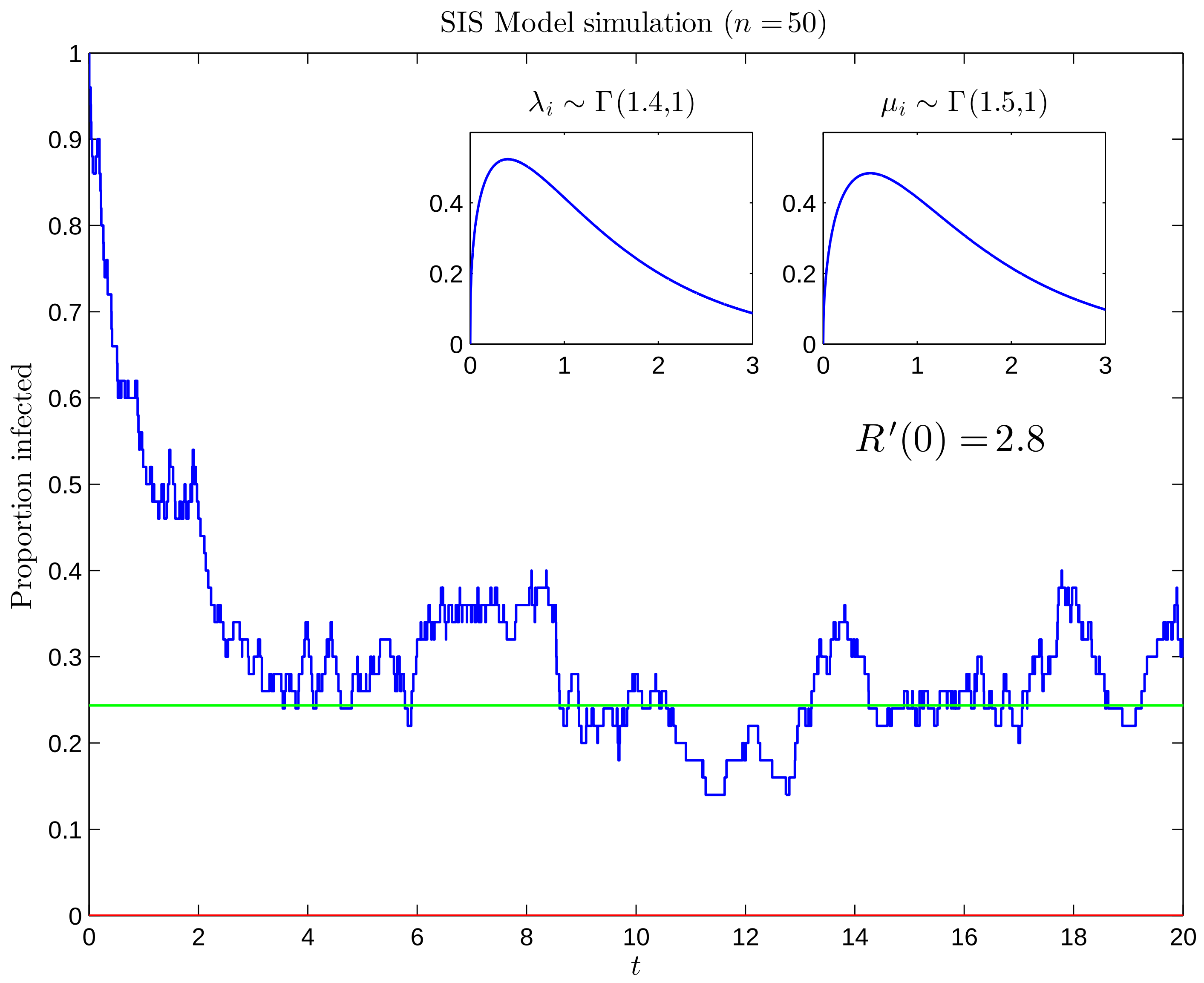


SIS Model simulation ($n = 50$)
Proportion infected
t
$R'(0) = 10$
$\lambda_i \sim \Gamma(10,1)$
$\mu_i \sim \Gamma(2,1)$
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0.5
1.5
2
2.5
3
10
20
4

Disease free state is globally stable



Endemicity!



SIS Model simulation ($n = 50$)
$\lambda_i \sim \Gamma(1.4,1)$
$\mu_i \sim \Gamma(1.5,1)$
$R'(0) = 2.8$
Proportion infected
t
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
2
4
6
8
10
12
14
16
18
20
0.4
0.2
0
1
2
3

Our approach - Point processes

Think of the individual characteristics $\theta_i := (\lambda_i, \mu_i)$ as (random) points in a subset S of $\mathbb{R}^2_+$.

Define sequences of random measures $(\sigma^{(n)})$ and random-measure-valued processes $(m_t^{(n)}, t \geq 0)$ by

$$\sigma^{(n)}(B) = \#\{\theta_i \in B\}/n, \qquad B \in \mathcal{B}(S),$$

$$m_t^{(n)}(B) = \#\{\theta_i \in B : X_{i,t}^{(n)} = 1\}/n, \qquad B \in \mathcal{B}(S).$$

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Our approach - Point processes

Equivalently, we may define $(\sigma^{(n)})$ and $(m_t^{(n)})$ by

$$\int h(\theta)\sigma^{(n)}(d\theta) = \frac{1}{n}\sum_{i=1}^{n} h(\theta_i)$$

$$\int h(\theta)m_t^{(n)}(d\theta) = \frac{1}{n}\sum_{i=1}^{n} X_{i,t}^{(n)}\, h(\theta_i),$$

for h in $C_b(S)$, the class of bounded continuous functions that map S to $\mathbb{R}$. (Here $\theta = (\lambda, \mu)$.)

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For example $(h \equiv 1)$,

$$m_t^{(n)}(S) = \int m_t^{(n)}(d\theta) = \frac{1}{n}\sum_{i=1}^{n} X_{i,t}^{(n)} \quad \text{(proportion infected)}.$$

A measure-valued limiting process

Theorem. [MP2] Suppose that $\sigma^{(n)} \xrightarrow{d} \sigma$ and $m_0^{(n)} \xrightarrow{d} m_0$ for some non-random measures σ and m_0. Then, the sequence of measure-valued processes $(m_t^{(n)}, t \geq 0)$ converges weakly to the unique solution $(m_t, t \geq 0)$ of

$$(h, m_t) = (h, m_0) + \int_0^t L(h, m_s)\, ds, \quad h \in C_b(S),$$

where (notation) $(h, m) = \int h(\theta) m(d\theta)$, and

$$L(h, m_t) := m_t(S) \left(\int \lambda h(\theta) \sigma(d\theta) - \int \lambda h(\theta) m_t(d\theta) \right) - \int \mu h(\theta) m_t(d\theta).$$

The limiting process

Lemma. For all $B \in \mathcal{B}(S)$ and $t \geq 0$, $m_t(B) \leq \sigma(B)$.

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In particular $m_t << \sigma$, and so m_t has a $($uniquely determined σ-a.e.$)$ Radon-Nikodym derivative ϕ_t (≥ 0) with respect to σ: $m_t(B) = \int_B \phi_t(\theta)\sigma(d\theta)$.

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Now, "differentiate" both sides of

$$(h, m_t) = (h, m_0) + \int_0^t L(h, m_s)\, ds,$$

with respect to σ. We get $\ldots$.

The limiting process

Corollary. The Radon-Nikodym derivative $\phi_t(\lambda, \mu)$ satisfies

$$\phi_t = \phi_0 + \int_0^t \Big(\lambda(1-\phi_s)\int \phi_s(\theta')\sigma(d\theta') - \mu\phi_s\Big)\, ds.$$

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An equilibrium ϕ_{eq} must satisfy

$$0 = \lambda(1 - \phi_{\mathrm{eq}}) \int \phi_{\mathrm{eq}}(\theta')\sigma(d\theta') - \mu\phi_{\mathrm{eq}}.$$

Equilibria of the limiting process

An equilibrium ϕ_{eq} must satisfy

$$0 = \lambda(1 - \phi_{\mathrm{eq}}) \int \phi_{\mathrm{eq}}(\theta)\sigma(d\theta) - \mu\phi_{\mathrm{eq}}\,.$$

On setting $\psi = \int \phi_{\mathrm{eq}}(\theta)\sigma(d\theta)$, we see that

$$\phi_{\mathrm{eq}}(\lambda,\mu)\ (\,=\phi_{\mathrm{eq}}(\theta)\ ) = \frac{\lambda\psi}{\lambda\psi+\mu},$$

and so, on integrating this over $(\lambda,\mu)\in S$, we find that ψ must solve the equation

$$\psi = R(\psi) := \int \frac{\lambda\psi}{\lambda\psi+\mu}\,\sigma(d\lambda,d\mu).$$

Stability

Theorem. (a) If $R'(0) \leq 1$, then $\psi = 0$ is the only fixed point of R, and $\phi_{\mathrm{eq}} = 0$ is globally stable, that is, for all ϕ_0, $\phi_t \to 0$ on S. The latter entails $m_t(B) \to 0$, for all $B \in \mathcal{B}(S)$, and hence *the disease free state is globally stable*.

Stability

Theorem. (b) If $R'(0) > 1$, then R has two fixed points, 0 and a positive fixed point ψ_*, and (subject to mild extra conditions), if $(m_0(S) =)\ (\phi_{\mathrm{o}}, \sigma) > 0$, then

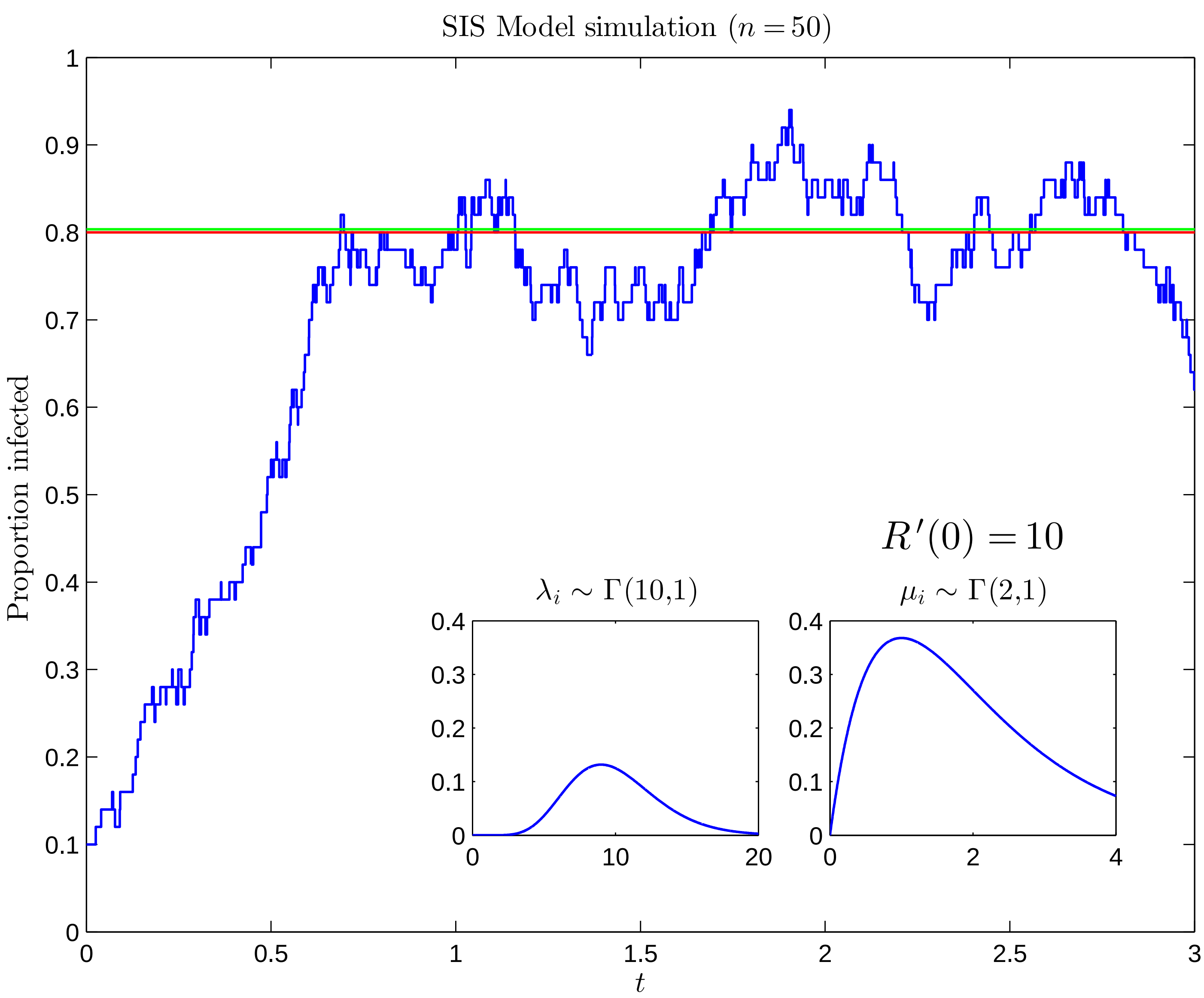
$$\phi_t \to \phi_* := \frac{\lambda\psi_*}{\lambda\psi_* + \mu}.$$

The latter entails $m_t(B) \to m_*(B)$, for all $B \in \mathcal{B}(S)$, where

$$m_*(B) = \int_B \phi_*(\theta)\sigma(d\theta) = \int_B \frac{\lambda\psi_*}{\lambda\psi_* + \mu}\sigma(d\lambda, d\mu),$$

implying *endemicity*.

Endemicity



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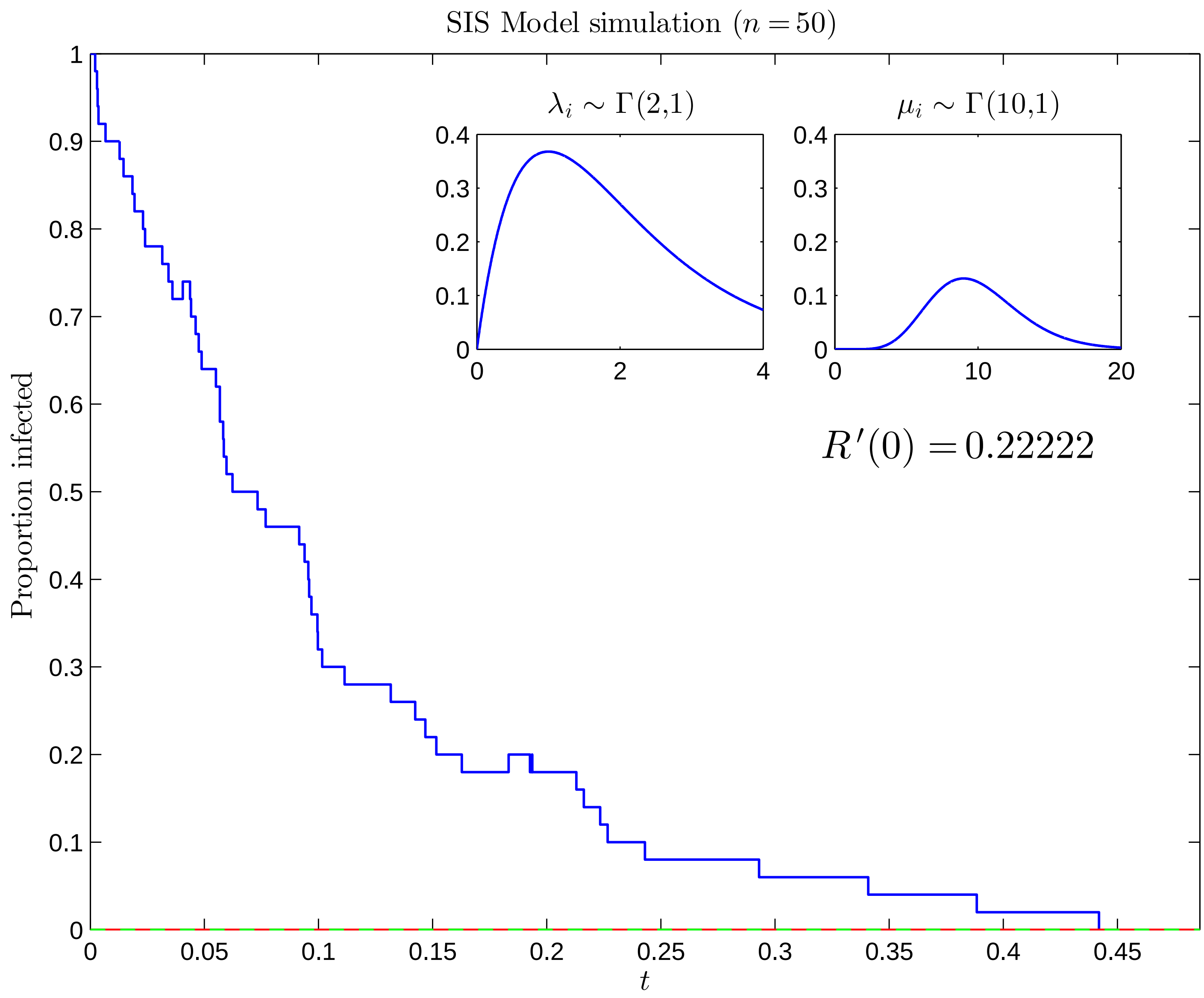

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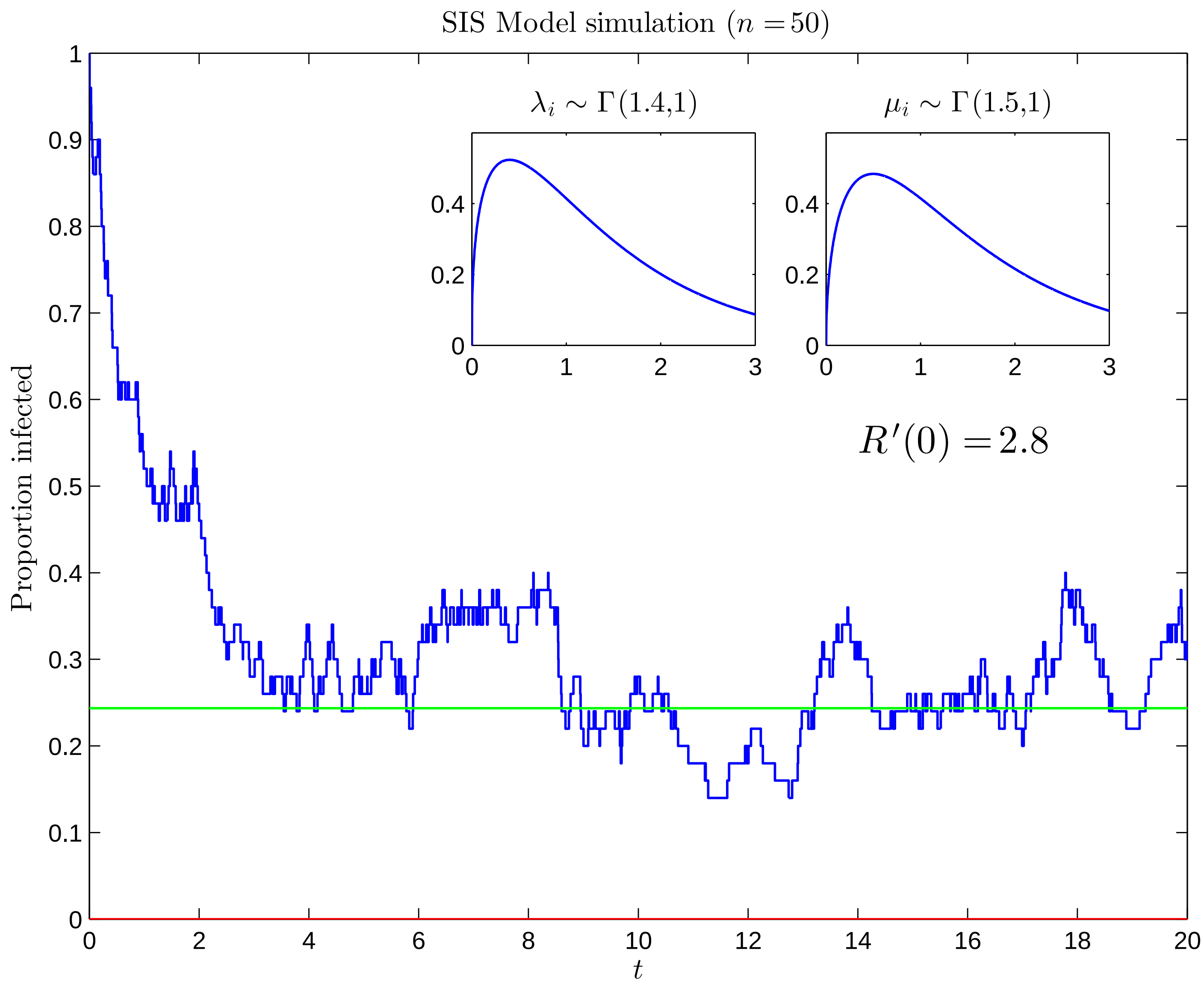

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