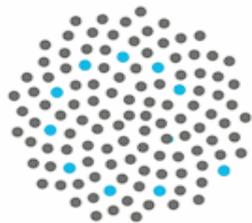


# Modelling population processes with random initial conditions

Phil Pollett

<http://www.maths.uq.edu.au/~pkp>



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University of Warwick



# Starting point

A paper by Bonnie Kegan (US Census Bureau Washington DC) and R. Webster West (now at Texas A&M University) ...

B. Kegan and R.W. West (2005) Modeling the simple epidemic with deterministic differential equations and random initial conditions. *Math. Biosci.* 194, 217–231.

# A simple epidemic

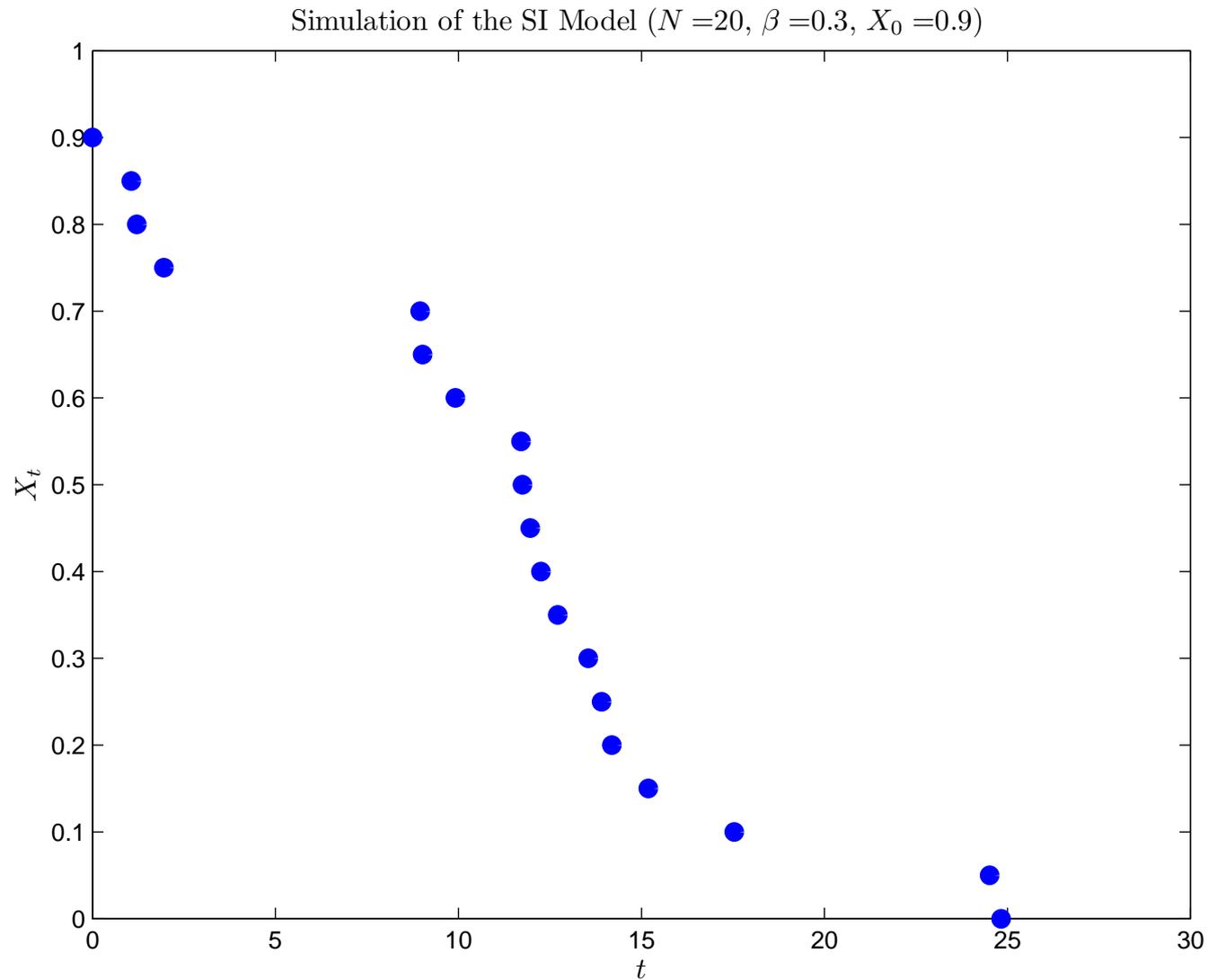
## The SI (*Susceptible-Infected*) Model

- $N$  individuals (fixed)
- $n_t$  susceptibles (random process in continuous time)
- $N - n_t$  infectives

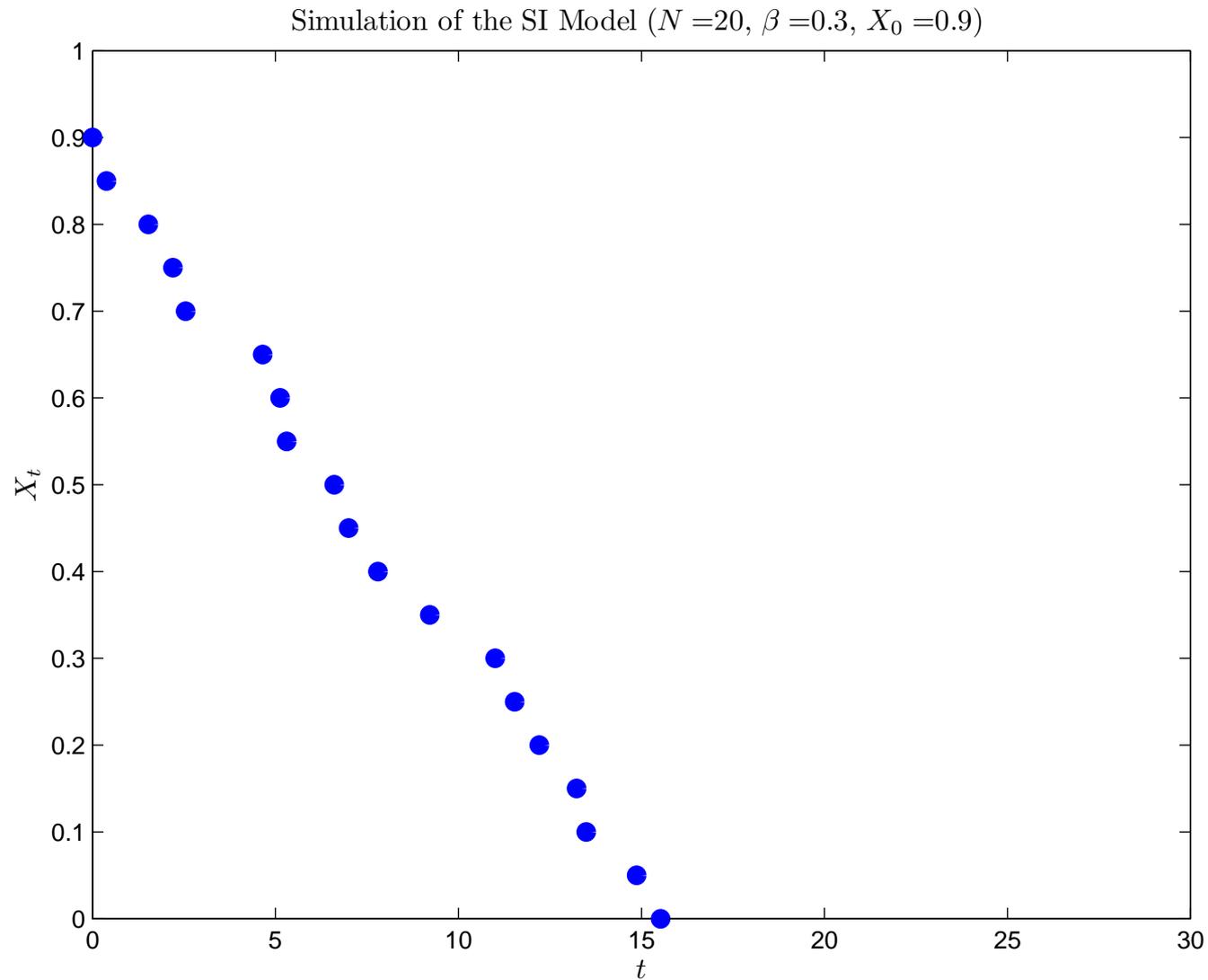
Start with a few infectives. Eventually everyone gets the disease. The per-encounter transmission rate  $\beta$  is specified.

Let  $X_t = n_t/N$  be the *proportion* of susceptibles.

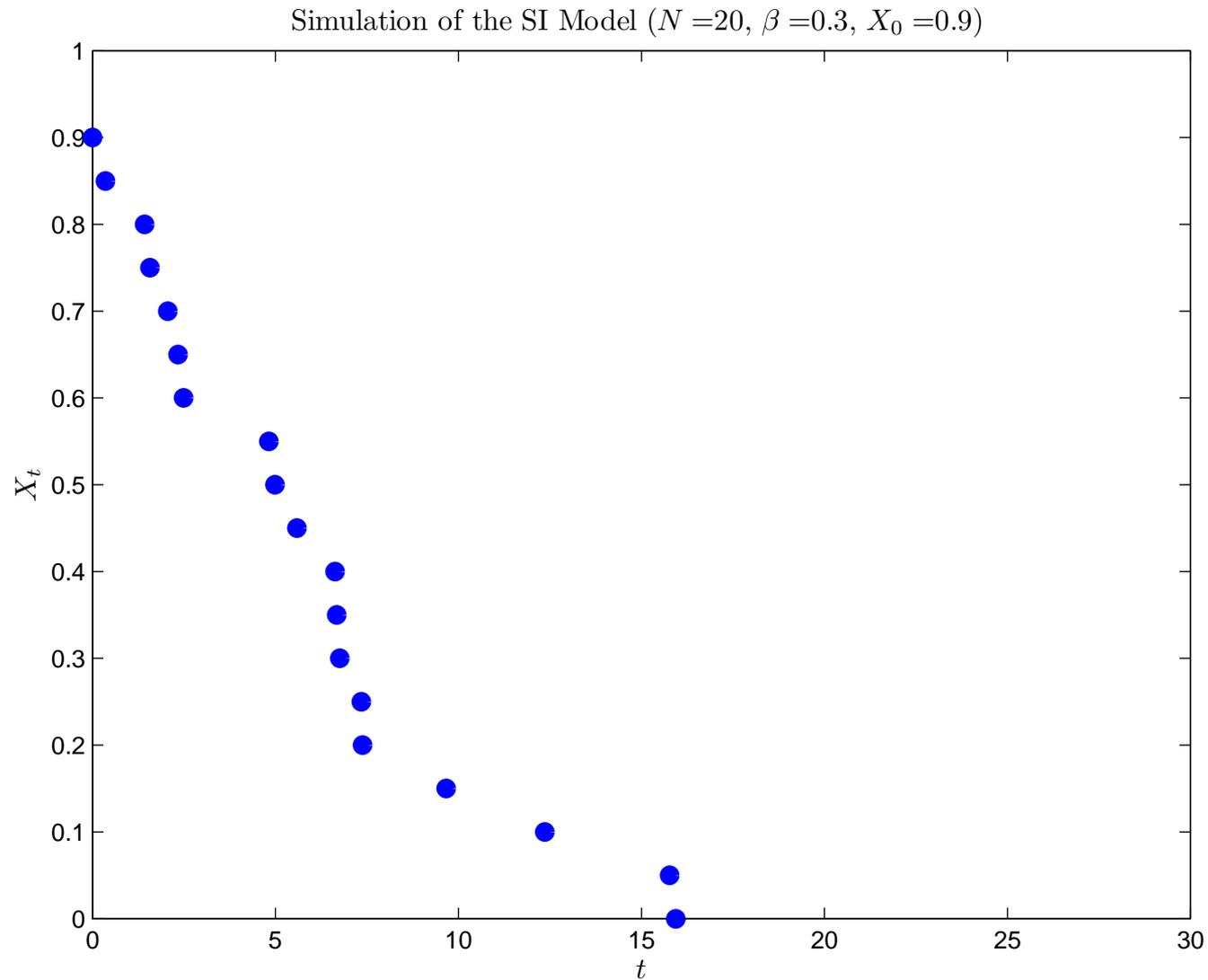
# Proportion of susceptibles



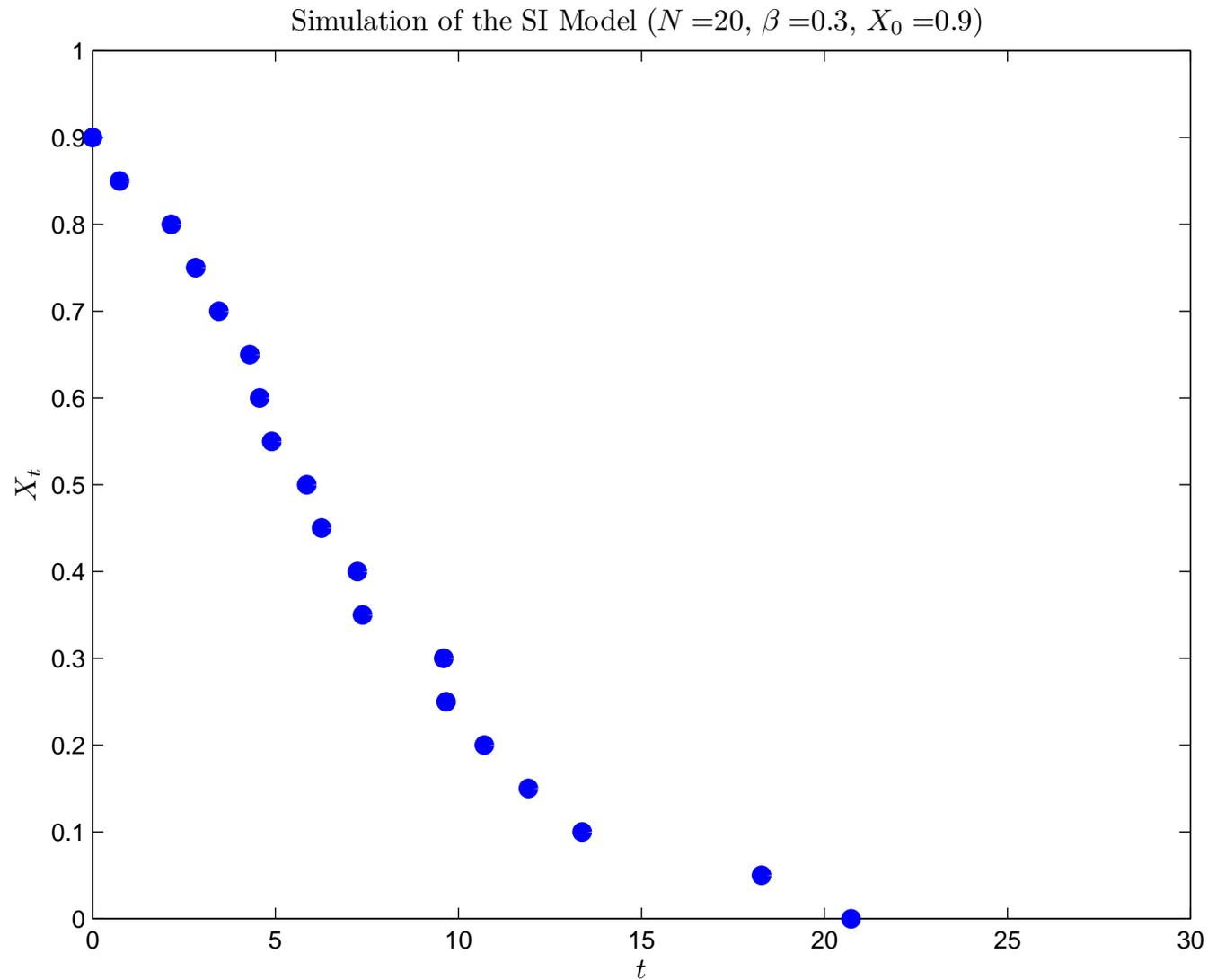
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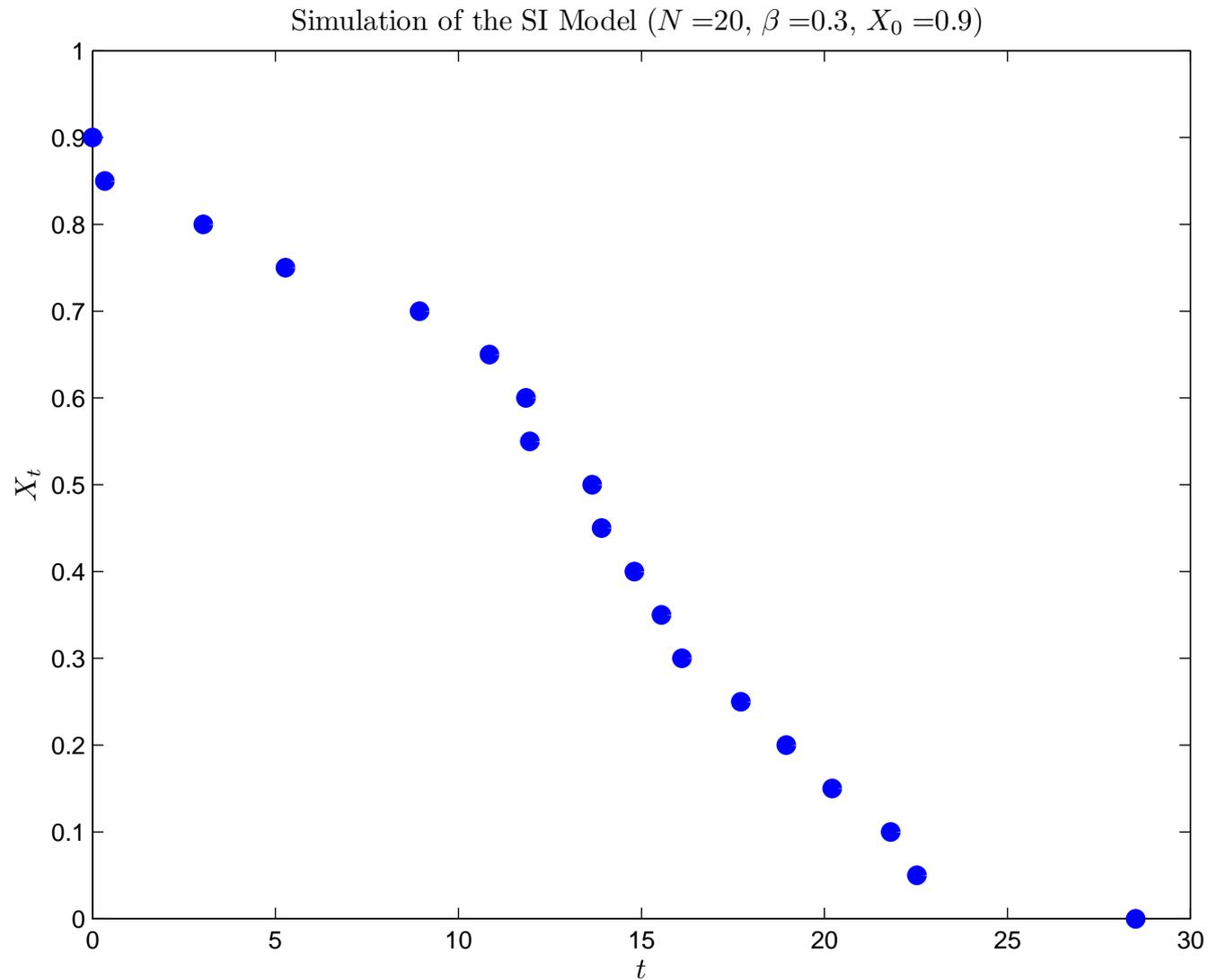
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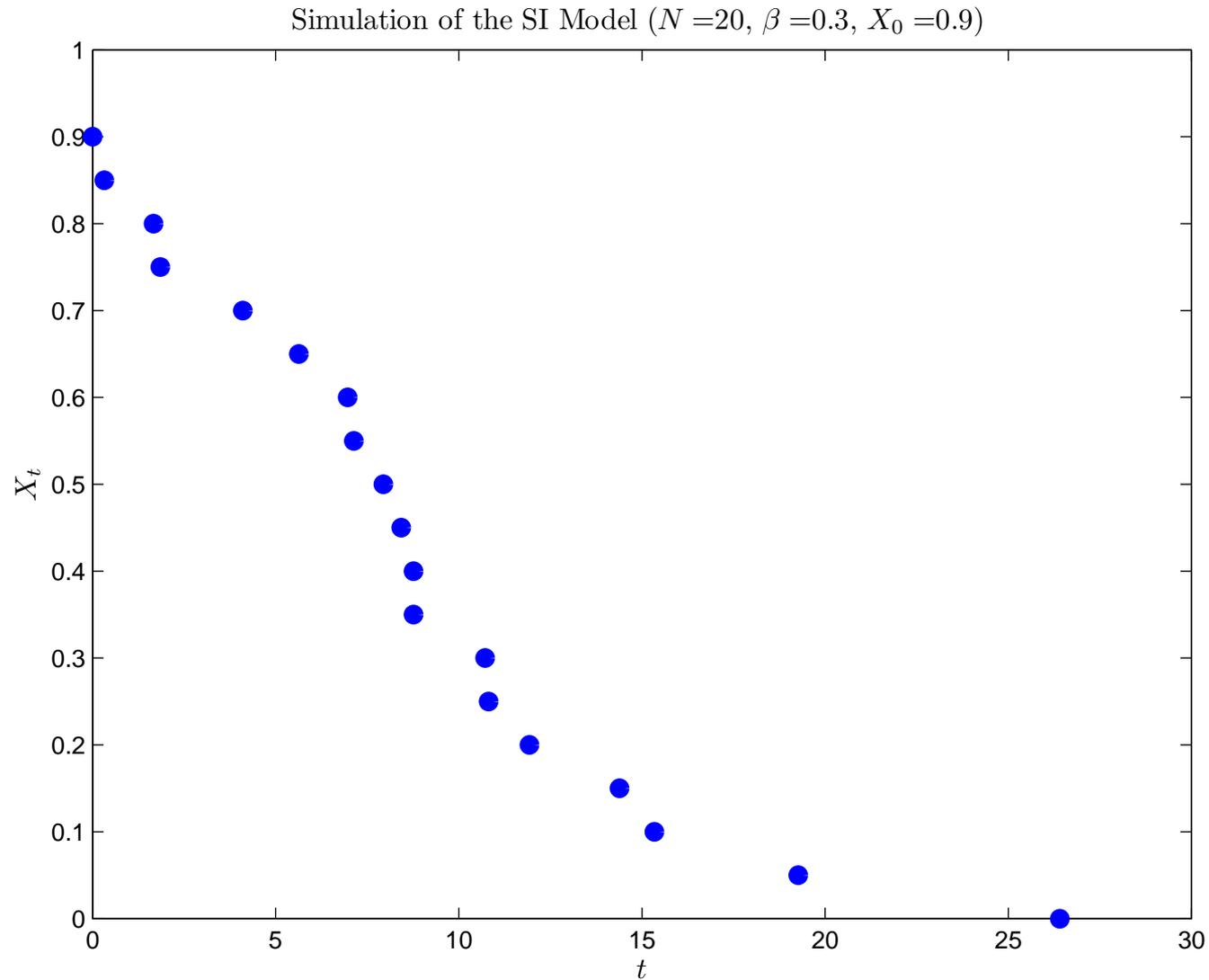
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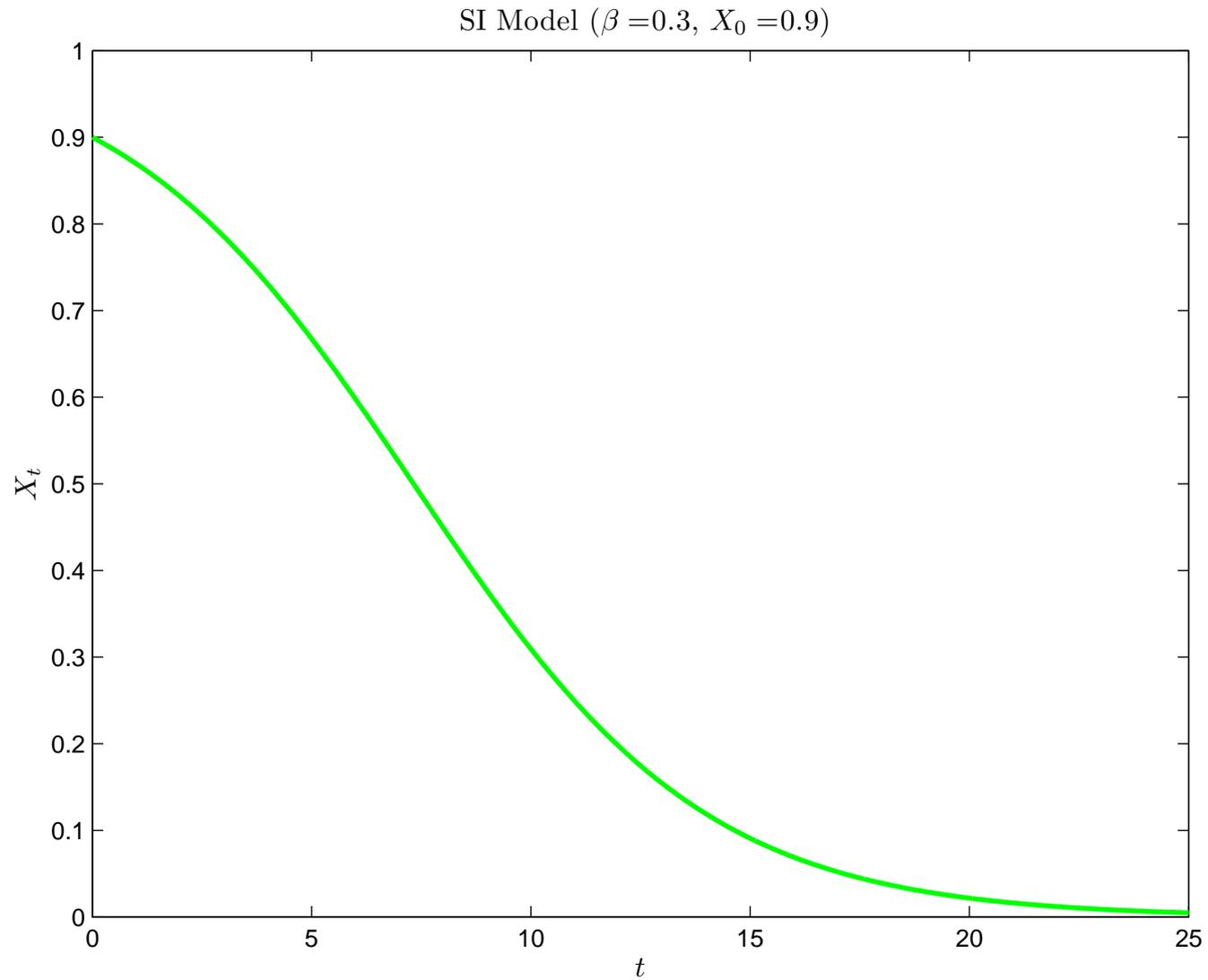
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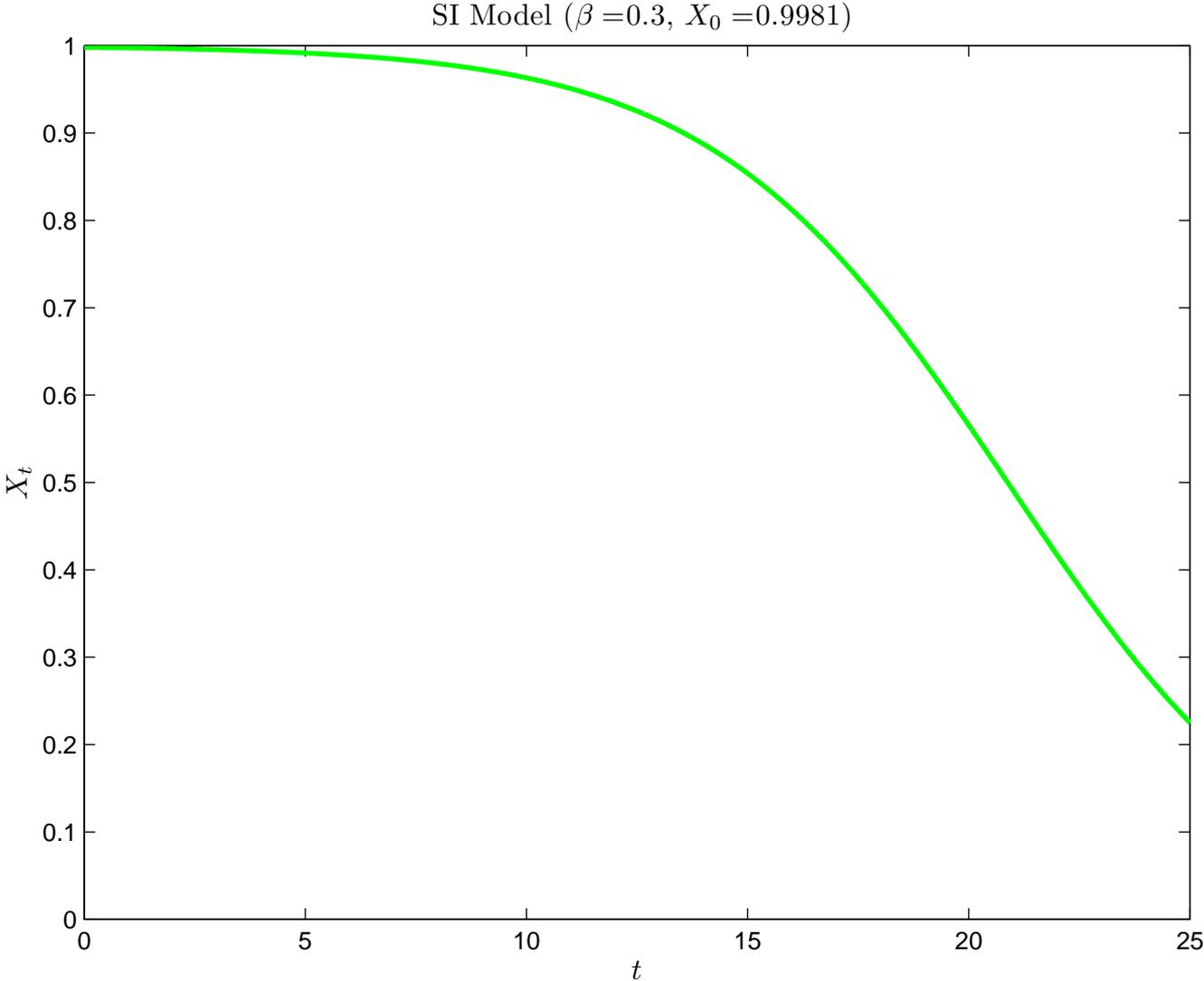
# Kegan and West



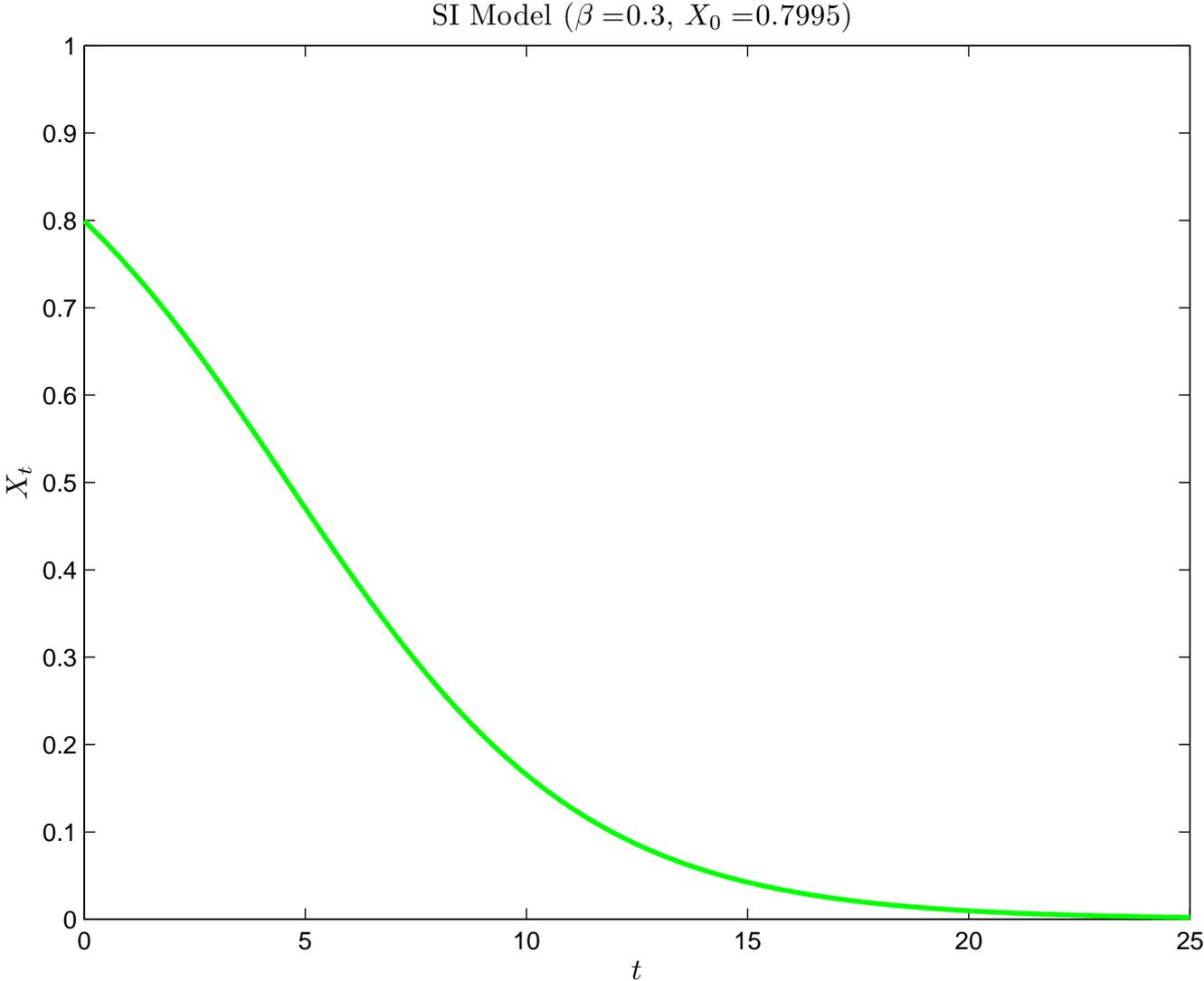
# Kegan and West

- Deterministic dynamics
- Randomness *only* in the initial state

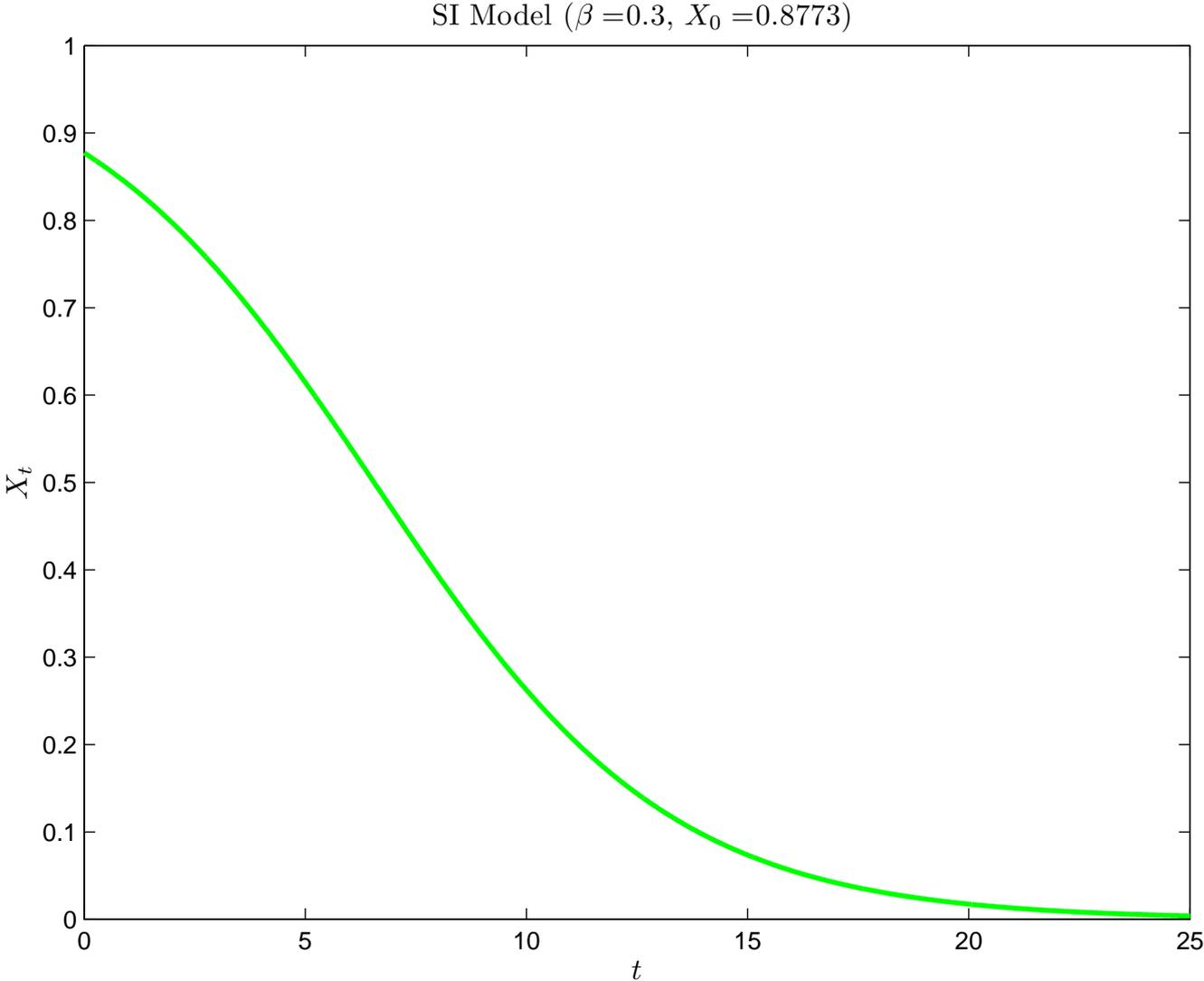
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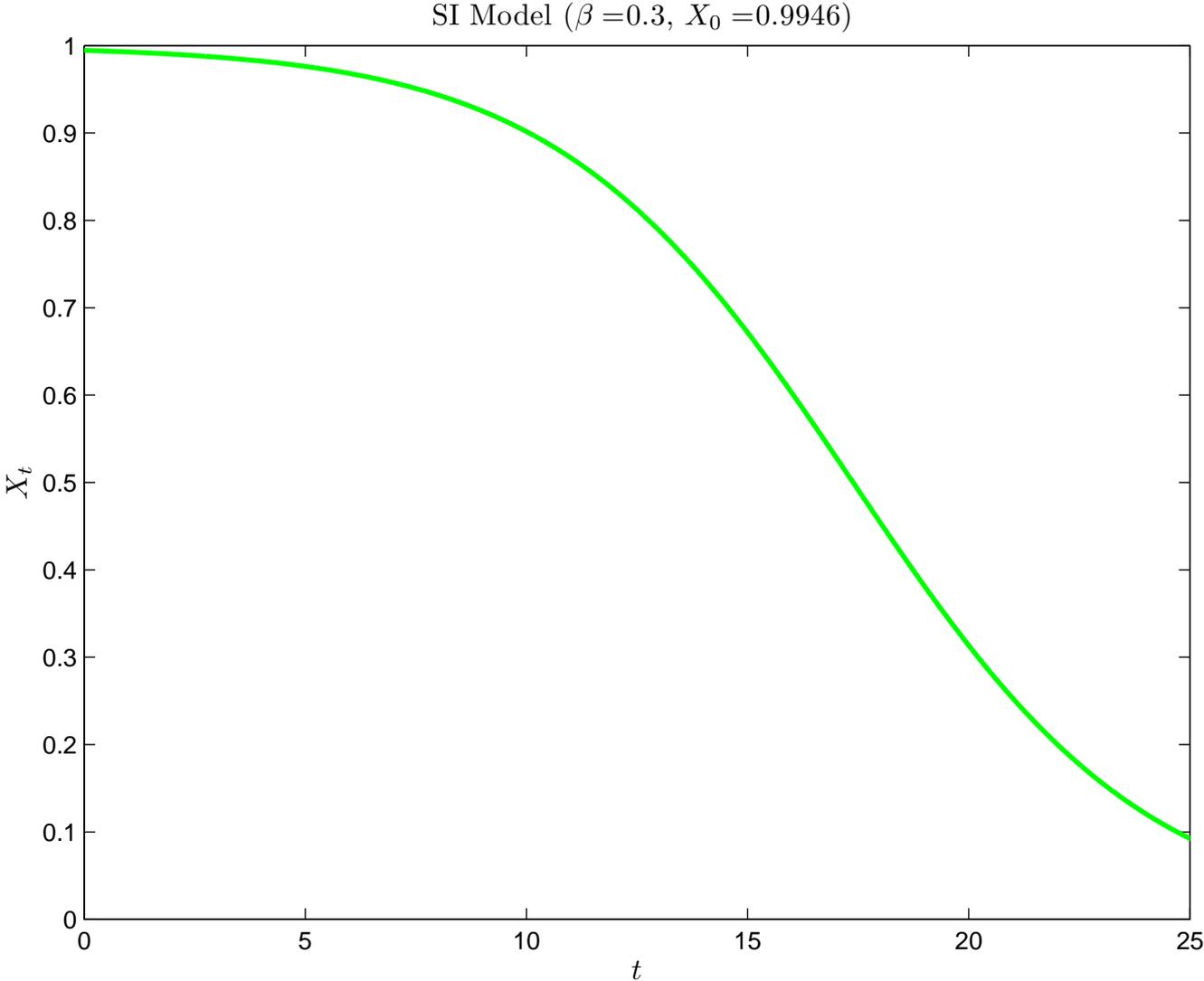
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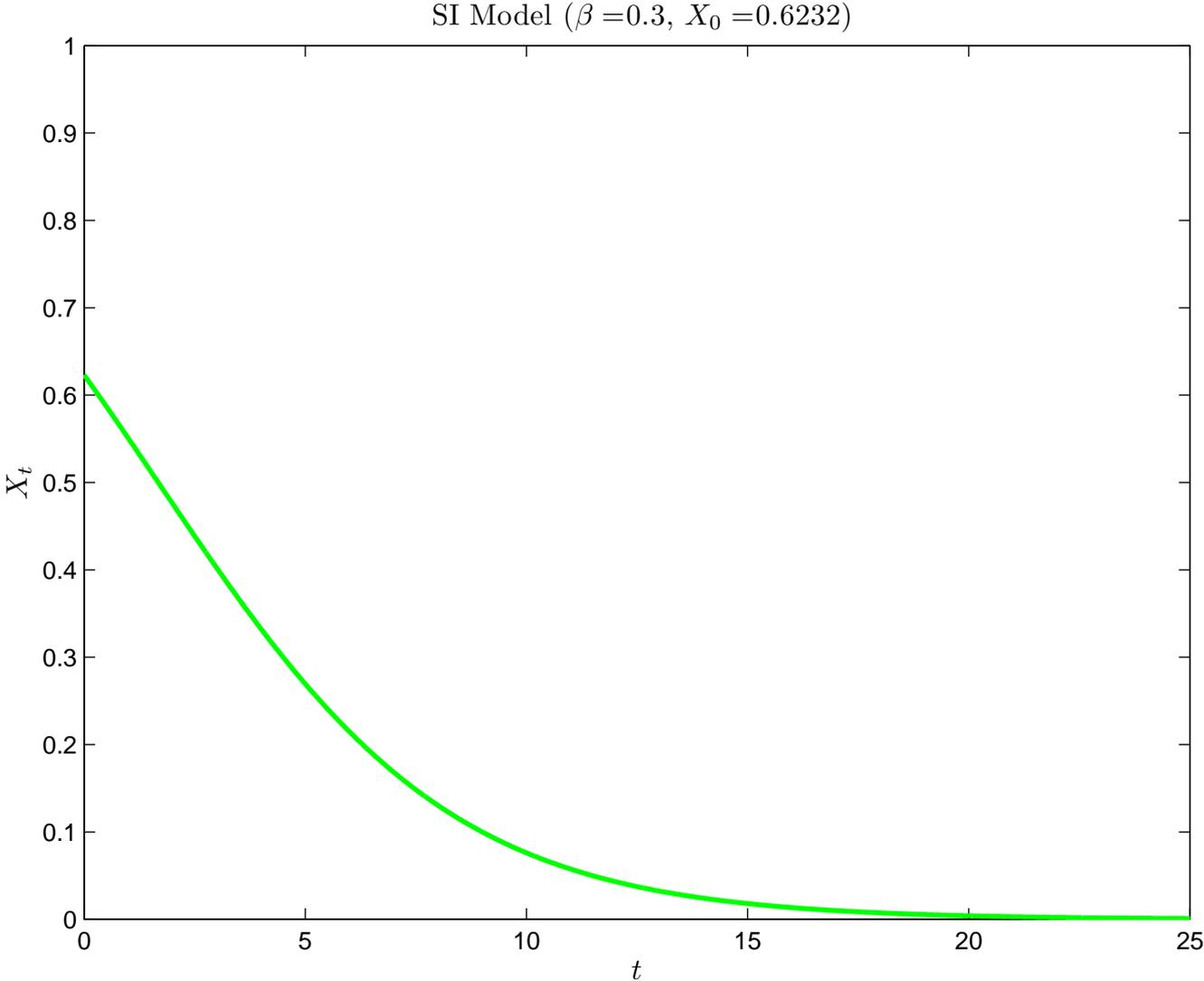
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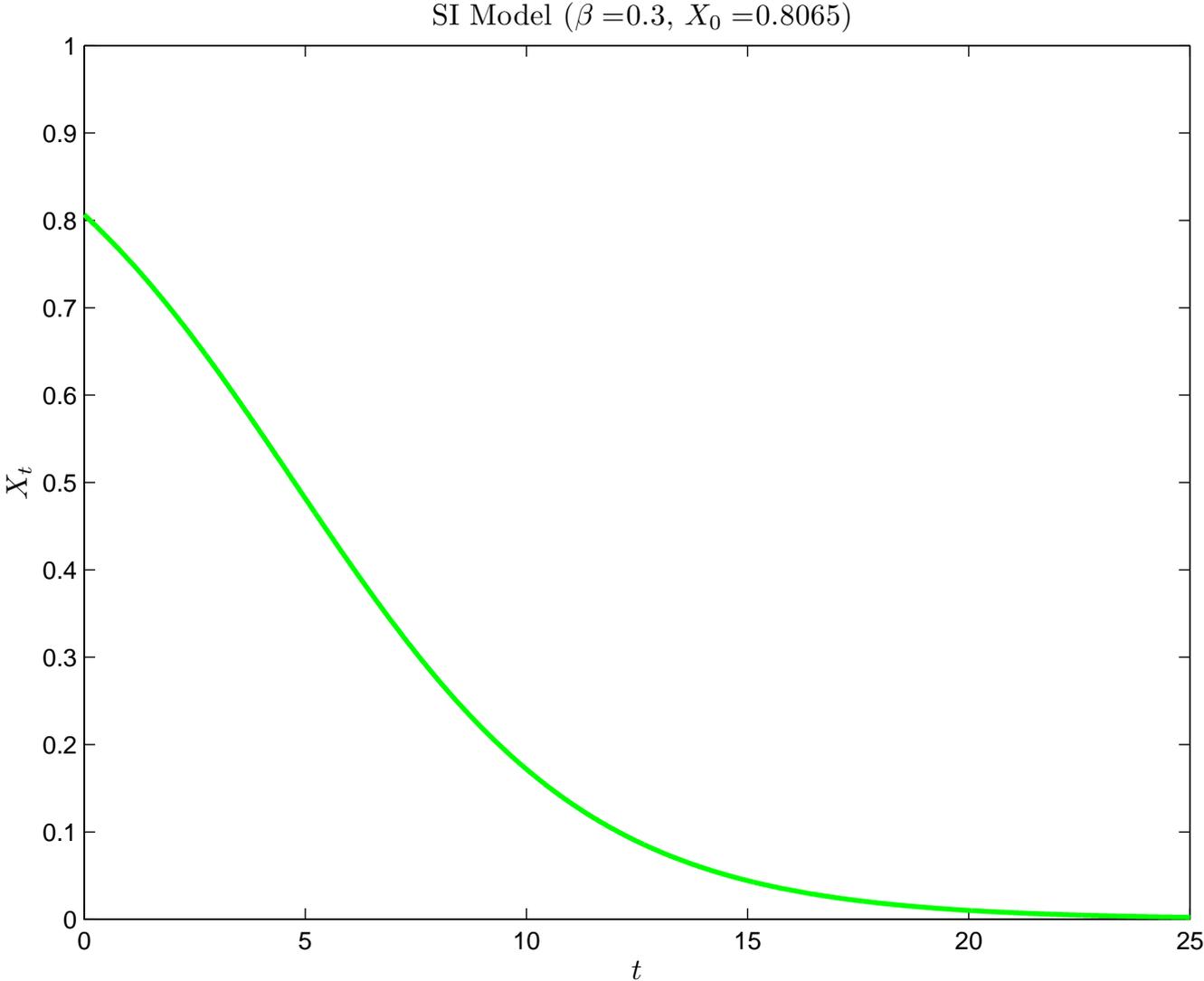
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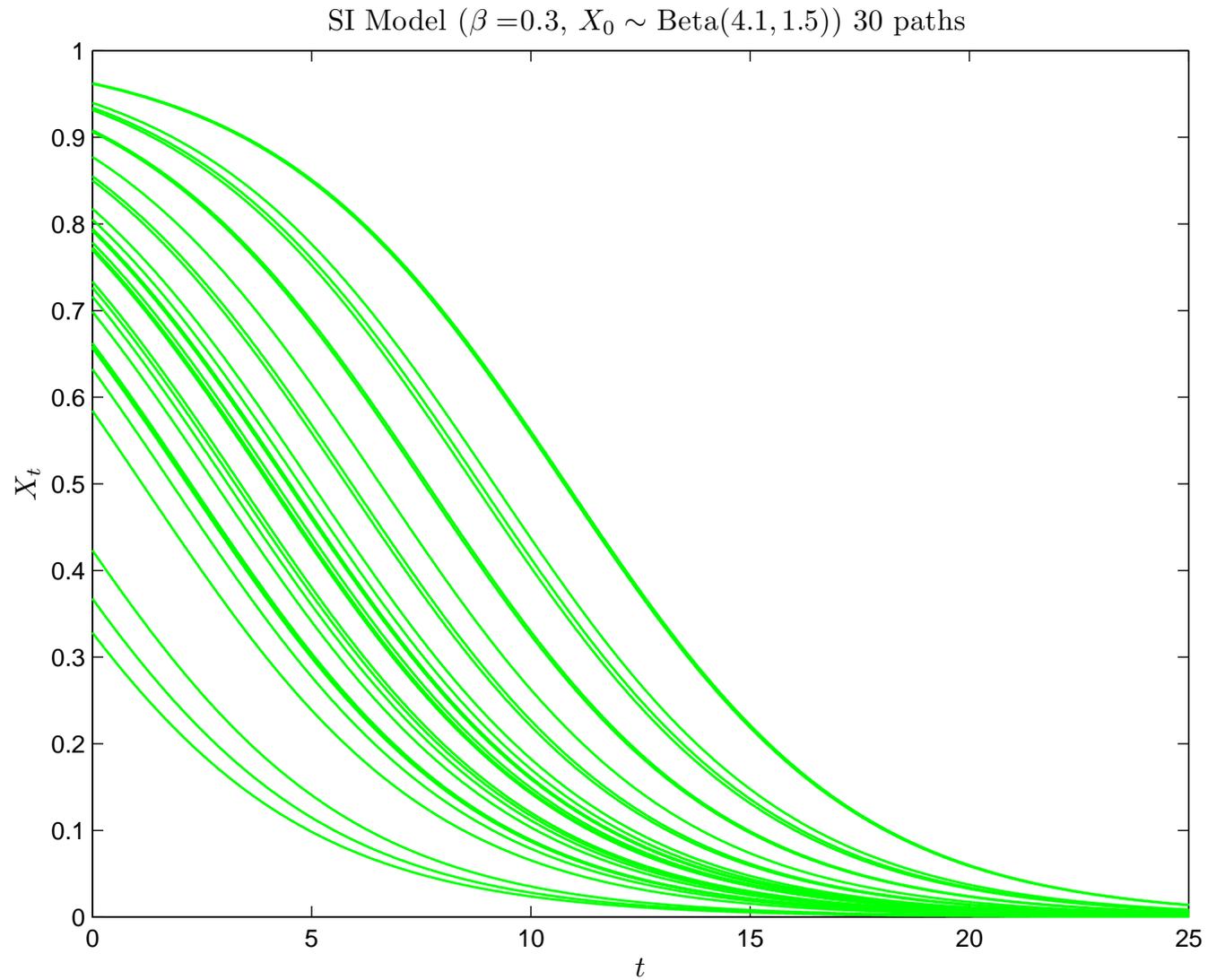
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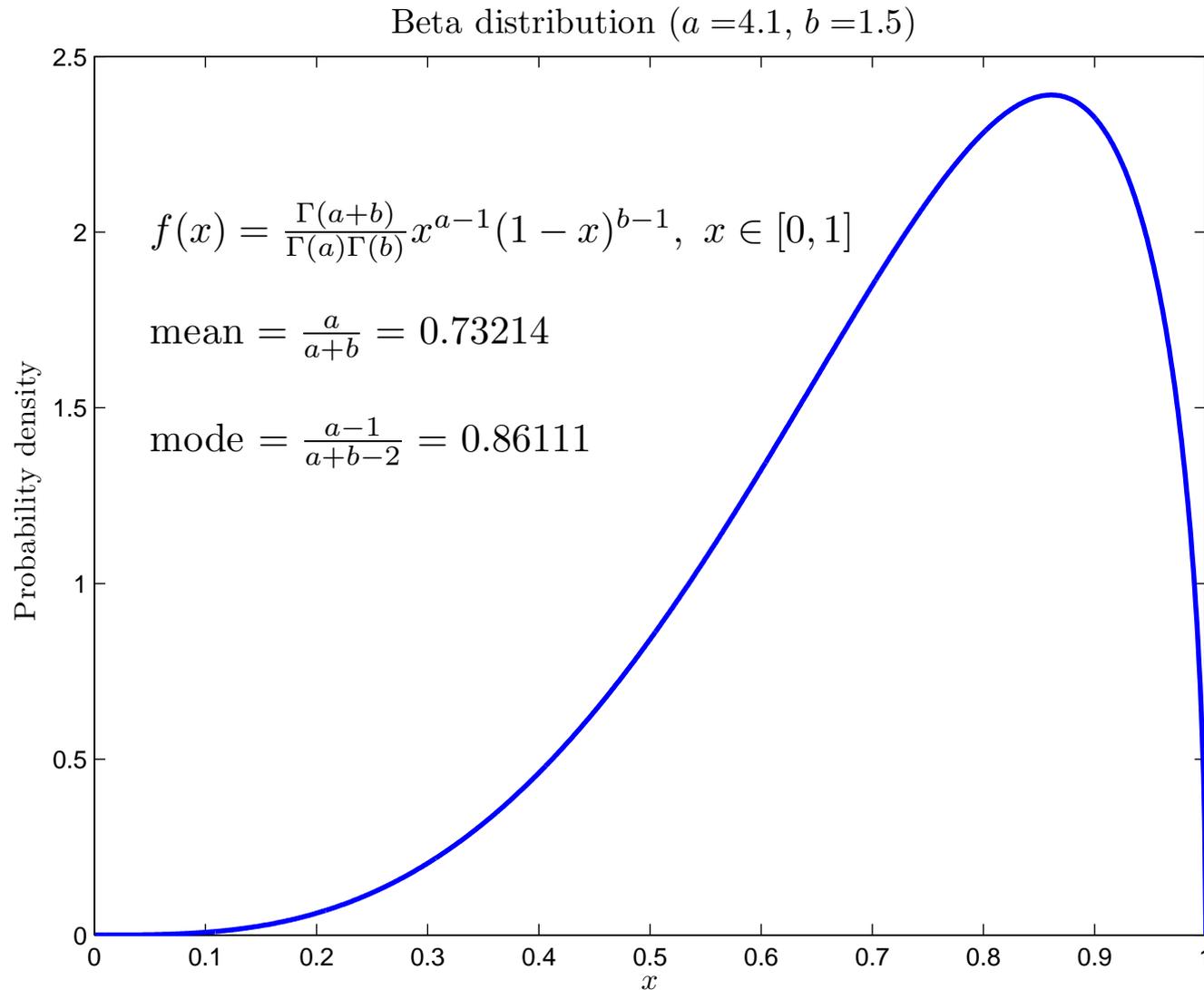
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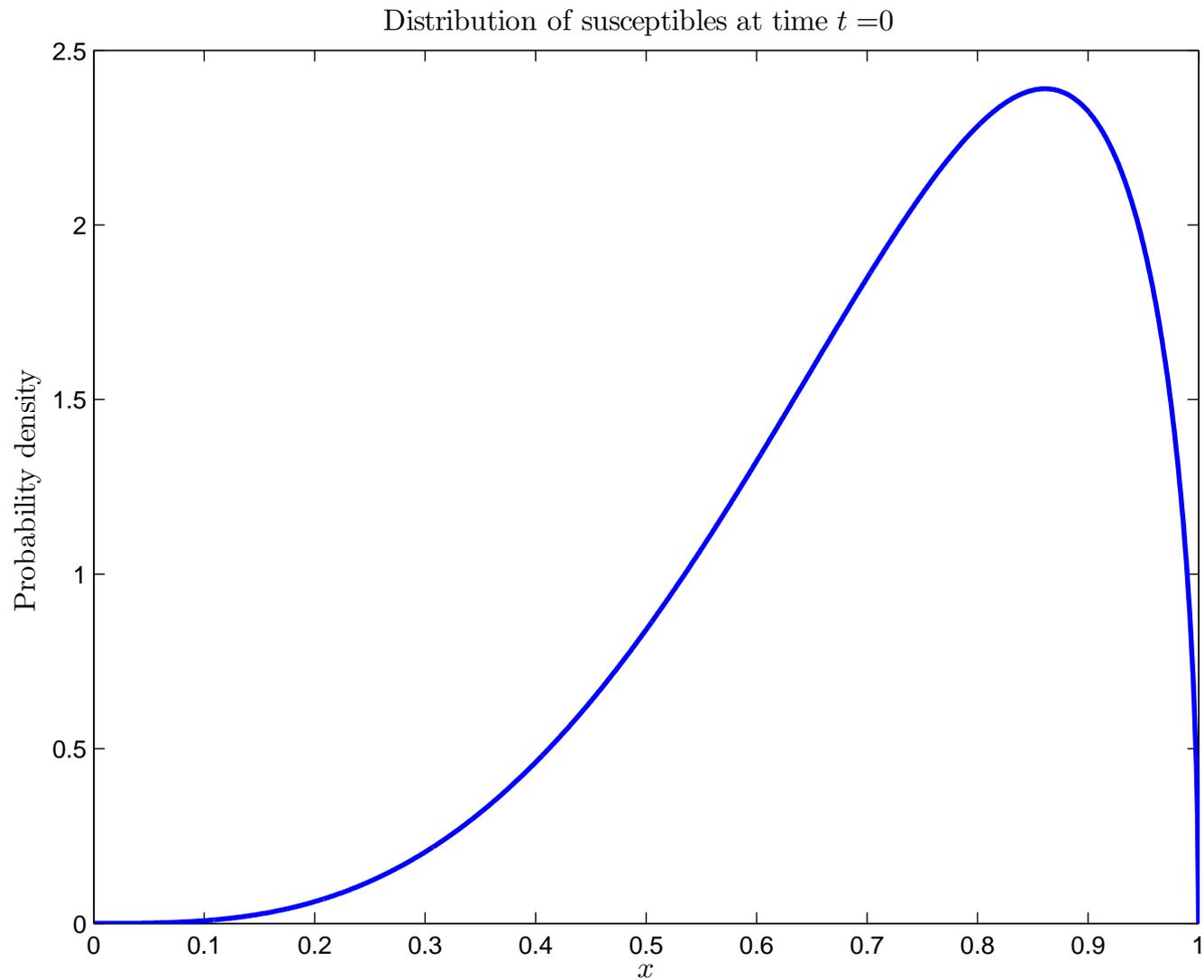
# Kegan and West



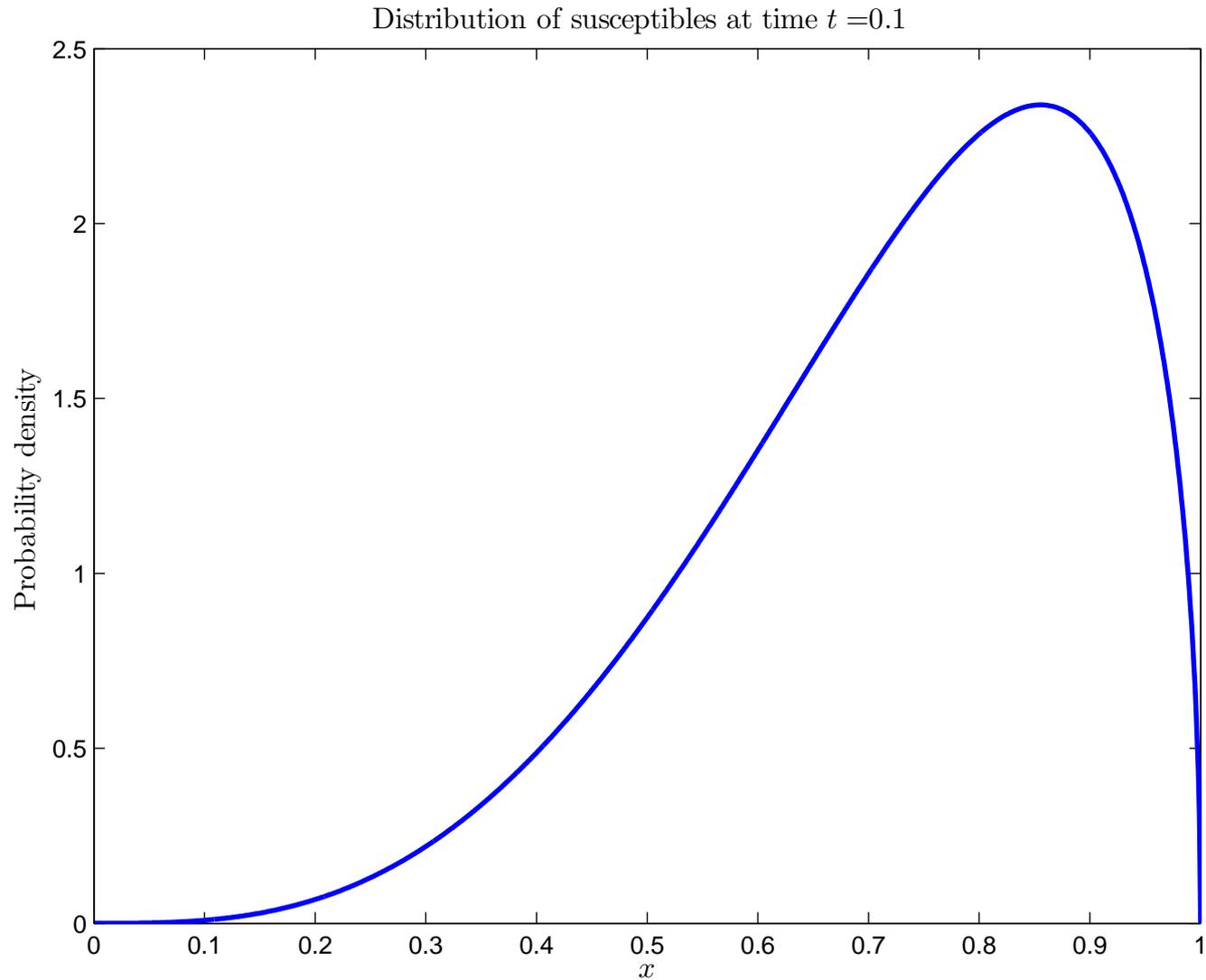
# Kegan and West initial distribution



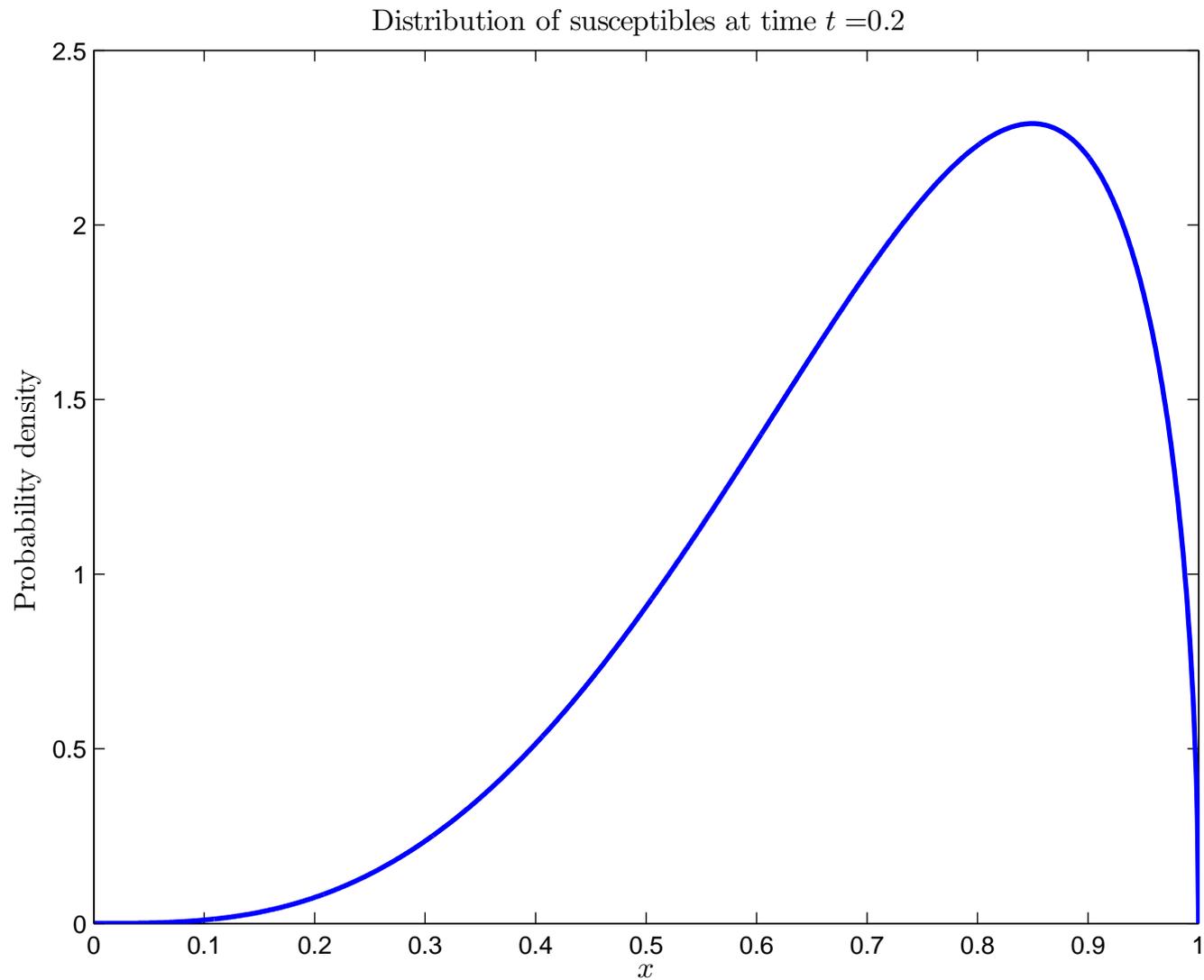
# Distribution at time $t$



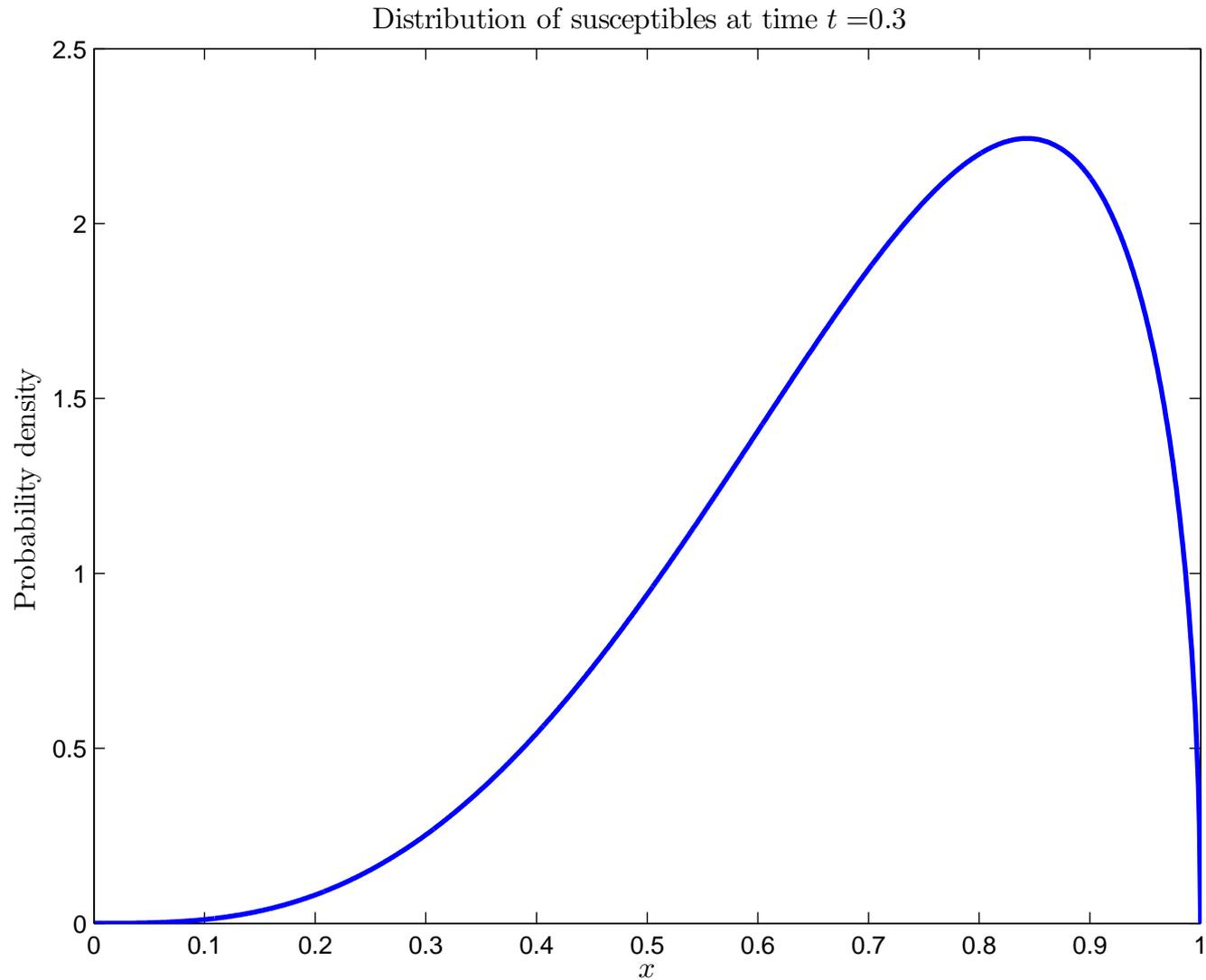
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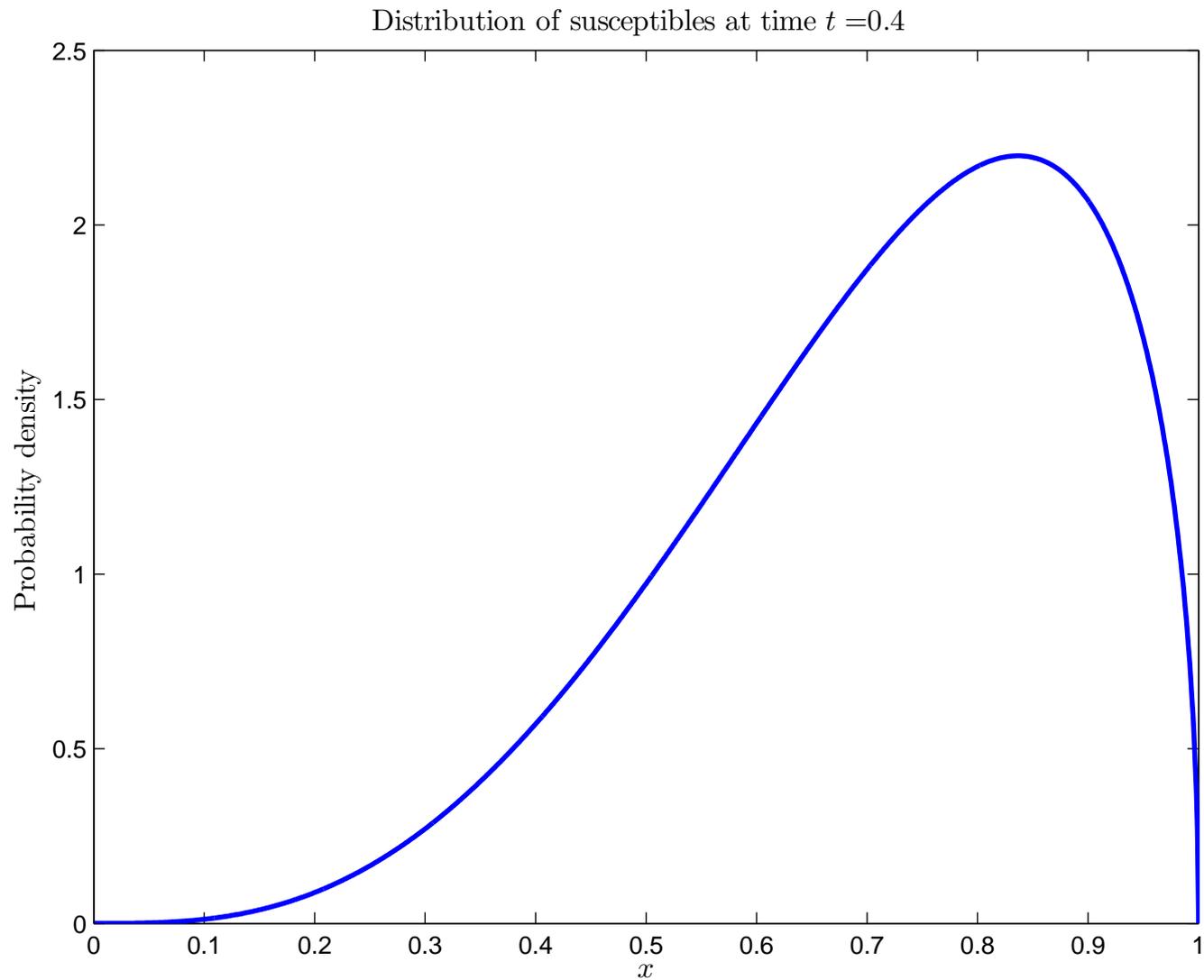
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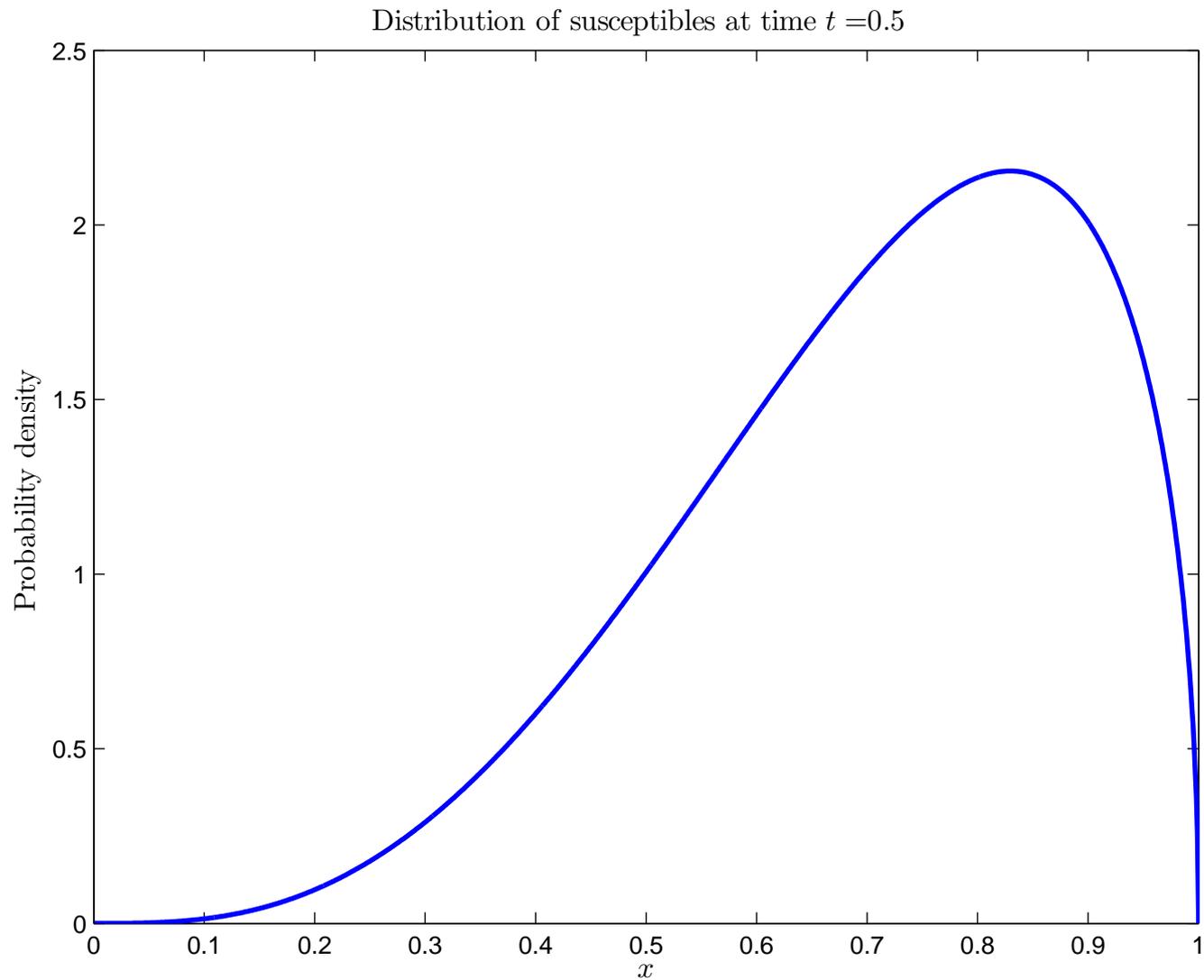
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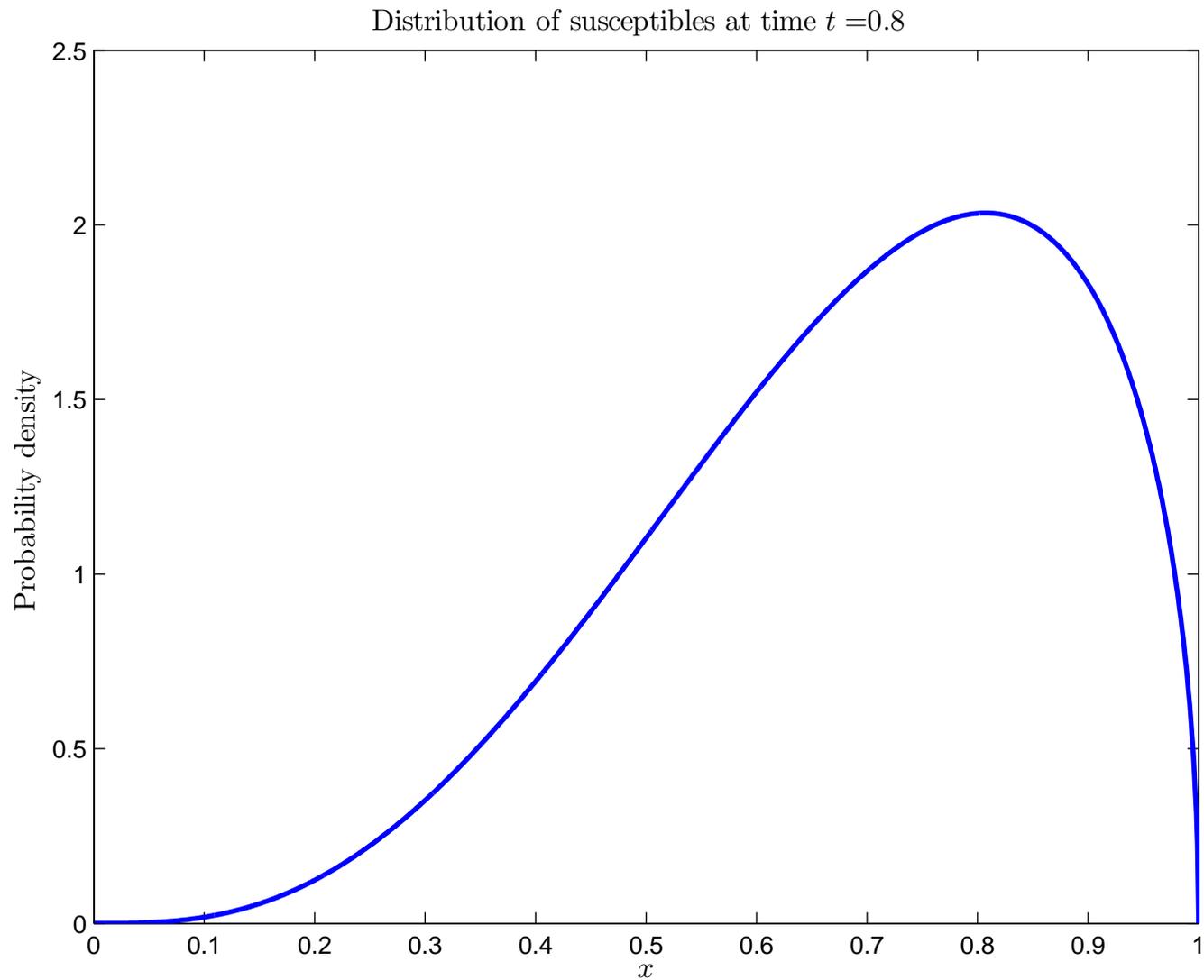
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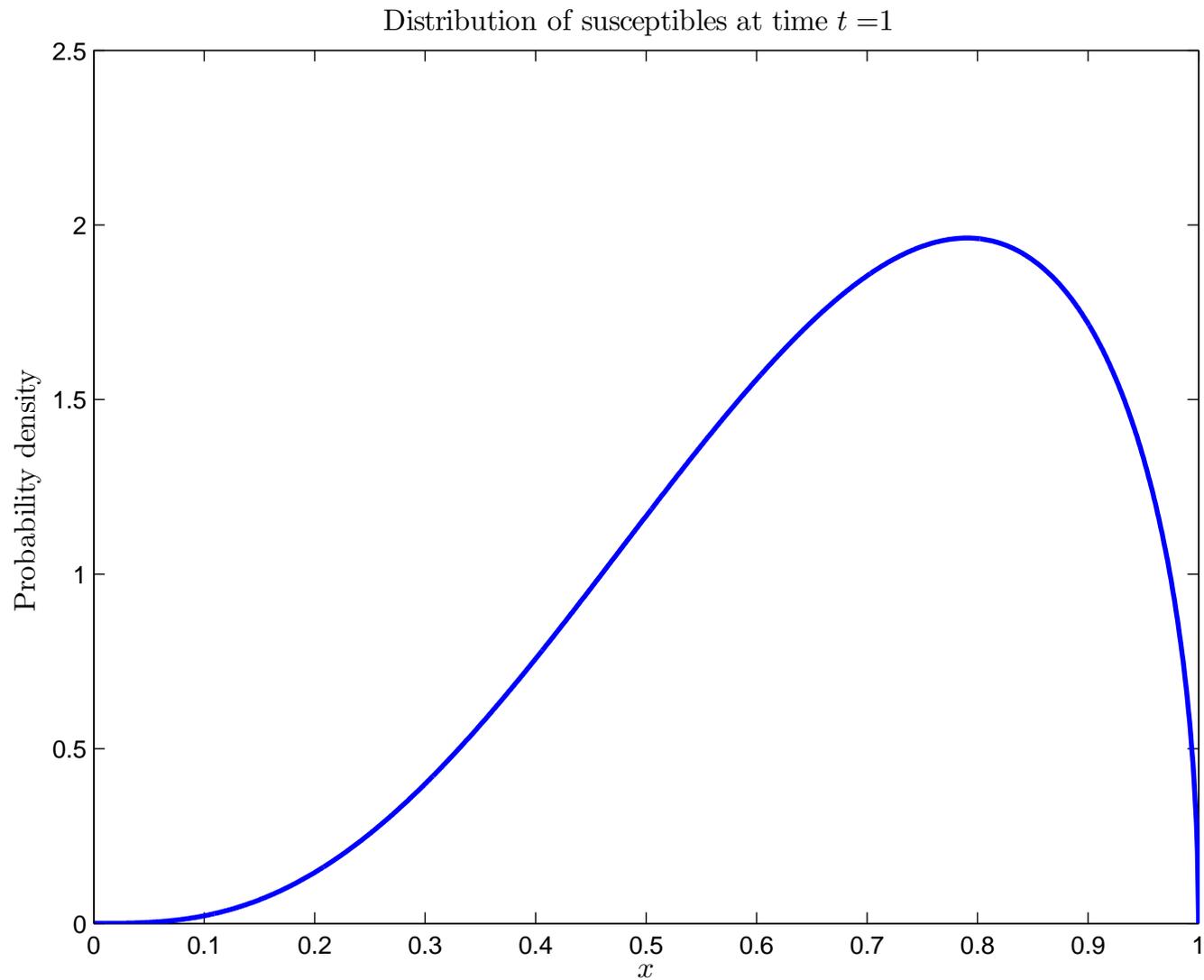
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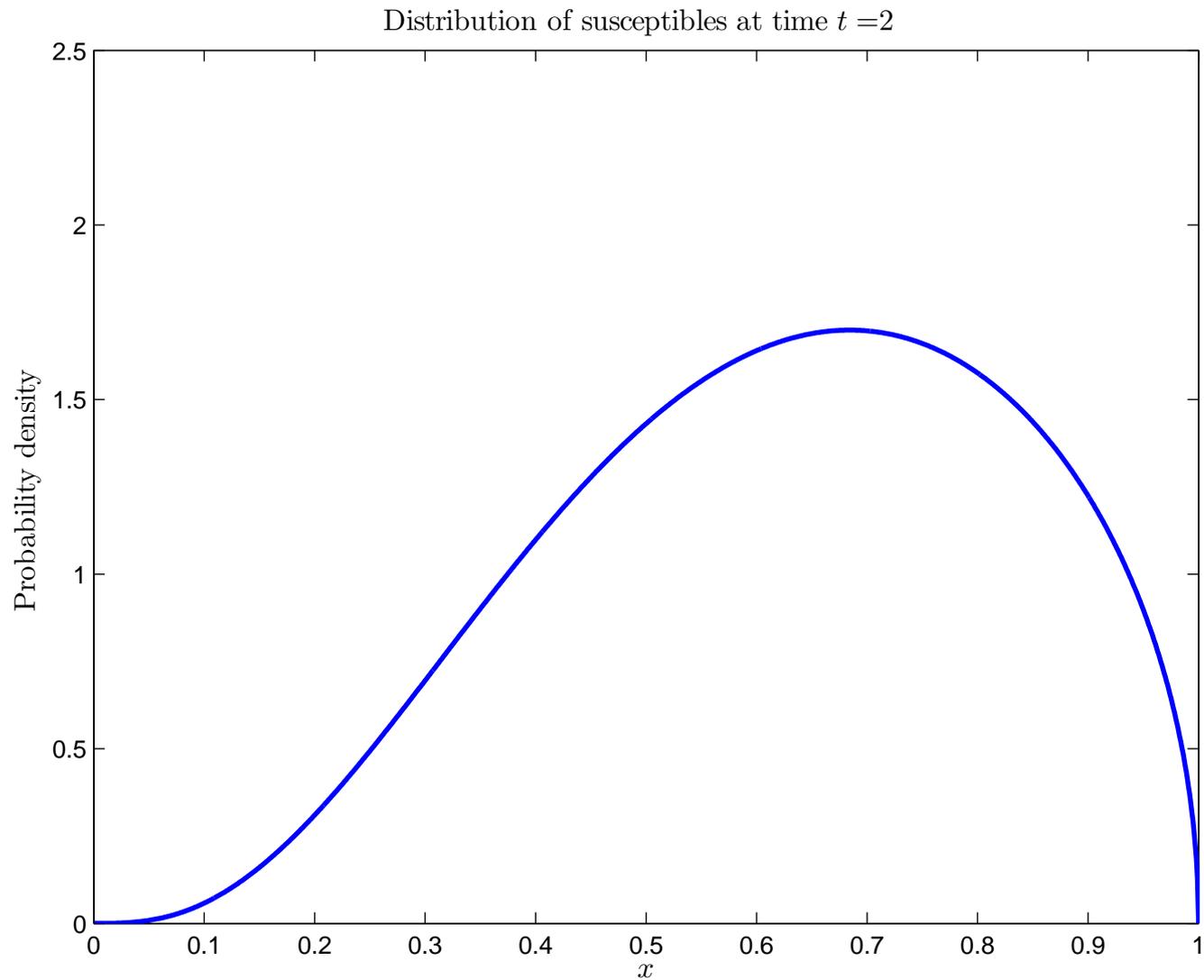
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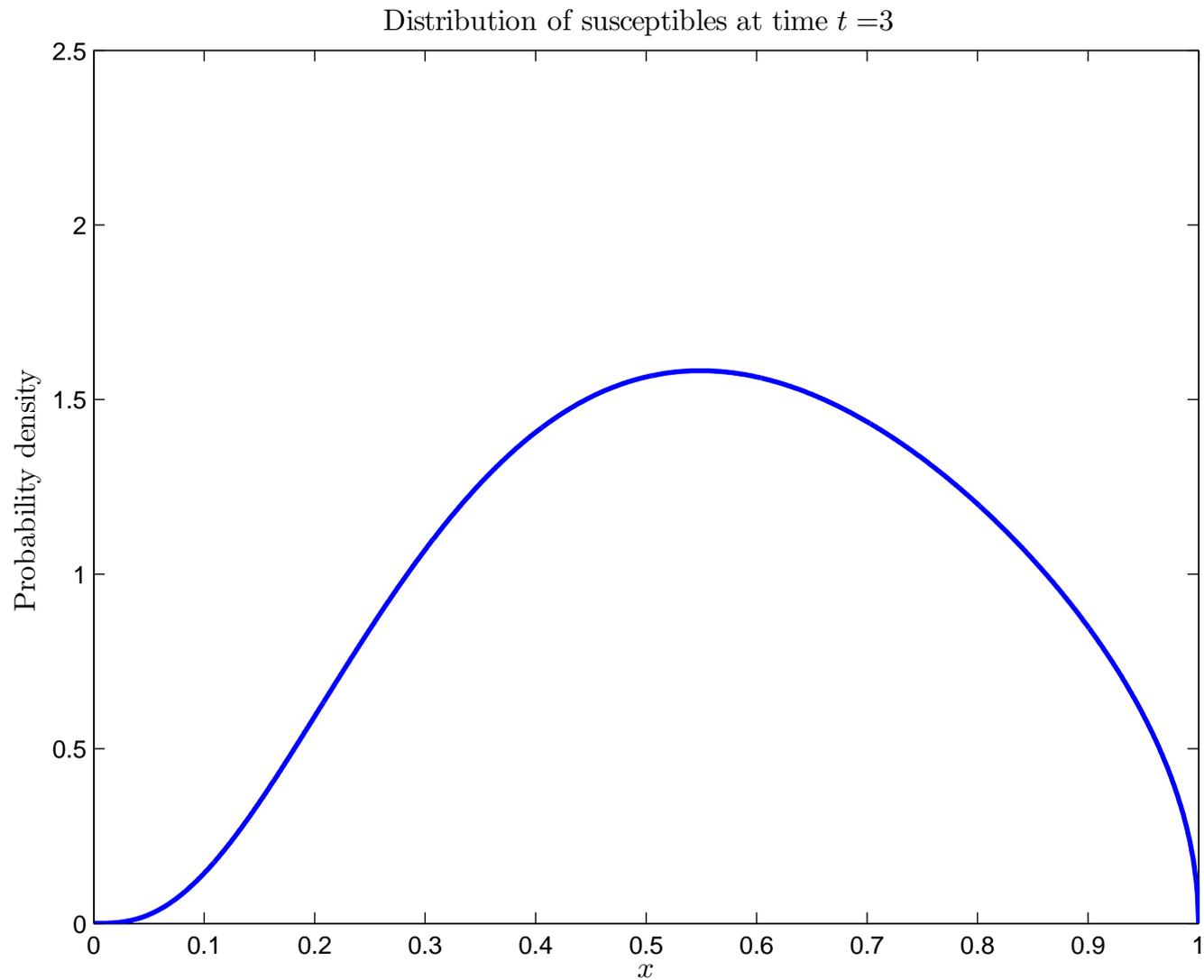
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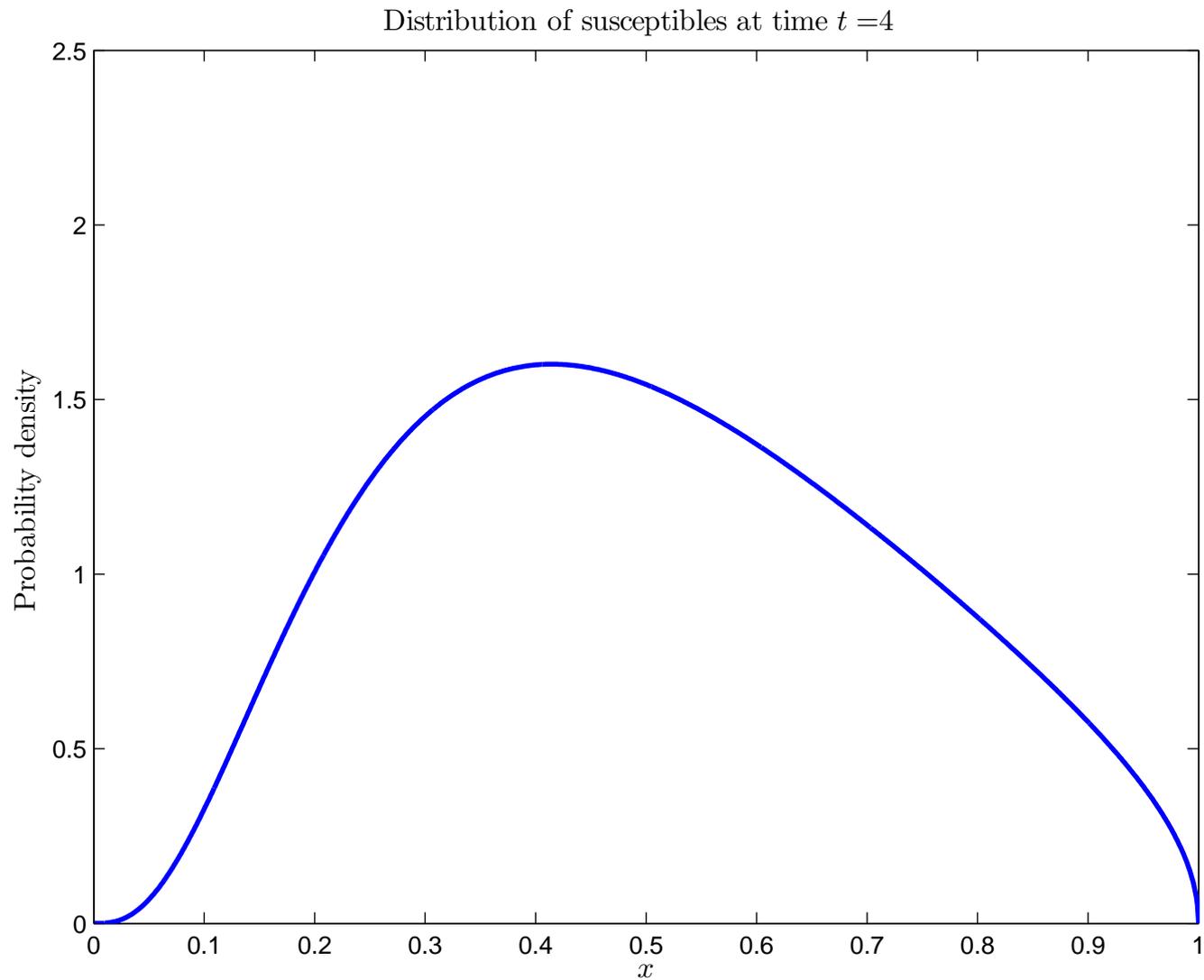
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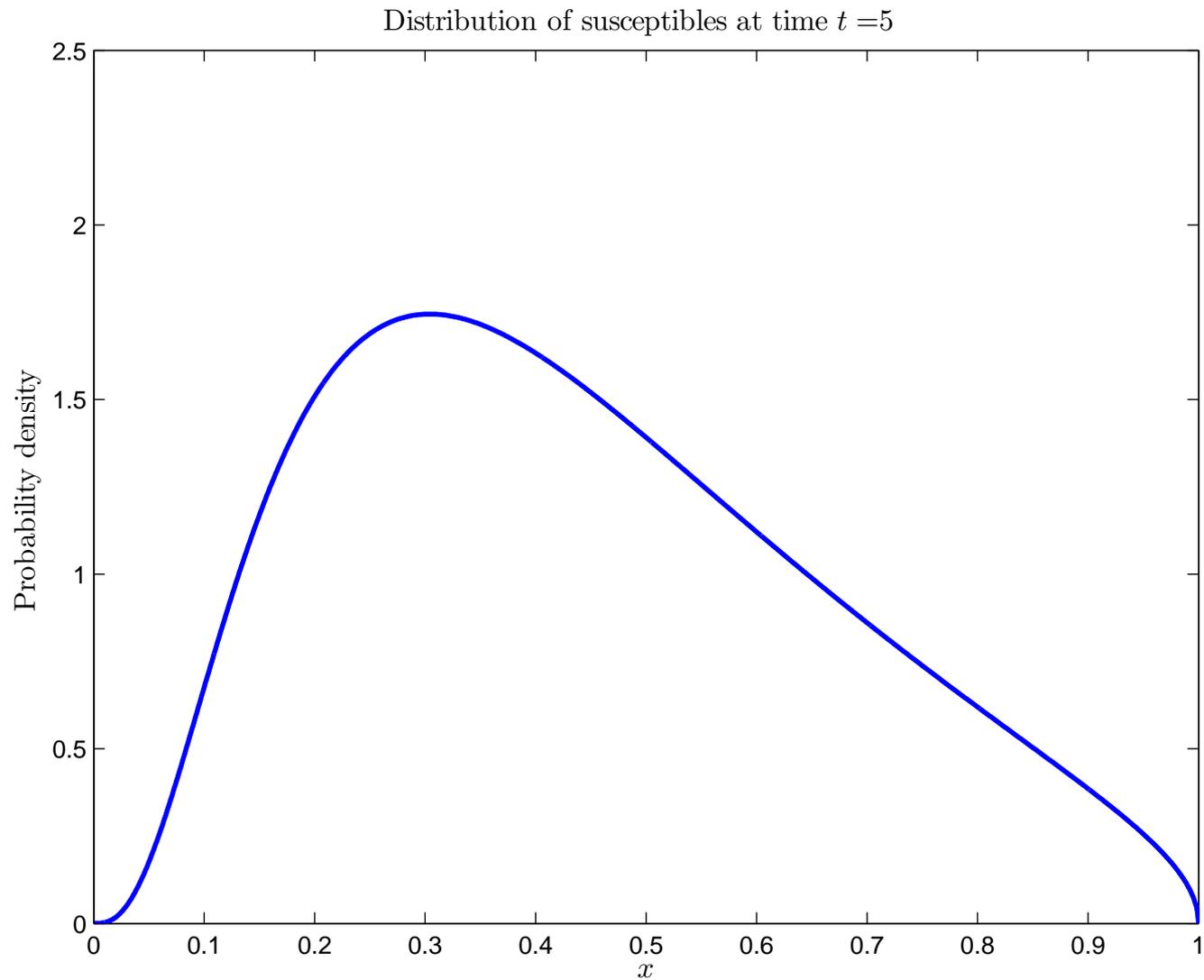
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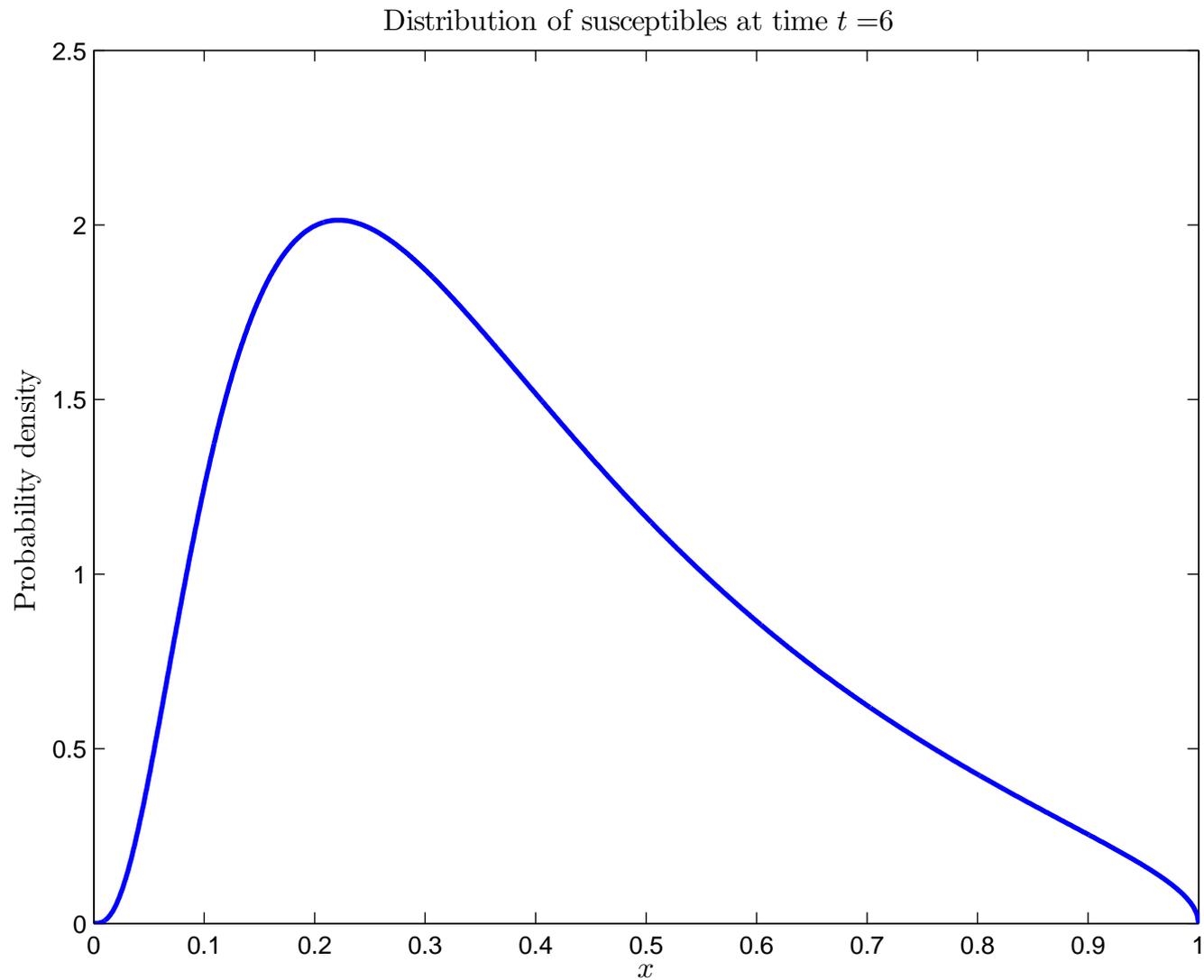
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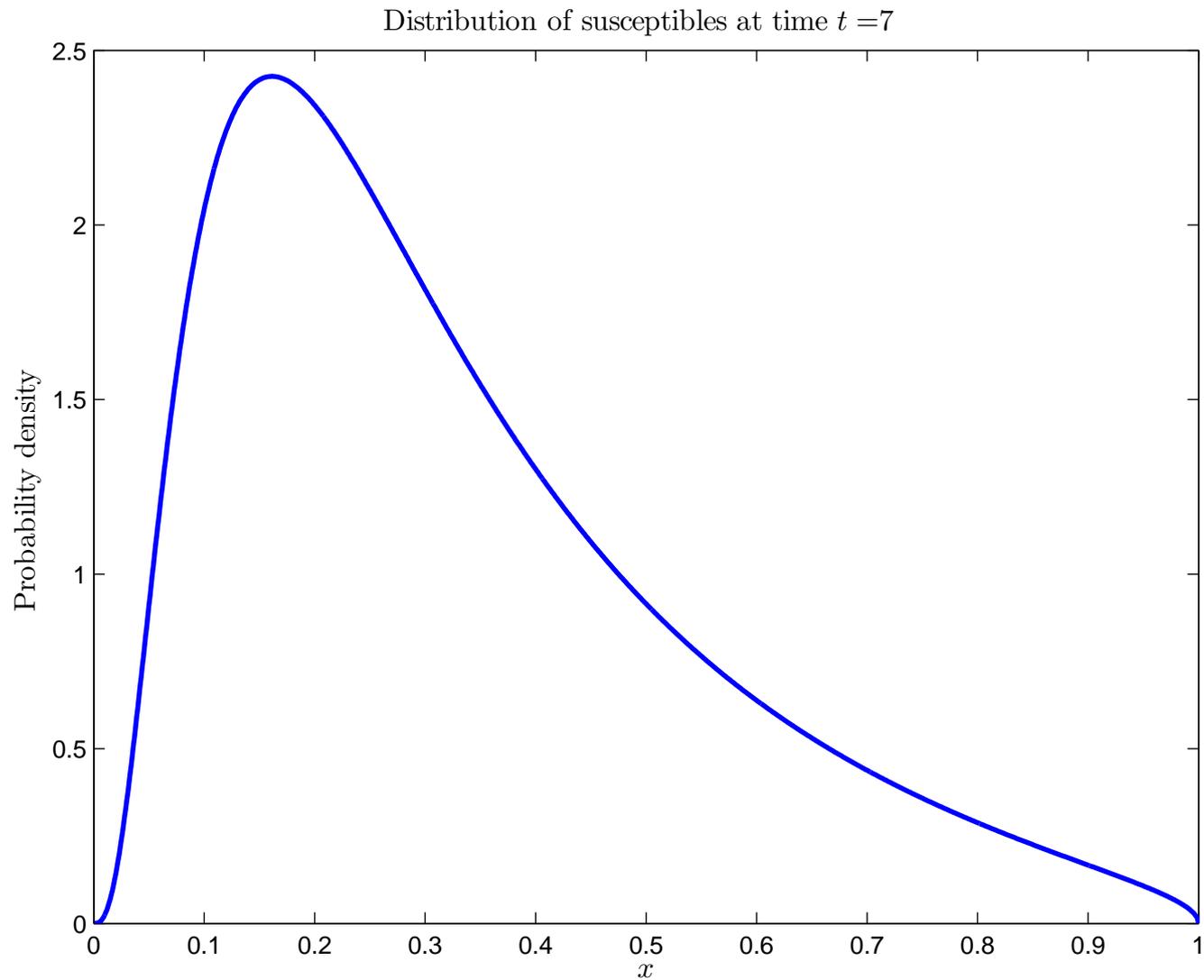
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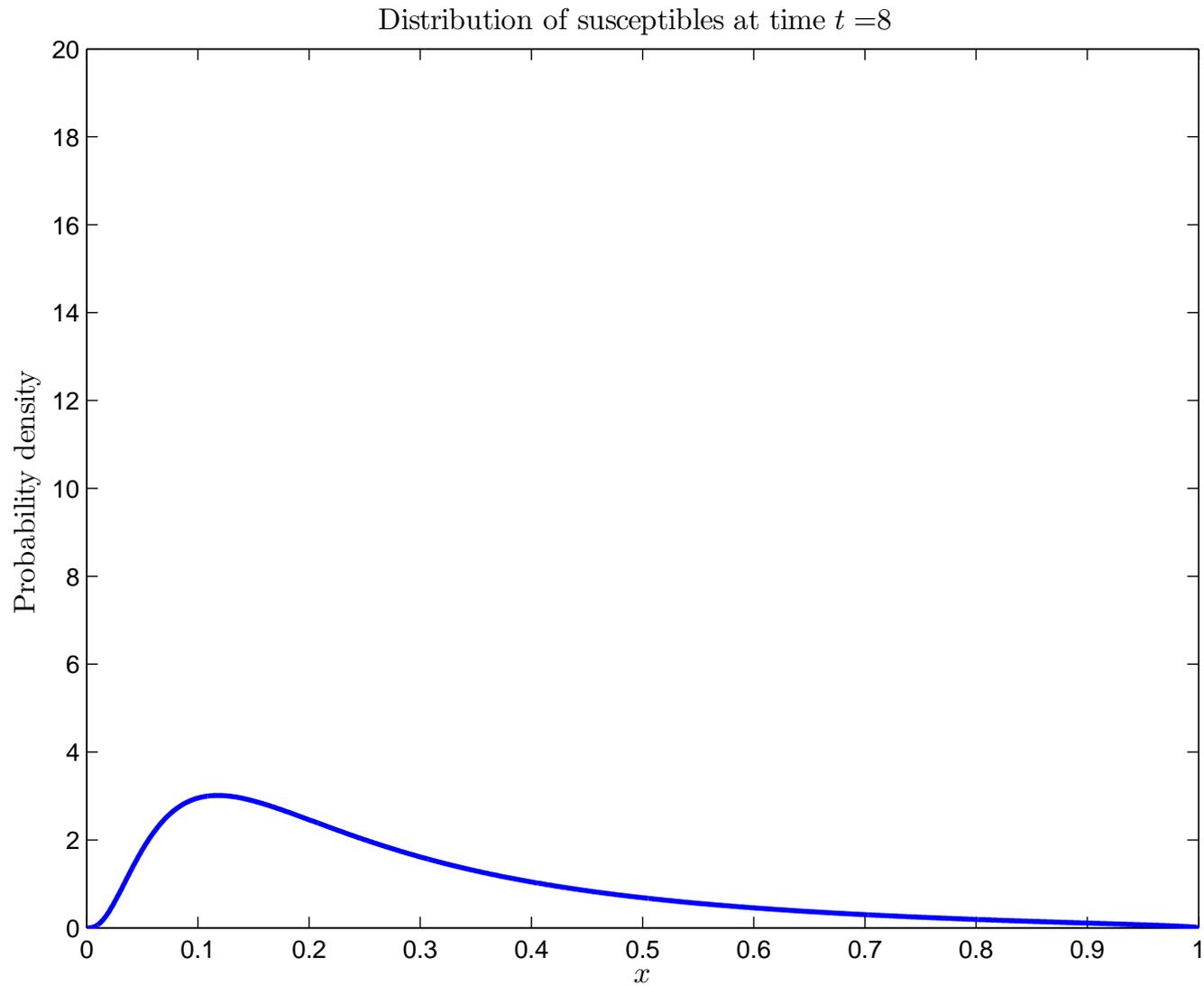
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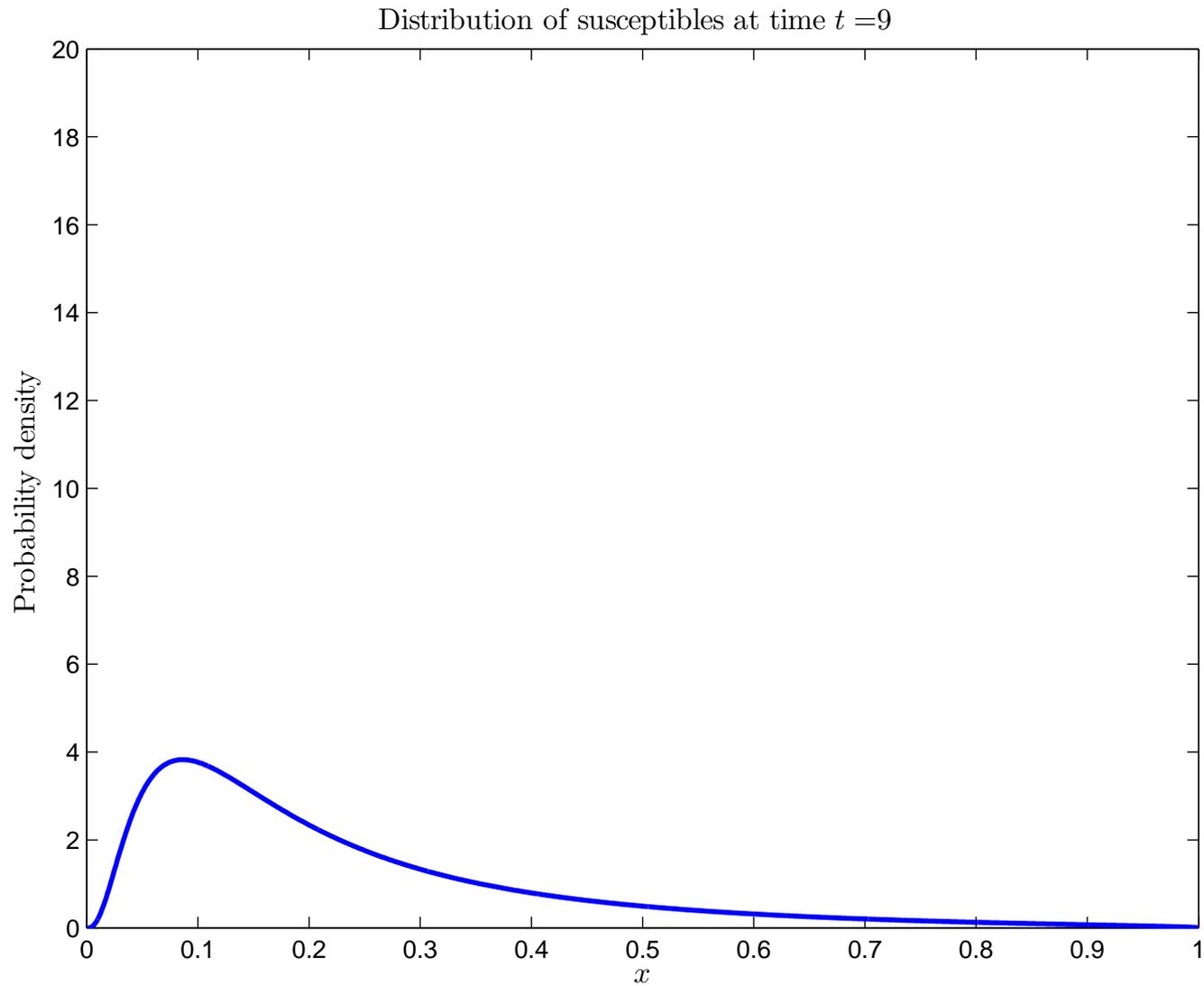
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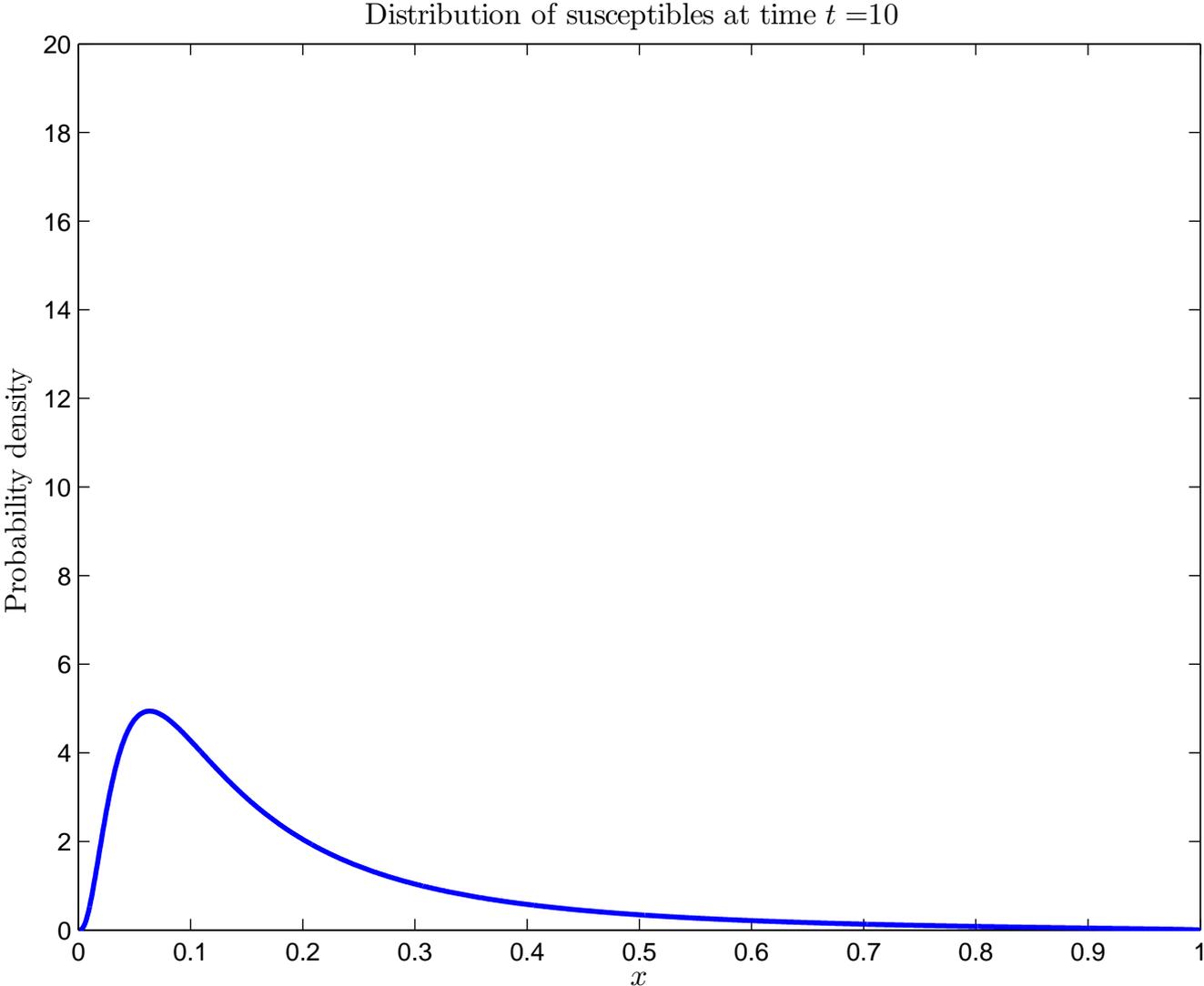
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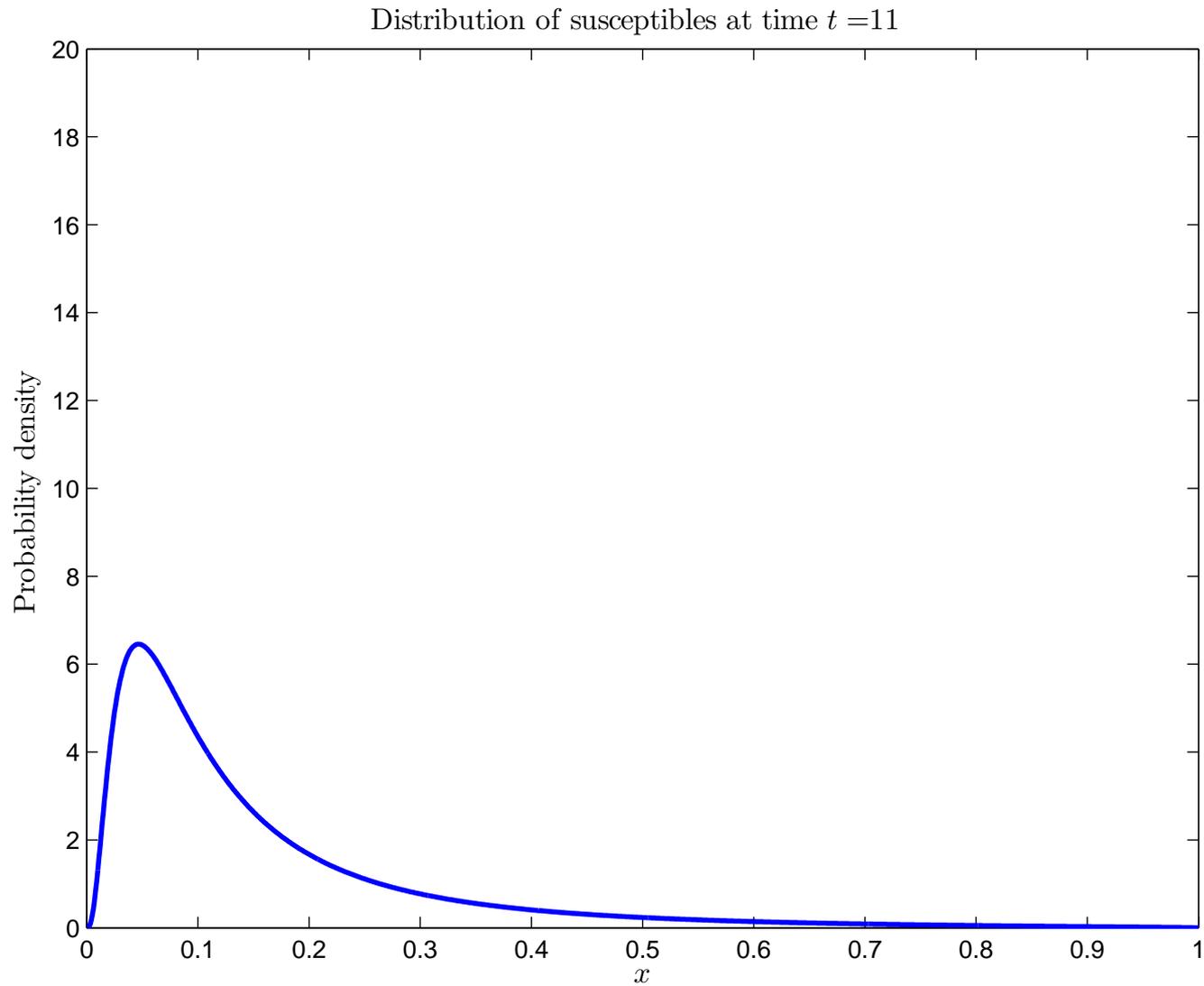
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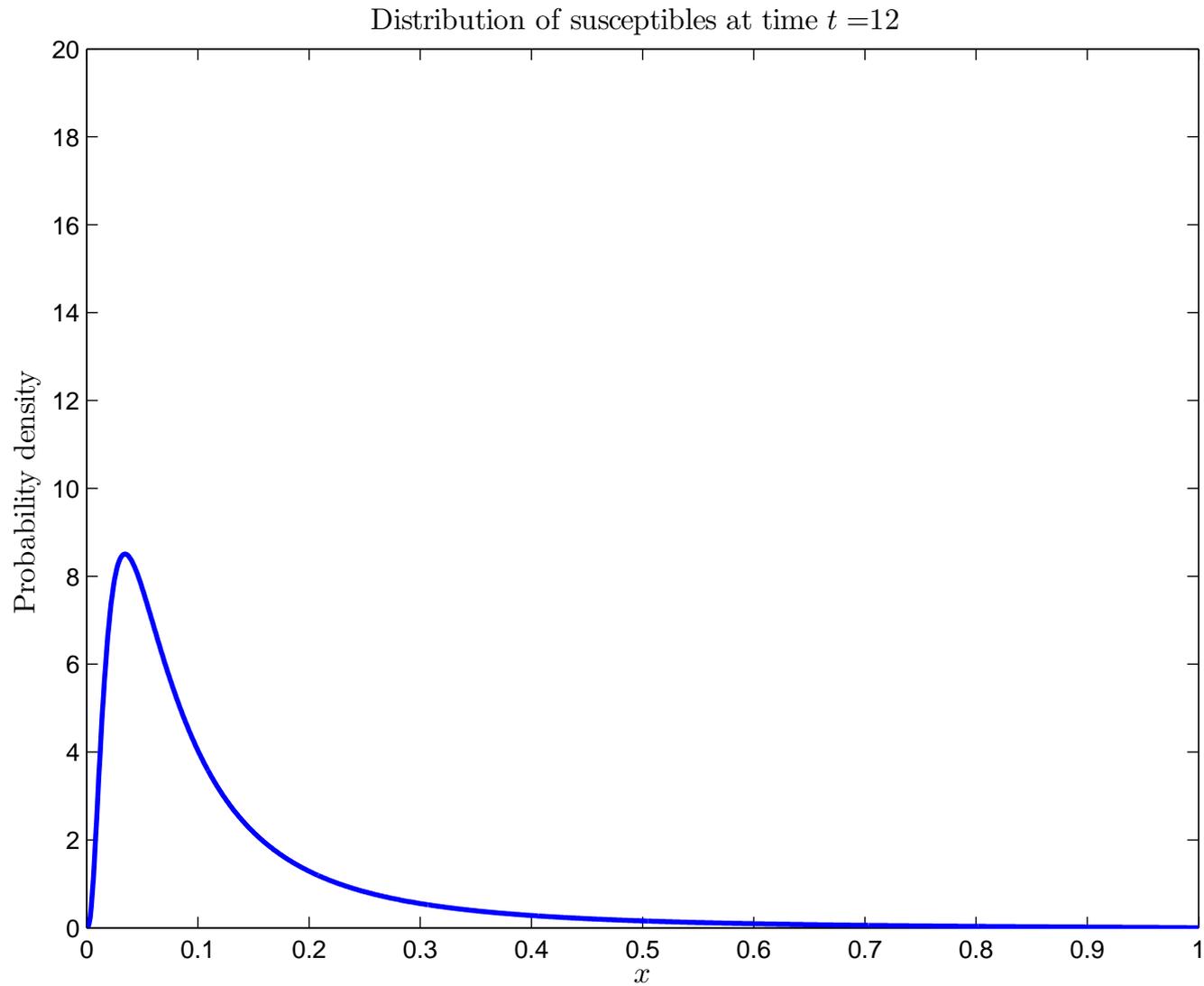
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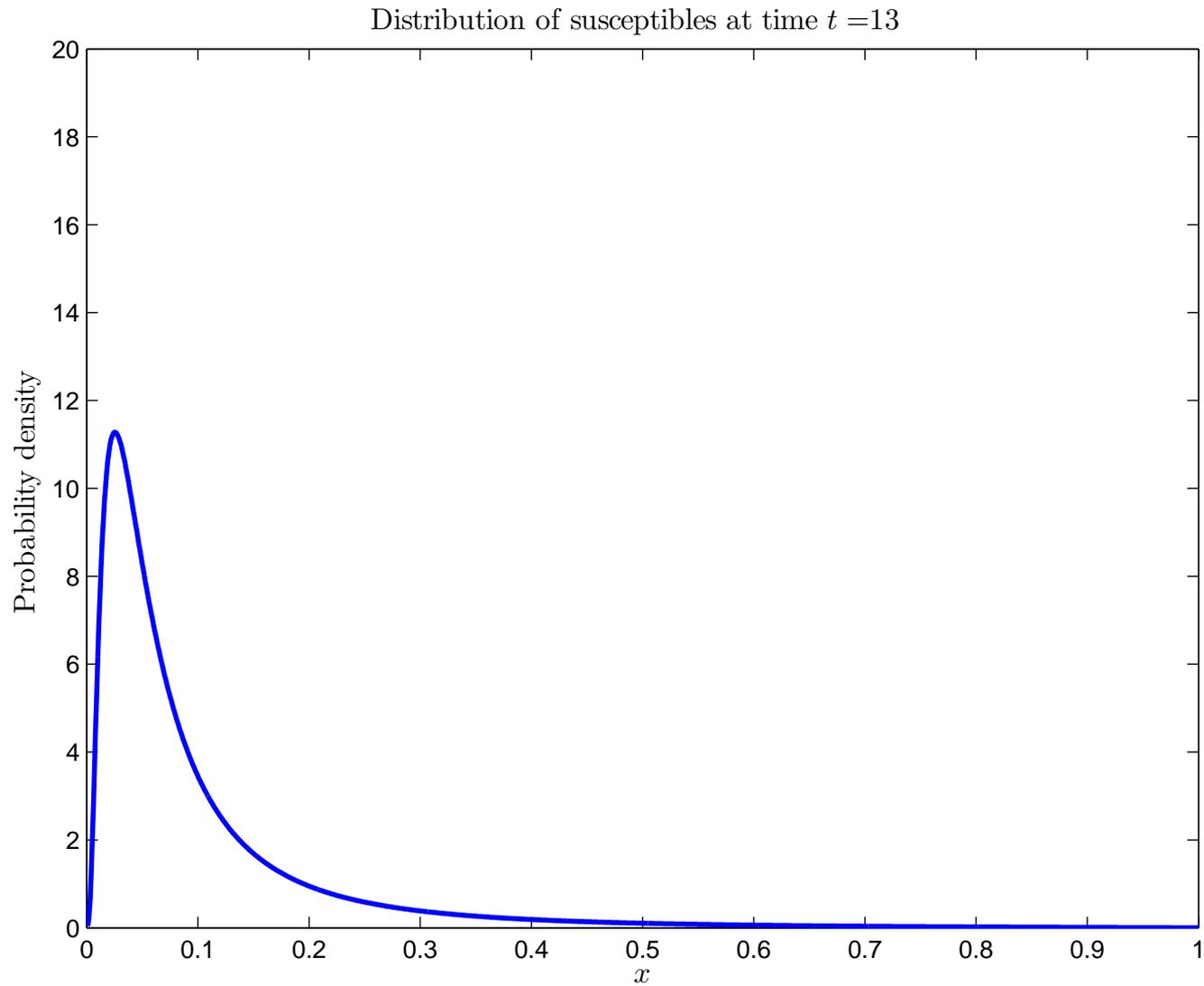
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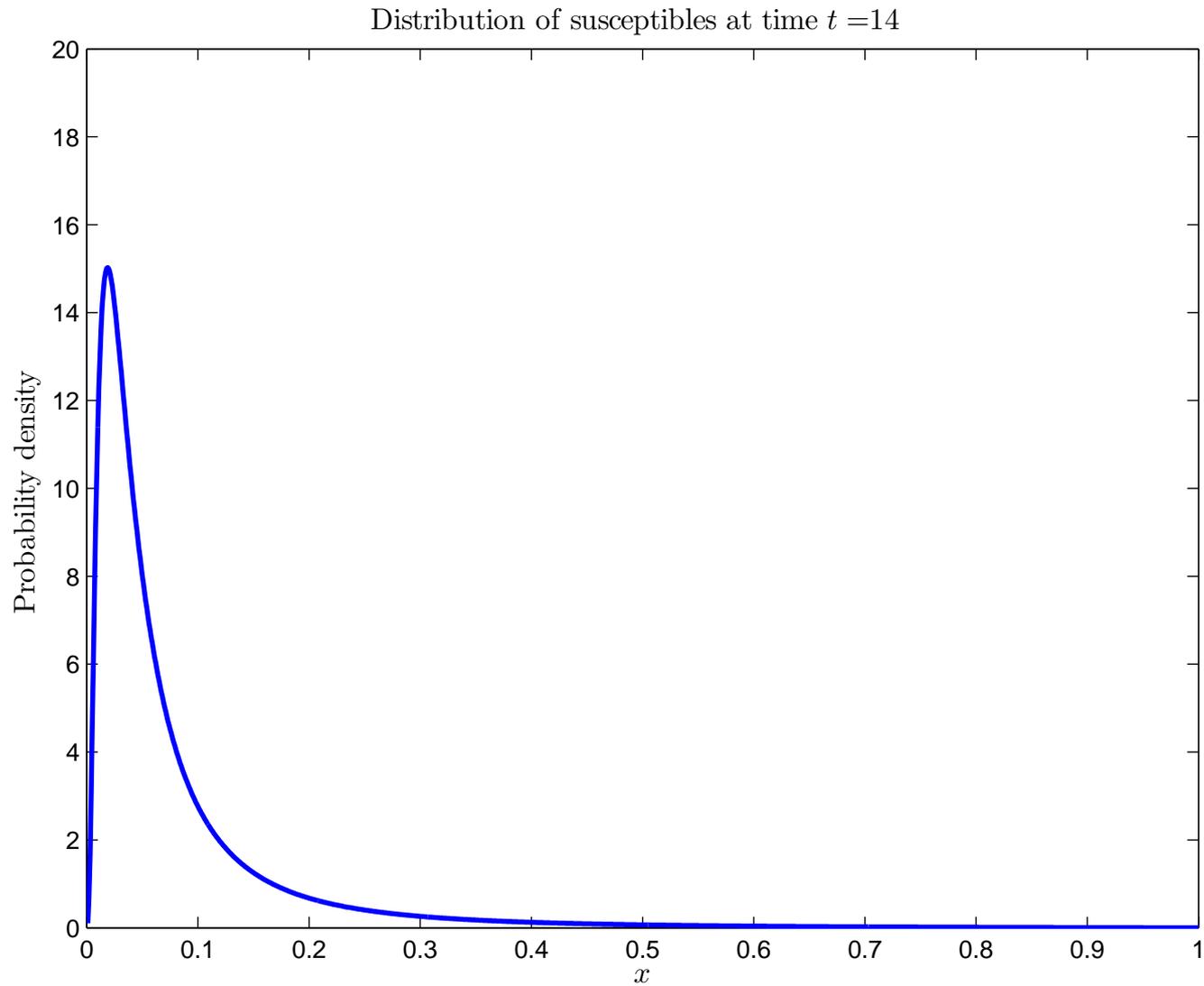
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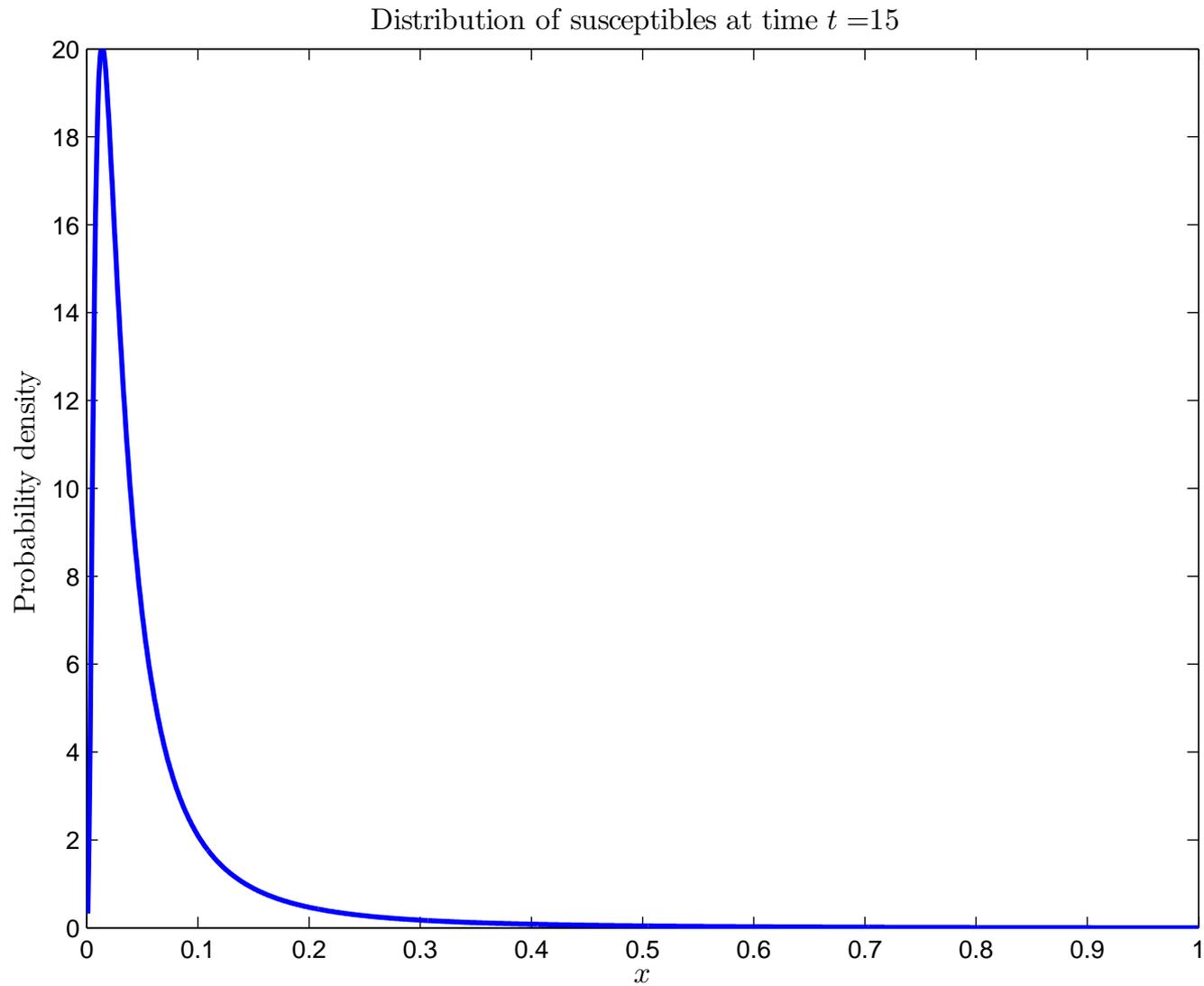
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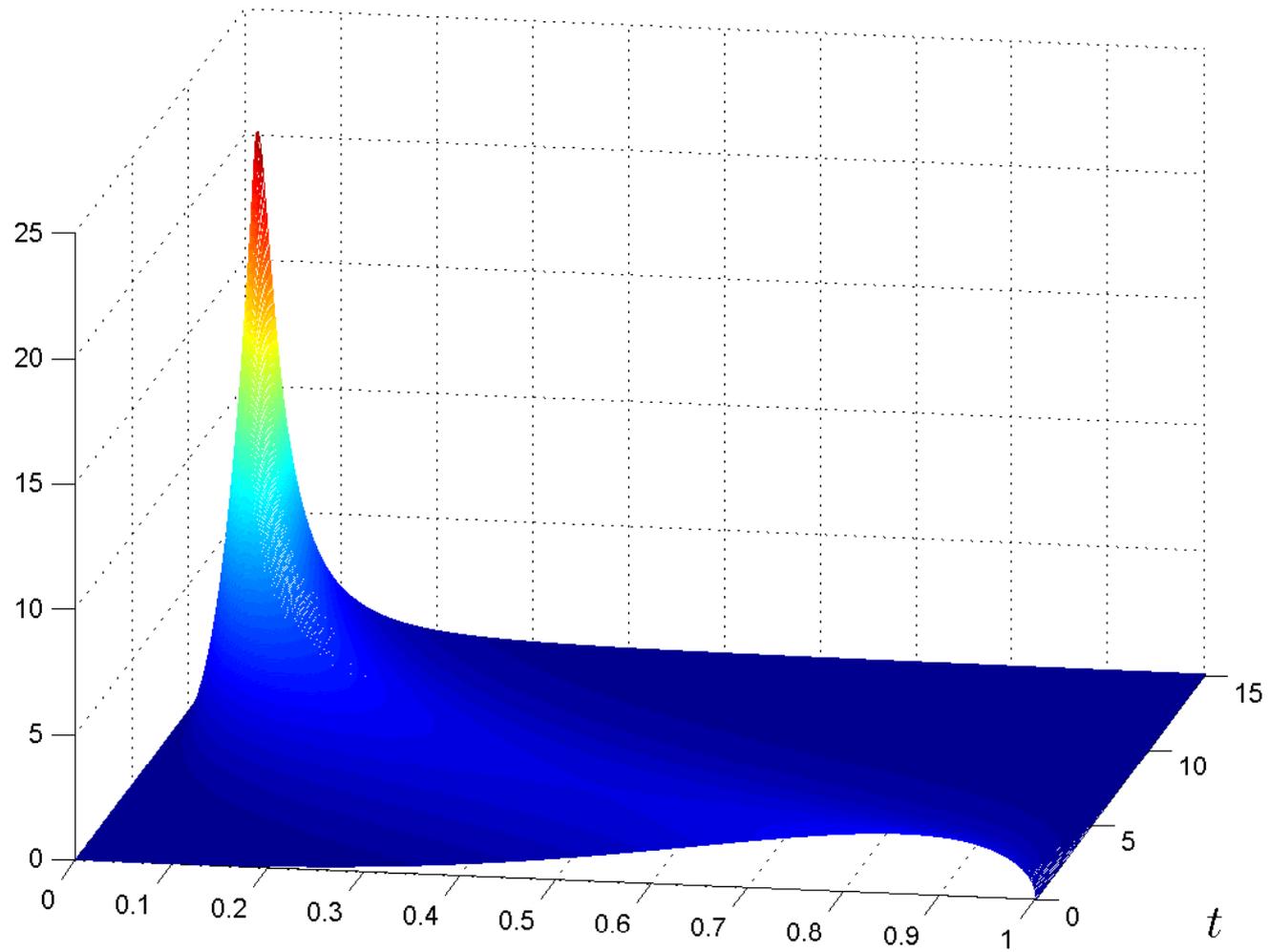
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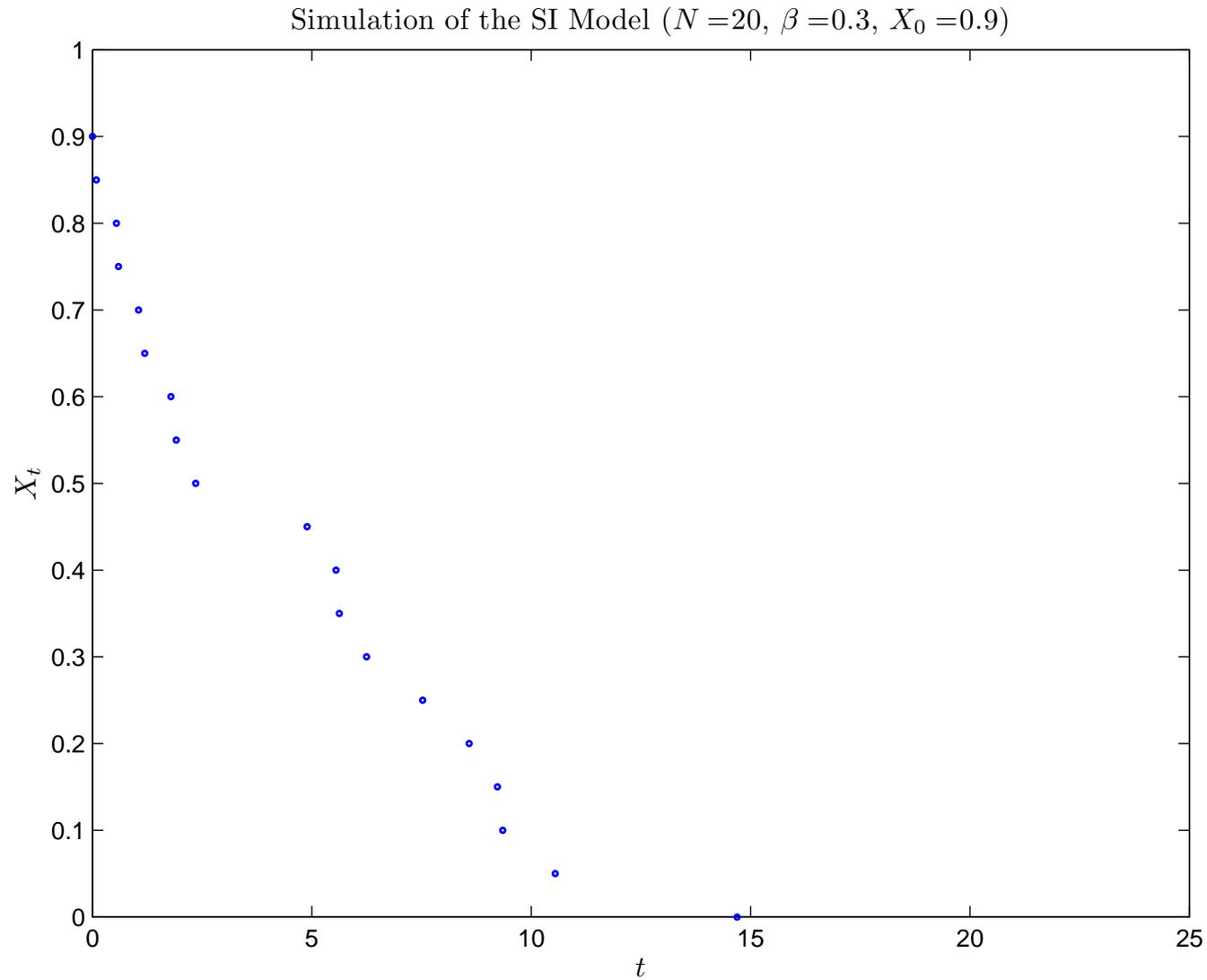
# Questions

- Is the deterministic approximation reasonable?

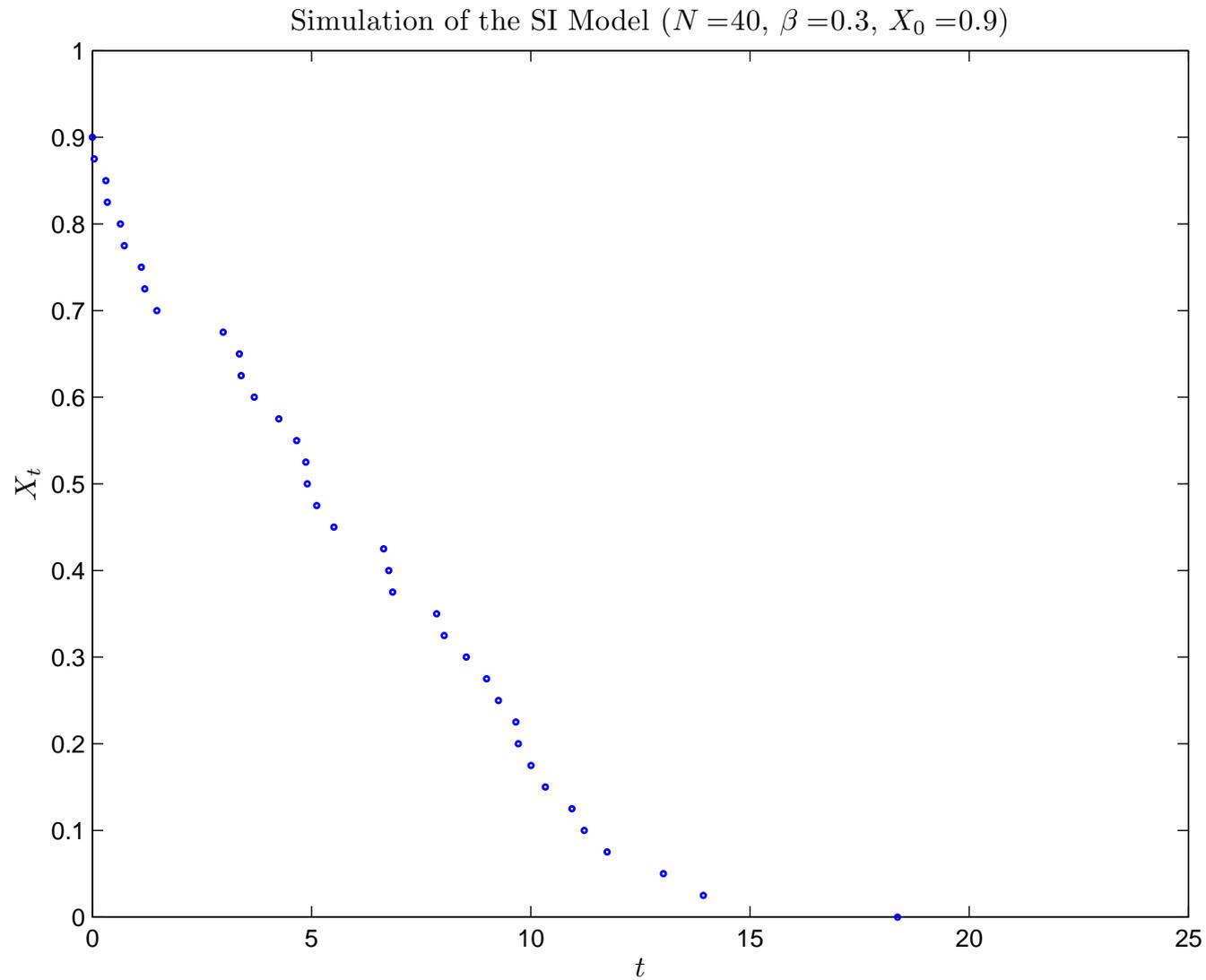
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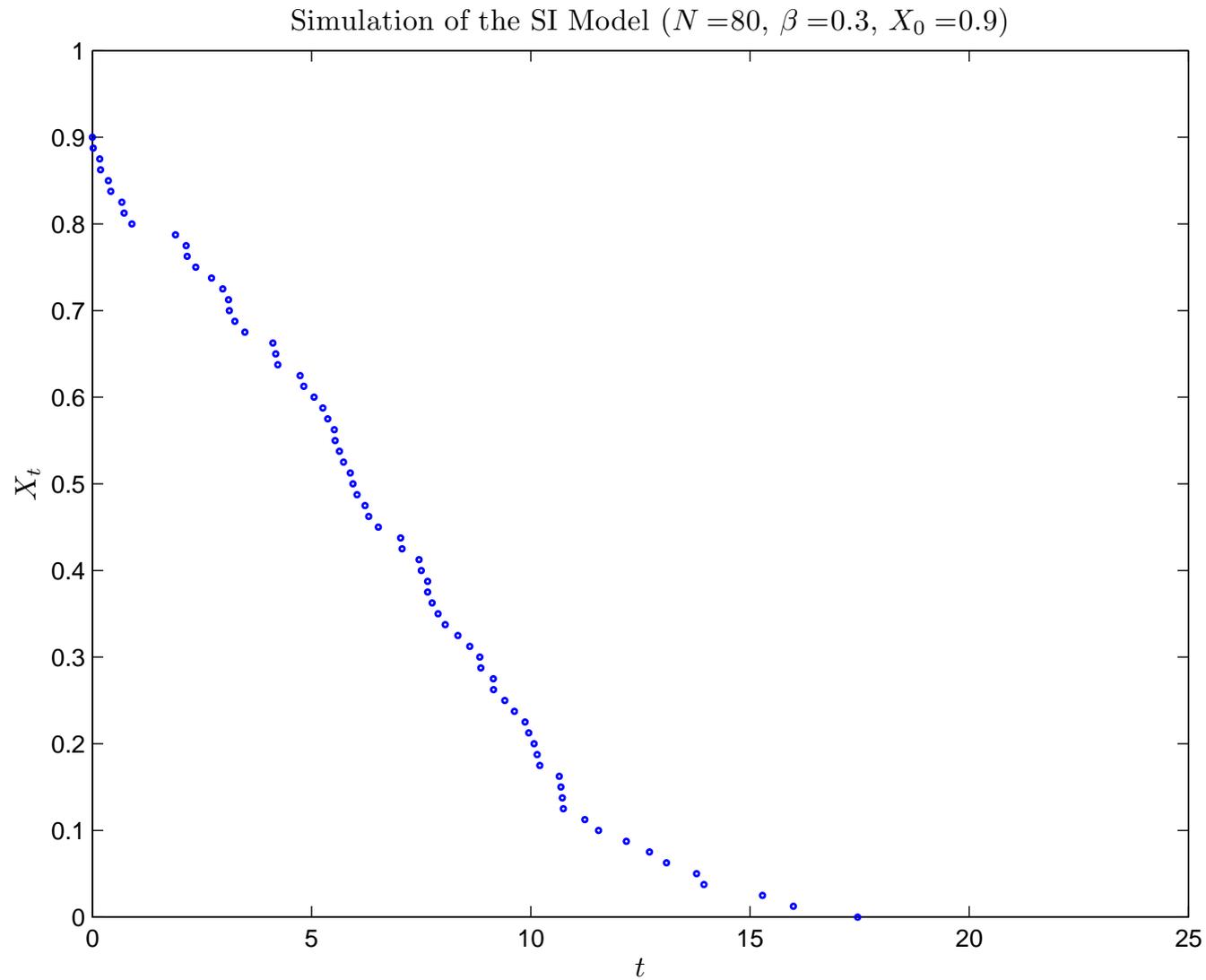
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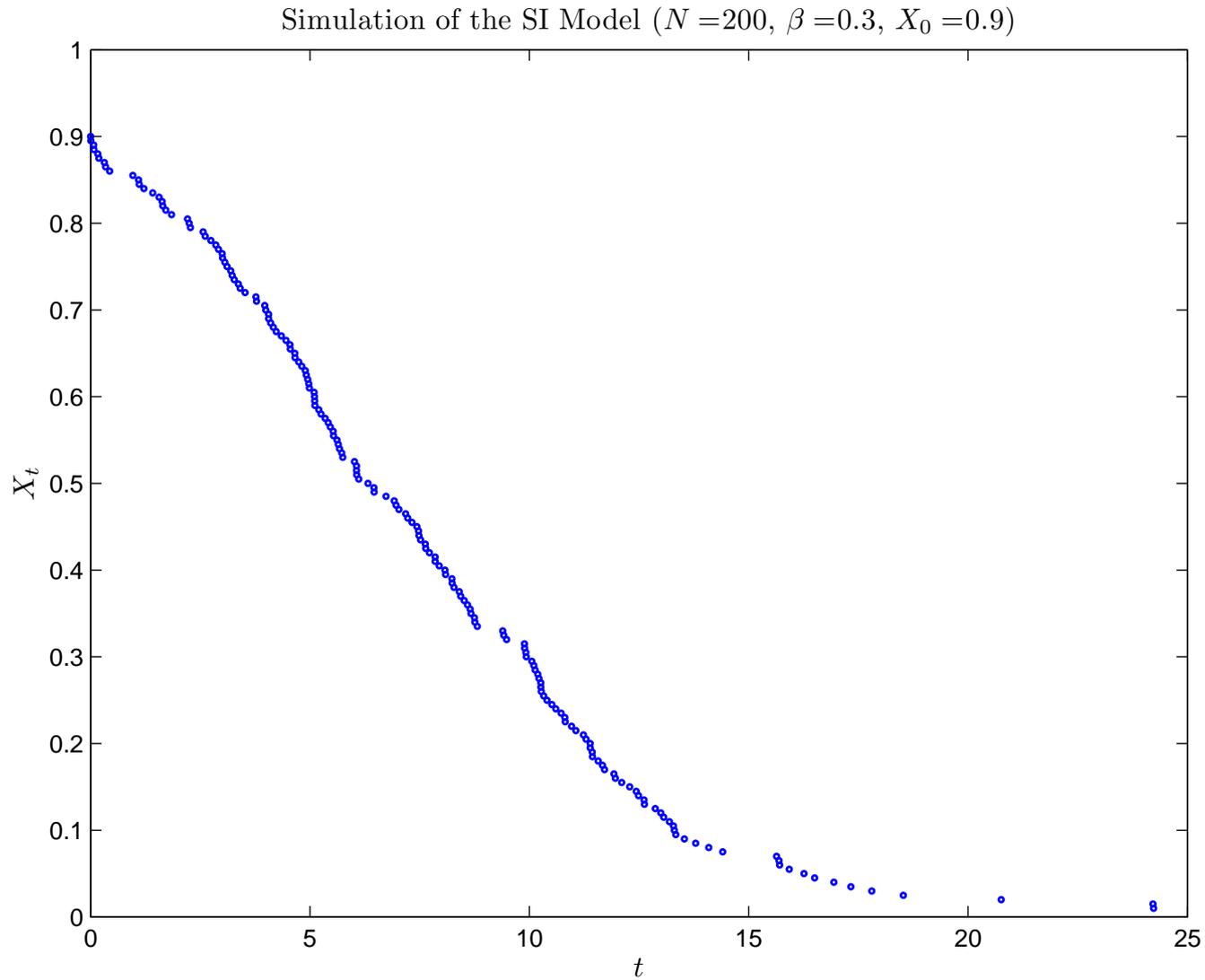
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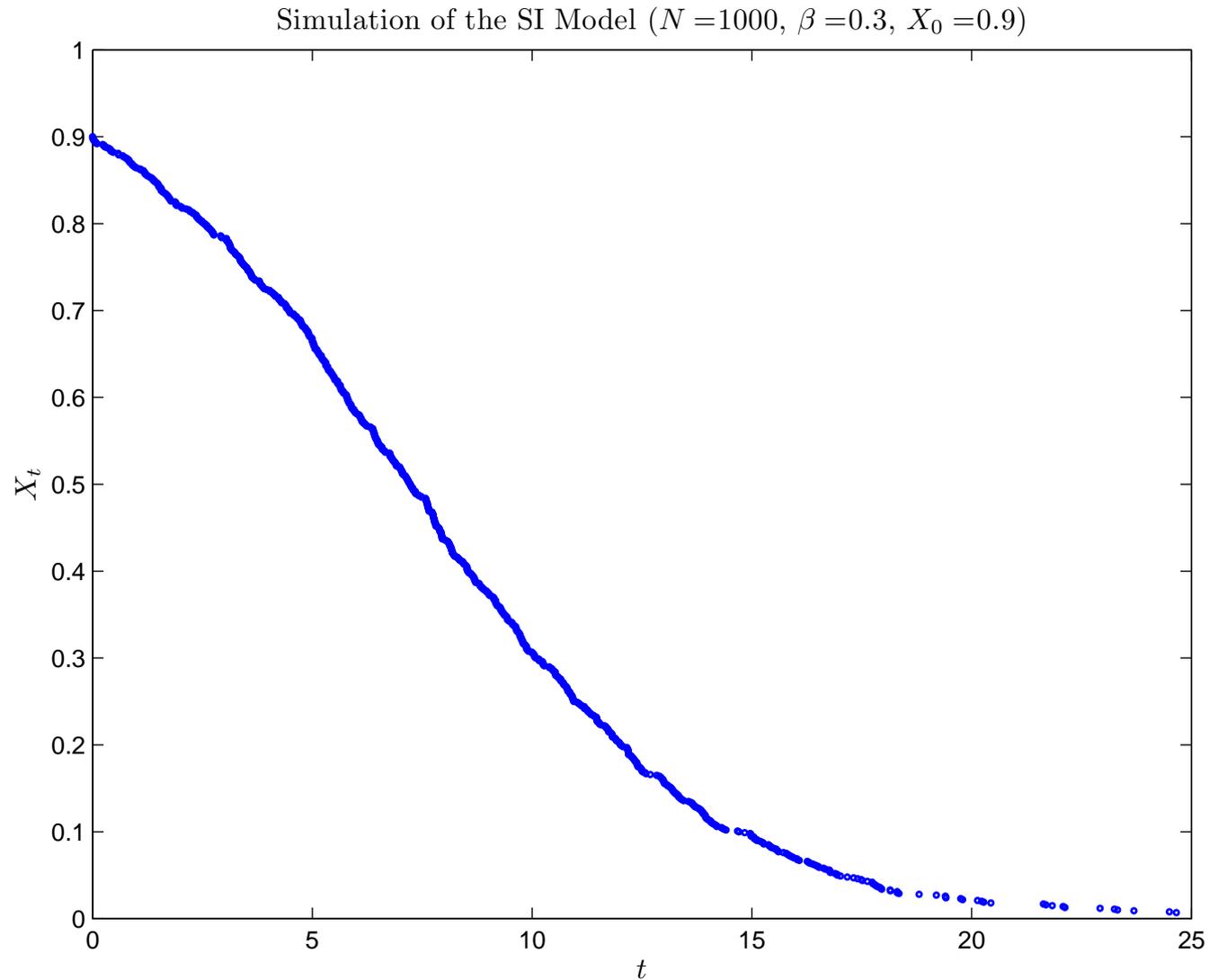
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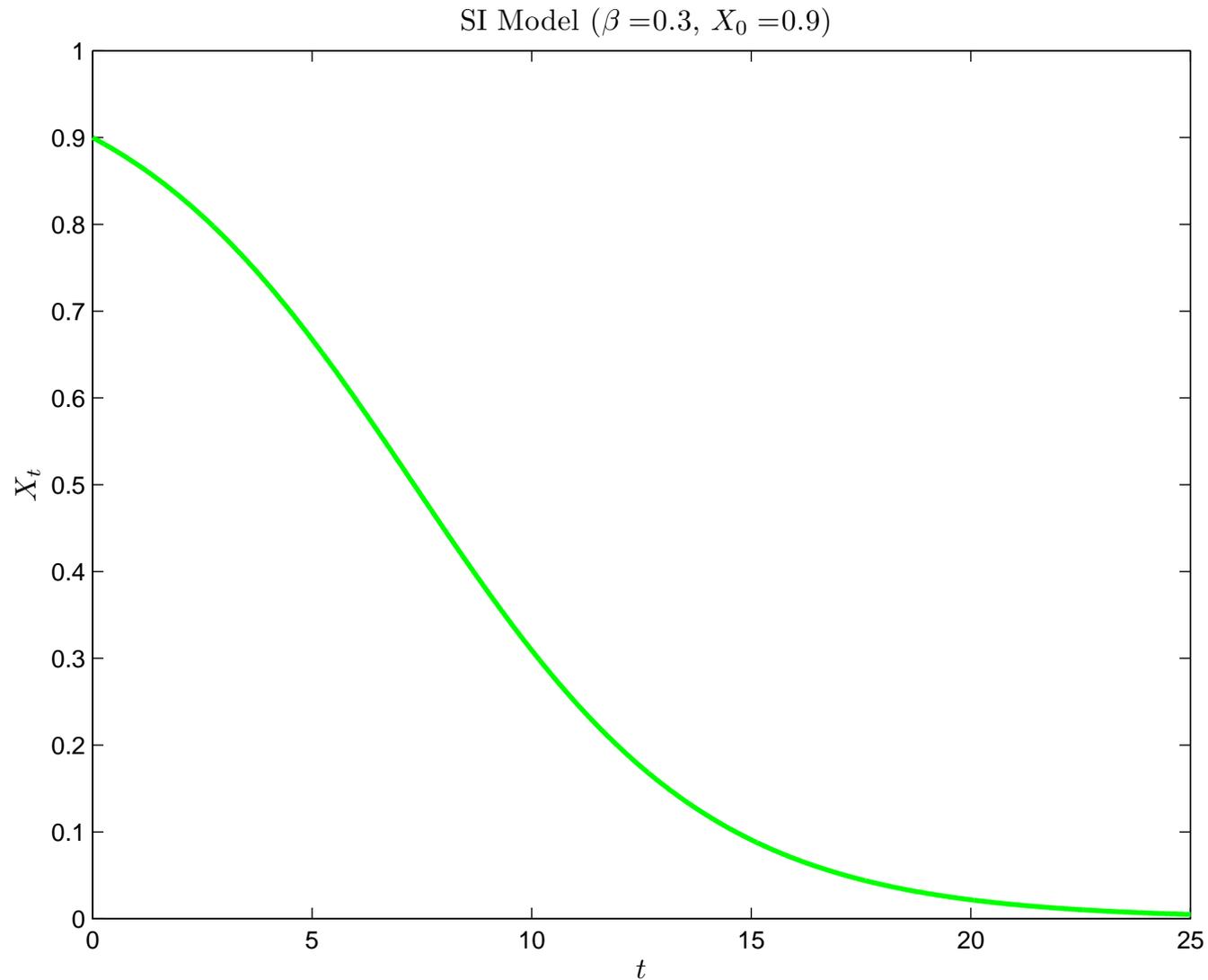
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We can do this (and more) for a very large class of stochastic models called *density dependent Markov chains*.

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We can do this (and more) for a very large class of stochastic models called *density dependent Markov chains*.

I will first explain how the Kegan and West approach (mapping an initial distribution) can be extended: *we do not need to evaluate the trajectories explicitly*.

# Our population process

Our population process  $(n_t, t \geq 0)$  is assumed to be a continuous-time Markov chain taking values in a subset  $S$  of  $\mathbb{Z}^D$ .

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It has a (stable and conservative) set of transition rates  $Q = (q(m, n), m, n \in S)$ , so that  $q(m, n)$  is the transition rate from  $m$  to  $n$  for  $n \neq m$  and  $q(m, m) = -q(m)$ , where  $q(m) = \sum_{n \neq m} q(m, n) (< \infty)$  is the total rate out of state  $m$ .

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For example, in the SI model  $n_t$  is the number of susceptibles at time  $t$ ,  $S = \{0, 1, \dots, N - 1\}$ , where  $N$  is total number of individuals (we assume that there is at least one infective), and  $q(n) = q(n, n - 1) = (\beta/N)n(N - n)$ , where  $\beta$  is the per-contact transmission rate.

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# Density dependent models

We suppose that the process is *density dependent* in the sense of Tom Kurtz (1970): there is a parameter  $N$  (usually a parameter of the model and often related to the size of the population) with the property that

$$q(n, n + l) = N f \left( \frac{n}{N}, l \right), \quad n, n + l \in S,$$

for suitable functions  $f(x, l)$ ,  $x \in E$ , where  $E \subseteq \mathbb{R}^D$ .

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The SI model is density dependent because

$$q(n, n - 1) = \frac{\beta}{N} n(N - n) = N\beta \frac{n}{N} \left(1 - \frac{n}{N}\right),$$

and hence  $f(x, -1) = \beta x(1 - x)$ ,  $x \in E = [0, 1)$ .

# Step I: Identify the deterministic model

Set  $X_t = n_t/N$  and call  $(X_t, t \geq 0)$  the *density process* (of course  $X_t$  would typically **be** a population density).

Set  $F(x) = \sum_{l \neq 0} l f(x, l)$ .

A deterministic model for  $X_t$  is

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**Theorem 1.** For every  $\epsilon > 0$ ,

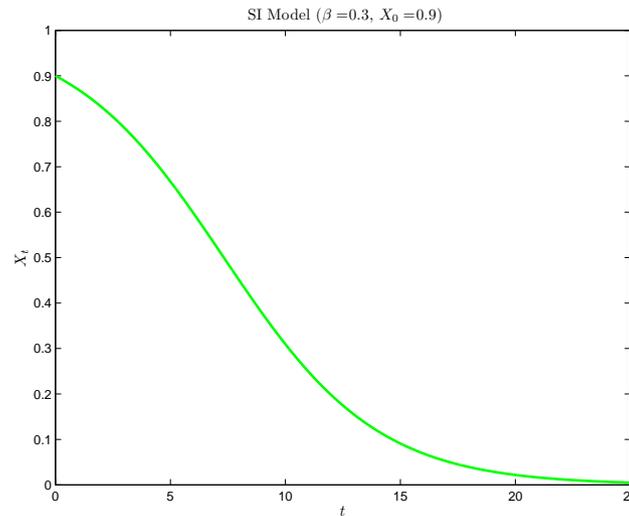
$$\Pr \left( \sup_{0 \leq s \leq t} |X_s^{(N)} - x(s)| > \epsilon \right) \rightarrow 0 \quad \text{as } N \rightarrow \infty.$$

# Step I: Identify the deterministic model

For the SI model

$$\frac{dx}{dt} = -\beta x(1-x) \quad x(0) = x_0.$$

$$x(t) = \frac{x_0}{x_0 + (1-x_0)e^{\beta t}} \quad (t \geq 0).$$



## Step II: Map the initial distribution

Think of the initial population density  $X_0$  as being a random variable with a specified probability density function (pdf)  $f_0$ .

Write  $x(t, x_0)$  for the trajectory starting at  $x_0$ .

Determining the action of the map  $g_t(x_0) = x(t, x_0)$  (assumed to be injective) on  $f_0$  to obtain a pdf  $f_t$  that summarizes the effect of random initial conditions in our population: for any  $t > 0$ ,

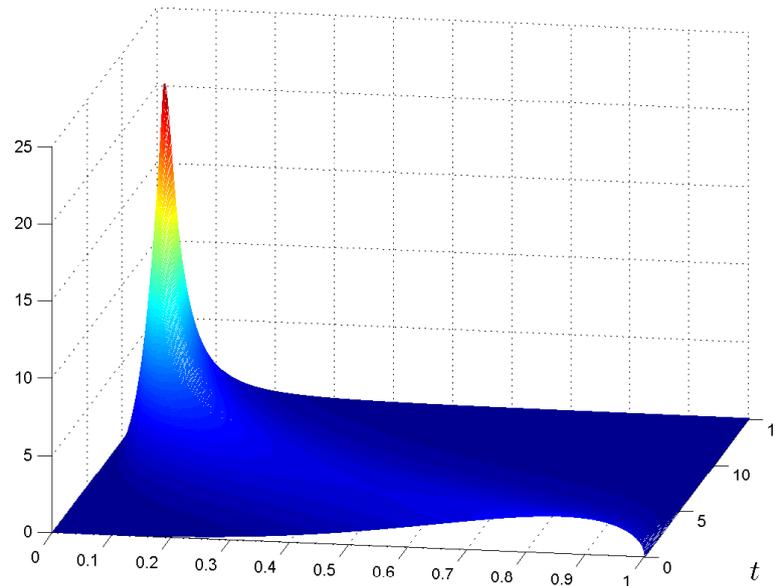
$$f_t(y) = |J_t(y)| f_0(g_t^{-1}(y)), \quad y \in \mathcal{R}_t,$$

where  $J_t$  is the Jacobian of  $g_t^{-1}$  and  $\mathcal{R}_t = g_t(E)$  is the image of  $E$  under  $g_t$ .

# Step II: Map the initial distribution

For the SI model,  $\mathcal{R}_t = E = [0, 1)$  for all  $t$ , and

$$f_t(y) = \frac{e^{-\beta t}}{(y + (1 - y)e^{-\beta t})^2} f_0 \left( \frac{y}{y + (1 - y)e^{-\beta t}} \right), \quad y \in [0, 1).$$



# Step II: Map the initial distribution

For one-dimensional models ( $D = 1$ ) this can be done without evaluating the trajectories explicitly.

We are given

$$\frac{dx}{dt} = F(x) \quad x(0) = x_0.$$

Let  $L(u)$  be the primitive  $L(u) = \int^u dw/F(w)$ . Suppose  $L$  is injective, so that  $L^{-1}$  is well defined (it is sufficient that  $F$  be everywhere positive or everywhere negative).

**Theorem 2.**

$$f_t(y) = \frac{F(L^{-1}(L(y) - t))}{F(y)} f_0(L^{-1}(L(y) - t)), \quad y \in \mathcal{R}_t.$$

# Step III: Unexplained variation

The following result quantifies the variation not accounted for when random dynamics are ignored.

**Theorem 3.** For  $N$  large,

$$\text{Cov}(X_s) \simeq V_s + \frac{1}{N} \int_E \Sigma_s(x_0) f_0(x_0) dx_0,$$

where  $V_s = \text{Cov}(x(s, X_0))$  (variation due to initial conditions)

$$\Sigma_s(x_0) = M_s \int_0^s M_u^{-1} G(x(u, x_0)) (M_u^{-1})^T du M_s^T,$$

$M_s = \exp(\int_0^s B_u du)$ ,  $B_s = \nabla F(x(s, x_0))$  and  $G(x)$  is the  $D \times D$  matrix with entries  $G_{ij}(x) = \sum_{l \neq 0} l_i l_j f_l(x)$ .

# Step III: The one-dimensional case

**Corollary.** Suppose  $D = 1$ . For  $N$  large,

$$\text{Var}(X_s) \simeq V_s + \frac{1}{N} \int_E \Sigma_s(x_0) f_0(x_0) dx_0,$$

where  $V_s = \text{Var}(x(s, X_0))$  (variation due to initial conditions),

$$\Sigma_s(x_0) = M_s^2 \int_0^s M_u^{-2} G(x(u, x_0)) du,$$

$M_s = \exp(\int_0^s B_u du)$ ,  $B_s = F'(x(s, x_0))$  and  $G(x) = \sum_{l \neq 0} l^2 f_l(x)$ .

For the SI model

$$\Sigma_t = e^{\beta t} x_0 (1 - x_0) \frac{(1 - x_0)^2 e^{2\beta t} - (1 - 2x_0 - 2\beta t x_0 (1 - x_0)) e^{\beta t} - x_0^2}{(x_0 + (1 - x_0) e^{\beta t})^4}.$$

# Unexplained variation in the SI model

