Modeling Epidemics: Introduction, Simple Model, and Linear Least Squares

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First Models

- Preliminary goal: Model the spread of an infectious (contagious) illness through a population.
- Simplifying assumptions:
  - The total population N is constant in time.
  - A newly infected person becomes infectious the next day and remains infectious forever.
  - Each infectious person is equally likely (probability p) to infect each noninfectious person on a given day.
- Let $\mathcal{I}(t)$ be the number of infectious people at the start of day t.

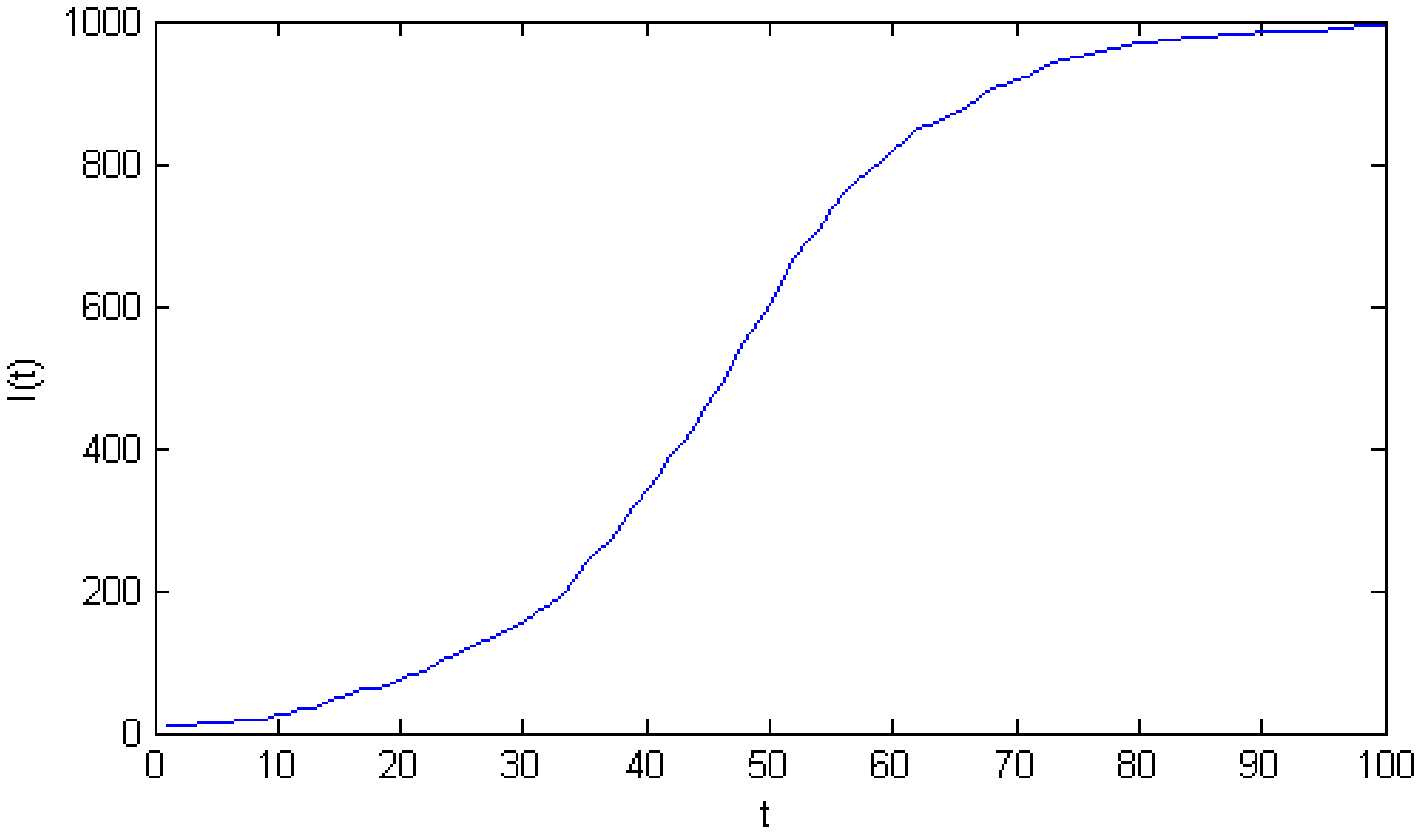
Stochastic Model

- Number the people from 1 to N.
- Let $x_n(t)$ be the infectious status (1 if infectious, 0 if not) of person n at the start of day t.
- We can simulate a possible spread of the illness with the following program ("rand"= random number):

```
for t=1:T-1
    for n=1:N
        let x(n,t+1)=x(n,t)
        for m=1:N
            if x(m,t)=1 and rand<p, then let x(n,t+1)=1
        end
    end
end
```

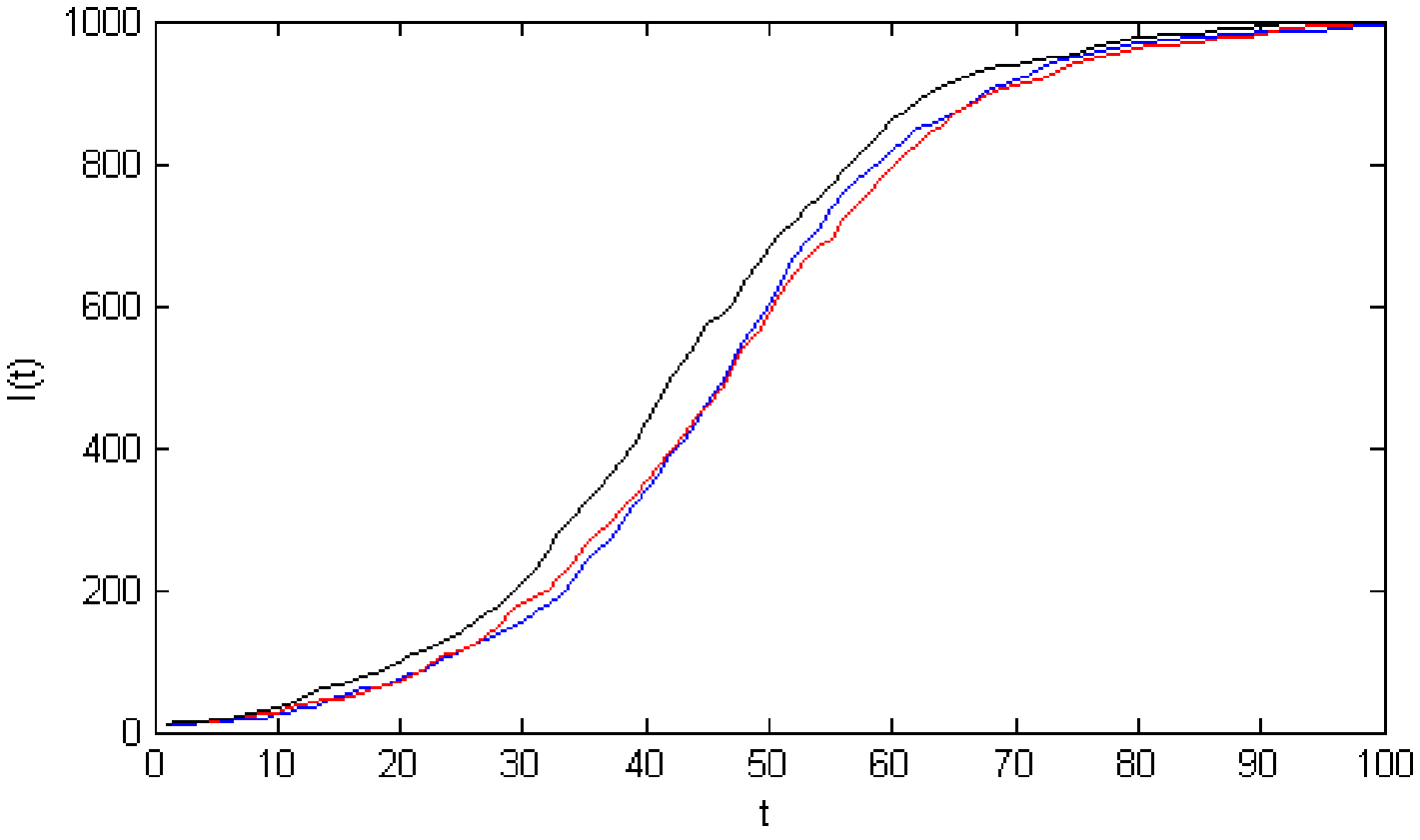
Simulation Results

- Notice that $\mathcal{I}(t) = \sum_{n=1}^{N} x_n(t)$.
- Here are the results of a simulation with $p = 10^{-4}$, $N = 1000$, and $\mathcal{I}(1) = 10$:



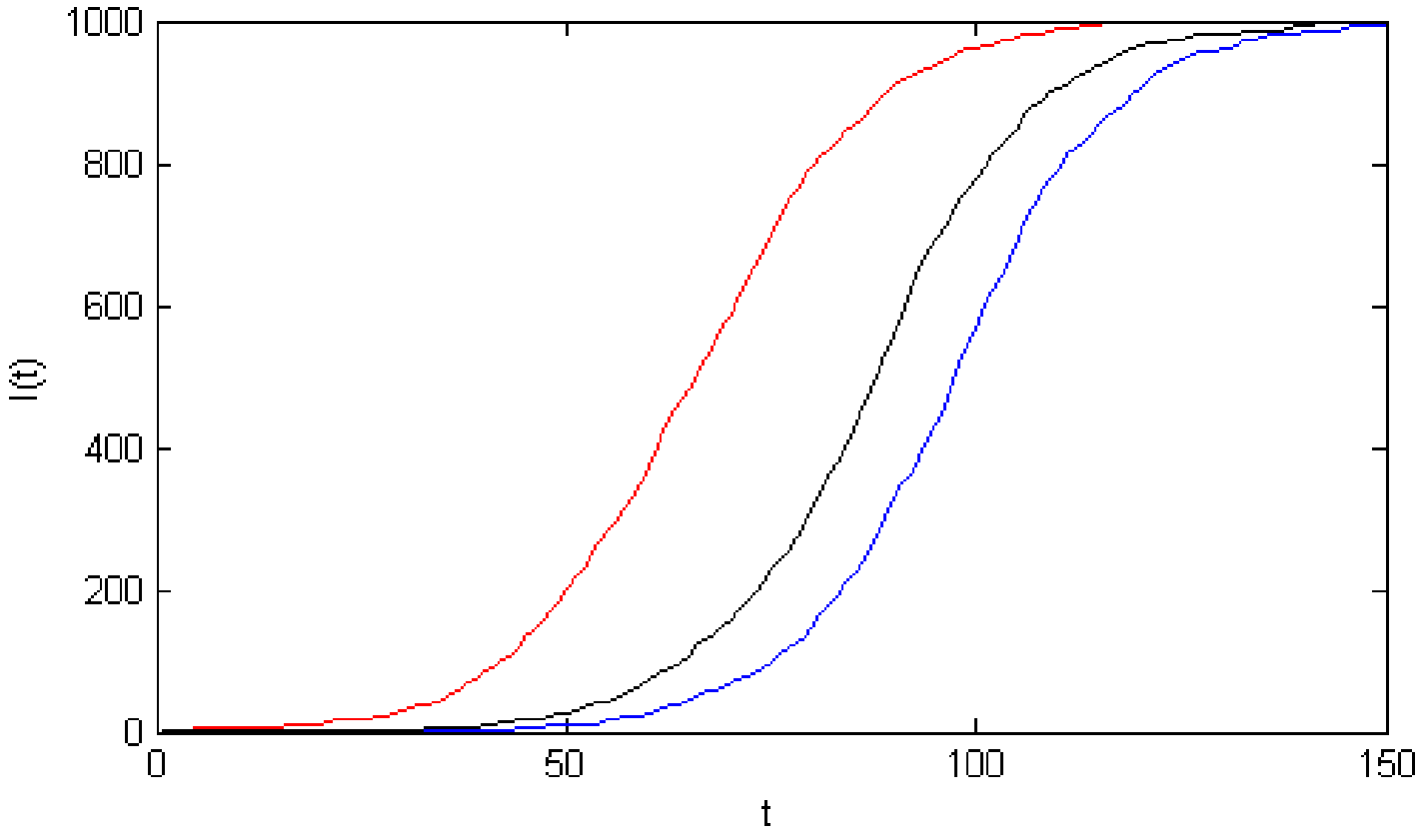
Simulation Results

- And here are the results of three different simulations with $p = 10^{-4}$, $N = 1000$, and $\mathcal{I}(1) = 10$:



Simulation Results

- Finally, here are the results of three different simulations with $p = 10^{-4}$, $N = 1000$, and $\mathcal{I}(1) = 1$:



Expected (Average) Daily Outcome

- Let's determine the expected number of people infected on a day t that starts with $\mathcal{I}(t)$ infectious people and $N - \mathcal{I}(t)$ who are susceptible to infection.
- A susceptible person n has probability $1 - p$ of NOT being infected on day t by a given infectious person m. Therefore, person n has probability $(1 - p)^{\mathcal{I}(t)}$ of NOT being infected on day t.
- The expected number of people who are infected on day t is then $[1 - (1 - p)^{\mathcal{I}(t)}][N - \mathcal{I}(t)]$, so

$$E[\mathcal{I}(t+1)] = \mathcal{I}(t) + [1 - (1 - p)^{\mathcal{I}(t)}][N - \mathcal{I}(t)]$$

Deterministic Models

- If both $\mathcal{I}(t)$ and $N - \mathcal{I}(t)$ are large enough, it may be reasonable to approximate $\mathcal{I}(t+1)$ by its expected value, resulting in a deterministic model:

$$\mathcal{I}(t+1) = \mathcal{I}(t) + [1 - (1-p)^{\mathcal{I}(t)}][N - \mathcal{I}(t)] \qquad (1)$$

- If $p\mathcal{I}(t)$ is small, we can approximate $(1-p)^{\mathcal{I}(t)}$ by $1 - p\mathcal{I}(t)$, yielding a simpler model:

$$\mathcal{I}(t+1) = \mathcal{I}(t) + p\mathcal{I}(t)[N - \mathcal{I}(t)] \qquad (2)$$

- For these models, given $\mathcal{I}(1)$ we can compute $\mathcal{I}(2)$, $\mathcal{I}(3)$, ...

Deterministic versus Stochastic

- These deterministic models are much more efficient to compute (1 calculation versus N^2 for the stochastic model). Their predictions may be just as reasonable as any particular simulation of the stochastic model.
- The stochastic model can give some idea of the uncertainty of its predictions via multiple simulations; the deterministic models we've written down say nothing about their uncertainty.

Continuous-Time Model

- The models we have discussed so far are called discrete-time models; time t takes on only integer values.
- We can approximate these models by continuous-time processes; approximating model (2), we get

$$\mathcal{I}'(t) = p\mathcal{I}(t)[N - \mathcal{I}(t)] \tag{3}$$

- We can write down an exact solution to this differential equation:

$$\mathcal{I}(t) = \frac{N\mathcal{I}(0)}{\mathcal{I}(0) + [N - \mathcal{I}(0)]e^{-pNt}}$$

Fitting the Model to Data

- The solution $\mathcal{I}(t)$ of model (3) has three parameters: N, p, and $\mathcal{I}(0)$. Suppose we know N but not the other two parameters. Given a set of data points $[t_j, \mathcal{I}_j]$, we can ask which values of p and $\mathcal{I}(0)$ best fit the data.
- [A more fundamental (but more difficult) question is whether the model can adequately fit the data at all; are there ANY parameters of the model that fit the data reasonably well?]
- We could try to minimize the sum of the squares of the residuals $\mathcal{I}_j - \mathcal{I}(t_j)$. However, this would be a NONlinear least squares problem, because $\mathcal{I}(t)$ does not depend linearly on p or $\mathcal{I}(0)$.

Way 1 to use Linear Least Squares

- If the data is given at consecutive values of t, say $t_j = j$, then one approach is to use model (2) and write

$$\mathcal{I}(t+1) - \mathcal{I}(t) = p\mathcal{I}(t)[N - \mathcal{I}(t)].$$

  The right-hand side is a linear function of the parameter p, and linear least squares yields the value of p that minimizes the sum of the squares of the residuals $\mathcal{I}_{j+1} - \mathcal{I}_j - p\mathcal{I}_j(N - \mathcal{I}_j)$.
- This doesn't resolve the question of which value of $\mathcal{I}(0)$ to use. If we let $t_0 = 0$ for the first data point, then we could let $\mathcal{I}(0) = \mathcal{I}_0$. However, this might not be the best choice of $\mathcal{I}(0)$ in order to make the residuals $\mathcal{I}_j - \mathcal{I}(t_j)$ small.

Way 2 to use Linear Least Squares

- Going back to the solution of model (3), we can make a transformation of variables so that the transformed solution does depend linearly on its parameters. First we divide both sides into N and simplify:

$$N/\mathcal{I}(t) = 1 + [N/\mathcal{I}(0) - 1]e^{-pNt}$$

- Next subtract 1 and take the logarithm:

$$\log[N/\mathcal{I}(t) - 1] = \log[N/\mathcal{I}(0) - 1] - pNt$$

- Let $Z(t) = \log[N/\mathcal{I}(t) - 1]$; then the model becomes $Z(t) = Z(0) - pNt$. This is a linear function of the parameters pN and $Z(0)$. One can transform the data to pairs (t_j, Z_j), use linear least squares to determine values for pN and $Z(0)$, and then solve for p and $\mathcal{I}(0)$.

Caveat

- Both ways of using linear least squares transform the model or its solution into a linear relationship between two quantities that can be computed from the data points $(t_j, \mathcal{I}_j)$; in the second way, the model predicts that Z_j is a linear function of t_j.
- Rather than simply accept the result of the least squares fit, one should graph the predicted relationship (e.g., Z_j versus t_j) and see if it actually looks linear. This gives some idea of how valid the model is.
- Regardless of how one determines values for p and $\mathcal{I}(0)$, one should also check directly how well the resulting $\mathcal{I}(t)$ fits the data.

More Sophisticated Models

- Let's re-examine the assumptions behind our first models and discuss how to make them more realistic.
- We assumed a fixed population size N that was isolated from other sources of the hypothetical illness we modeled.
- We assumed that a single number p represents the probability of an infectious person infecting a susceptible person on each day, for each such pair of people.
- A more realistic model would allow p to depend on a number of factors.

Modeling the Infection Probability p

- In real life, the infection probability p depends on the pair of people. However, introducing an independent probability p_{mn} for each pair of people m and n results in way too many parameters.
- Also, p depends on time; for example, day of week.
- Perhaps most importantly, p depends on how long the infectious person has had the illness. Typically it peaks a certain amount of time after infection, then decreases to 0.
- To keep the number of parameters manageable, we need to have a model for how p depends on these factors.

Compartmental Models

- Many models divide the population into a relatively small number of categories (“compartments”) and keep track of the number of people in each compartment.
- Our first deterministic models had two compartments: “susceptible” and “infectuous”. We’ll call the continuous time model (3) the SI model.
- A widely studied model is the SIR model, which introduces a third compartment: “recovered”. People in this category are no longer infectious.
- Other possible compartments can take into account more stages in the progression of the illness, different behavior patterns, different biological characteristics, etc.

Fitting to Data, Revisited

- In our earlier discussion, we assumed that the number of infectious people at a given time could be measured. But how would we ever know this number?
- The number of infectious people is often inferred from data on new diagnoses of the illness. However:
  - Not all people who get the illness see a doctor.
  - Diagnosis may come well after a person becomes infectious.
  - Data is not always reported (e.g., to CDC) promptly or reliably.
- A common problem in modeling is to relate the quantities of interest to the available data.