

Mathematical Modeling Lecture

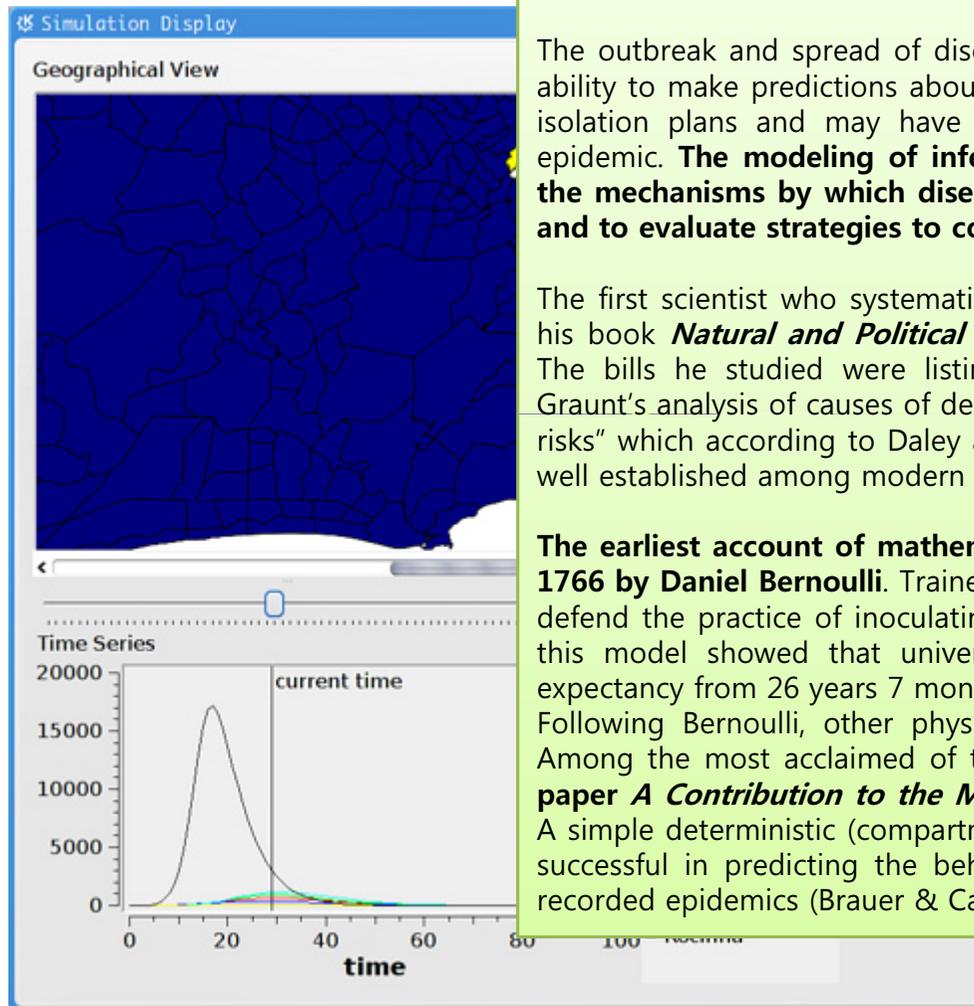
Epidemic Models

– an examples of the mathematical modeling

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Epidemic model



An **Epidemic model** is a simplified means of describing the transmission of communicable disease through individuals.

The outbreak and spread of disease has been questioned and studied for many years. The ability to make predictions about diseases could enable scientists to evaluate inoculation or isolation plans and may have a significant effect on the mortality rate of a particular epidemic. **The modeling of infectious diseases is a tool which has been used to study the mechanisms by which diseases spread, to predict the future course of an outbreak and to evaluate strategies to control an epidemic (Daley & Gani, 2005).**

The first scientist who systematically tried to quantify causes of death was **John Graunt** in his book ***Natural and Political Observations made upon the Bills of Mortality, in 1662.*** The bills he studied were listings of numbers and causes of deaths published weekly. Graunt's analysis of causes of death is considered the beginning of the "theory of competing risks" which according to Daley and Gani (Daley & Gani, 2005, p. 2) is "a theory that is now well established among modern epidemiologists".

The earliest account of mathematical modeling of spread of disease was carried out in 1766 by Daniel Bernoulli. Trained as a physician, Bernoulli created a mathematical model to defend the practice of inoculating against smallpox (Hethcote, 2000). The calculations from this model showed that universal inoculation against smallpox would increase the life expectancy from 26 years 7 months to 29 years 9 months (Bernoulli & Blower, 2004). Following Bernoulli, other physicians contributed to modern mathematical epidemiology. Among the most acclaimed of these were **A. G. McKendrick and W. O. Kermack, whose paper *A Contribution to the Mathematical Theory of Epidemics* was published in 1927.** A simple deterministic (compartmental) model was formulated in this paper. The model was successful in predicting the behavior of outbreaks very similar to that observed in many recorded epidemics (Brauer & Castillo-Chavez, 2001).

Types of Epidemic Models

"Stochastic" means being or having a random variable. **A stochastic model is a tool for estimating probability distributions of potential outcomes by allowing for random variation in one or more inputs over time.** Stochastic models depend on the chance variations in risk of exposure, disease and other illness dynamics. They are used when these fluctuations are important, as in small populations (Trottier & Philippe, 2001).

Stochastic

TYPES
Epidemic Models

Deterministic

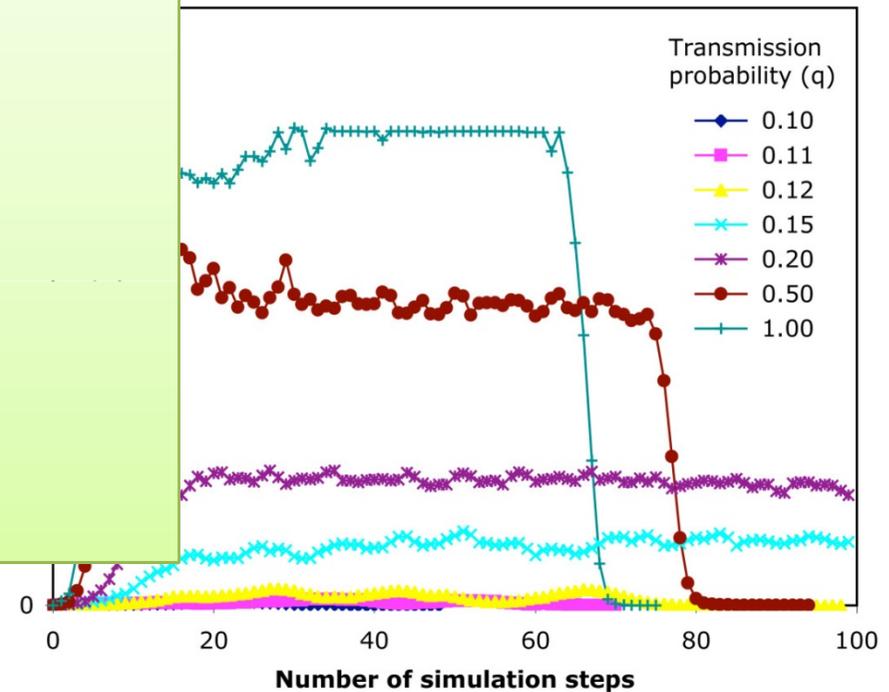
When dealing with large populations, as in the case of tuberculosis, deterministic or compartmental mathematical models are used. **In the deterministic model, individuals in the population are assigned to different subgroups or compartments, each representing a specific stage of the epidemic. Letters such as M, S, E, I, and R are often used to represent different stage.**

The transition rates from one class to another are mathematically expressed as derivatives, hence the model is formulated using differential equations. While building such models, it must be assumed that the population size in a compartment is differentiable with respect to time and that the epidemic process is deterministic. In other words, the changes in population of a compartment can be calculated using only the history used to develop the model (Brauer & Castillo-Chavez, 2001).

Terminology

The following is a summary of the notation used in this:

M -- Passively Immune Infants
 S -- Susceptibles
 E -- Exposed Individuals in the Latent Period
 I -- Infectives
 R -- Removed with Immunity
 β -- Contact Rate
 μ -- Average Death Rate
 B -- Average Birth Rate
 $1/\varepsilon$ -- Average Latent Period
 $1/\gamma$ -- Average Infectious Period
 R_0 -- Basic Reproduction Number
 N -- Total Population
 f -- Average Loss of Immunity Rate of Recovered Individuals
 δ -- Average Temporary Immunity Period



The SIR Model : Deterministic Compartmental Models

In 1927, W. O. Kermack and A. G. McKendrick created a model in which they considered a fixed population with only three compartments, susceptible: $S(t)$, infected, $I(t)$, and removed, $R(t)$. The compartments used for this model consist of three classes:

- $S(t)$ is used to represent the number of individuals not yet infected with the disease at time t , or those susceptible to the disease
- $I(t)$ denotes the number of individuals who have been infected with the disease and are capable of spreading the disease to those in the susceptible category
- $R(t)$ is the compartment used for those individuals who have been infected and then recovered from the disease. Those in this category are not able to be infected again or to transmit the infection to others.



Component Analysis Diagram
(Compartmental Models)

The SIR Model : Deterministic Compartmental Models

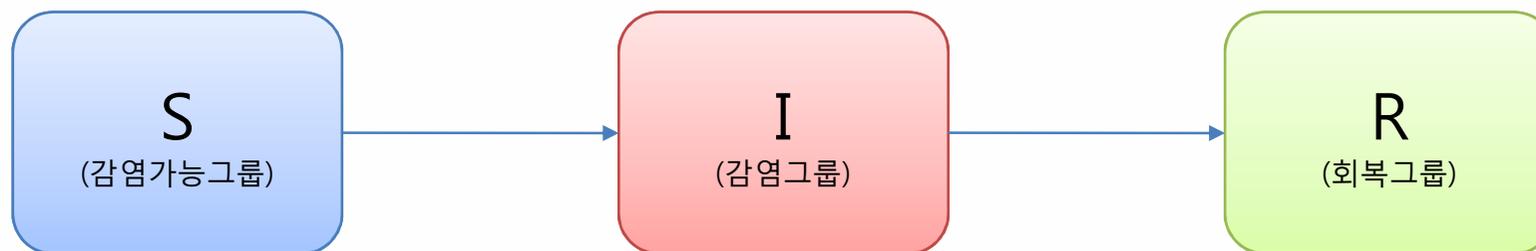
$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

The following is a summary of the notation used in this:

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Component Analysis Diagram
(Compartmental Models)

The SIR Model with Excel

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	A	B	C	D	E	F	G
1	beta	0.002					
2	y	1					
3							
4		S	I	R	dS	dI	dR
5		1000	1	0	-2	1	1
6		998	2	1	-3.992	1.992	2
7		994.008	3.992	3	-7.93616	3.94116	3.992
8		986.0718	7.93616	6.992	-15.6512	7.715088	
9		970.4206	15.65125	14.92816	-30.3766	14.71534	
10		940.044	30.37659	30.57941	-57.1107	26.73407	
11		882.9334	57.11065	60.95599	-100.85	43.73915	57.11065
12		782.0835	100.8498	118.0666	-157.746	56.89614	100.8498
		624.3376	157.7459	218.9165	-196.973	39.22751	157.7459
		427.3642	196.9735	376.6624	-168.359	-28.6147	196.9735
		259.0054	168.3588	573.6358	-87.2117	-81.1471	168.3588
		171.7937	87.21166	741.9946	-29.9648	-57.2468	87.21166
		141.8289	29.96483	829.2063	-8.49976	-21.4651	29.96483
		133.3291	8.499756	859.1711	-2.26653	-6.23323	8.499756
		131.0626	2.26653	867.6709	-0.59411	-1.67242	2.26653
		130.4685	0.594115	869.9374	-0.15503	-0.43909	0.594115

=\$B\$1*B5*C5

=\$B\$1*B5*C5-\$B\$2*C5

=\$B\$2*C5

In this example, we will use following parameters:
 β -- Contact Rate : 0.002
 γ -- Recovery Rate (or Removed Rate) : 1

The SIR Model with Excel

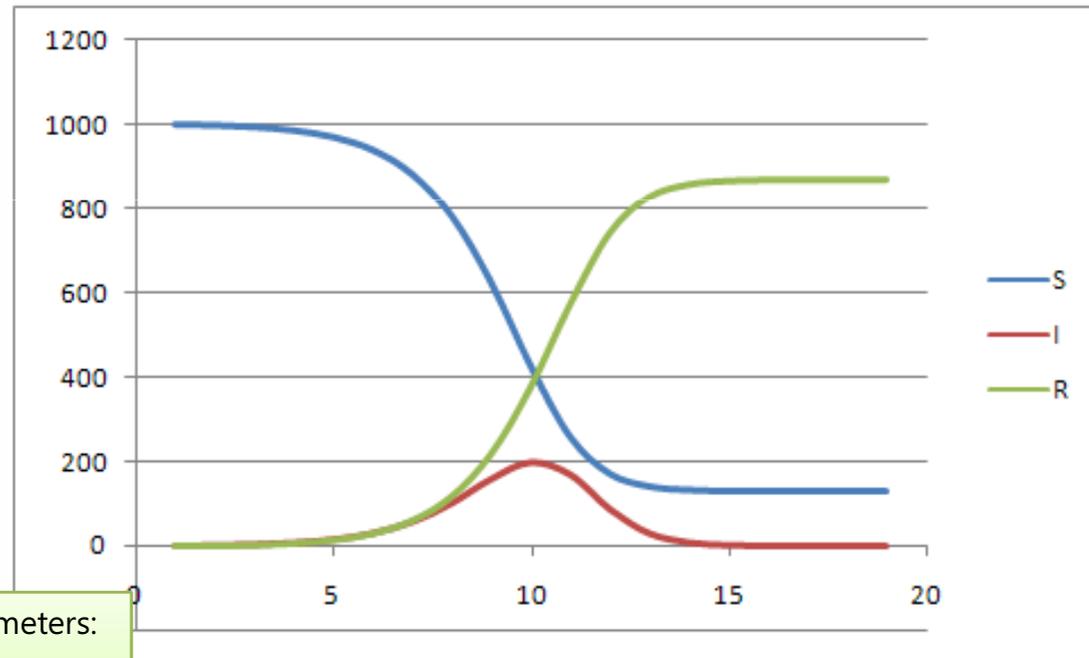
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병에 걸리지 않을 확률 = $(1 - \text{접촉비율})^{\text{병에 걸린 사람의 수}}$

→ 병에 걸릴 확률 = $1 - (1 - \text{접촉비율})^{\text{병에 걸린 사람의 수}}$

→ 감염되는 사람 수 = 이전 감염자 $\times (1 - (1 - \text{접촉비율})^{\text{병에 걸린 사람의 수}})$

This formular is a general solution of this differential equation

The SIR Model with Births and Deaths

Using the case of measles, for example, there is an arrival of new susceptible individuals into the population. For this type of situation births and deaths must be included in the model. The following differential equations represent this model:

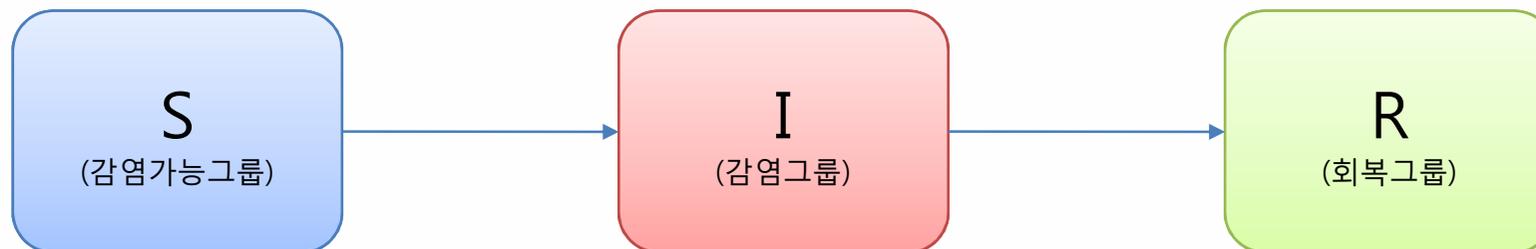
$$\frac{dS}{dt} = -\beta SI + B(S + I + R) - \mu S$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

The following is a summary of the notation used in this:

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Component Analysis Diagram
(Compartmental Models)

The SIR Model with Births and Deaths

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- μ -- Average Death Rate
- N -- Total Population
- B -- Average Birth Rate

=-\$B\$1*B6*C6+\$D\$1*(B6+C6+D6)-\$B\$3*B6

=\$B\$1*B6*C6-\$B\$2*C6-\$B\$3*C6

=\$B\$2*C6-\$B\$3*D6

In this example, we will use following parameters:

- β -- Contact Rate : 0.002
- $1/\gamma$ -- Average Infectious Period : 1
- μ -- Average Death Rate : 0.2
- N -- Total Population : 1000
- B -- Average Birth Rate : 0.2

The SIR Model with Births and Deaths

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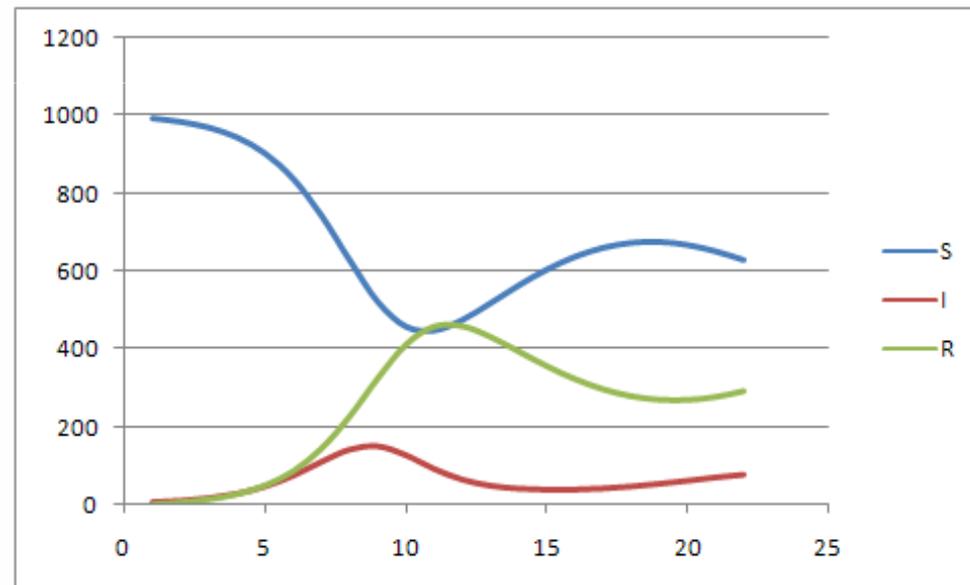
$$\frac{dR}{dt} = \gamma I - \mu R$$

The following is a summary of the notation used in this:

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 β -- Contact Rate
 $1/\gamma$ -- Average Infectious Period
 μ -- Average Death Rate
 N -- Total Population
 B -- Average Birth Rate

In this example, we will use following parameters:

β -- Contact Rate : 0.002
 $1/\gamma$ -- Average Infectious Period : 1
 μ -- Average Death Rate : 0.2
 N -- Total Population : 1000
 B -- Average Birth Rate : 0.2



<http://math.colgate.edu/~wweckesser/solver/DiseaseSIRwBD.shtml>

The SIS Model with Births and Deaths

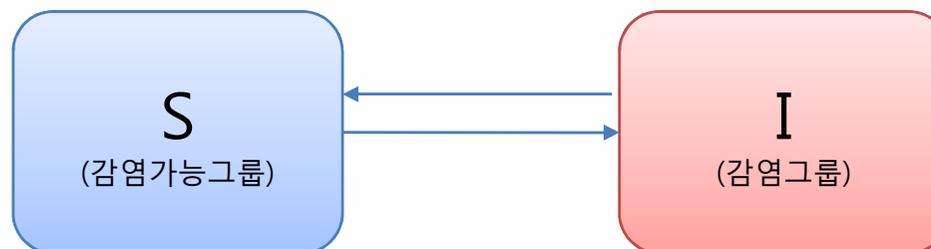
The SIS model can be easily derived from the SIR model by simply considering that the individuals recover with no immunity to the disease, that is, individuals are immediately susceptible once they have recovered. Removing the equation representing the recovered population from the SIR model and adding those removed from the infected population into the susceptible population gives the following differential equations:

$$\frac{dS}{dt} = -\beta SI + B(S + I + R) + \gamma I - \mu S$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

The following is a summary of the notation used in this:

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Component Analysis Diagram
(Compartmental Models)

The SIS Model with Births and Deaths

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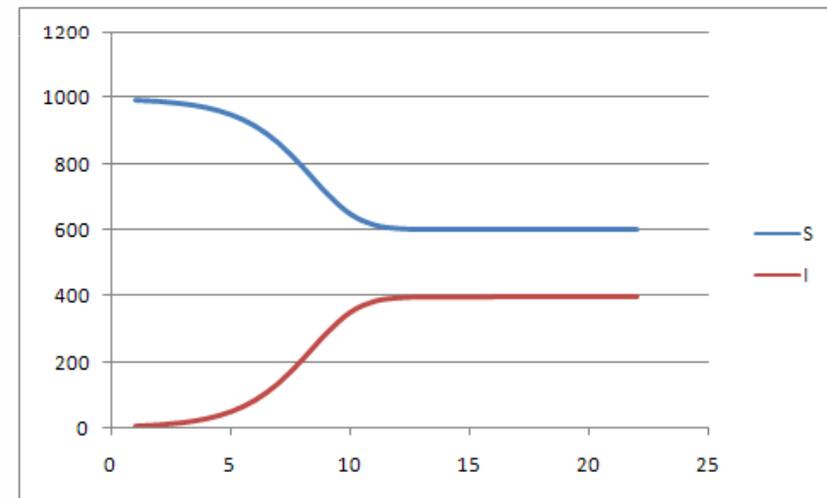
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In this example, we will use following parameters:

β -- Contact Rate : 0.002
 $1/\gamma$ -- Average Infectious Period : 1
 μ -- Average Death Rate : 0.2
 N -- Total Population : 1000
 B -- Average Birth Rate : 0.2



The SEIR Model

The SIR model discussed above takes into account only those diseases which cause an individual to be able to infect others immediately upon their infection. Many diseases have what is termed a latent or exposed phase, during which the individual is said to be infected but not infectious. In this model the host population (N) is broken into four compartments: susceptible, exposed, infectious, and recovered, with the numbers of individuals in a compartment, or their densities denoted respectively by S(t), E(t), I(t), R(t), that is $N = S(t) + E(t) + I(t) + R(t)$

$$\frac{dS}{dt} = -\beta SI$$

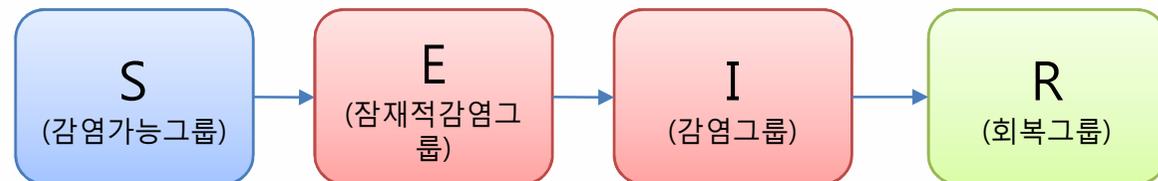
$$\frac{dE}{dt} = \beta SI - \epsilon E$$

$$\frac{dI}{dt} = \epsilon E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

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 I -- Infectives
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 μ -- Average Death Rate
 $1/\epsilon$ -- Average Latent Period



Component Analysis Diagram
(Compartmental Models)

The SEIR Model

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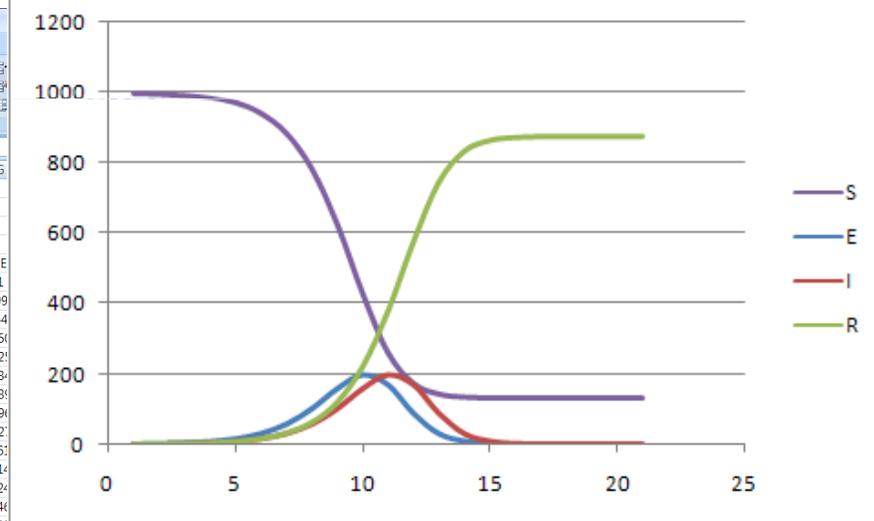
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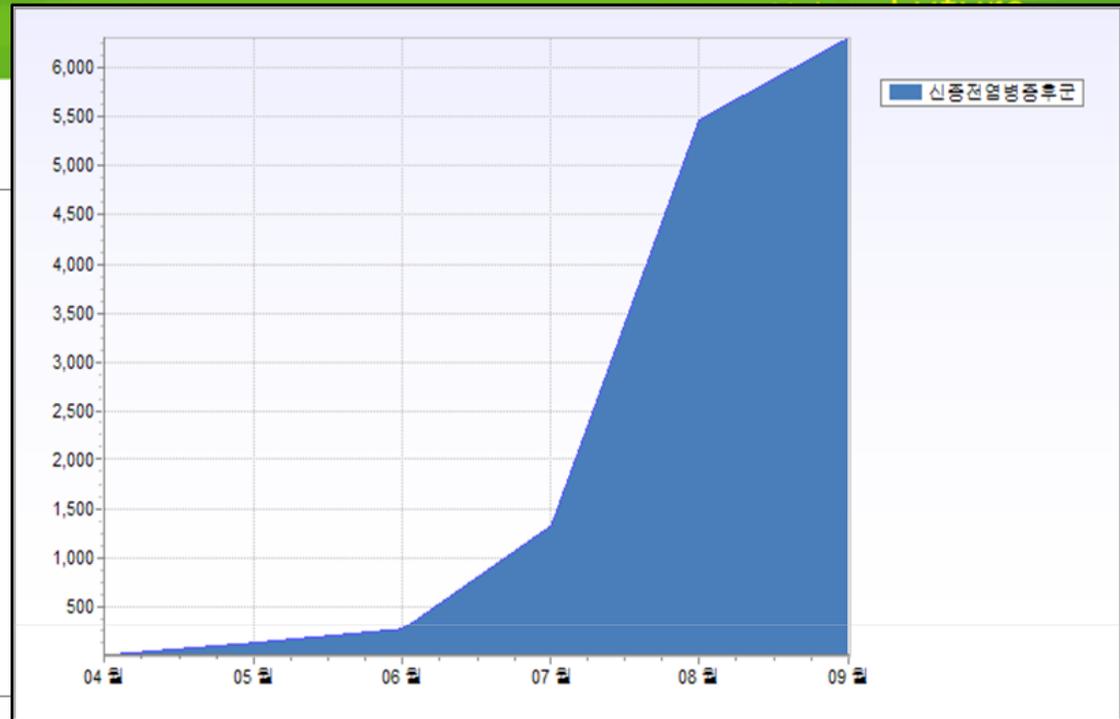
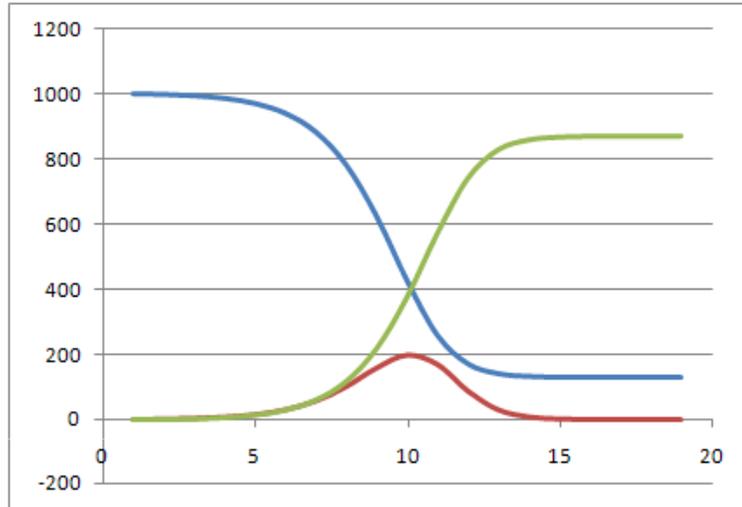
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21	130.4685	0.594115	2.26653	868.6709	-0.15503	-0.43909
22	130.3135	0.155026	0.594115	870.9374	-0.0404	-0.11462
23	130.2731	0.040404	0.155026	871.5315	-0.01053	-0.02988
24	130.2625	0.010527	0.040404	871.6865	-0.00274	-0.00778
25	130.2598	0.002743	0.010527	871.7269	-0.00071	-0.00203
26	130.2591	0.000714	0.002743	871.7375	-0.00019	-0.00053



Discussion : H1N1 Influenza



http://www.cdc.go.kr/kcdchome/jsp/observation/stat/dgt/STATDGT0600List.jsp?menuid=110161&contentid=null&boardid=null&appid=kcdcobs&pageNum=1&sub=3&tabinx=4&q_had01=A&q_had02=2009&q_gunCode_tmp=null&q_disCode_tmp=null&q_popupOn=null&q_disguntxts_tmp=&q_discodetexts_tmp=

<http://stat.cdc.go.kr/>

