

# COVID-19 SIR, SQEAIR, DDE Sigmoidal Models

Created with Mathcad 14 Math Software: Documentation, Model Creation, and Math Calculations

Mathcad Program File (COVID-19 SIR Sigmoid Model.xmcd) and Data can be found at: [VXPhysics.com/COVID-19](http://VXPhysics.com/COVID-19)

This work was sparked by the desire to understand the basic dynamics of the Novel COVID-19 Pandemic. With the exception of the Sigmoidal Incidence Model that was created, this work is mostly a review of existing research. This is not a formal paper and attribution to sources are sketchy. Epidemiological models are commonly stochastic, diffusive-spatial, network based, with heterogeneous sub-populations. However, the parameters of Dynamic Equation Models, such as SIR and SQEAIR, are more directly related to and interpretable as physical processes. The intent of this work was to build a simple epidemiological "toy model" to estimate the period before the peak infection and the total number of infected cases. The methodology employed was, first, application of Dynamic Deterministic Discrete SIR, SEIR, & DDE Models to characterize infection data from Wuhan China, USA, UK, Italy, Spain, N.

Korea, NY, FL, New Orleans. Next, a Sigmoidal Incidence Function was used to give an Empirical Transmission/Contact Model that **can successfully fit the observational data** from China. The Levenberg-Marquardt Method was used to extract the Empirical Epidemiological Parameters of the Epidemic Isolation Policies that were successfully employed by China and S.

Korea. The insights gained from analysis of these successful interventions were then used to Analyze and Predict Results for the Mitigation Policies of the US, NY, & UK.

NOTE: Current State of Modeling is such that projections are "good" for **only about 2 weeks**.

## Table of Contents (\*Page Number Description)

- \*1 Analysis of the COVID-19 Pandemic and Page Outline
- \*2-3 Methodology of the Investigation and Preview: Mitigation Model Match
- \*4-5 General Description of the SARS-CoV-2 Virus and Conclusions, Factors in Spread
- \*6-7 COVID-19 Epidemiology and Forecasting Impact on Hospitals
- \*8-9 SIR Compartmental Disease Model, Deterministic Mathematical Modeling
- \*9-11 Continuous SIR, SEIR, and **Delayed Differential Equation (DDE)** Solution Methods
- \*12-14 Discrete SIRD & SEIR Models and Algorithms. Analyze Typical Flu Season
- \*15 Some Different Possible Compartmental Models: SIR, SEIR, SQEAIR
- \*16 COVID-19 SIRD Data, Log Curve, Model & Predictions for Hubei, China
- \*17-18 Mitigation: Rationale for **Empirical Sigmoidal Transmission/Contact Phase Model**
- \*19 Algorithm for Discrete SIR Transmission Sigmoidal Transition Model: SIRM
- \*20 Algorithm for Discrete SEIR Transmission Sigmoidal Transition Model: SEIRM
- \*21-22 SEIR Sigmoidal Transition Model Successful Fit for Hubei Data. Extract  $R_0$
- \*23-24 SPATIAL AGGREGATION by US States: Estimate Model Parameters
- \*25-26 New York City and State COVID19 Cases Feb 15 - April
- \*27 Project Outcome New York Epidemic: No Mitigation-Worst Case Scenarios
- \*28 Mitigation Modeling for NY: No Mitigation vs. Mitigation Scenarios
- \*29 USA Data Directly From Johns Hopkins
- \*30 Extract SIR Parameters from US Data, Apply IHME Projections, Project Deaths
- \*31 Data on USA Total Confirmed Deaths to March 19
- \*32-35 Florida Cases & Deaths, Prob of Infection **36** New Orleans COVID19 Cases
- \*37-38 UK COVID19 Cases, Extract UK SIR Parameters
- \*39-40 Italy Cases, Spain Cases and Deaths
- \*41-42 S. Korea Cases, Sigmoidal Model: Extract Mitigation Parameters
- \*43-45 World Cases and Deaths/Million
- \*46-47 Computational Tools, Bibliography

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May 6, 2020



# Particulars of the Methodology for the COVID-19 Investigation

This work starts with a general description of the SARS-CoV-2 Virus and the associated COVID-19 disease. Its Epidemiology (Transmission and Model Parameters), Infection Cycle, Risks, and Estimate of Required Hospital Services are investigated.

Next the SIRD and SEIRD Mathematical Models and their parameters, and general epidemiological behavior are discussed. Also, the basic assumptions of the SIRD/SEIR models are examined. The model is demonstrated by its application to a typical flu season. The detailed characteristics of a typical flu season and the range of its parameters are discussed. **We will use whichever model (SEIR or SIR) works best.**

COVID-19 outbreaks in Wuhan China, NY, USA, FL, New Orleans, UK, Italy, Spain, N. Korea, and the World are presented. This was done in the following fashion. First, data on the total infections for each region were obtained. The rate of change, days to double, and a fit to the data with two types of exponential curves was made. The data was plotted with two types of exponential curve fits and with the number of new cases of infection. The infection data on a semi-log plot to observe its exponential behavior were also plotted. A fundamental and key concept in epidemiology and demography is the Basic Reproduction Number,  $R_0$ . It is a threshold, and it is defined such that if  $R_0 > 1$ , the infectious disease will result in an outbreak, i.e. unstable exponential growth.  $R_0 < 1$  would imply its disappearance.  $R_0$  is the ratio new secondary/primary infections.

## **A Sigmoidal Transition Model was created to model Mitigation by Governmental Intervention.**

An attempt was made to do a spatial analysis by looking at the model behavior in all 50 states. Estimates of the Reproduction Number,  $R_0$ , for each of the states were made. However, keeping up with, aggregating, updating, processing, and doing a spatial analysis in a timely manner was beyond the time and scope of this basic investigation.

A deeper investigation on the outbreaks in Wuhan, NY, USA, and the UK was made. For these locations, the parameters for the SIRD infection model were abstracted. Using the SIRD model and abstracted parameters, observations on how well the model compares with the infection data, and the projected behavior/growth of the epidemic was made. The model gave Projected Numbers of the Susceptibles, Infections, Recovered, and Fatalities.

**The initial projected numbers for infections and deaths were horrendous.** Projections gave 2 million deaths in the US. These initial models agreed with the assessment of other earlier epidemiological models. Clearly, governmental intervention was needed to reduce these epidemic numbers.

Based on interventions in Wuhan China, a Sigmoidal Model was created for this investigation to reflect the effects of the Wuhan intervention. This intervention model was then applied to our SIRD epidemiological model. A preview of the model results/plot is shown at the bottom of the following page. It is formulated to model the reduction in the transmission rate,  $\beta$ , resulting from the intervention.

## COVID-19 Situation (April 8, 2020) of the World at Large

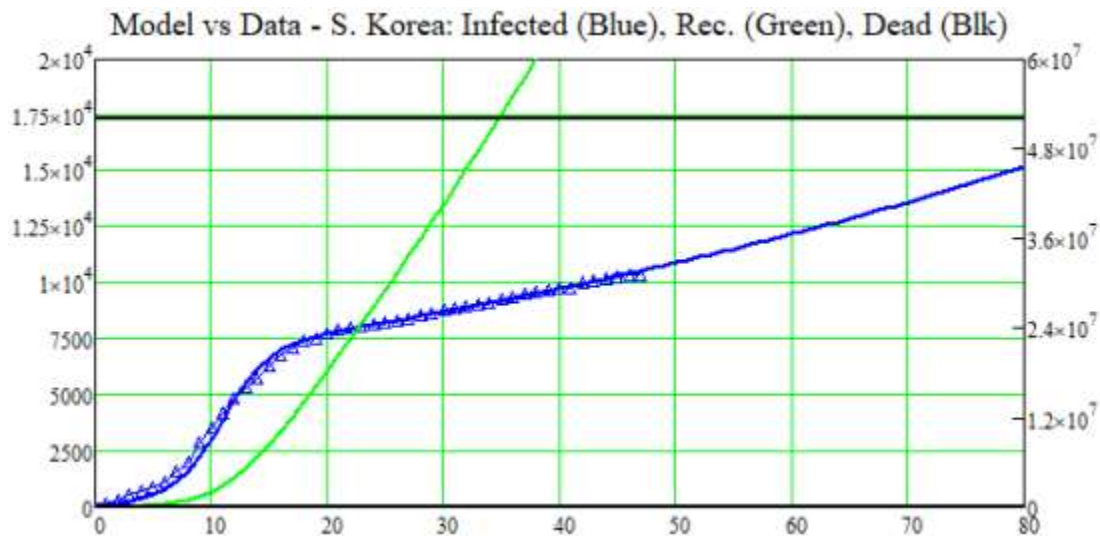
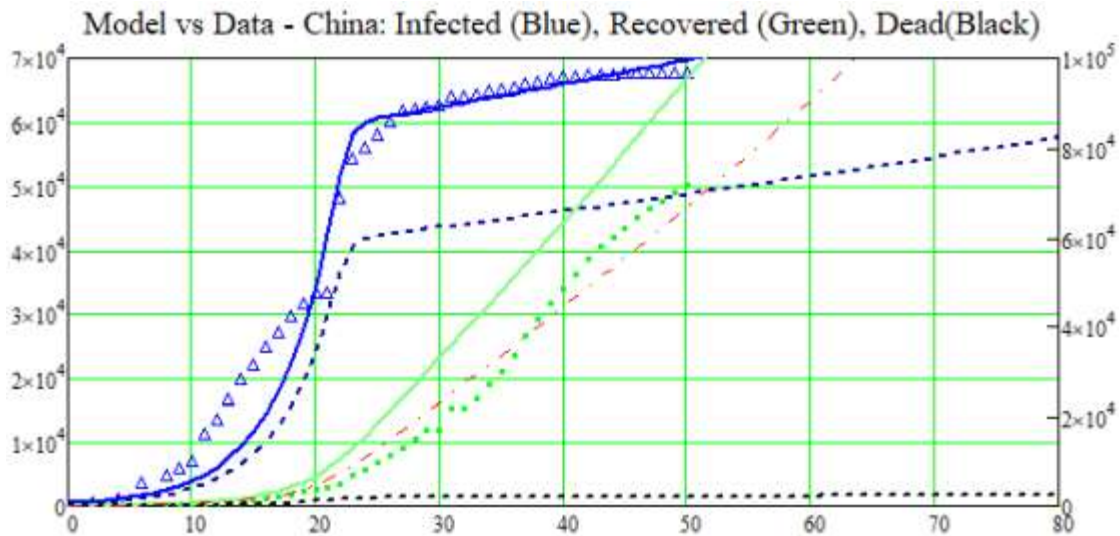
Epidemiological Mathematical Models are important. They are based on our knowledge of the dynamics of epidemics. Often, there are phenomena that can only be comprehended with math models. Generalization models have been used to estimate the demand for hospital beds, ICU days, number of ventilators and also, importantly, the need and required extent of governmental intervention. To date, the number of infections and deaths are **far below** the projections of earlier models. A Model is only as good as the assumptions put into the Model. Clearly, there are phenomena of the COVID-19 epidemic that are as yet not understood. Models are constantly being updated and improved.

The story of the COVID-19 outbreak is ongoing. Our knowledge of this novel virus, is in a state of flux. Every week seems to bring additional important medical and epidemiological information.

# Preview: Mitigation Models for China, S. Korea, USA

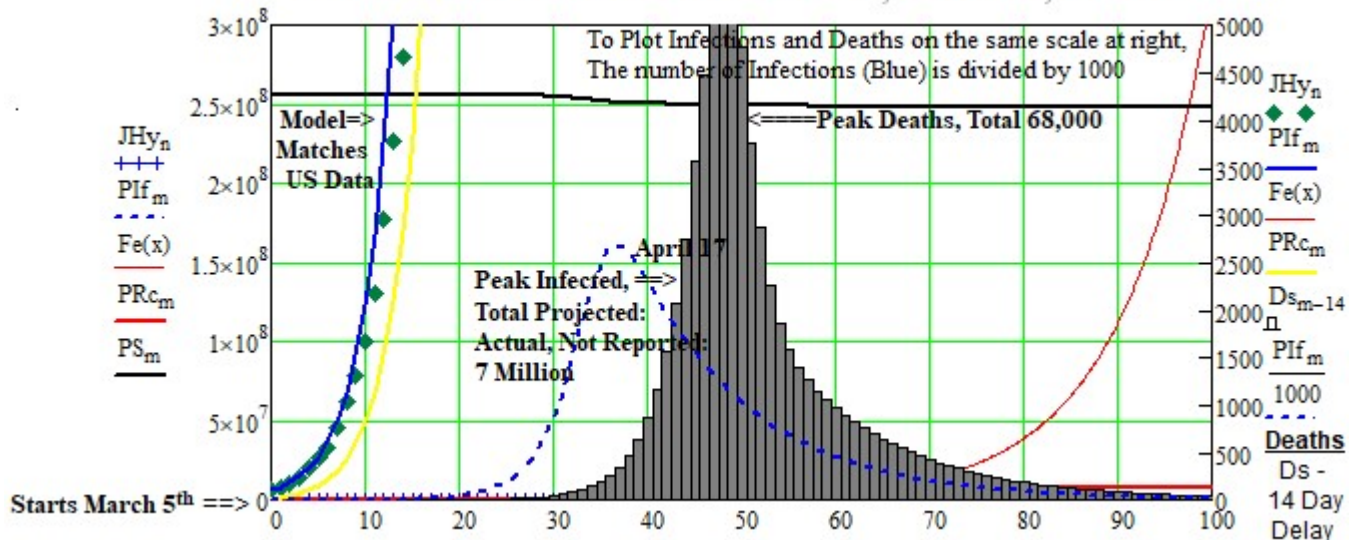
Shows Daily Match Between Infection Data (Blue ▲) vs Sigmoidal Model (Blue Line)

See Pages 18, 36, and 27 for the Methodology to Extract Mitigation Model Parameters



What is the predicted infection rate after the April 17th peak? We see that in 30 days, a month later, May 19th, the number of infections drops down to 11% of the peak, but this is a very very big number.

## USA: Infection Cases vs. SIR Model Sus, Infections, and Rec



# General Description of Virus and Conclusions

## Some Characteristics of the COVID-19 Disease

The SARS-CoV-2 Virus is an enveloped, single-stranded RNA virus. It is commonly referred to by the name of the disease it causes, which is COVID-19. The later name was chosen by the WHO for PR purposes. This virus was first discovered in China by observing that hospital patients were showing a very virulent type of pneumonia. (Historically, the most general cause of pneumonia the *Streptococcus pneumoniae* bacterium.) Currently, according to the CDC, the incubation period for the novel coronavirus is somewhere between **2 to 10 days after exposure, mean**. More than 97 percent of people who contract SARS-CoV-2 show **symptoms within 11.5 days of exposure**. The **average incubation period seems to be around 5.2 days**. For many people, COVID-19 symptoms start as mild symptoms and gradually get worse over a few days. **Transmission occurs primarily:** via respiratory droplets from coughs and sneezes within a range of about 6 feet (1.8 m). Indirect contact via contaminated surfaces is another possible cause of infection. Preliminary research indicates that the virus may remain **viable on plastic and steel** for up to **three days**, but does not survive on **cardboard for more than one day** or on copper for more than four hours. Models show that 1/3 each of transmission occurs in household, schools-workplaces, and in the community.

### Additional Data on Model Parameters:

The paper: "*The effect of travel restrictions on the spread of the 2019 novel coronavirus outbreak*", by Ira M. Longini and Alessandro Vespignani give the **following data for the World Pandemic**. A **generation time ( $T_g$ ) ranging from 6 to 11 days** based on plausible ranges from the SARS epidemic and recent analysis of COVID-19 data. The results for generation time  $T_g = 7.5$  days. The obtained posterior distribution provides an average reproductive number  $R_0 = 2.57$ , and a **doubling time measured at  $T_d = 4.2$  days**.

They reported that the median ascertainment rate of detecting an infected individual in Mainland China is equal to **24.4%**. In other words, the modeling results suggest that in Mainland China **only one out of four cases are detected and confirmed**. Studies in Germany suggest **only 6%** of cases are reported. A recent study in the US, suggests that as few as **2%** of infections are confirmed. Reported Cases, at best, are only **10%** of Actual Number.

**Let Q equal the % of the Population that, if Infected, could be Reportable Cases.**

Q := 10.0%

Allowing for a 7 day incubation period, Bayesian Spectral Fusion Analysis of 5 countries shows wavelengths of 2.7, 4.1, and 6.7 days. After lockdown the 2.7 and 4.1 day cycles are suppressed, suggesting that they are related to virus dynamics. See: *Rapidly evaluating lockdown strategies using spectral analysis*, Nason.

In reality, model parameters, such as  $R_0$ , have different types of statistical distributions. The generation interval distribution for an infectious disease is the probability distribution function for the time from infection of an individual to the infection of a secondary case by that individual. Generation interval distributions uniquely characterize the relationship between the reproductive number  $R$  and the growth rate  $r$ . Different infectious diseases have at least 5 different possible distributions. See: *How generation intervals shape the relationship between growth rates and reproductive numbers*, Wallinga.

## The Susceptible, Infected, Recovered (SIR) Model

COVID-19 has a latent or incubation period, during which the individual is said to be infected but not infectious. Members of this population in this latent stage are labelled as Exposed (but not infectious). The model with this Exposed group is the Susceptible, Exposed, Infected, Recovered, SEIR Model. However, for this study, given the decision to use a deterministic discrete differential equation model and the limited amount of data, the model that most successfully matched the published Confirmed Infectious Case Data is the SIR model.

**We will use an SIR Model for Wuhan and the USA. This is shown** two pages after this. **For the Wuhan Virus**, we found that the Basic Reproductive Ratio,  $R_0$ , was 2.74 and that the time to recover is 41 days, days to double of 3.62  $\Rightarrow$  **Exponential Transmission**. During the initial exponential phase of growth, the **USA data** gave the number of days for infections to double as 2.309 and the Basic Reproductive Ratio as 2.74.



# Epidemic Spread: Factors, Herd Immunity, Prognosis

*Infectious Disease Dynamics, Derek Cummings*

- The number of individuals infected by each infectious case. ( $R_0$ )
- The time it takes between when a case is infected and when that case infects other people.

## **Difference in the Serial Interval**

The average length of time between when a case is infected and when s/he infects others,  
This serial interval is different for these two pathogens

- Influenza ~2.5 days
- Measles ~ 18 days

## **A Third Factor, $\theta$**

- Defined as the proportion of transmission occurring prior to symptoms
- Measure of how much shorter latent period is than incubation period
- Proposed by Fraser and colleagues

## **Reproduction Ratio, $R_0$ : Example - Sexually Transmitted Infection**

$$R_0 = \alpha \times c \times \beta$$

$\beta$  is the proportion of contacts that become infected

$c$  is the number of contacts per day

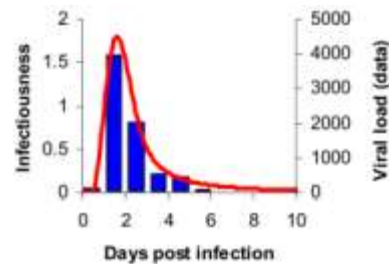
$\alpha$  is the duration of infectiousness

## **Estimates of $R_0$ of several pathogens**

Measles – 12	Scarlet Fever – 6	Smallpox – 6
Pertussis – 15	Mumps – 10	Influenza – 2
Chicken Pox – 9	Rubella – 8	HIV – 5
Diphtheria – 4	Polio – 6	Dengue – 4
Schistosoma japonicum – 3		

## **Death Rate, Extent**

Flu: 0.1%, 8%/year  
COVID-19: 0.5%, 70%



Could also use a proxy for infectiousness, viral load  $\implies$   
infectiousness, viral load in oropharyngeal secretions,  
for example

## **Targeted interventions to stop transmission depend upon [being able to identify cases](#)**

- Isolation, quarantine, screening travelers, prophylactic use drugs all depend on identifying people before transmit
- **Delays dramatically reduce effectiveness**
  - if your interventions don't identify people until after they've done the bulk of their transmission, they don't work
- The serial interval identifies the time-scale of response
- How quickly can we identify cases?

## **The Critical Immunization or Infection Rate to Eradicate a Disease (Herd Immunity %)**

### **COVID-19 Herd Immunity %**

$$HI(R_0) := 100 \cdot \left(1 - \frac{1}{R_0}\right) \quad HI(2.8) = 64.286$$

### **Herd Immunity %**

Measles and whooping cough, 90-95%  
chicken pox and mumps 85-90% coverage  
polio and scarlet fever 82-97% coverage  
smallpox 70-80% coverage

**US Herd Immunity:** This projects to 200 million infected in USA.

## **PROGNOSIS:**

When social isolation ends, the epidemic will start up again. Based on our current knowledge of the virus, without social isolation or a vaccine, the number of potential infections in USA is still 200 million.

It is still very infectious. It will probably be two years before the epidemic is under control in the US.

# COVID-19 Epidemiology State of Flux (Time Dependent)

## Perspective on Number of COVID-19 Deaths in USA

### Categories of Annual Deaths in the US

2,813,503 registered deaths (8,000/year) in the United States in 2017

Heart Disease: 647,000/ 23.5%

Cancer: 99,108/ 21.3%

Unintentional injuries: 169,936/ 6%

Chronic lower respiratory disease: 160,201/ 5.7%

Stroke and cerebrovascular diseases: 146,383/ 5.2%

Alzheimer's disease: 121,404/ 4.3%

Diabetes: 83,564/ 3%

**COVID-19: 82,000/3%**

Influenza and pneumonia: 55,672/ 2%

Suicide: 47,173

## April 7, 2020: IHME Revised Estimate of Number of COVID-19 US Deaths:

**82,000 deaths** from the first wave of infection, although the number could range from 49,000 to 136,000.

## Model Limitations: Old February 2020 AHA COVID-19 BEST GUESS

2020 Webinar of the American Hospital Association (AHA)

- |  |  |
|--|--|
| * $R_0 = 2.5$ ; Doubling time 7-10 days    | Community epidemic wave 2 months             |
| * Community attack rate = 30-40%           | <b>US: 96 million cases (27% Population)</b> |
| * Cases requiring hospitalization = 5%     | US: 4.8 million admissions                   |
| * Cases requiring ICU care = 1-2%          | US: 1.9 million ICU                          |
| * Cases requiring ventilatory support = 1% | US: 1 PPV                                    |
| * CFR = 0.5%                               | <b>US: 480,000 deaths</b>                    |

## Study: Nowcasting and Forecasting the International Spread of COVID-19

*Nowcasting and forecasting the potential domestic and international spread of the*

*2019-CoV outbreak originating in Wuhan, China: a modeling study, Wu, Leung, January 31, 2020*

### Nowcasting Findings:

In our baseline scenario, we estimated that the **basic reproductive number** for 2019-nCoV was **2.68 Confidence Level (95% CL 2.47–2.86)** and that 75,815 individuals (95% CL 37 304–130 330) have been infected in Wuhan as of Jan 25, 2020. The epidemic **doubling time** was **6.4 days** (95% CL 5.8–7.1). We estimated that in the baseline scenario, Chongqing, Beijing, Shanghai, and Shenzhen had imported 461 (95% CL 227–805), 113 (57–193), 98 (49–168), 111 (56–191), and 80 (40–139) infections from Wuhan, respectively. If the transmissibility of 2019-nCoV were similar everywhere domestically and over time, we inferred that epidemics are **already growing exponentially in multiple major cities of China** with a **lag time behind the Wuhan outbreak** of about 1–2 weeks.

*Nowcasting and forecasting the potential domestic and international spread of the*

*2019-nCoV outbreak originating in Wuhan, China: a modeling study, Wu, Leung, January 31, 2020*

**Transmission occurs primarily via respiratory droplets** from coughs and sneezes within a range of about 6 feet (1.8 m). Indirect contact via contaminated surfaces is another possible cause of infection. Preliminary research indicates that the virus may remain **viable on plastic and steel** for up to **three days**, but does not survive on **cardboard for more than one day** or on copper for more than four hours

The **incubation period** of COVID-19 can last for **2 weeks or longer**.

Incubation rate  $\sigma$ , is the rate of latent individuals becoming infectious.

Given the **known average duration of incubation Y**,  $\sigma = 1/Y$ .

The average incubation duration us **5.2 days**.

# IHME COVID-19 health service utilization forecasting team

## Forecasting COVID-19 Impact on Hospital bed-days, ICU-days, Ventilator-days and deaths by US state in the next 4 months

### Estimate for Required Hospital Needs Generated April 2, 2020

#### Goal:

Develop a statistical model forecasting deaths and hospital utilization against capacity by state for the US over the next 4 months.

#### Statistical model for the cumulative death rate.

We developed a curve-fitting tool to fit a nonlinear mixed effects model to the **available admin cumulative death data**. The cumulative death rate for each location is assumed to follow a **parametrized Gaussian error function**:

$$D(t; \alpha, \beta, p) = \frac{p}{2} (\Psi(\alpha(t - \beta))) = \frac{p}{2} \left( 1 + \frac{2}{\sqrt{\pi}} \int_0^{\alpha(t-\beta)} \exp(-\tau^2) d\tau \right)$$

$$H(t, \alpha, \beta, p) := \frac{p}{2} \cdot \left[ \operatorname{erfc} \left[ \alpha \cdot (t - \beta) \right]^2 \right] \quad ICU(t, \alpha, \beta, p) := \frac{p}{2} \cdot \left[ \operatorname{erfc} \left[ \alpha \cdot (t - \beta) \right]^2 \right]$$

Where the function Y is the Gaussian error function (written explicitly above),

p controls the maximum death rate at each location,

t is the time since death rate exceeded  $1e^{-15}$ ,

$\beta$  (beta) is location-specific inflection point (time at which rate of increase of the death rate is maximum), and

$\alpha$  (alpha) is a location-specific growth parameter.

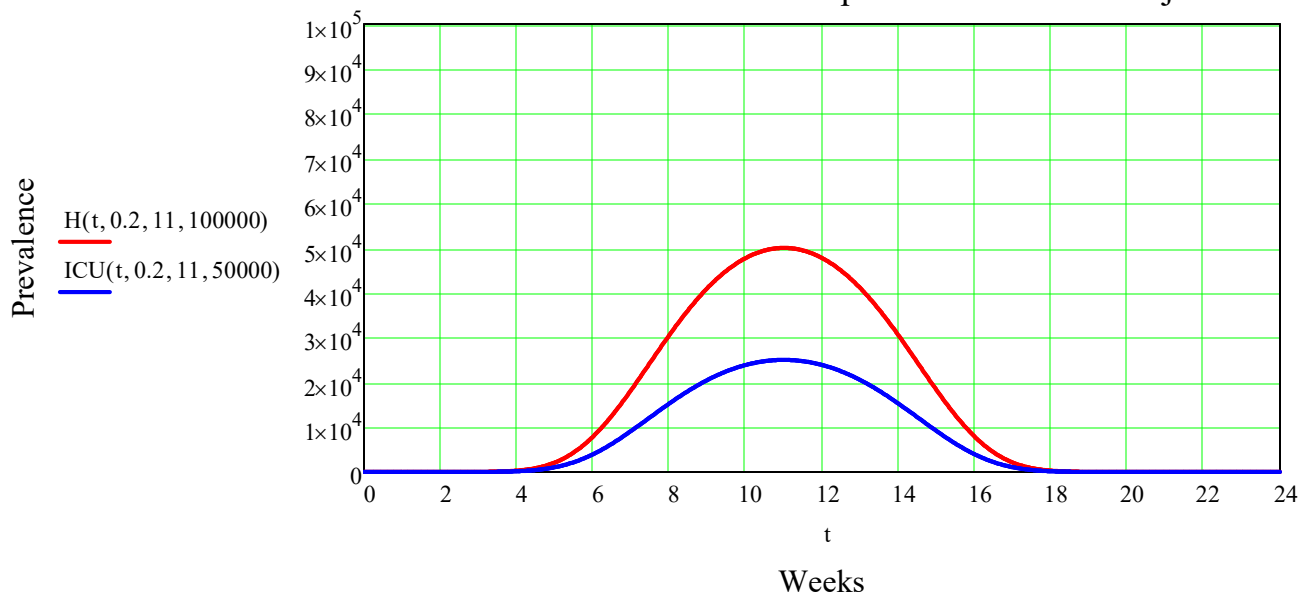
Other sigmoidal functional forms (alternatives to Y) were considered but did not fit the data as well. Data were fit to the log of the death rate in the available data, using an optimization framework described in the appendix.

The date of peak excess demand by state varies from the **second week of April through May**. We estimate that there will be a total of **81,114** (95% UI 38,242 to 162,106) **deaths from COVID-19 over the next 4 months** in the US. Deaths from COVID-19 are estimated to **drop below 10 deaths per day between May 31 and June 6**. Given current estimates of the basic reproductive rate (the number of cases caused by each case in a susceptible population), **25% to 70% of the population** will eventually become infected. Based on reported case-fatality rates, these projections imply that there would be millions of deaths in the United States due to COVID-19.

A covariate of days with expected exponential growth in the cumulative death rate was created using information on the number of days **after the death rate exceeded 0.31 per million to the day when 4 different social distancing measures were mandated**

### Projection: Excess demand for services above capacity available currently

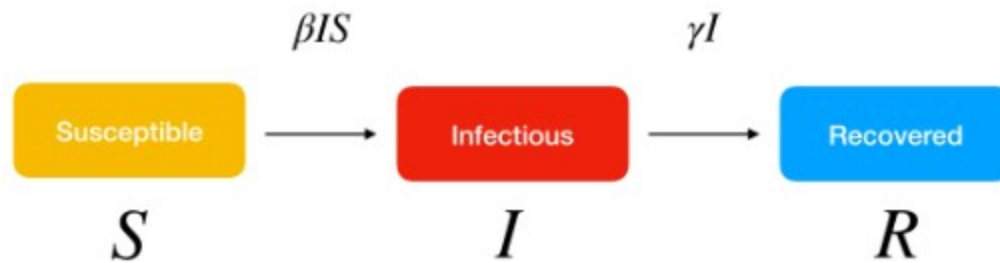
COVID-19 Death Curves - Hospital and ICU Bed Projection



# SIR Compartmental Disease Transmission Model: Susceptible, Infected, Removed

Data-Based Analysis, Modeling and Forecasting of the COVID-19 outbreak

<https://www.medrxiv.org/content/10.1101/2020.02.11.20022186v4.full.pdf> - March 5, 2020



## Phenomena involving rates of change often can only be comprehended through Mathematical Models.

The oldest and most common **Epidemiological Model** is the **SIRD model**, consisting of a set of four coupled **nonlinear differential equations**, which assigns every person in a population to be in one of 4 conditions or categories. The advantage of SIR model over more detailed models, is that SIR uses only known surveillance data.

**S = Susceptible to becoming infected.**  $S_0$ , **Initial population** (initial # of people who are susceptible),

**I = Infected through contact with someone already infected.**  $I_0$ , **Initial number of infected people**

**R = Removed or Removal Group, either in isolation or dead, or no longer sick or infected.**

**D = Fatalities**

Through time a person may **move from being Susceptible to Infected to Removed**, so that the number of people in each category changes, but the total of  $S + I + R$  remains some constant,  $N$ .

This is a Compartmental Model, with S, I, R, and D being compartments of subpopulations. Every person starts off in a given compartment and may then, in time, move to another. Graphically the compartment model looks like the plots starting on page 11, with the rates of movement between the compartments designated by the parameters:  $\alpha$ ,  $\beta$ , and  $\gamma$ .

This model assumes that once someone recovers they are immune and can't be infected again. The model also assumes that a disease is passed from person to person. The SIRD model can't be used for diseases that spread by other modalities, such as eating exotic animals or being bitten by insects.

**REMEMBER:** *A Model is only as good as the assumptions put into the Model.*

**Potential Error Sources:** There are two major of potential sources of error: Process Error and Observation Error. The source of Process Error is the disease dynamics. It is inherently stochastic.

The observation error is the error in the observation process. A number investigations to measure the true rate of COVID-19 infections have been done. Actual cases may be 10 to 50 times larger than reported. **The major source of error is observational.**

## Epidemiological Parameters (Different Author May Use Different Symbols)

**Infection rate,**  $\beta$ : Transmission rate, rate (number per day) that susceptible people become infected

**Recovery rate,**  $\gamma$ : Recovery rate (number per day) that infected people recover. Portion - Removal Rate

CDC - Flu in USA: 36 million flu illnesses, 370,000 hospitalizations & 22,000 deaths.

**NOTE:** Since the population size,  $N$ , is constant,  
 $N = S + I + R$  these constraints can be used to  
 $N = S + E + I + R$  eliminate the equation for R in the Models.



# Deterministic Mathematical Modeling of Disease

## Bio-mathematical deterministic treatment of the SIR or SEIR model

This SIR system of ordinary differential equations is **non-linear**, and **does not admit a generic analytic solution**. Nevertheless, significant results can be derived analytically.

$$\frac{d}{dt}S = \frac{-\beta IS}{N}$$

$$\frac{d}{dt}I = \frac{-\beta IS}{N} - \gamma I$$

$$\frac{d}{dt}R = \gamma I$$

Initially, when  $S \sim N$

$$I(t) = I_0 \cdot e^{(\beta - \gamma)t}$$

### Transition Rates of SIR Movement between adjacent Compartments

- The terms  $dS/dt$ ,  $dI/dt$ ,  $dR/dt$  in the Nonlinear Differential Equations indicate the rates of change of the susceptible population size, the infected population size and the Removed population size, respectively. It is a mechanistic model.
- The term  **$\beta$  is the transmission rate** and  $\beta \sim 2.8 * 1/10 \text{ days} = 0.199$
- The rates are nonlinear, determined by the law of mass action, rate  $\sim \beta IS$
- $1/\gamma$  is the period when infected people are contagious.
- High value of  $\beta$  means the epidemic will spread quickly.
- **$\gamma$  recovery rate** (inverse of the **number of days until recovery ( $1/\beta$ )**)
- The median number of days until recovery is about **6.8 days:  $\gamma = 1/6.8$**
- High value of  $\gamma$  means a person will remain infected for more days
- SIR model basic reproduction number,  **$R_0 = \beta/\gamma$**  when everyone is susceptible.
- Rate at which compartments move from one to another depends on the fraction of population in each compartment and transmission rate,  $\beta$  and recovery rate,  $\gamma$ . The SIR model does not allow for those who are exposed, but not infected or infected but asymptomatic, or time period when latent and also infectious.

## Continuous SIRD Model: System of Differential Equations, DE

Given  $\delta := 0.005$

$$\frac{d}{dt}S(t) = \frac{-\beta \cdot I(t) \cdot S(t)}{N}$$

$$\frac{d}{dt}I(t) = \frac{\beta \cdot I(t) \cdot S(t)}{N} - (\gamma + \delta) \cdot I(t)$$

$$\frac{d}{dt}R(t) = \gamma \cdot I(t)$$

$$\frac{d}{dt}D(t) = \delta \cdot I(t)$$

Initial Conditions:

$$S(0) = S_0$$

$$I(0) = I_0$$

$$R(0) = R_0$$

$$D(0) = 0$$

Terminal Point, T:

$$T := 40$$

Mathcad Odesolve Solver: Solution for a System of Ordinary Differential Equations

$$DE\_SIR(S_0, I_0, R_0, D_0, \beta, \gamma, N, T) := \text{Odesolve} \left[ \begin{pmatrix} S \\ I \\ R \\ D \end{pmatrix}, t, T \right]$$

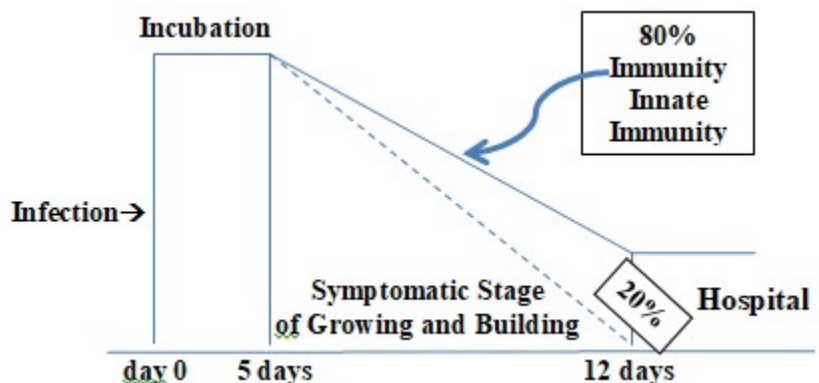
## SEIR Model (E is Exposed) Infection Cycle Outcomes

MedCram: COVID Pandemic Update 49: New Data COVID-19 vs Other Viral Infections (Ventilator Outcomes)

SEIR has two (EI) infected Classes.  
30% of all transmissions occur from symptomatic or minimally symptomatic carriers.

**Note:**

A SEIR model does not give a good fit for Confirmed Infection Case data, which manifests only when the carrier is symptomatic.



# Continuous SEIR Model

This is an SEIR Model for China Data from Mathematica: "SEIR model of the coronavirus infection in China"  
 Mathematica Notebook: SEIR model C 27 march 2020.nb  
<https://community.wolfram.com/groups/-/m/t/1888335>

```
InfM := READPRN("China Cases -SEIR MMica-13332.txt")    RecM := READPRN("China Recovered -SEIR MMica.txt")
Rc := rows(InfM)    Rc = 68    m := 1..Rc - 1    IR_m := InfM_m - RecM_m
Ifnc_m := InfM_m - InfM_{m-1}
SEIR(S0,I0,E0,β,ε,γ,N)    τ := 1.1    Terminal Point, T:
T := 100    n := 0..140
```

## Continuous SEIR Model: System of Differential Equations, DE

Given

$$\frac{d}{dt}S(t) = \frac{-\beta \cdot I(t) \cdot S(t)}{N}$$

$$\frac{d}{dt}E(t) = \frac{\beta \cdot I(t) \cdot S(t)}{N} - \varepsilon \cdot E(t)$$

$$\frac{d}{dt}I(t) = \varepsilon \cdot E(t) - (\gamma + \delta) \cdot I(t)$$

$$\frac{d}{dt}R(t) = \gamma \cdot I(t)$$

**Initial Conditions:**

$$S(0) = 80900$$

$$E(0) = 1$$

$$I(0) = 1$$

$$R(0) = 0$$

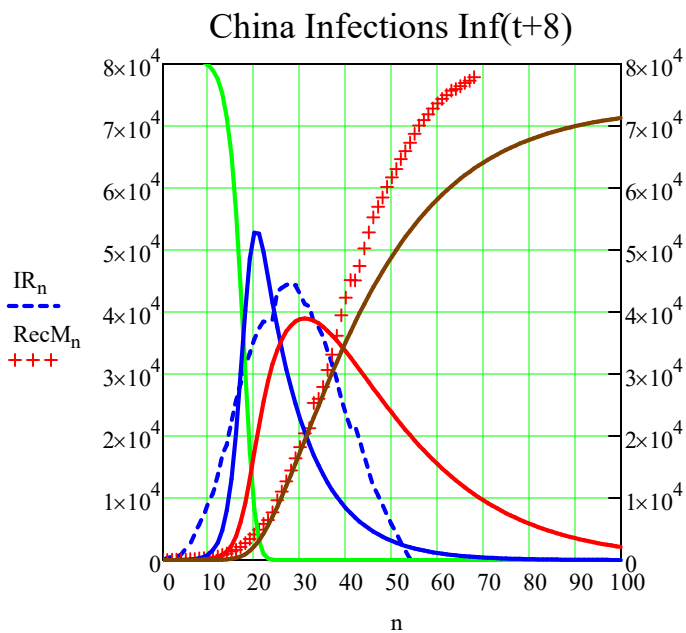
obreak = **Mathematica/Maple SEIR DDE**

```
{s'[t] == -β*s[t]*i[t]/p,
 e'[t] == β*s[t]*i[t]/p - σ*e[t-1.1],
 i'[t] == σ*e[t-1.1] - γ*i[t-8.7],
 r'[t] == γ*i[t-8.7]};
```

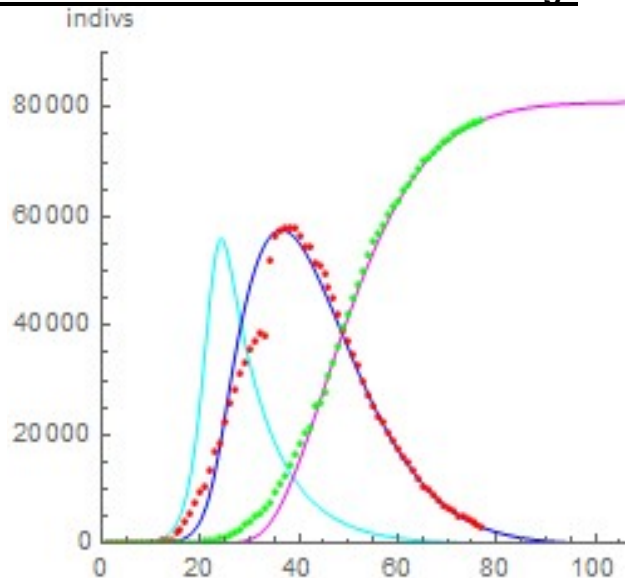
## Mathcad Odesolve Solver: Solution for a System of Ordinary Differential Equations

$$DE\_SEIR(S_0, E_0, I_0, R_0, \beta, \varepsilon, \gamma, N, T) := \text{Odesolve} \left[ \begin{pmatrix} S \\ E \\ I \\ R \end{pmatrix}, t, T \right]$$

$$(S, E, I, R) := DE\_SEIR(80899, 1, 1, 0, 4, 0.1, 0.0478, 80900, 100)^T \quad t := 0..140$$



## Mathematica Solution Plot -See Next Page



**Good Match Between Data and DDE SEIR Model**

## Difference Compartmental Models: SEIR Delayed (Maple) v.s. Mathcad SEIR No Delay

This Delayed SEIR Model was developed in Mathematica and Executed in Maple:

"SEIR model C 27 China march 2020.nb" From Mathematica

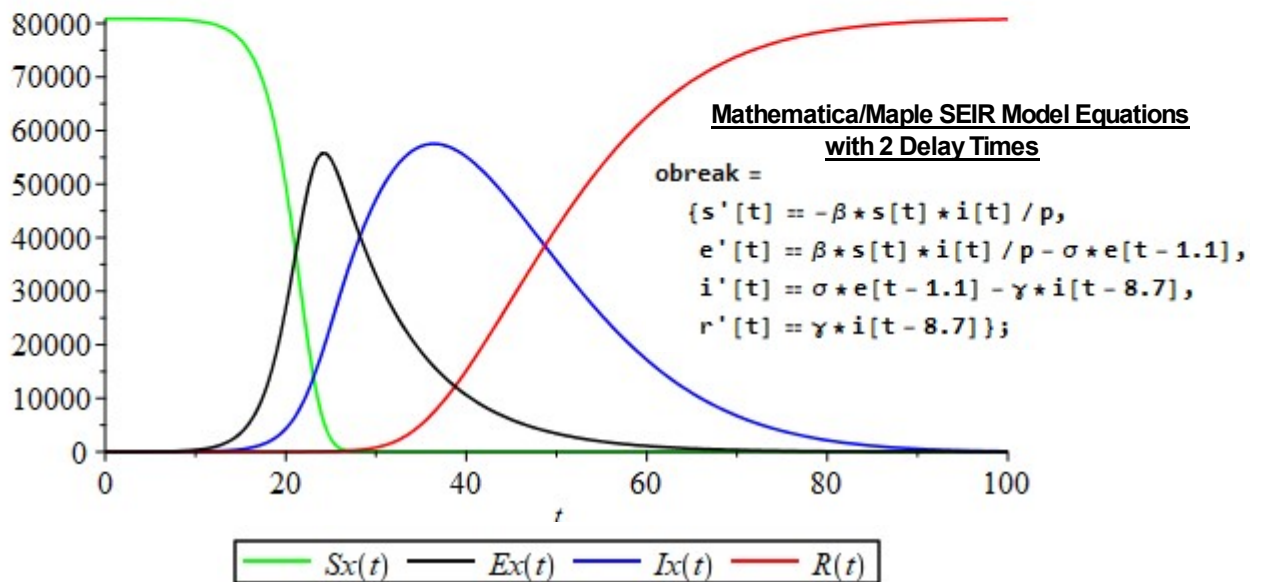
NOTE: The Mathematica and Maple Delayed SEIR Plots are Identical.

$$\begin{aligned}
 ddesys := & \left\{ Dx(0) = 0, Ex(0) = 1, Ix(0) = 1, R(0) = 0, Sx(0) = 80900, \frac{d}{dt} Dx(t) = \delta Ix(t), \frac{d}{dt} Ex(t) \right. \\
 & = \frac{\beta Sx(t) Ix(t)}{N} - \sigma Ex(t - \tau_1), \frac{d}{dt} Ix(t) = \sigma Ex(t - \tau_1) - \gamma Ix(t - \tau_2), \frac{d}{dt} R(t) = \gamma Ix(t \\
 & \left. - \tau_2), \frac{d}{dt} Sx(t) = -\frac{\beta Sx(t) Ix(t)}{N} \right\}
 \end{aligned}$$

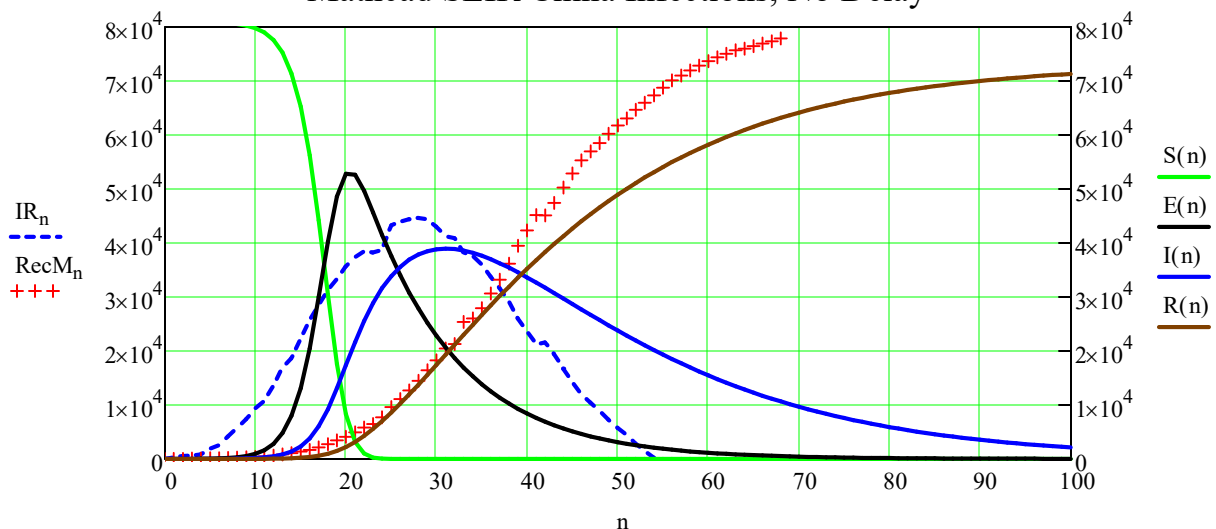
```

> dsn := dsolve(eval(ddesys, {beta = 4, gamma = 0.0478, sigma = 0.10,
delta = 0.0005, N=80900, tau 1 = 1.1,tau 2 = 8.7,tau 3 = 0}),
numeric);
> plots[odeplot](dsn, [[t, Sx(t), color = green], [t, Ex(t), color =
black]], [t, Ix(t), color = blue],[t, R(t), color = red], 0 .. 100,
legend = [ Sx(t), Ex(t), Ix(t), Rx(t)], labels = [t,""]);

```



Mathcad SEIR China Infections, No Delay



# Discrete SIRD and SEIR Models - Infectious Disease Outbreak Equations

The number of people at any day, n, who are:

$$R_0 = \beta/\gamma$$

**# Susceptible-S**

**Number (#) Infected - I**

**# Removed - R**

**# Dead - D**

$$S_t = S_{t-1} - \frac{\beta}{N} \cdot S_{t-1} \cdot I_{t-1}$$

$$I_t = I_{t-1} + \frac{\beta}{N} S_{t-1} \cdot I_{t-1} - \beta \cdot I_{t-1} - \gamma \cdot I_{t-1}$$

$$R_t = R_{t-1} + \gamma \cdot I_{t-1}$$

$$D_t = \delta \cdot I_{t-1}$$

## Algorithms to Calculate the Values of S, I, R, D and S, E, I, R from Model Parameters

### Governmental Mitigation is not Modeled

Outputs S, E, I, R, but Shown without the R term below

SIRD(S0, I0, β, γ, δ, N) :=

```

S0 ← S0
I0 ← I0
D0 ← R0 ← 0
(M0,0 M0,1 M0,2 M0,3) ← (S0 I0 0 0)
for n ∈ 0..N
    Sn+1 ← Sn - (Sn / S0) · β · In
    In+1 ← In + (Sn / S0) · β · In - In · (γ + δ)
    Rn+1 ← Rn + In · γ
    Dn+1 ← In · δ
    Mn+1,0 ← Sn+1
    Mn+1,1 ← In+1
    Mn+1,2 ← Rn+1
    Mn+1,3 ← Dn+1
M
    
```

, γ, N) :=

```

S0 ← S0
I0 ← I0
E0 ← E0
δ ← 0.005
R0 ← 0
(M0,0 M0,1 M0,2) ← (S0 I0 E0)
for n ∈ 0..N
    Sn+1 ← Sn - (Sn / S0) · |β| · In
    En+1 ← En - ε · En + (Sn / S0) · |β| · In
    In+1 ← In + ε · En - (|γ| + δ) · In
    Mn+1,0 ← Sn+1
    Mn+1,1 ← In+1
    Mn+1,2 ← En+1
M
    
```

### Let's look at the example of a typical flu season virus outbreak, α, β, γ, R0

**Typical Flu Outbreak Parameters:**     β := 0.2     γ := 0.10     1/γ = 10     δ := 0.005     R0 := β / (γ + δ)     R0 = 1.905

A typical flu season lasts about 35 weeks (245 days). Week 1 generally is the first week of October and lasts until week 35 or the end of May. See plots of a typical flu season on the following page.

The basic reproductive ratio, R0 is defined by epidemiologists as "R0" represents the **average number** of secondary cases that result from the introduction of a **single infectious** case in a totally susceptible population during the infectiousness period". The **product** of the infection rate and mean infection duration.

As such R0 can tell us about the initial increase of number of the those infected/carrier over a generation.

A typical flu season lasts about 35 weeks (245 days). Week 1 generally is the first week of October and lasts until week 35 or the end of May. See plots of a typical flu season on the following page.

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As such R0 can tell us about the initial increase of number of the those infected/carrier over a generation.

# Compare Solutions: SID Parameters for Typical Flu Virus

The Flu Season parameters are  $\beta = 0.2$  and  $\gamma = 1.4$ .  $S_{\text{final}}$  is about 0.52 and Infected peaks at 0.024. If  $S_0 < \beta/\lambda$  then Infections decrease monotonically to zero - this designates the season as nonepidemic.

Below is a model for a **typical flu virus**. Because of **mutation, new strains** of influenza make **most people susceptible** ( $S_n, \alpha = 29\%$ ) at the beginning of an outbreak. Interestingly, it shows that the number of infected people (blue curves) has reached a **peak after about 54 days (7 1/2 weeks)** and then falls to after 100-120 days (3 - 4 months).

**This demonstrates that the SIR model is a good representation for a flu season.**

## Compare Solution Methods

### Continuous Solution:

$$(S, I, R, D) := \text{DE\_SIR}(999, 1, 0, 0, \beta, \gamma, 1000, 120)^T \quad t := 0, 0.01 \dots 120$$

**NOTE:** The Continuous Model gives the total number of dead. So D does not hide I in plots, Discrete gives New Deaths.

### Discrete Solution:

$$\text{FluSIRD} := \text{SIRD}(999, 1, \beta, \gamma, \delta, 130) \quad n := 0 \dots 130$$

<u>Susceptible</u>	<u>Infected</u>	<u>Removed</u>	<u>Dead</u>
$S_d := \text{FluSIRD}^{(0)}$	$I_d := \text{FluSIRD}^{(1)}$	$R_d := \text{FluSIRD}^{(2)}$	$\text{Ded} := \text{FluSIRD}^{(3)}$

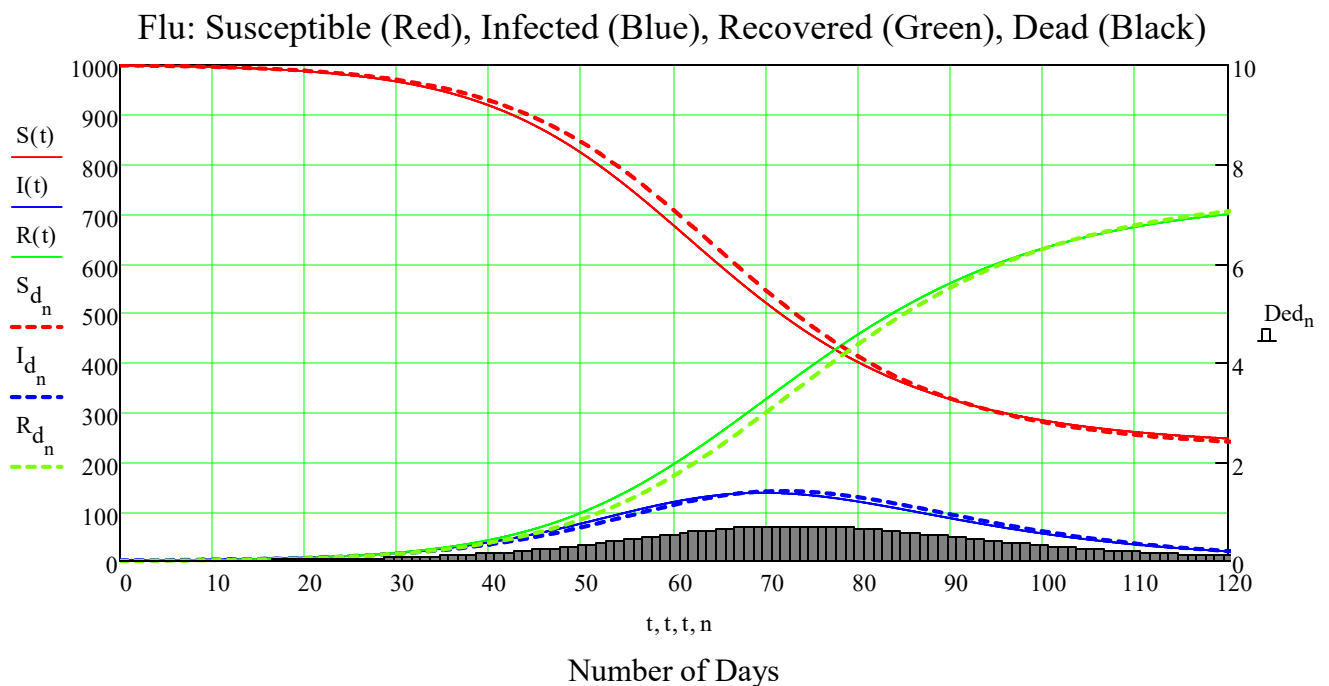
### Compare Continuous vs. Discrete Solutions Percent Difference at the Infection Peak:

$$\Delta\text{PC} := \left( I(70) - I_{d70} \right) \cdot \frac{100}{I(70)} \quad \Delta\text{PC} = -2.119$$

Given the uncertainty in Epidemic Data, a 2.1% difference is acceptable

Note that there **two different sized scales**, the scale shown at the left is larger than the one at the right.

The S, I, R solutions are shown with the scale on the left, Scale Max = 1000  
The black curve for the number of deaths uses the scale on the right only. Scale Max = 10



**From Flu: Notice the number of infections drops off with the flu season.**



The number of those that are susceptible drops below new infections

## SIR Model Normalized: Flu Season 2002-2007 and 2010-2013

Parameters and graphs are from the paper: "Forecasting seasonal influenza with a state-space SIR model", 2017

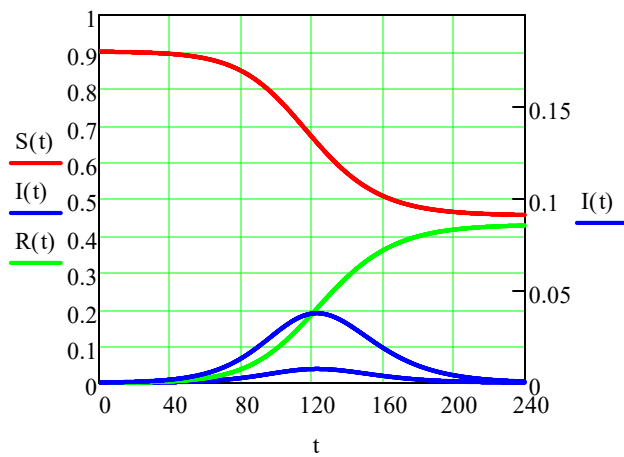
$$\begin{pmatrix} S \\ I \\ R \end{pmatrix} := \text{DE\_SIR}(0.9, 0.0002, 0, 0, 0.2, 0.14, 0.9, 240)$$

t := 0, 0.1.. 240

Plots From: "Forecasting seasonal influenza with a state-space SIR model", Osthus

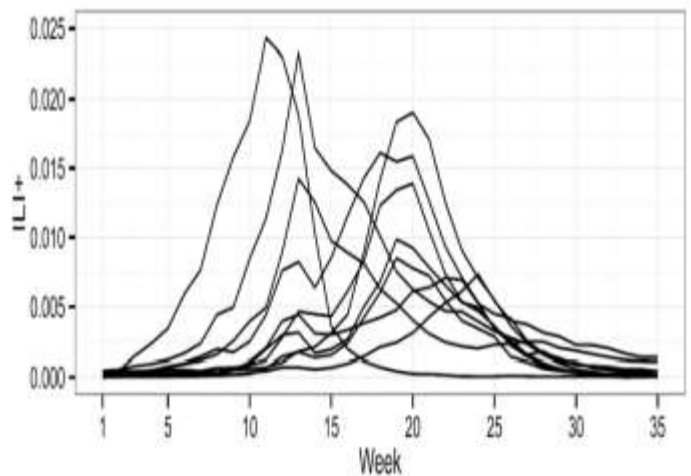
Sus (Red), Infected (Blue), Removed (Green), Dead (Black)

Flu: Susceptible



Number of Days

Plot of Fraction of Infections/S<sub>0</sub> for Flu seasons 2002-2007 and 2010-2013



Season: 35(Wks) x 7 = 245 days

$$\frac{125}{7} = 17.857$$

**NOTE:** In the below Osthus paper,  $R_0$  represents the proportion of the population in the recovered compartment at time  $t = 0$  for the SIR model and **does not represent the "basic reproductive number"**

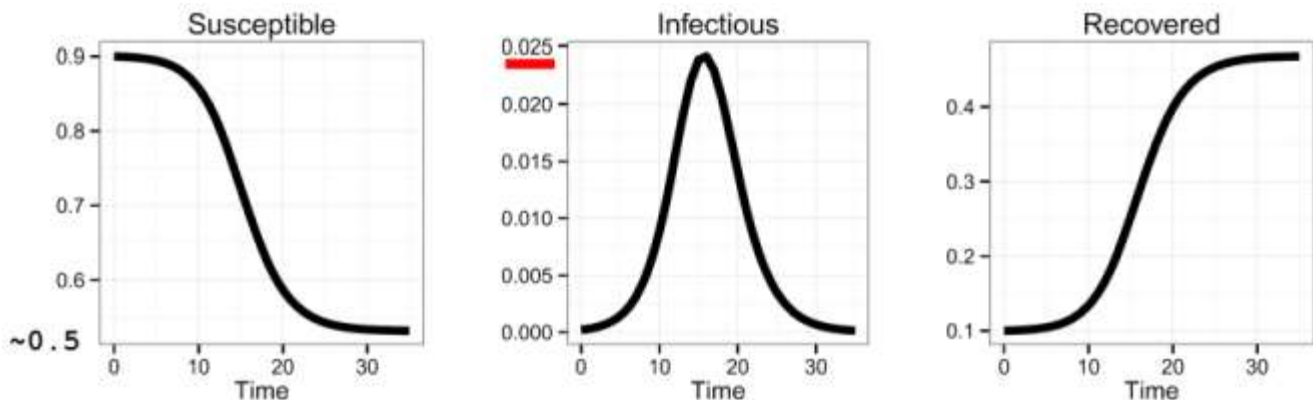


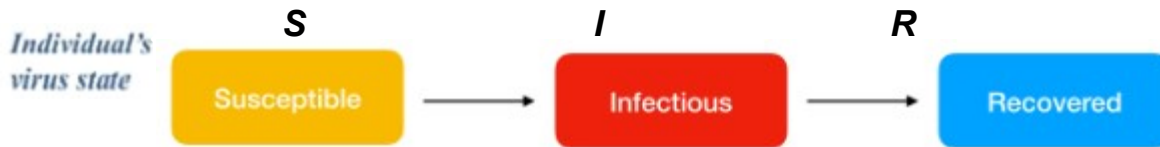
Fig. 2.

Simulated SIR Curve with  $S_0 = 0.9$ ,  $I_0 = 0.0002$ ,  $R_0 = 0.0998$ ,  $\alpha = 2$ , and  $\beta = 1.4$

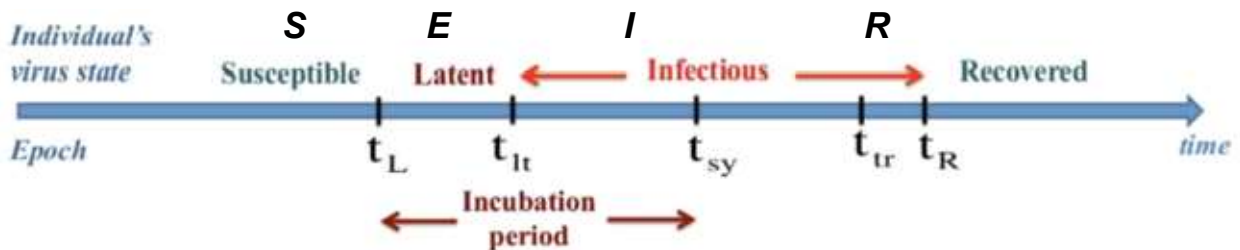
# Some Different Possible Compartmental Models

No One Model is Superior to the Others. They all have their uses. It all depends on the application or goal. The SIR model, generally, is the only one in which all the compartments (S, I, R) are observable and documented.

## Classical SIR Model of an Epidemic: Susceptible, Infectious, and Recovered



## Classical SEIR Model: Susceptible, Exposed (Latent), Infectious, Recovered



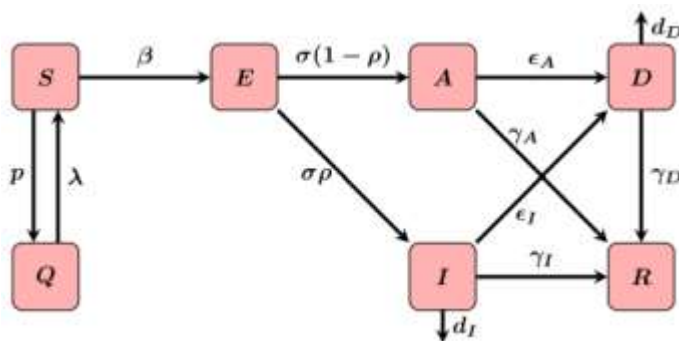
## Here is an Extension of the SEIR Model, the SQEAIIRD Model

### Proposed by Jai for Modeling the Wuhan COVID-19 Epidemic Control Policy

#### *Modeling the Control of COVID-19:*

#### *Impact of Policy Interventions and Meteorological Factors, Jai*

This Model was extended to include the influence of Quarantine (Q) and Non-Infectious Asymptomatic Hosts, A. A more comprehensive model would also include Infections by Asymptomatic Hosts.



### SQEAIIRD Quarantine Model

$$\frac{dS}{dt} = -\beta S(I + \theta A) - pS + \lambda Q$$

$$\frac{dQ}{dt} = pS - \lambda Q$$

$$\frac{dE}{dt} = \beta S(I + \theta A) - \sigma E$$

$$\frac{dA}{dt} = \sigma(1 - \rho)E - \epsilon_A A - \gamma_A A$$

$$\frac{dI}{dt} = \sigma\rho E - \gamma_I I - d_I I - \epsilon_I I$$

$$\frac{dD}{dt} = \epsilon_A A + \epsilon_I I - d_D D - \gamma_D D$$

$$\frac{dR}{dt} = \gamma_A A + \gamma_I I + \gamma_D D$$

### Compartmental Model: Transmission Spread Dynamics

Some models may have many more compartments to account for heterogeneity. For example: "A mathematical model (Network) for simulating Transmission COVID" has 14. Some models may have compartments for demographic characteristics (age, gender, location), different modes of transmission, mitigation policies, zoonotic routes, symptoms, types of hospitalization, public risk avoidance behavior, states of infectiousness, or different methods of case confirmation.

# COVID-19 SIRD Data, Model & Predictions Hubei Province, China

An outbreak of “pneumonia of unknown etiology” in Wuhan, Hubei Province, China in early December 2019 has spiraled into an epidemic. The virus is SARS-CoV-2, a coronavirus.

Simulations until the 29th of February of the cumulative number of Removed as obtained using the SIRD model. Dots correspond to the number of confirmed cases from the 16th of January to the 10th of February. The initial date of the simulations was the 16th of November with one infected, zero Removed and zero deaths. Solid lines correspond to the dynamics obtained using the estimated expected values of the epidemiological parameters

$$S_0 = 59 \times 10^6, \beta = 0.193, \gamma = 0.063/\text{day}, \delta = 0.01;$$

## Data from Hubei Province China from 1-22-2020 to 3-12-2020 - Population 58.5 Million

China := READPRN("OWiD China 19 Jan - April 12.txt")  
 Hubei := READPRN("K-COVID19-Hubei-Complete.txt")    HPop :=  $58.5 \cdot 10^6$     rows(Hubei) = 51  
 Data from Kaggle    <https://www.kaggle.com/kimjihoo/coronavirusdataset>

COVID Data:    Infected    Dead    Removed  
 HInf := Hubei<sup>(3)</sup>    HDed := Hubei<sup>(4)</sup>    HRec := Hubei<sup>(5)</sup>    **HInf<sub>50</sub> = 67781**

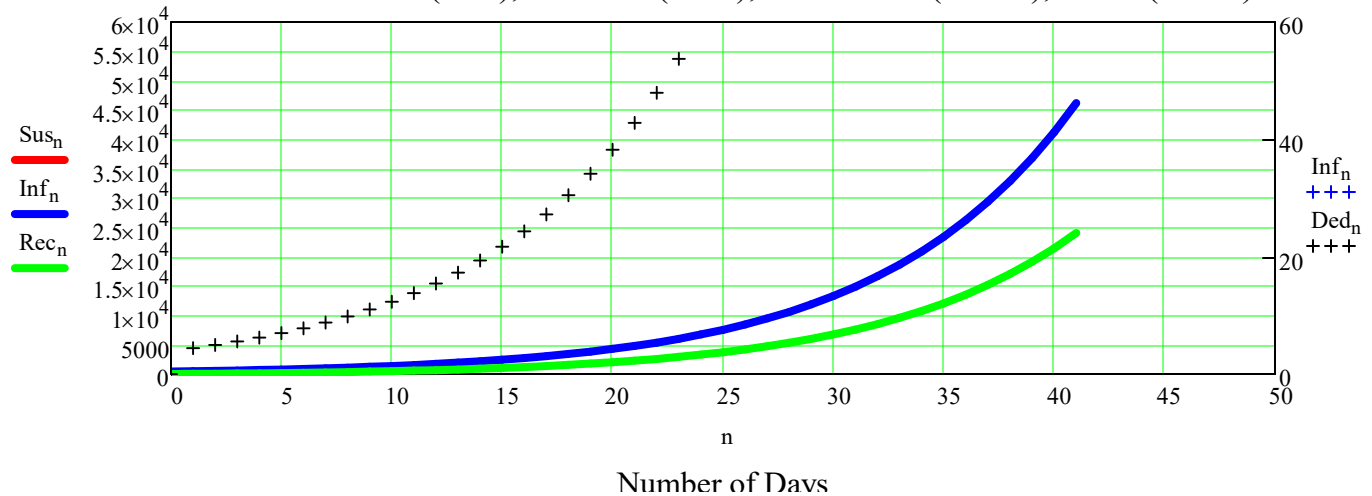
### Calculate SIRD Model Values for Wuhan of COVID-19 to Feb 10, 2020

$$\text{SIRD}(S_0, I_0, \beta, \gamma, \delta, N) \quad W19 := \text{SIRD}(59 \cdot 10^6, 444, 0.193, 0.063, 0.01, 40)$$

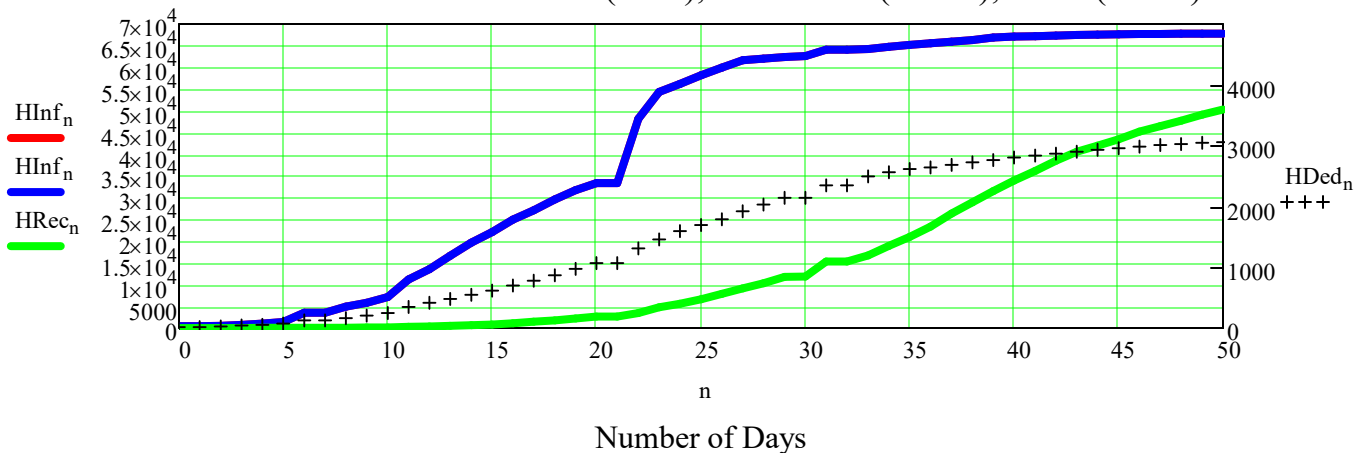
Model Results:    Susceptible-Sus,    Infected - Inf,    Removed - Rec,    Dead - D  
 Sus := W19<sup>(0)</sup>    Inf := W19<sup>(1)</sup>    Rec := W19<sup>(2)</sup>    Ded := W19<sup>(3)</sup>

Inf<sub>40</sub> = 41252.059     $\beta = 0.193$      $\gamma = 0.063$      $\delta = 0.01$      $R_0 = \frac{\beta}{\gamma + \delta} = 2.644$

SIR Model: Sus (Red), Infected (Blue), Recovered (Green), Dead (Black)



Hubei COVID-19: Infected (Blue), Recovered (Green), Dead (Black)



## **Mitigation: Rationale for Phase Transition, Segmented Terminate, Function**

The spread of a disease is a physical process with many different contributing factors. Some examples of different types of physical growth are found in processes such as: the law of mass action, growth in a petri dish, crop growth, population growth, nuclear reactions, and current saturation in an a MOSFet transistor. As a generalization, there are three approximate phases of growth: exponential growth, linear transition, and saturation. Saturation occurs when a growth system runs out of finite buildable land area for the growth of cities. Extended growth has occurred for 50 years in the semiconductor industry. This has been fueled by extensive research which resulted in extended sequences of sigmoidal growths of one technology succeeded by a new one.

Different researchers have added their own wrinkles to functional growth such as asymmetrical growth, an inflection point, and application of limits/bounds through integration. There is a plethora of Functional Growth Distributions: sigmoidal, logistic growth, beta function, expolinear, and eponymous functions such as: Gompertz, Richards, Weibull, and Goudriaan. More abstract formulations based on Physics (Hamiltonian, Wave Velocity), and a host of statistical distributions and curve fitting formulations. There are a variety of different approaches: deterministic, stochastic, Markov Chain, numerical, discrete, linearization, network theory, engineering solutions, and approaches such as control theory. Recently, there has been an explosion and spectacular accomplishments in the application of neural networks and big data techniques to challenging problems. Problems can also be crunched with modeling packages such as COMSOL Multiphysics, SPSS, SAS, R, Stata, and so on.

**Modeling Mitigation - What to do?** We will use an amalgamation of the two models. First combining our data of the daily growth of the initial number (initial exponential growth) of total confirmed cases in the US. Second applying the known range of  $R_0$  values for COVID-19 dataset (reflects their mitigation work) from Wuhan. There is a caveat to this data. The epidemic in Wuhan was mitigated by action of an authoritarian government. They closed roads, locked people in rooms, totally shut down events, had people and healthcare workers with access to an inadequate supply of masks and respirators, built hospitals in two weeks, and had policemen and drones patrolling the streets arresting those who did not comply. These are steps that cannot be strictly enforced in a democratic society. The resultant low Mitigation  $R_{mit}$  values achievable in an autocratic government are not achievable in a democratic society. Also our concern for the economic and business life of our citizens imposes limits on extremes and duration of mitigation measures.

### **The Bottom Line:**

What is a reasonable and tractable methodology that can be used to transition from exponential to mitigation case models? As noted, there are three approximate phases of growth: exponential growth, linear transition, and saturation. The initial phase of exponential growth needs to transition, to lower  $R_{mit}$  via a viable epidemiological model constrained by knowledge of the Range in Values of  $R_0$ . ( $R_0$  is a viable parameter because it has an epidemiological interpretation.) The bottom line is: What is a good way to transition between growth phases?

Einstein espoused a principle for the construction of theories: "A scientific theory should be as simple as possible, but no simpler". We will apply this principle of parsimony. We will transition from the large  $R_{effective}$  value extracted from the initial exponential growth data coupled through a linear region via a decreasing sigmoidal curve to the region of a smaller overall average mitigation  $R_{mit}$  value. A sigmoidal curve has some nice features such as a smooth transitions and a zero slope at the ends of the phases. We use the average value of  $R_0$  (includes the results of their mitigation policy) calculated for the Wuhan epidemic. The model is to be consistent with the dynamic epidemiological SIR model. We will now work out the details and parameters of the transition.

### **Sigmoidal Segmented Terminate Transition Function.**

Our sigmoidal transition function has two parameters: The time of transition from the exponential growth rate to the linear rate,  $t_{el}$  and the time in days to transition from exponential to the saturation phase/mitigation region,  $t_{es}$ . Of these, the most critical is the time for the end of exponential growth, and enforcement of mitigation policy,  $t_{el}$ . We will use multiples of the transition time for one doubling of infections cases, or 2.5 days to transition from the exponential phase to the  $R_0$  saturation/mitigation phase.

# Limits to Exponential Growth: The Sigmoidal Transition Function

The Transmission Rate,  $\beta$ , for Infectious Diseases generally changes with the spread of an epidemic.

Some different possible ways in which the Transmission Rate can change are:

- (1) The bilinear incidence rate  $\beta SI$  where  $\beta$  is the average number of contacts per infected individual per day.
- (2) The standard incidence rate  $\beta SI/N$
- (3) The Holling type incidence rate of the form  $\beta SI/(1 + \alpha_1 S)$ .
- (4) The saturated incidence rate of the form  $\beta SI/(1 + \alpha_2 I)$
- (5) The saturated incidence rate of the form  $\beta SI/(1 + \alpha_1 S + \alpha_2 I)$

The bilinear rate is the Law of Mass Action.

## 2 Scenarios: Worst Case - Exponential $R_{eff}$ vs. Government Intervention/Mitigation to Lower $R_{mit}$

Consider two different scenarios for epidemic growth. A worst case model that matches the initial exponential growth well, but then gives a large estimate of both infectious growth and the effective reproductive number,  $R_{effective}$ . Then we have a best case model where we use the **mean  $R_0$  value of 2.6 (range of 2.4 to 2.8)**

**estimated for the Wuhan COVID-19 breakout**, which was obtained with strong Government Intervention.

Is there a more general way to model a transition from Wuhan  $R_{init}$  Exponential Growth to a Final Mitigation  $R_{mit}$ ?

### Below is sigmoidal transition function, $\beta(t, t_{el}, \alpha_m, z)$ , to Model Mitigation to $\beta_{mit}$ at time, $t_{el}$ Model Government Mitigation as Transitioning Between Two Transmission/Contact Rates, $\beta_{int}$ & $\beta_{mit}$

$s_{es}$  is the approximate period that doubles the total number of infections  $s_{es} := 2$

$t_{el}$ , time to transition from the end of the exponential phase,  $\beta_{exp}$  to a lower  $\beta_{mit}$ , at the start of mitigation

Somewhat equivalently, think of this as transitioning  $R_{effective}$

#### Length of Transition

Variable  $z$  gives multiples of 2 days of transition periods for the transition to the final mitigation,  $R_{mit}$

$$R_{SM}(t, t_{el}, R_{exp}, R_{mit}, z) := R_{exp} - \frac{R_{exp} - R_{mit}}{1 + e^{-\left[ \left( t \cdot s_{es} \cdot z^{-1} \right) - \left( 4 + t_{el} \cdot s_{es} \cdot z^{-1} \right) \right]}}$$

#### In the SIR Model, the parameter of greatest interest is the Transmission rate, $\beta$

$$R = \frac{\beta}{\gamma} \quad \lambda := \frac{1}{10} = 0.1 \quad s_{es} := 2 \quad \beta_{sm}(t, t_{el}, \beta_{initial}, \beta_{mit}, z) := \beta_{initial} - \frac{\beta_{initial} - \beta_{mit}}{1 + e^{-\left[ t \cdot s_{es} \cdot z^{-1} - \left( 4 + t_{el} \cdot s_{es} \cdot z^{-1} \right) \right]}}$$

$\beta_{mit}$  is some fraction, (30 to 90%), of  $\beta_{initial}$

### "Phase-adjusted estimation of number of CPVID 2019 cases in Wuhan, China", Wang

#### R\_wks: Reproduction Number Data from Phase-Adjusted Rt Study of Wuhan

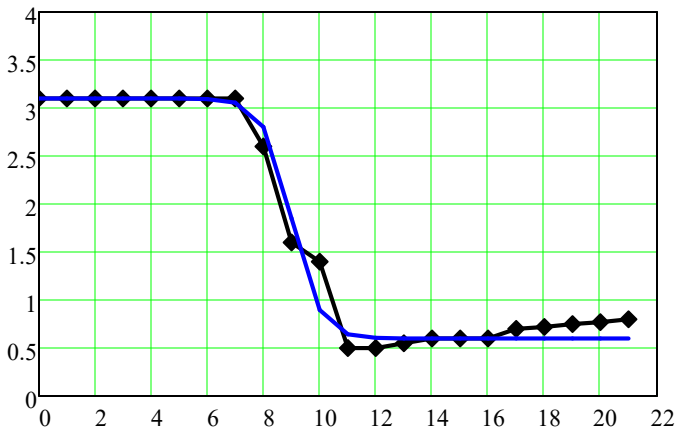
$R\_wks := \text{READPRN}(\text{"Phase-adjusted estimation of Rt COVID 1-1-19 to 4-26-20 cases in Wuhan China.txt"})$

$RR := \text{rows}(R\_wks)$

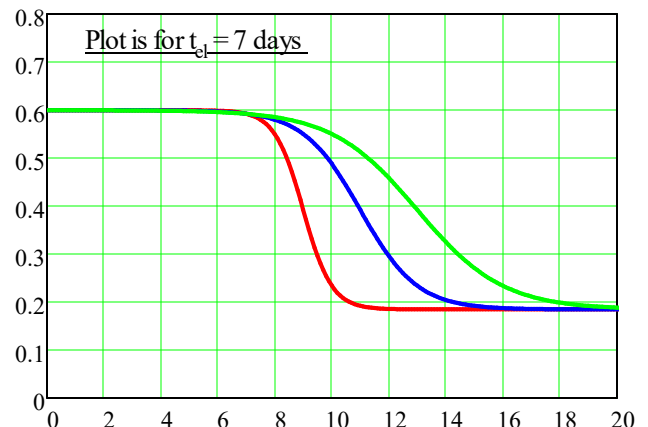
$RR = 22$

$wks := 0..RR - 1$

Wuhan Mitigation: Phase-Adjusted Rt



Phase Adjusted  $\beta$  Model,  $z = 1 \ 2 \ 3$





## Below is the Discrete Algorithm for Implementing the SIR (SIRM) Sigmoidal Transition Mitigation Model

We will refer to this as the SIR Mitigation Model or SIRM

$$\begin{array}{l}
 \text{SIRM}(S_0, I_0, \beta, \beta_{\text{mit}}, t_{\text{el}}, z, \gamma, N) := \\
 \left. \begin{array}{l}
 S_0 \leftarrow S_0 \\
 I_0 \leftarrow I_0 \\
 D_0 \leftarrow R_0 \leftarrow 0 \\
 \delta \leftarrow 0.009 \\
 (M_{0,0} \ M_{0,1} \ M_{0,2} \ M_{0,3}) \leftarrow (S_0 \ I_0 \ 0 \ 0) \\
 \text{for } n \in 0..N \\
 \left| \begin{array}{l}
 S_{n+1} \leftarrow S_n - \frac{S_n}{S_0} \cdot \beta_{\text{sm}}(n, t_{\text{el}}, \beta, \beta_{\text{mit}}, z) \cdot I_n \\
 I_{n+1} \leftarrow I_n + \frac{S_n}{S_0} \cdot \beta_{\text{sm}}(n, t_{\text{el}}, \beta, \beta_{\text{mit}}, z) \cdot I_n - (\gamma + \delta) \cdot I_n \\
 R_{n+1} \leftarrow R_n + I_n \cdot \gamma \\
 D_{n+1} \leftarrow I_n \cdot \delta \\
 M_{n+1,0} \leftarrow S_{n+1} \\
 M_{n+1,1} \leftarrow I_{n+1} \\
 M_{n+1,2} \leftarrow R_{n+1} \\
 M_{n+1,3} \leftarrow D_{n+1}
 \end{array} \right. \\
 M
 \end{array}
 \right.
 \end{array}$$

## Below is the Discrete Algorithm for Implementing the SEIR (SEIRM) Sigmoidal Transition Mitigation Model

The SEIRM Model is the SEIR Model with  $\beta$  replaced by the Sigmoidal Function:

$$\begin{array}{l}
 \text{SEIRM}(S_0, I_0, \beta, \beta_{\text{mit}}, t_{\text{el}}, z, \gamma, N) := \left\{ \begin{array}{l}
 S_0 \leftarrow S_0 \\
 E_0 \leftarrow I_0 \cdot 1.23 \\
 I_0 \leftarrow I_0 \\
 \varepsilon \leftarrow \frac{1}{3} \\
 \delta \leftarrow 0.009 \\
 R_0 \leftarrow 0 \\
 (M_{0,0} \ M_{0,1} \ M_{0,2} \ M_{0,3} \ M_{0,3}) \leftarrow (S_0 \ I_0 \ 0 \ 0 \ E_0) \\
 \text{for } n \in 0..N \\
 \left\{ \begin{array}{l}
 S_{n+1} \leftarrow S_n - \frac{S_n}{S_0} \cdot \beta_{\text{sm}}(n, t_{\text{el}}, \beta, \beta_{\text{mit}}, z) \cdot I_n \\
 E_{n+1} \leftarrow E_n - \varepsilon \cdot E_n + \frac{S_n}{S_0} \cdot \beta_{\text{sm}}(n, t_{\text{el}}, \beta, \beta_{\text{mit}}, z) \cdot I_n \\
 I_{n+1} \leftarrow I_n + \varepsilon \cdot E_n - (\gamma + \delta) \cdot I_n \\
 R_{n+1} \leftarrow R_n + |\gamma| \cdot I_n \\
 D_{n+1} \leftarrow I_n \cdot \delta \\
 M_{n+1,0} \leftarrow S_{n+1} \\
 M_{n+1,1} \leftarrow I_{n+1} \\
 M_{n+1,2} \leftarrow R_{n+1} \\
 M_{n+1,3} \leftarrow D_{n+1} \\
 M_{n+1,4} \leftarrow E_{n+1}
 \end{array} \right. \\
 M
 \end{array} \right.
 \end{array}$$

# Methodology to Extract Mitigation Parameters for Hubei

China Applied Mitigation to Contain their COVID -19 Epidemic. Can we Model Mitigation?

**SEIRM Model**  $Mdl(\beta, \beta_m, t_e, N) := SEIRM\left(59 \cdot 10^6, 444, \beta, \beta_m, t_e, 1, \frac{1}{6.8}, N\right)$   $Mod(\beta, \beta_m, t_e) := Mdl(\beta, \beta_m, t_e, 49)^{(1)}$   
 $SIRM(S_0, I_0, \beta, \beta_{mit}, t_{el}, z, \gamma, N)$

**Initial Guess (SEIRM Params):**  $(\beta, \beta_m, t_e) := (0.19, 0.063, 20)$

## Use Levenberg-Marquardt Method: Minimize Least Squares Error to Residual

Define a Residual to be the difference between the current data points HInf, HRec, HDed and SIRModel

$Residual(\beta, \beta_m, t_e) := HInf - Mod(\beta, \beta_m, t_e)$   $R := rows(HInf)$   $R = 51$

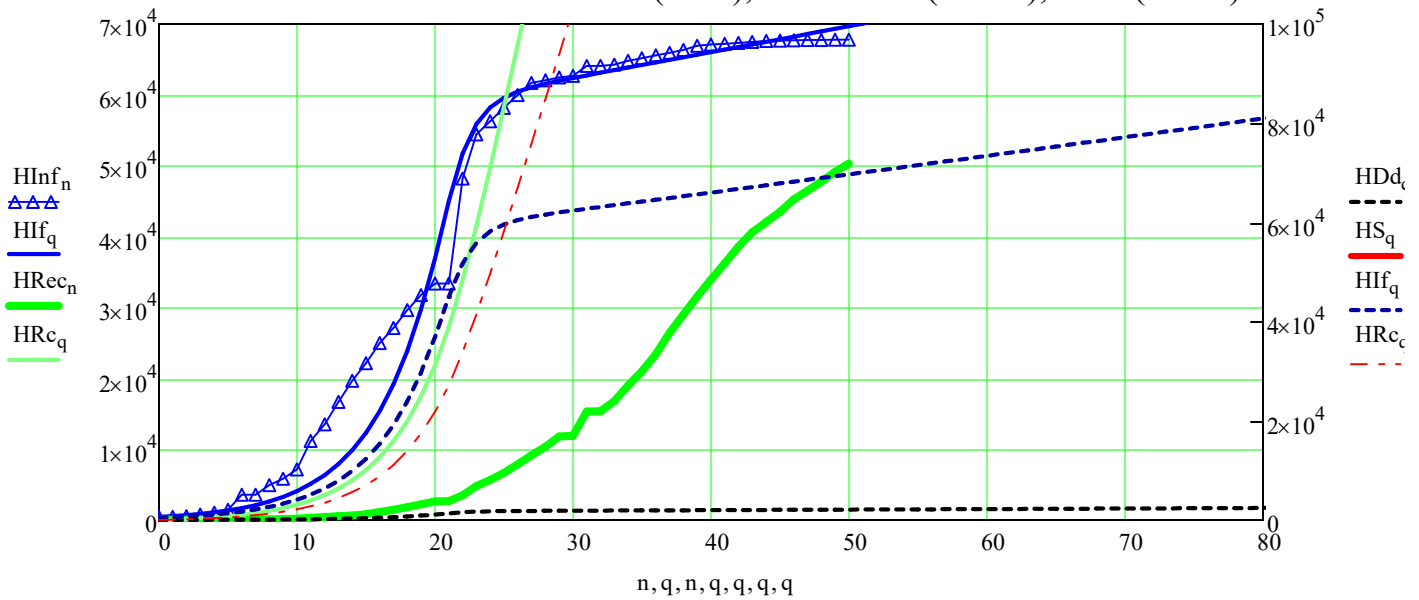
### Condition to Minimize the Residual Least Squares Fit Error Using L-V Minerr Method

Given  $0 = Residual(\beta, \beta_m, t_e)$   $(b, \beta_m, t_e) := Minerr(\beta, \beta_m, t_e)^T$   $(b, \beta_m, t_e) = (0.703, 0.165, 17.732)$

**Infected**  
 $Hif := Mdl(b, \beta_m, t_e, 140)^{(1)}$   $HRec := Mdl(b, \beta_m, t_e, 140)^{(2)}$   $HDd := Hif \cdot 0.03$   $\frac{ERR}{R} = 543.934$   
 $HS := Mdl(b, \beta_m, t_e, 140)^{(0)}$   $R_p := rows(Hif) = 142$   $q := 0..R_p - 1$   $HDe := submatrix(HDd, 0, 21, 0, 0)$

## Good Match of SEIRM Mitigation Model (Curves) to Data (Symbols $\Delta$ )

Model vs Data - China: Infected (Blue), Recovered (Green), Dead(Black)



$\delta := 0.005$

## Extracted Parameters of Hubei/Wuhan COVID-19 Epidemic

The number of days it takes infections to double,  $t_{2x}$   $t_{2x} := \frac{1}{b}$   $t_{2x} = 1.423$

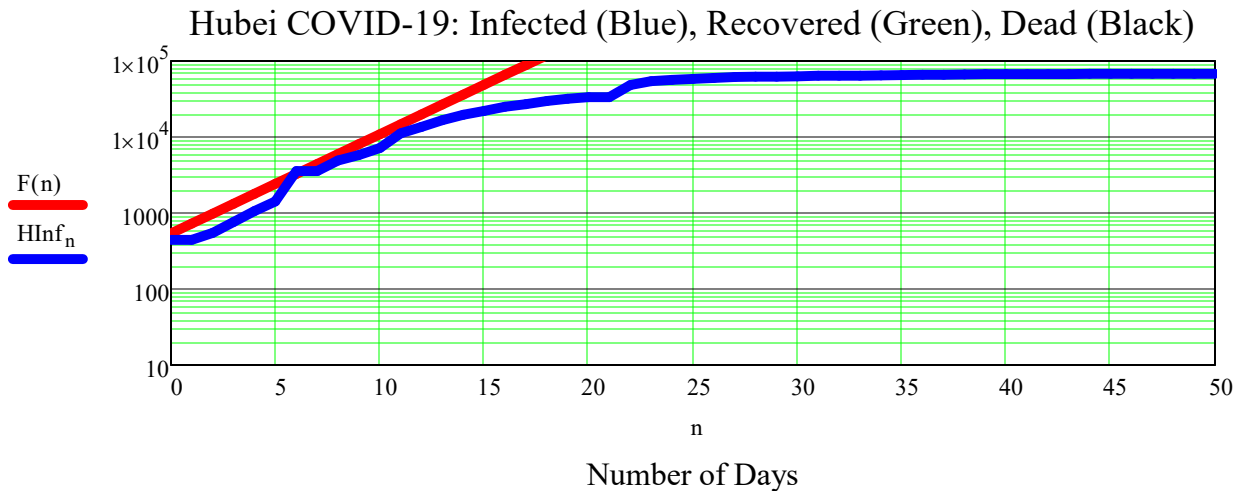
The number of days it takes to recover,  $t_{rec}$   $t_{rec} := 6.8$   $t_{rec} = 6.8$

Basic Reproductive Ratio before and after Intervention:  $R_0 := \frac{b}{\delta + \gamma}$   $R_{0\delta} := \frac{b}{\delta + \gamma}$   $R_0 = 10.333$   $R_{0\delta} = 10.333$

# Extracting R0 from Log Plots of Hubei Infected

$$\text{Inf}(t) = \text{Inf}_0 \cdot e^{(R-1) \cdot \left( \frac{t}{\text{Infectious\_Period}} \right)} \quad \log(\text{Inf}(t)) = \log(I_0) + (R-1) \cdot \frac{t}{\text{Infectious\_Period}}$$

$\text{HInf20} := \text{submatrix}(\text{HInf}, 0, 20, 0, 0) \quad k := 0..20 \quad X_k := k + 1 \quad F(k) := 400 \exp\left[ (4-1) \cdot \frac{X_k}{10} \right]$



## Find the Slope to the Log Plot of Infected to Get an Estimate of R0

$m := 0..15 \quad \text{HIm}_m := \text{HInf}_m \quad \text{daz}_m := m \quad \text{Assume Infectious Period is 10 days}$

$\text{LM} := \overrightarrow{\log(\text{HIm})} \quad \text{LN} := \overrightarrow{\log(\text{HInf})} \quad y(x) = s \cdot x + \text{int} \quad F(x) := (x-1)^T$

$\text{linfit}(\text{daz}, \text{LM}, \text{F}) = \begin{pmatrix} 0.126 \\ 2.587 \end{pmatrix} \quad \text{slope}(\text{daz}, \text{LM}) = 0.126 \quad \text{slope} = \frac{R-1}{\text{Infectious\_Period}}$

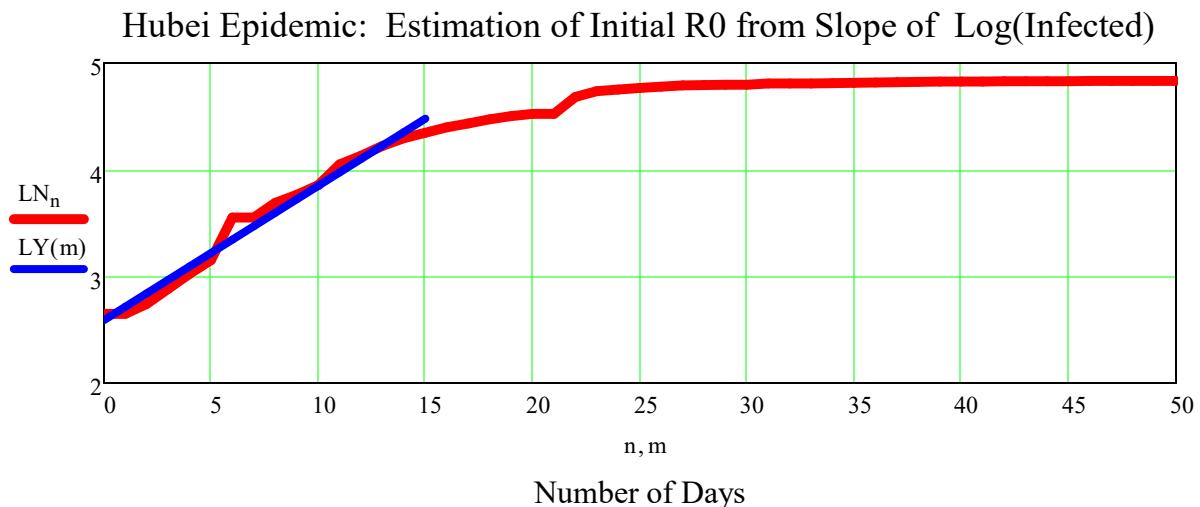
### Linear Fit, LY, to Log of the Curve of Initial Infected:

$\text{LY}(m) := 0.126 \cdot m + 2.587$

$R_{0L}(\text{slope}, \text{Infectious\_Period}) := \text{slope} \cdot (\text{Infectious\_Period}) + 1$

$R_{0L}(0.126, 10) = 2.26$

**The semi-log plot below of Hubei Infected vs. Time reveals that after 15 days, the epidemic was no longer exponential ==> Containment was successful.**



# Spatial Aggregation by State: Estimate Infect Growth Rate

Downloaded Johns Hopkins Data From: March 10 to March 22 2020 Row 0 JH\_SP is # of State  
[https://github.com/CSSEGISandData/COVID-19/blob/master/csse\\_covid\\_19\\_data/csse\\_covid\\_19\\_time\\_series/](https://github.com/CSSEGISandData/COVID-19/blob/master/csse_covid_19_data/csse_covid_19_time_series/)

**Read Data Files:** JH\_SP := READPRN("JHU State-DCUSNo, Index, Confirmed Sort 0toP1 3-10- to 3-22-Pop A P-A.txt")<sup>T</sup>

JH\_s := submatrix(JH\_SP, 1, 13, 0, 50) **Data from March 10 to March 22** **Sort by Number of Cases**

$\overset{\text{R}}{\text{R}} := \text{rows}(\text{JH\_s}) = 13$      $r := 0..R - 1$      $z := R - 1$      $\text{dayz}_T := r$      $\overset{\text{C}}{\text{C}} := \text{cols}(\text{JH\_s}) = 51$      $\overset{\text{c}}{\text{c}} := 0..C - 1$

## Compare All States: Normalize Infection Curves for all States so Each has a Maximum Value of "1"

**Increase Resolution: Multiply Infection Exponential Rate Values X 10**

$\overset{\text{gx}}{\text{gx}} := (1 \ 0.3)^T \overset{\text{F}}{\text{F}}(\text{x}, \text{v}, \text{m}) := \text{v} \cdot \text{e}^{\text{m} \cdot \text{x}}$

$\overset{\text{JXy}}{\text{JXy}}_{r,c} := \frac{\text{JH\_s}_{r,c}}{\text{JH\_s}_{12,c}}$      $(\text{v}_c \ \text{m}_c) := \text{genfit}(\text{dayz}, \overset{\text{JXy}}{\text{JXy}}^{\langle \text{c} \rangle}, \overset{\text{gx}}{\text{gx}}, \text{F})^T$   
 $\text{m}_{\text{avg}} := \text{mean}(\text{m}) = 0.292$

$\overset{\text{X}}{\text{X}}(\text{j}, \text{k}) := \text{submatrix}(\text{m}, \text{j}, \text{k}, 0, 0)^T \cdot 10$   
 $\text{m}_{\text{avg}} \cdot 10 = 2.917$

## All States: Estimate the Growth Rate from Slope of Log of the Infected vs Days Data

**Increase Resolution: Multiply Slope of Log Number Infected vs Time Rate Values X 10**

$\overset{\text{LY}}{\text{LY}} := \log(\text{JH\_s})$      $\overset{\text{SLP}_c}{\text{SLP}_c} := \text{slope}(\text{dayz}, \overset{\text{LY}}{\text{LY}}^{\langle \text{c} \rangle}) \cdot 10$      $\overset{\text{S}}{\text{S}}(\text{j}, \text{k}) := \text{submatrix}(\text{SLP}, \text{j}, \text{k}, 0, 0)^T$

## State Growth Rates Estimates -2 Methods: Exponents\*10 ==> X, Slopes\*10 ==> S

**NY-1 FL-7 USA-50 CA-3 WA-0 CO-6 NJ-2**

	NY	WA	NJ	CA	IL	MI	LA	FK	MA	TX	GE	
X(0,10) =	0	1	2	3	4	5	6	7	8	9	10	
	0	3.966	1.51	3.921	1.912	3.566	4.294	2.921	2.686	1.986	3.127	2.701

	0	1	2	3	4	5	6	7	8	9	10	
S(0,10) =	0	1.706	0.699	1.825	0.888	1.54	2.864	2.076	1.451	0.71	1.399	1.328

	PE	TE	CO	WI	OH	NC	MY	CN	VG	MI	IN	
X(11,21) =	0	1	2	3	4	5	6	7	8	9	10	
	0	2.993	3.92	2.115	3.317	3.478	3.221	2.811	2.622	2.427	4.596	3.784

	0	1	2	3	4	5	6	7	8	9	10	
S(11,21) =	0	1.354	1.486	1.143	1.693	1.744	1.408	1.295	1.791	1.148	2.756	1.138

	SC	NV	UT	MN	AR	OR	AZ	MO	KY	IO	MN	
X(22,32) =	0	1	2	3	4	5	6	7	8	9	10	
	0	2.968	2.687	2.972	2.293	3.477	1.965	3.716	3.977	2.738	2.221	2.591

	0	1	2	3	4	5	6	7	8	9	10	
S(11,21) =	0	1.354	1.486	1.143	1.693	1.744	1.408	1.295	1.791	1.148	2.756	1.138

	RI	OK	NH	KN	NM	VT	NB	HA	DL	ID	MT	
X(33,43) =	0	1	2	3	4	5	6	7	8	9	10	
	0	2.231	2.732	2.222	2.779	2.089	2.76	1.695	3.201	2.503	3.637	2.686

	0	1	2	3	4	5	6	7	8	9	10	
S(33,43) =	0	1.12	1.519	1.097	1.634	1.575	1.465	0.861	1.269	1.901	2.341	1.658

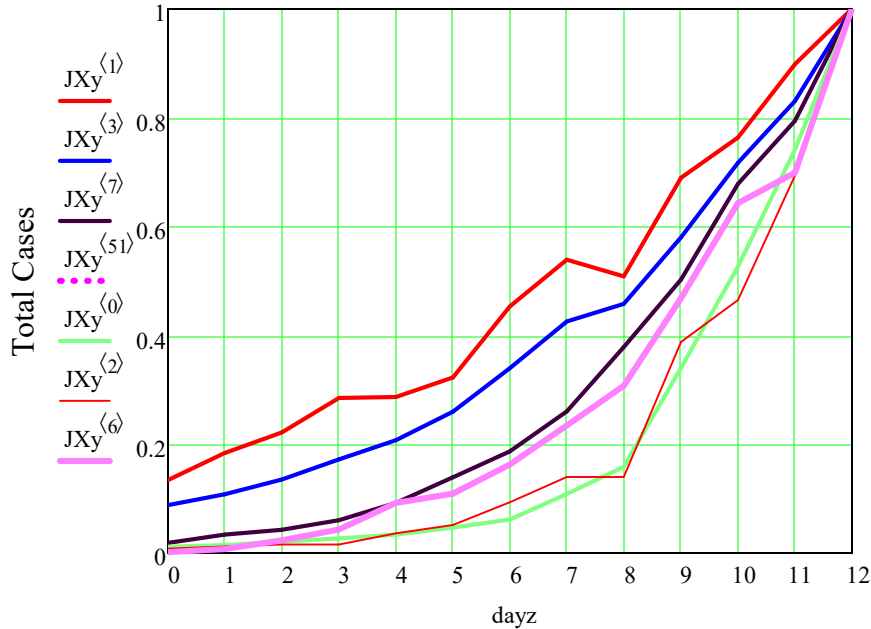
$\overset{\text{ND}}{\text{ND}}$   $\overset{\text{WY}}{\text{WY}}$   $\overset{\text{AL}}{\text{AL}}$   $\overset{\text{SD}}{\text{SD}}$   $\overset{\text{WV}}{\text{WV}}$   $\overset{\text{DC}}{\text{DC}}$   $\overset{\text{US}}{\text{US}}$   
 $\overset{\text{X}}{\text{X}}(44,50) = (3.281 \ 2.328 \ 3.459 \ 1.062 \ 4.699 \ 2.71 \ 3.211)$   
 $\overset{\text{S}}{\text{S}}(44,50) = (2.079 \ 2.049 \ 2.089 \ 0.923 \ 1.993 \ 1.023 \ 1.313)$

Note the **Wide Range of Growth Rates** between the States. Physical/Social isolation/distance makes some State populations less inaccessible.



**STATE PLOTS ARE IN THIS ORDER TOP TO BOTTOM**  
**WA-1 CA-3 FL-7 USA-51 NY-0 NJ-2 LA-6**

States and USA - Total CVID-19 Cases/Day



**Estimate the Basic Reproduction Ratio  $R_0$  for the Four States and USA:**

**Reproductive Ratio  $R_{0L}$  Rank (Listed in Order Below): NY, FL, USA, CA, WA**

$\text{slope}(\text{dayz}, LY^{\langle 1 \rangle}) = 0.07$	$R_{0L}(0.164, 10) = 2.64$	$\text{slope}(\text{dayz}, LY^{\langle 2 \rangle}) = 0.183$	$R_{0L}(0.092, 10) = 1.92$
$\text{slope}(\text{dayz}, LY^{\langle 3 \rangle}) = 0.089$	$R_{0L}(0.155, 10) = 2.55$	$\text{slope}(\text{dayz}, LY^{\langle 0 \rangle}) = 0.171$	$R_{0L}(0.074, 10) = 1.74$
$\text{slope}(\text{dayz}, LY^{\langle 4 \rangle}) = 0.154$	$R_{0L}(0.128, 10) = 2.28$		

**Assumptions Used for SIR Mathematical Epidemiological Model**

Refer to the SIR Model given on page 7.

The Dynamics of an epidemic can be expressed by the rates of change of three Compartments or groups: Susceptibles or Healthy (S), those that are Infected (I), and those Recovered (R). The dynamics of S, I, R, can be described by three non-linear deterministic differential equations.

**Some Assumptions of Compartmental SIR Model:**

The model's transmission rate probabilities ( $\beta, \gamma$ ) and the Basic Reproductive Ratio  $R_0$  are constant during the outbreak.

A person who transitions to the infected group immediately becomes infectious. There is no latent period.

All individual have the same rate of recovery,  $\gamma$ . If the duration of the infection is D days, then the transition rate,  $\gamma$ , from I to R is the reciprocal of D. The duration (average generation) of the infection for COVID-19 is  $\sim 10$  days.

The population is homogenous and well mixed (homogenous mixing within the populations I and S). In actuality, people interact in complex social networks (communities) that have different fundamental structural properties.

In a Population, N, spread is by the Law of Mass Action, that is, the number of new cases per unit time, or rate, is proportional to the product of the number of Susceptible and the number of Infections people,  $= \beta * I * S/N$

The rate of decrease of the healthy population,  $dS/dt$ , is proportional to the product of the number of healthy people and the fraction of the total population that is infected.

People are no longer infectious after  $1/\gamma$  days and are afterwards immune. The I and R case records are accurate and can be used to extract the magnitude of  $\beta$ .

# New York City Data

<https://www1.nyc.gov/assets/doh/downloads/pdf/imm/covid-19-daily-data-summary.pdf>

Cases := READPRN("NYC Inf 3-13 to 3-30 2020.txt")      R<sub>c</sub> := rows(Cases)    j := 0..R<sub>c</sub> - 1    JNy := Cases  
 R<sub>c</sub> = 18      i := 1..R<sub>c</sub> - 1      New\_Cases<sub>i</sub> := Cases<sub>i</sub> - Cases<sub>i-1</sub>      JNx<sub>j</sub> := j      NCs := New\_Cases

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

rate<sub>avg</sub> := 100 \*  $\frac{NCs_i}{Cases_{i-1}}$       Cases<sub>R<sub>c</sub>-1</sub> = 38087      rate := rate + 1      rate<sub>avg</sub> := mean(rate) = 41.189

## Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{rate_{avg}}{100}\right)}$$

**Days to Double:**    Dbl = 2.01

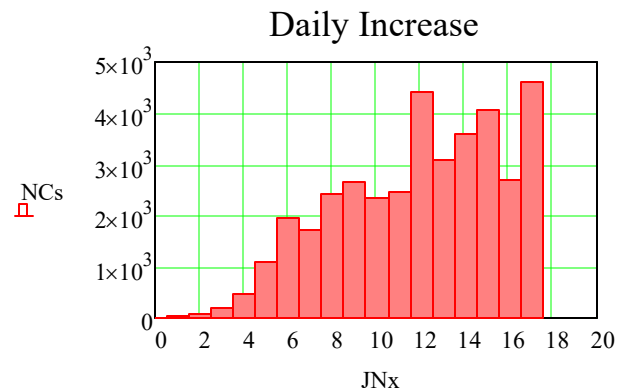
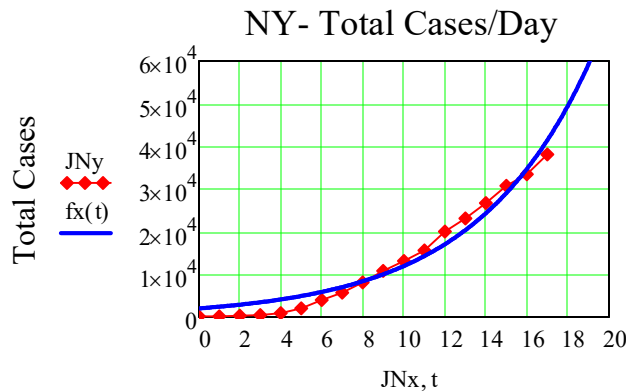
Dbl\_Days(JNy<sub>R<sub>c</sub>-1</sub>, 100, R<sub>c</sub>, 0) = 2.1

gx := (100 0.3)<sup>T</sup>    F(x, v, m) := v \* e<sup>m \* x</sup>    (v m) := genfit(JNx, JNy, gx, F)<sup>T</sup>    m = 0.178    fx(t) := v \* e<sup>m \* t</sup>

guess := (1 0.01 1)<sup>T</sup>    (a k c) := expfit(JNx, JNy, guess)<sup>T</sup>    (a k c) = (7398.75 0.111 -9307.034)    Fe(x) := a \* e<sup>k \* x</sup> + c

## Exponential Growth ==> NY Epidemic

$$I(t) = I(0)e^{(\beta - \gamma)t} \quad R_{0m} := m \cdot 10 - 1 = 0.776$$



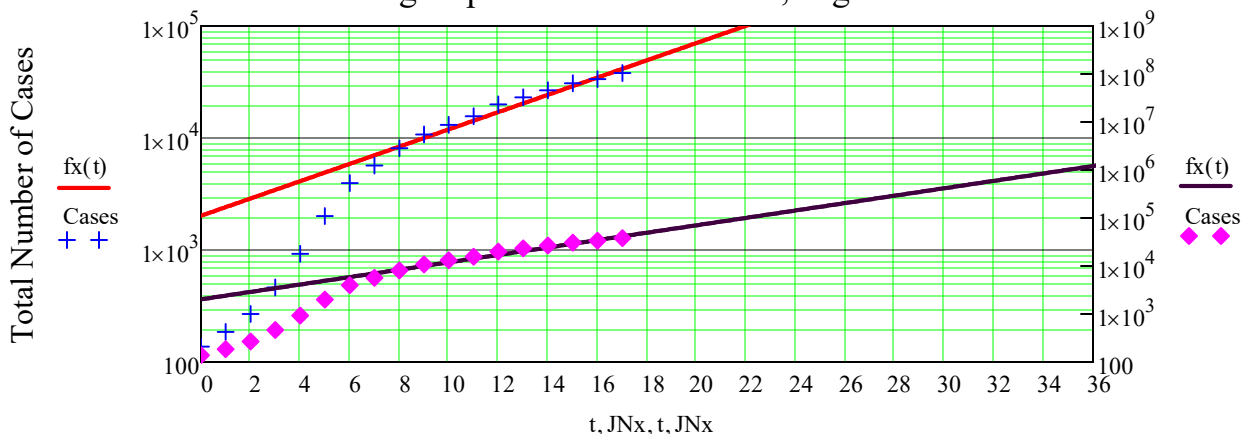
## NY Reproductive Ratio R<sub>0L</sub>:

$$LM := \log(Cases)$$

$$\text{slope}(JNy, LM) = 5.548 \times 10^{-5}$$

$$R_{0L}(0.137, 10) = 2.37$$

## NY: Left Log Exponential Fit & Cases, Right Linear Cases



Number of Days from Initial 100 Cases

# New York State Data

[https://en.wikipedia.org/wiki/2020\\_coronavirus\\_pandemic\\_in\\_New\\_York\\_\(state\)](https://en.wikipedia.org/wiki/2020_coronavirus_pandemic_in_New_York_(state))

Cases := READPRN("NY CV-19 Inf 3-3 to 4-12 2020.txt")      Rc := rows(Cases)    j := 0..Rc - 1    JNy := Cases  
 Rc = 41      i := 1..Rc - 1      New\_Cases\_i := Cases\_i - Cases\_{i-1}      JNx\_j := j      NCs := New\_Cases

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

rate := 100 \*  $\frac{NCs_i}{Cases_{i-1}}$       Cases\_{Rc-1} =  $1.867 \times 10^5$       rate := rate + 1      rate\_avg := mean(rate) = 41.786

## Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{rate\_avg}{100}\right)}$$

**Days to Double:**      Dbl = 1.985

Dbl\_Days(JNy\_{Rc-1}, 100, Rc, 0) = 3.773

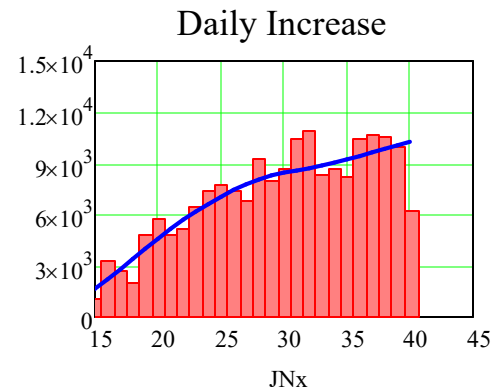
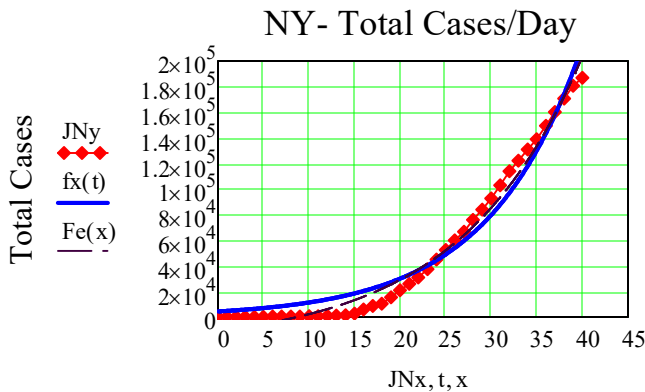
gx := (100 0.3)^T    F(x, v, m) := v \* e^{m \* x}    (v, m) := genfit(JNx, JNy, gx, F)^T    m = 0.098    fx(t) := v \* e^{m \* t}

(a, k, c) := expfit(JNx, JNy, guess)^T    (a k c) = (11641.922 0.074 -22313.21)    Fe(x) := a \* e^{k \* x} + c

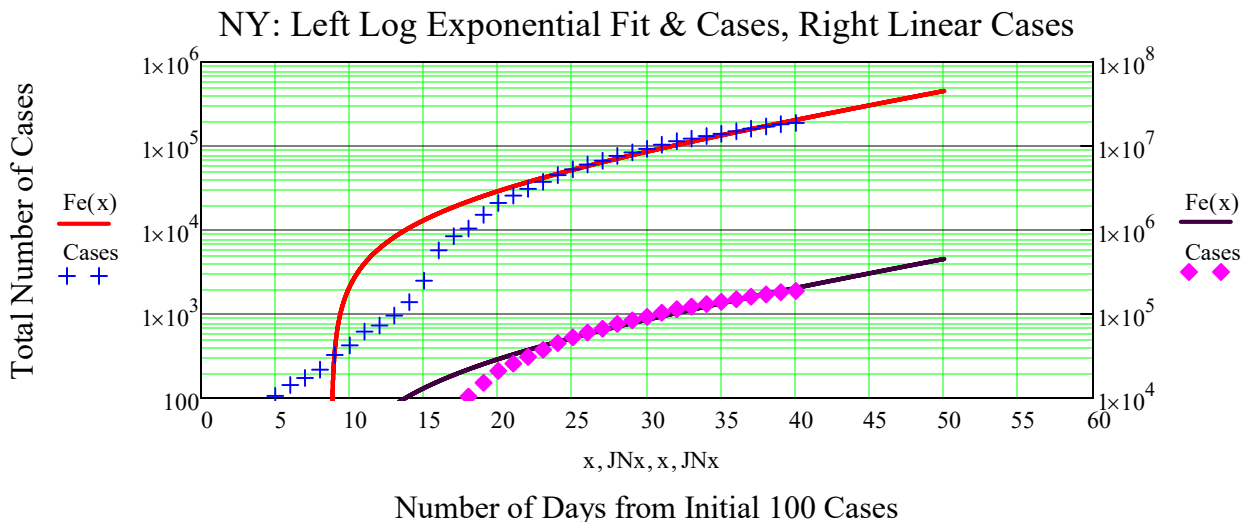
R\_{0m} := m \* 10 - 1 = -0.02

## Exponential Growth ==> NY Epidemic

Nsm := supsmooth(JNx, NCs)



**NY Reproductive Ratio R\_{0L}:**      LM := log(Cases)      slope(JNy, LM) =  $1.761 \times 10^{-5}$       R\_{0L}(0.137, 10) = 2.37



# Methodology to Estimate the Outcome of the NY Epidemic

Our methodology is similar to most papers, the major difference is we use Mathcad's Error Minimization function Minerr, not Python, R, or MATLAB's Minimization Tool.

USA:  $m = 0.248$

$\beta = 0.1$

$\alpha = 0.248 + 0.1$

$\alpha = 0.319, R_0 = 4.49$

Assume that 80% of the Population is Either Not Susceptible nor Accessible

$$L := 11^{-1}$$

SIR Model  $S_0 := 19.5 \cdot 10^6 \cdot 0.8$   $S_0$  is Population ModN( $\beta$ ) := SIRD( $S_0, 2, \beta, L, \delta, Rc - 2$ )

InfN( $\beta$ ) := ModN( $\beta$ )<sup><1></sup> SU( $\beta$ ) := ModN( $\beta$ )<sup><0></sup> ISU( $\beta$ ) := stack(InfN( $\beta$ ), SU( $\beta$ ))

$$I(t) = I_0 \cdot e^{(\beta - \gamma)t}$$

## Use Levenberg-Marquardt Method: Minimize Least Squares Error to Residual

Define a Residual to be the difference between the current data points JNy and SIRD Model

JNS := stack[JNy, (S<sub>0</sub> - JNy)] ResidJN( $\beta$ ) := JNS - ISU( $\beta$ ) Given 0 = ResidJN( $\beta$ )

Use Minerr to Extract Optimal Parameters:

$$b := \text{Minerr}(\beta)^T$$

$b = 0.435$

$$R_{0w} := \frac{b}{L} = 4.79$$

Infected

UIf := ModN(b)<sup><1></sup>

Removed

URc := ModN(b)<sup><2></sup>

Dead

UDd := UIf · 0.03

$$\frac{ERR}{R} = 31075.158$$

$n := 0..Rc - 1$

$$R_{0SIR} := \frac{b}{L + 0.015} = 4.112$$

UDe := submatrix(UDd, 0, 13, 0, 0)

## Extracted Parameters of NY COVID-19 Epidemic

### Imax, Calculate Days to Double, D2X and Fit Power Function to USA JH Data

Guess  $ex := 1.4$  FitPwr(ex, t) := JNy<sub>0</sub> · ex<sup>t</sup>  $I_{max} = I(0) + S(0) - \sqrt{\beta} \log S(0) - \sqrt{\beta} + \sqrt{\beta} \log \sqrt{\beta}$

ResidJN<sub>2</sub>(ex) := JNy - FitPwr(ex, JNx) Given 0 = ResidJN<sub>2</sub>(ex) Ex := Minerr(ex) Ex = 1.344

### Fit JHy with a Power Function, PWR(t):

$$Pwr(t) := JNy_0 \cdot Ex^t$$

$$D2X(Ex) := \frac{\ln(2)}{\ln(Ex)}$$

$D2X(Ex) = 2.345$

$$Dbl\_Days(9415, 100, 15, 0) = 2.288$$

The number of days it takes infections to double,  $t_{2x}$

$$t_{2x} := \frac{1}{b}$$

$t_{2x} = 2.296$

$b = 0.435$

The number of days it takes to recover,  $t_{rec}$

$\gamma = 0.063$

$$t_{rec} := \frac{1}{L}$$

$t_{rec} = 11$

$$R_{0w} := \frac{b}{L + \delta} = 4.541$$

Proj := SIR( $S_0, 2, 0.186, L, 180$ ) PIf := Proj<sup><1></sup>

PRc := Proj<sup><2></sup>

PS := Proj<sup><0></sup>

$R_{mpv} := \text{rows}(PIf) = 182$

$$m := 0..R_p - 1 \quad R_p - 1 = 181$$

## No Mitigation Scenario: Approximate Match to Early NY Total # Cases

Proj := SIR( $S_0, 2, b, \frac{1}{6.8}, 60$ )

PIf := Proj<sup><1></sup>

PRc := Proj<sup><2></sup>

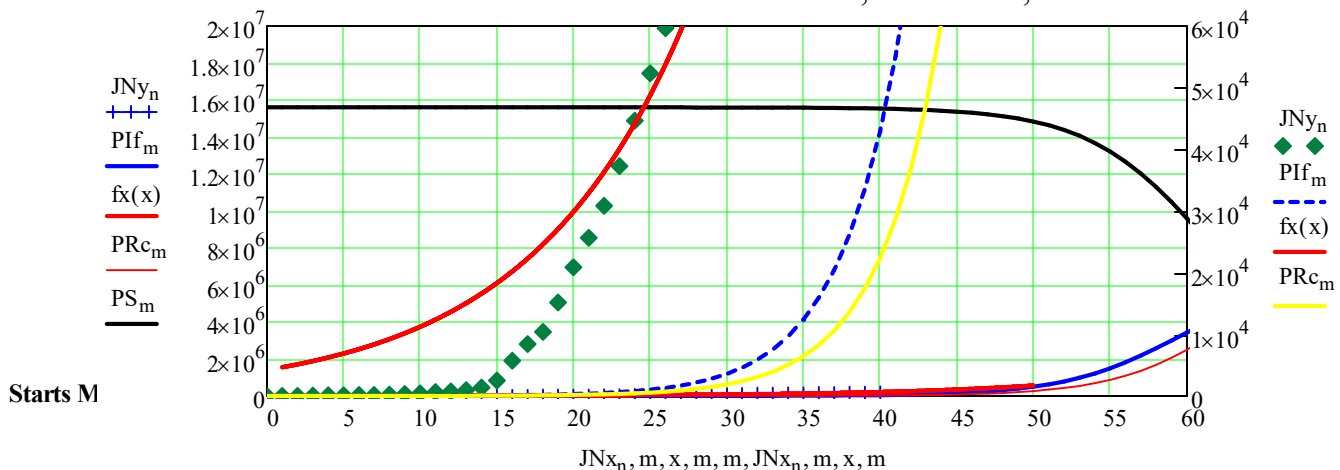
PS := Proj<sup><0></sup>

$R_{mpv} := \text{rows}(PIf) = 62$

$$m := 0..R_p - 1 \quad R_p - 1 = 61$$

$$\max(PIf) = 3.819 \times 10^6$$

NY: Infection Cases vs. SIR Model Sus, Infections, and Rec

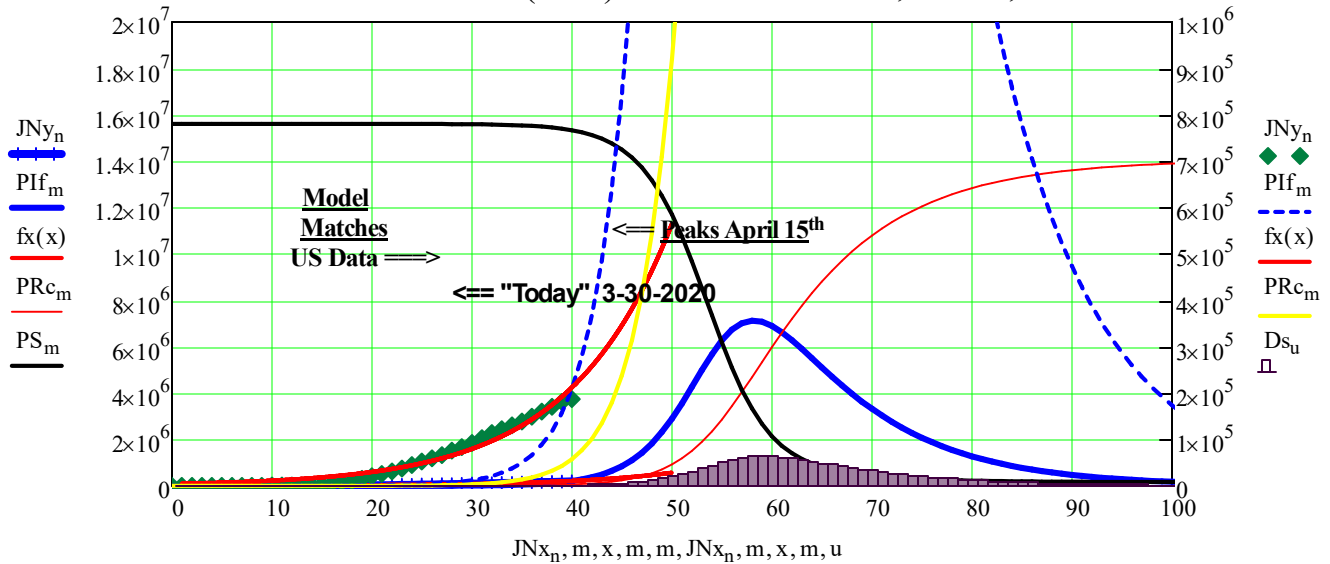


# Mitigation: Model with Sigmoid Transition to a Lower $R_{eff}$

$$\begin{aligned}
 \text{ProM} &:= \text{SIRM}\left(S_0, 2, b, b, 180, 7, \frac{1}{11}, 180\right) & \text{Pif} &:= \text{ProM}^{(1)} & \text{PRc} &:= \text{ProM}^{(2)} & \text{PS} &:= \text{ProM}^{(0)} & R_{p,v} &:= \text{rows}(\text{Pif}) = 182 \\
 Ds &:= \text{ProM}^{(3)} & R_d &:= \text{rows}(Ds) = 182 & u &:= 1..R_d - 1 & \text{Total\_Deaths} &:= \sum Ds & \text{Total\_Deaths} &= 1.391 \times 10^6 \\
 R_c &= 41 & m &:= 0..R_p - 1 & R_p - 1 &= 181 & \text{Imax} &:= \max(\text{Pif}) & \text{Imax} &= 7.124 \times 10^6
 \end{aligned}$$

## No Mitigation: NY Infection Peaks by April 15th - It has infected everybody

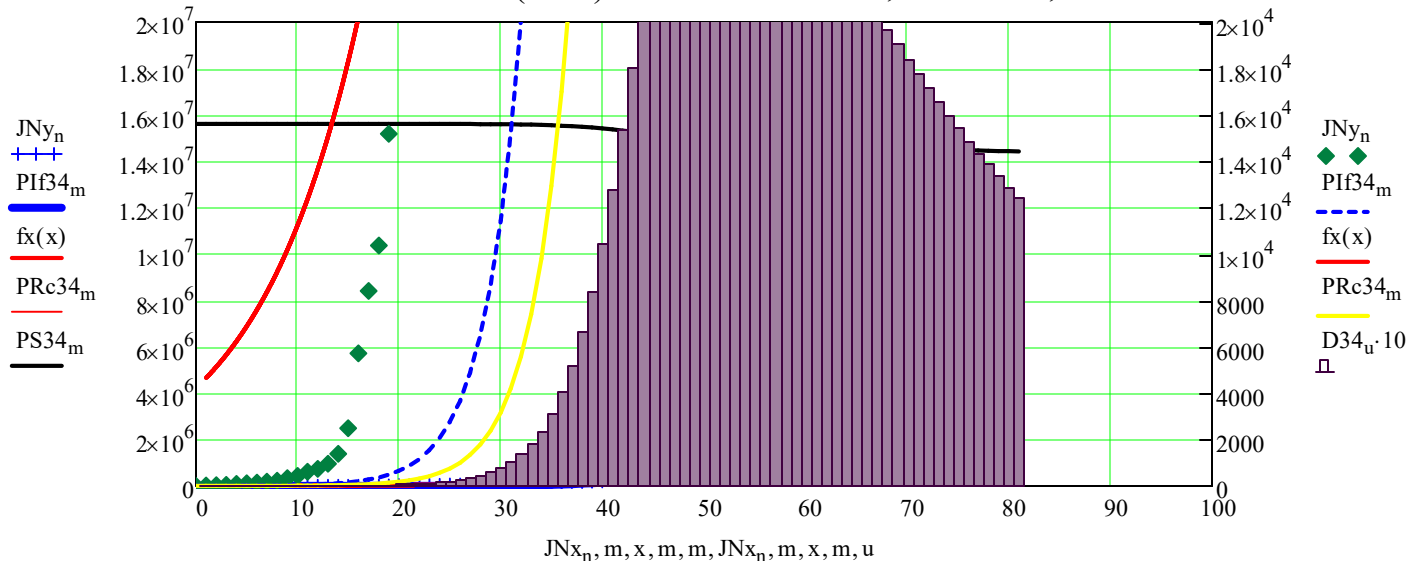
TWK: Infection Cases (Blue) vs. SIR Model Sus, Infecti, and Rec



## Mitigation $R_{eff} \Rightarrow 0.476$ @ 47 Days: NY State Infection Peak with Transition

$$\begin{aligned}
 R_c = 41 & \quad \text{MR34} := \text{SIRM}\left(S_0, 2, b, 0.07, 28, 7, \frac{1}{11}, 80\right) & \text{Pif34} &:= \text{MR34}^{(1)} & \text{PRc34} &:= \text{MR34}^{(2)} & \text{PS34} &:= \text{MR34}^{(0)} \\
 D34 &:= \text{MR34}^{(3)} & \text{Total\_Deaths} &:= \sum D34 & \text{Total\_Deaths} &= 94783.722 \\
 \text{\# Infected at the Exponential Transition Point} & & \text{Imax} &:= \max(\text{Pif34}) & \text{Nmax} &:= \text{match}(\text{Imax}, \text{Pif34}) & \text{Nmax} &= (50) & \text{Imax} &= 3.42 \times 10^5
 \end{aligned}$$

TK: Infection Cases (Blue) vs. SIR Model Sus, Infections, and Rec



# USA Data Directly Our World in Data

<https://ourworldindata.org/coronavirus>

Read Data File: JH\_USA := READPRN("OWD US Date, TC NC TD ND 3-3 to 4-29.txt")

March 3 to April 25

JHy := JH\_USA<sup>(3)</sup> Cases := JHy R<sub>c</sub> := rows(JHy) JHy<sub>R<sub>c</sub>-1</sub> = 1.013 × 10<sup>6</sup> j := 0..R<sub>c</sub> - 1  
 R<sub>c</sub> = 58 i := 1..R<sub>c</sub> - 1 JHx<sub>j</sub> := j days<sub>i</sub> := i rows(days) = 58

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

rate := 100 \*  $\frac{\text{New\_Cases}_i - \text{Cases}_{i-1}}{\text{Cases}_{i-1}}$  New\_Cases<sub>i</sub> := Cases<sub>i</sub> - Cases<sub>i-1</sub> NC := New\_Cases  
 Cases<sub>R<sub>c</sub>-1</sub> = 1.013 × 10<sup>6</sup> rate := rate + 1 rate<sub>avg</sub> := mean(rate) = 19.012

## Calculate the Number of Days for Cases to Double - Dbl:

$$\text{Dbl} := \frac{\ln(2)}{\ln\left(1 + \frac{\text{rate}_{\text{avg}}}{100}\right)}$$

Days to Double: Dbl = 3.982

Dbl\_Days(26138, 100, 17, 0) = 2.117

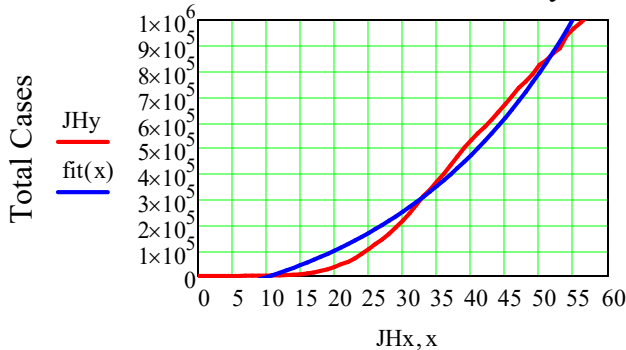
a := 1 b := 0.01 c := 1 guess := (a b c)<sup>T</sup> gx := (100 0.3)<sup>T</sup> F(x, v, m) := v · e<sup>m·x</sup> (v m) := genfit(JHx, JHy, gx, F)<sup>T</sup>  
 m = 0.059 R<sub>0</sub> := m · 10 - 1 = -0.409

## Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

(a. b. c.) := expfit(JHx, JHy, guess)<sup>T</sup> (a b c) = (1.573 × 10<sup>5</sup> 0.038 -2.342 × 10<sup>5</sup>) Fe(x) := v · e<sup>m·x</sup> ln( $\frac{N}{v}$ )  
 fit(x) := a e<sup>b·x</sup> + c v = 40282.182 b = 0.038 Days to Number, N: dy(N) :=  $\frac{\ln\left(\frac{N}{v}\right)}{m}$   
 x := 0..100

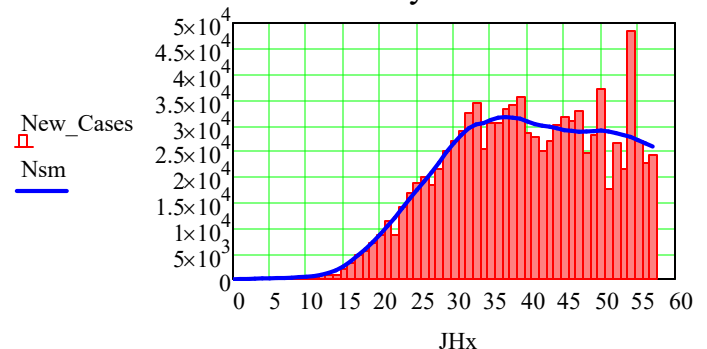
## Exponential Growth ==> US Endemic

USA- Total Cases/Day



Nsm := supsmooth(JHx, NC)

Daily Increase



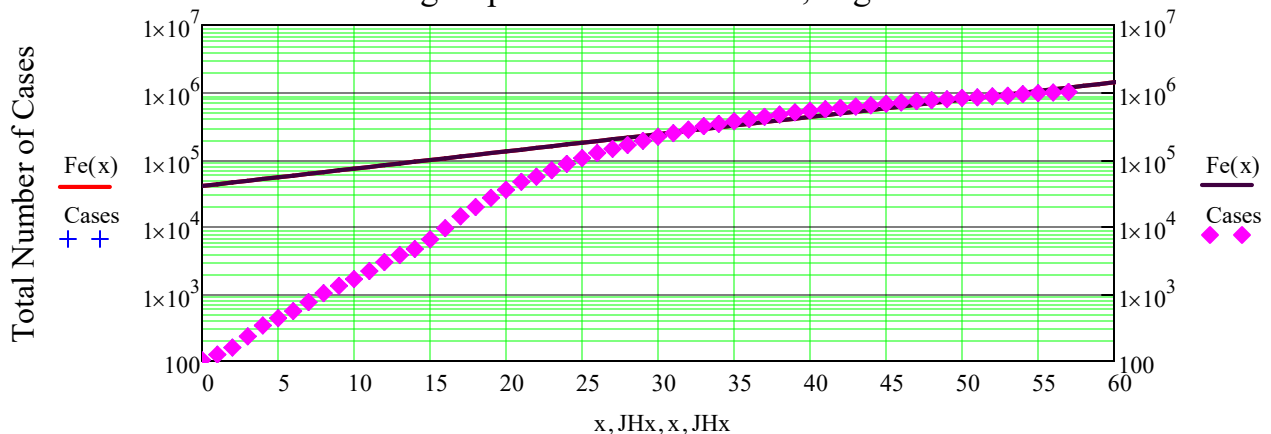
## US Reproductive Ratio R<sub>0L</sub>:

LM := log(Cases)

slope(JHx, LM) = 0.07

R<sub>0L</sub>(0.137, 10) = 2.37

## USA: Left Log Exponential Fit & Cases, Right Linear Cases



Number of Days from Initial 100 Cases



# Methodology to Estimate the Outcome of the USA Epidemic

Our methodology is similar to most papers, the major difference is we use Mathcad's Error Minimization function Minerr, not Python, R, or MATLAB's Minimization Tool.

Assume that 80% of the Population is Either Not Susceptible nor Accessible

**SIR Model**  $S_0 := 3.2 \cdot 10^8 \cdot 0.8$  S<sub>0</sub> is Population  $\text{ModU}(\beta) := \text{SIRD}\left(S_0, 100, \beta, \frac{1}{6.8}, \delta, R_c - 2\right)$   
 $\text{InfU}(\beta) := \text{ModU}(\beta)^{\langle 1 \rangle}$   $\text{SU}(\beta) := \text{ModU}(\beta)^{\langle 0 \rangle}$   $\text{ISU}(\beta) := \text{stack}(\text{InfU}(\beta), \text{SU}(\beta))$

## Use Levenberg-Marquardt Method: Minimize Least Squares Error to Residual

Define a Residual to be the difference between the current data points JHy and SIRModel

$\text{ResidJH}(\beta) := \text{JHy} - \text{InfU}(\beta)$  Given  $0 = \text{ResidJH}(\beta)$

Use Minerr to Extract Optimal Parameters:

$b := \text{Minerr}(\beta)^T$   $b = 0.337$   $R_0 := \frac{b}{L} = 3.703$

**Infected**  $\text{Uif} := \text{ModU}(b)^{\langle 1 \rangle}$  **Removed**  $\text{URc} := \text{ModU}(b)^{\langle 2 \rangle}$  **Dead**  $\text{UDd} := \text{Uif} \cdot 0.03$   $\frac{\text{ERR}}{R} = 1.503 \times 10^5$   
 $n := 0..R_c - 1$   $R_{0\text{SIR}} := \frac{b}{L + 0.015} = 3.179$   $\text{UDe} := \text{submatrix}(\text{UDd}, 0, 13, 0, 0)$

## Extracted Parameters of USA COVID-19 Epidemic

Imax, Calculate Days to Double, D2X and Fit Power Function to USA JH Data

Guess  $ex := 1.4$   $\text{FitPwr}(ex, t) := \text{JHy}_0 \cdot ex^t$   $I_{\text{max}} = I(0) + S(0) - v/\beta \log S(0) - v/\beta + v/\beta \log v/\beta$   
 $\text{ResidJH}_2(ex) := \text{JHy} - \text{FitPwr}(ex, \text{JHx})$  Given  $0 = \text{ResidJH}_2(ex)$   $Ex := \text{Minerr}(ex)$   $Ex = 1.184$

Fit JHy with a Power Function, PWR(t):  $\text{Pwr}(t) := \text{JHy}_0 \cdot Ex^t$   $\text{Dbl\_Days}(9415, 100, 15, 0) = 2.288$   $\text{D2X}(Ex) = 4.111$

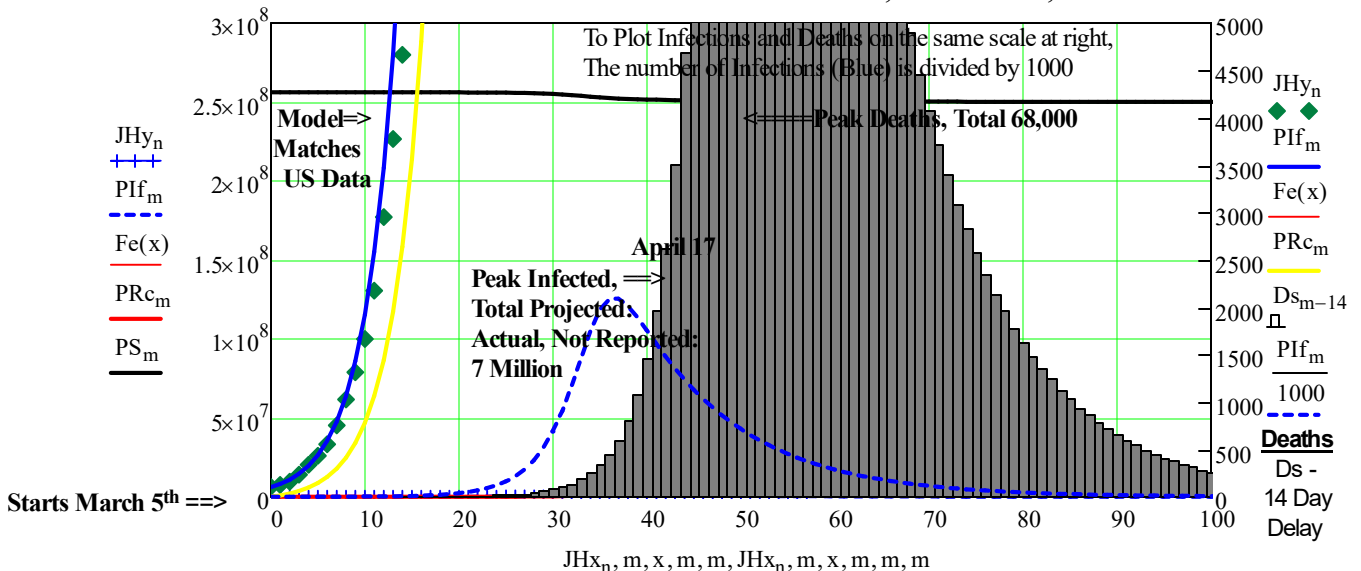
The number of days it takes infections to double,  $t_{2x}$   $t_{2x} := \frac{1}{h}$   $t_{2x} = 2.97$   $L = 0.091$   
 The number of days it takes to recover,  $t_{\text{rec}}$   $\gamma = 0.063$   $t_{\text{rec}} := \frac{1}{L}$   $t_{\text{rec}} = 11$   $R_0 := \frac{b}{L + \delta} = 3.51$

## USA Mitigation R0 => 0.476 @ 28 Days: Infection Peak with Transition

$\text{Proj} := \text{SIRM}\left(S_0, 100, 0.5, 0.07, 28, 3, \frac{1}{6.8}, 120\right)$   $\text{Pif} := \text{Proj}^{\langle 1 \rangle}$   $\text{PRc} := \text{Proj}^{\langle 2 \rangle}$   $\text{Ds} := \text{Proj}^{\langle 3 \rangle}$   $\text{PS} := \text{Proj}^{\langle 0 \rangle}$   $R_{\text{pw}} := \text{rows}(\text{Pif})$   
 $I_{\text{max}} := \max(\text{Pif})$   $I_{\text{max}} = 2.089 \times 10^6$   $N_{\text{max}} := \text{match}(I_{\text{max}}, \text{Pif})$   $\text{Total\_Deaths} := \sum \text{Ds}$   $\text{Total\_Deaths} = 3.458 \times 10^5$

## TWK Mitigation Scenario: Reasonably Good Match to USA Cases to Date

USA: Infection Cases vs. SIR Model Sus, Infections, and Rec



# CDC: Data on USA Total Confirmed Deaths

<https://ourworldindata.org/coronavirus>

Today := 57

**Read Data File:** FL\_Deaths := READPRN("US HD Deaths MLH 3-1 to 4-27.txt") Rc := rows(FL\_Deaths)

FND\_m := FL\_Deaths <sup>(0)</sup> Rc = 137 i := 1..Rc - 1 j := 0..Rc - 1 JFx\_i := j D\_now := submatrix(FL\_Deaths, 0, 33, 0, 0)

$$FD_m_j := \sum_{i=0}^j FDN_m_i \quad FD_L_j := \sum_{i=0}^j FL_Deaths_{i,1} \quad FD_H_j := \sum_{i=0}^j FL_Deaths_{i,2}$$

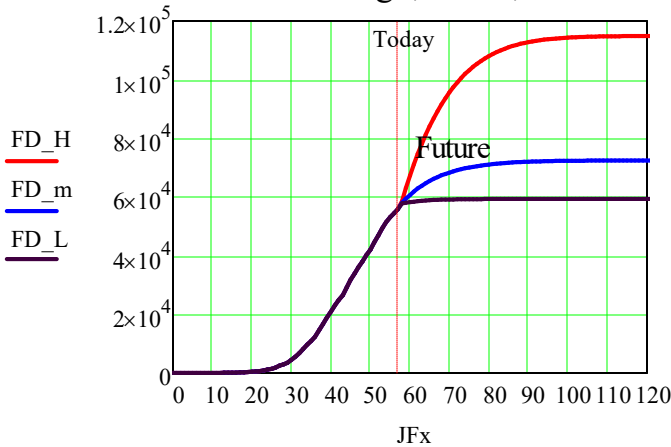
## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

$$rate_i := 100 \frac{FDN_m_i}{FD_m_{i-1}} \quad rate := rate + 1 \quad rate_{avg} := mean(rate) = 9.406$$

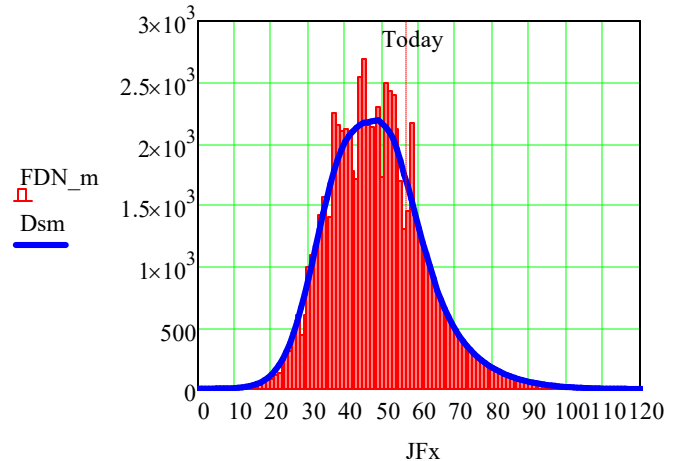
## Deaths to Data and Range Projections

Dsm := supsmooth(JFx, FDN\_m)

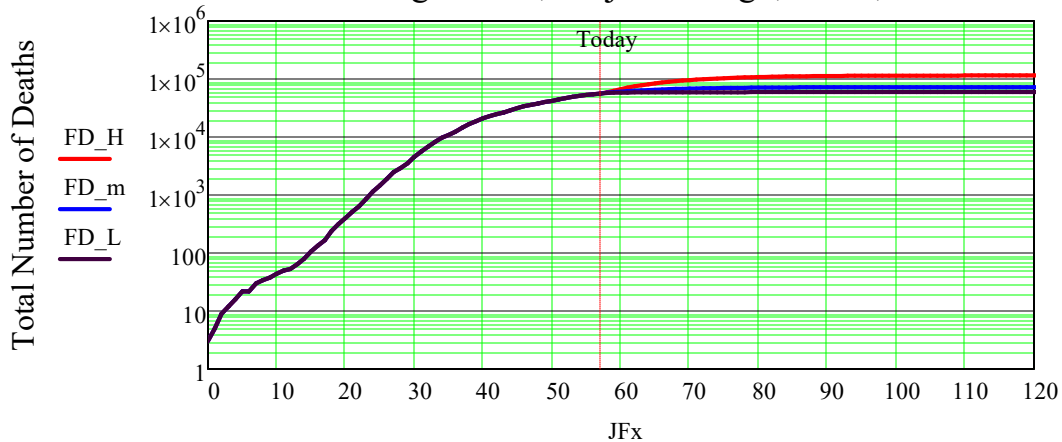
Deaths: High, Mean, Low



New Deaths & Smoothed



USA: Log Deaths, Projected High, Mean, Low



Number of Days from One Death

# Florida Data

Update New Cases from Bar Chart: <https://experience.arcgis.com/experience/96dd742462124fa0b38ddedb9b25e429>

**Read Data File:** `NCfs := READPRN("FL Cases 3-11 to 5-5.txt")` `Rc := rows(NCfs)` `Rc = 55` `NCfsRc-1 = 589`

`i := 1..Rc - 1` `j := 0..Rc - 1` `JFyj := ∑i=0j NCfsi` `JFxxj := j` `JFyRc-1 = 37760`

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

`ratei := 100 * (NCfsi / JFyi-1)` `rate := rate + 1` `rateavg := mean(rate) = 10.544`

### Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{rate_{avg}}{100}\right)}$$

**Days to Double:** `Dbl = 6.915`

`Dbl_Days(JFyRc-1, JFy0, Rc, 0) = 4.436`

## Exponential Growth ==> FL Epidemic

### Days to Number, N:

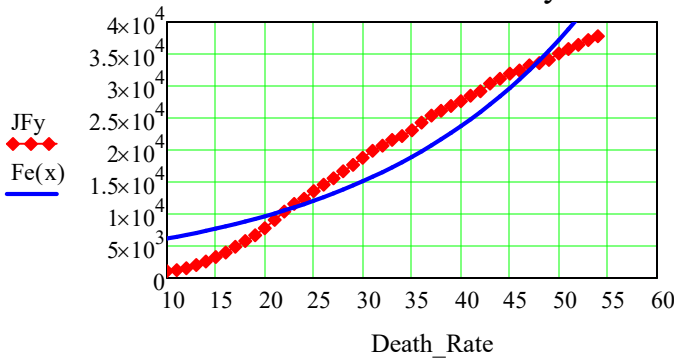
`gx := (100 0.3)T` `F(x, v, m) := v * em*x` `v = 3908.15` `m = 0.045`

`(v, m) := genfit(JFxx, JFy, gx, F)T` `R0 := m * 10 - 1 = -0.55`

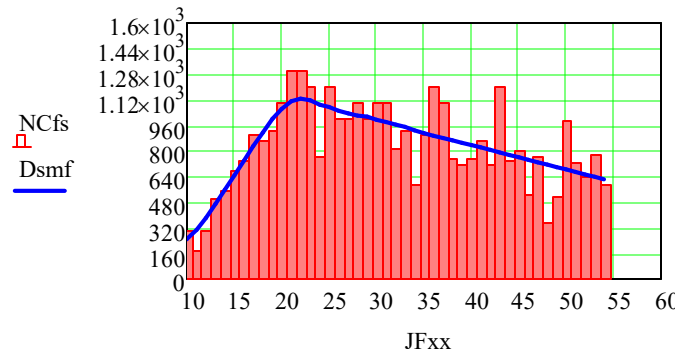
`Fe(x) := v * em*x` `dy(N) := ln(N/v) / m`

`Dsmf := supsmooth(JFxx, NCf)`

FL- Total Cases/Day



New Cases

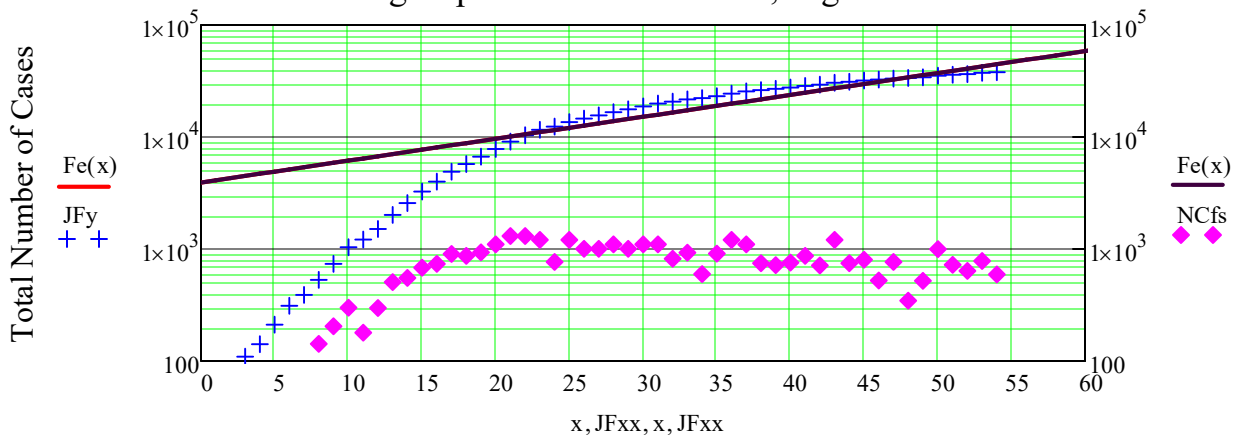


### FL Reproductive Ratio $R_{0L}$ :

`LM := log(JFy)` `slope(JFxx, LM) = 0.05`

`R0L(0.137, 10) = 2.37`

## FL: Left Log Exponential Fit & Cases, Right Linear Cases



Number of Days from Initial 100 Cases

# Florida Deaths: IHME Projection Mean, High, Low

IHME <https://covid19.healthdata.org/united-states-of-america/florida>

```

Read Data File:  FL_Deaths := READPRN("FL Deaths MLU Total MLU 3-14 to 4-27 to 6-25.txt")  Rc := rows(FL_Deaths)
FND_m := FL_Deaths<0>  Rc = 104  i := 1..Rc - 1  j := 0..Rc - 1  JFx_i := j  D_now := submatrix(FL_Deaths, 0, 33, 0, 0)
FD_m_j := sum_{i=0}^j FND_m_i  FD_L_j := sum_{i=0}^j FL_Deaths_{i,1}  FD_H_j := sum_{i=0}^j FL_Deaths_{i,2}  April 16:  sum D_now = 666
    
```

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

```

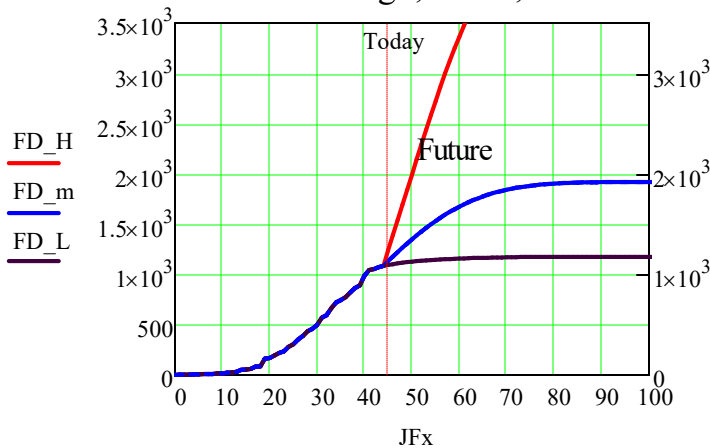
rate := 100 * FND_m_1 / FD_m_{i-1}  rate := rate + 1  rate_avg := mean(rate) = 8.009  Today := 45  JFx_j := j
    
```

## Deaths to Data and Range Projections

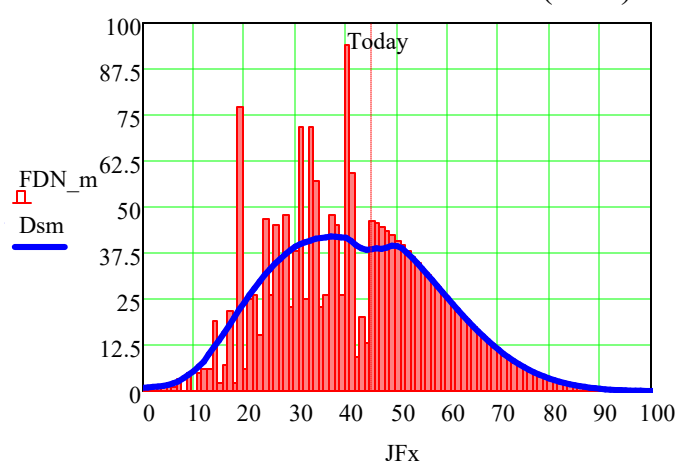
```

Dsm := supsmooth(JFx, FND_m)
    
```

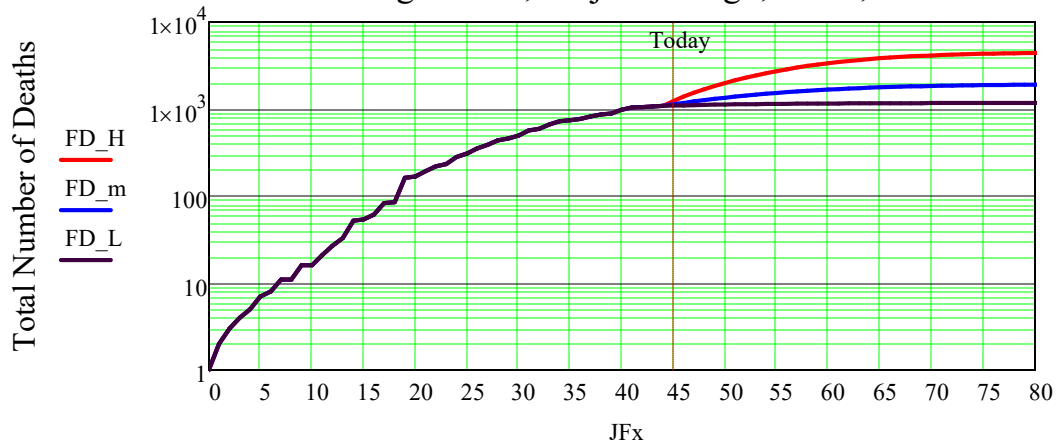
Deaths: High, Mean, Low



New Deaths & Smoothed (Blue)



FL: Log Deaths, Projected High, Mean, Low



Number of Days from One Death

# Lee County Florida Data - Download From Github

[https://github.com/CSSEGISandData/COVID-19/blob/master/csse\\_covid\\_19\\_data/csse\\_covid\\_19\\_time\\_series/time\\_series\\_covid19\\_confirmed\\_US.csv](https://github.com/CSSEGISandData/COVID-19/blob/master/csse_covid_19_data/csse_covid_19_time_series/time_series_covid19_confirmed_US.csv)

```

Read Data File:  JFy := READPRN("FL Lee County Total Cases to 5-6.txt")  Rc := rows(JFy)  JFyRc-1 = 1176
i := 1..Rc - 1  j := 0..Rc - 1  New_Casesi := JFyi - JFyi-1  NC := New_Cases  JFxxj := j  Rc = 61
    
```

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

```

ratei := 100 * (NCi / JFyi-1)  rate := rate + 1  rateavg := mean(rate) = 7.575
    
```

## Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{rate_{avg}}{100}\right)}$$

**Days to Double:** Dbl = 9.492

Dbl\_Days(JFy<sub>Rc-1</sub>, JFy<sub>0</sub>, Rc, 0) = 6.631

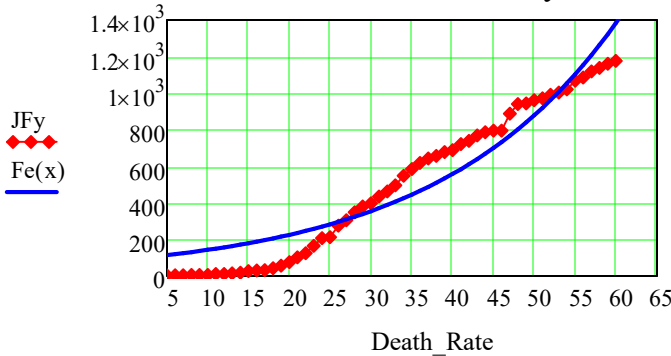
## Exponential Growth ==> FL Epidemic

## Days to Number, N:

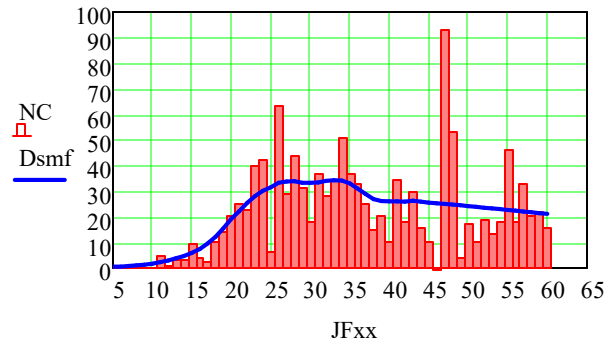
```

gx := (100 0.3)^T  F(x,v,m) := v * e^(m*x)  (v,m) := genfit(JFxx,JFy,gx,F)  Fe(x) := v * e^(m*x)  dy(N) := ln(N/v) / m
x := 0..100  v = 90.642  m = 0.045  R0max := m * 10 - 1 = -0.546  Dsmf := supsmooth(JFxx,NC)
    
```

FL- Total Cases/Day



Lee County New Cases

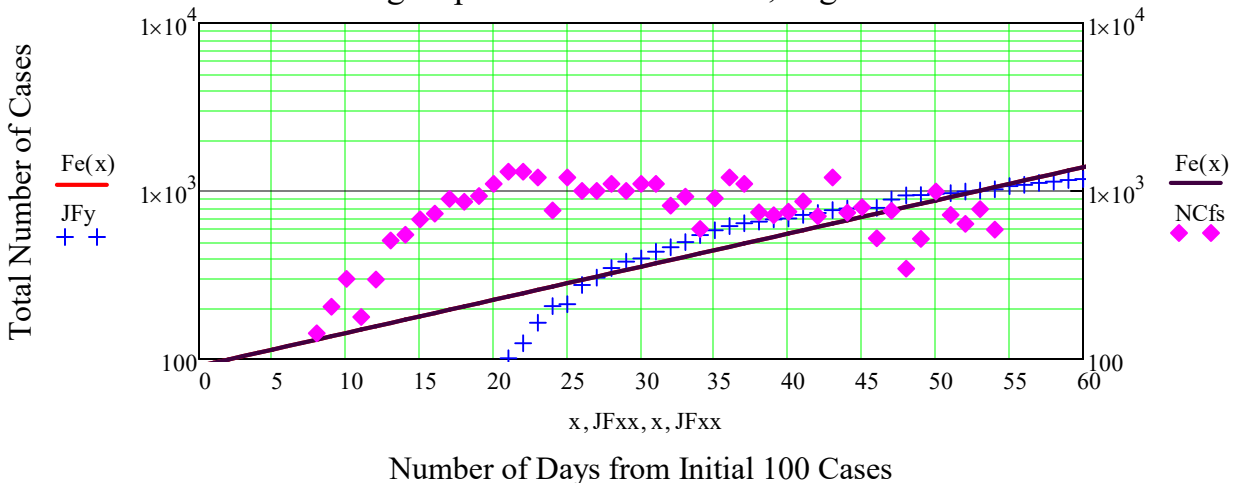


## FL Reproductive Ratio R<sub>OL</sub>:

```

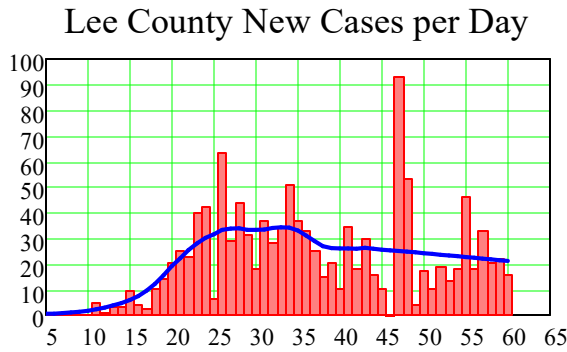
LM := log(JFy)  slope(JFxx,LM) = 0.051  R0L(0.137,10) = 2.37
    
```

FL: Left Log Exponential Fit & Cases, Right Linear Cases

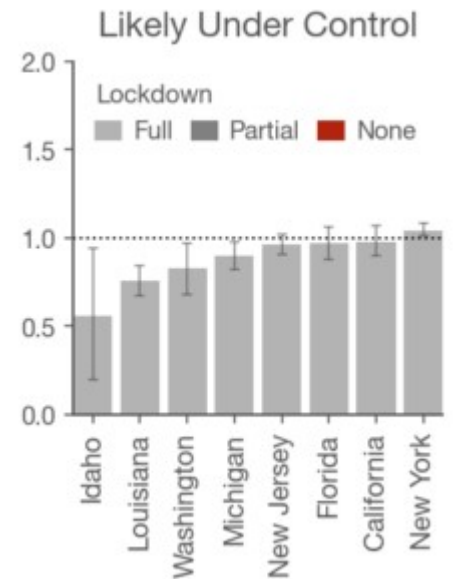


# Lee County, Cape Coral: Risk of Getting Infected

## Chance that any One person we meet in Lee County has COVID-19



**Florida R Values vs. Time**  
<http://system.com/topic/coronavirus/>



**Estimate People are Infectious for 14 Days**

$$N_{\text{Infectious}} := \sum_{n=0}^{13} NC_{Rc-n-1} = 382$$

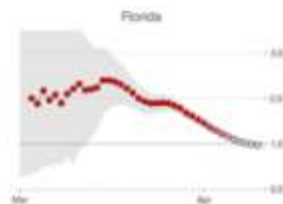
Dx is Factor for Confirmed vs Detected Infections

$$Lee\_Pop := 771 \cdot 10^3 \quad Prob_{LeeFL}(Dx) := \frac{N_{\text{Infectious}} \cdot Dx}{Lee\_Pop}$$

Probability Being Infected in Lee Co.

**Prob<sub>LeeFL</sub> = 1.0%**

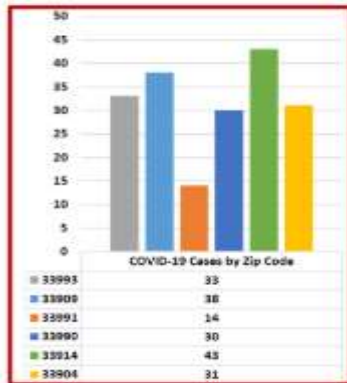
### R Numbers in FL



## Chance that any one person we meet in Zip 33991 has COVID-19

[https://www.capecoral.net/government/city\\_government/city\\_manager/covid-19\\_info/index.php](https://www.capecoral.net/government/city_government/city_manager/covid-19_info/index.php)

### Cape Coral Zip 33991 Number Cases



### Calculate Probability of Being Infected in Zip 33991

Pop in Zip in 33991: Pop<sub>Zip</sub> := 29075

$$Prob_{33991} := \frac{14}{Pop\_Zip}$$

**Prob<sub>33991</sub> = 0.048%**

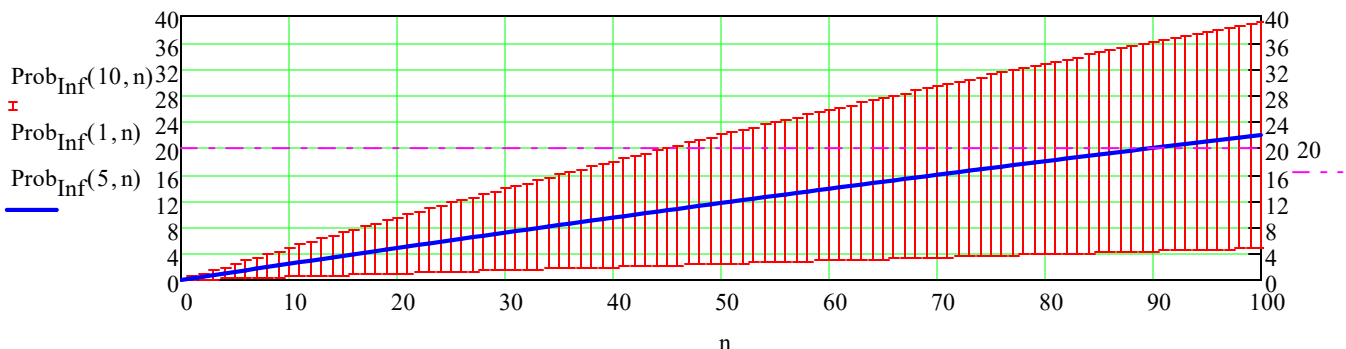
### Probability of Being Infected by Group of N People in Lee Co

Assumptions: Infectious for 14 Days, Dx is Range Confirmed vs. Actual Infected

$$Prob_{Inf}(Dx, N) := \left[ 1 - \left( 1 - Prob_{LeeFL}(Dx) \right)^N \right] \cdot 100$$

## Probability (%) of Getting Infected in a Group of N people in Lee County, FL

### Probability Spread (%) Becoming Infected vs. Number People in Group





# New Orleans Cases

[https://en.wikipedia.org/wiki/2020\\_coronavirus\\_pandemic\\_in\\_Louisiana](https://en.wikipedia.org/wiki/2020_coronavirus_pandemic_in_Louisiana)

NO := READPRN("New Orleans 3-10 to 4-1-2020.txt")      Cases := NO      JHy := Cases      Rc := rows(Cases)  
 Rc = 23    rows(Cases) = 23    p := 0..Rc - 1      i := 1..Rc - 1    dx\_p := p      rows(dx) = 23  
 New\_Cases\_i := Cases\_i - Cases\_{i-1}      Nc := New\_Cases      rows(New\_Cases) = 61

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

rate := 100 \*  $\frac{\text{New\_Cases}_1}{\text{Cases}_{1-1}}$       Cases\_{Rc-1} = 6424      rate := rate + 1      rate\_avg := mean(rate) = 11.498

### Calculate the Number of Days for Cases to Double - Dbl:

$$\text{Dbl} := \frac{\ln(2)}{\ln\left(1 + \frac{\text{rate\_avg}}{100}\right)}$$

**Days to Double:**      Dbl = 6.369

Dbl\_Days(JHy\_{Rc-1}, JHy\_0, Rc, 0) = 2.227

## Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

a := 1    k := 0.01    c := 1    guess := (a k c)^T    gx := (100 0.3)^T    F(x,v,m) := v \* e^{m\*x}    (v m) := genfit(dx, JHy, gx, F)^T

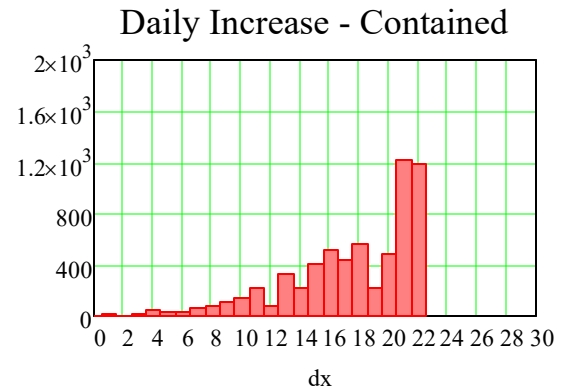
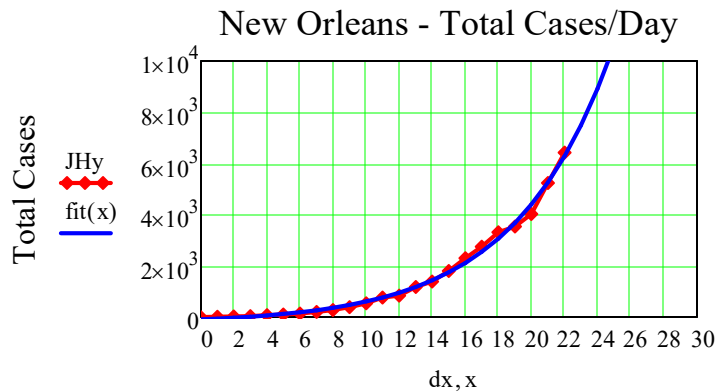
(a k c) := expfit(dx, JHy, guess)^T      (a k c) = (155.916 0.17 -244.651)^T      Fe(x) := v \* e^{m\*x}

fit(x) := a e^{k\*x} + c      m = 0.191      v = 96.221

**Pop of S Korea: 51.5 Million**

$$\frac{dy(N)}{m} := \frac{\ln\left(\frac{N}{v}\right)}{m}$$

R\_{0m} := m \* 10 - 1 = 0.908

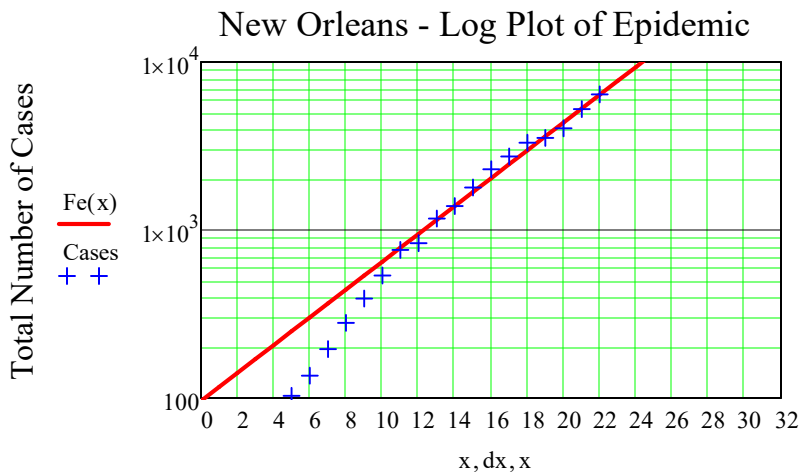


### SK Reproductive Ratio R\_{0L}:

$$\text{LM} := \log(\text{Cases})$$

slope(dx, LM) = 0.129

R\_{0L}(0.053, 10) = 1.53



# UK Data

<https://ourworldindata.org/coronavirus-source-data>

```
Cases := READPRN("UK Cases 3-1 to 4-19.txt")
Rc := rows(Cases)  j := 0..Rc - 1  JGy := Cases
Rc = 50  i := 1..Rc - 1  New_Cases_i := Cases_i - Cases_{i-1}  JGx_j := j  NCs := New_Cases
```

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

```
rate_i := 100 * (NCs_i / Cases_{i-1})
Cases_{Rc-1} = 1.142 * 10^5
rate := rate + 1
rate_avg := mean(rate) = 10.673
```

## Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{rate_{avg}}{100}\right)}$$

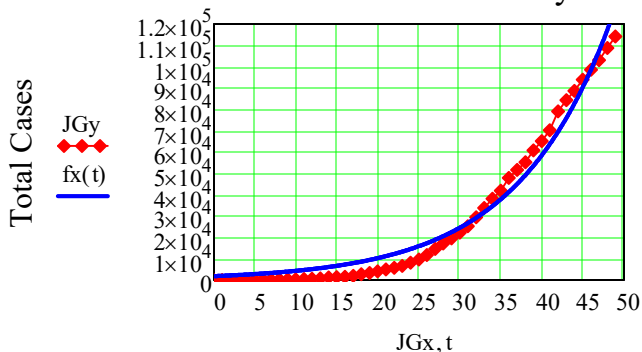
**Days to Double:** Dbl = 6.835

Dbl\_Days(JNy\_{Rc-1}, 100, Rc, 0) = ■

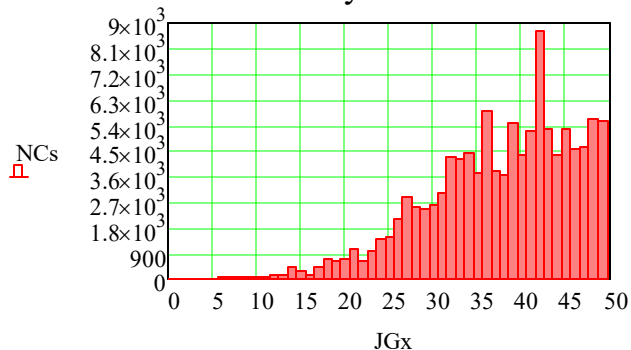
```
gx := (20 0.2)^T
F(x, v, m) := v * e^{m * x}
(v, m) := genfit(JGx, JGy, gx, F)
fx(t) := v * e^{m * t}
m = 0.087
R_{0L} := m * 10 - 1 = -0.13
```

## Exponential Growth ==> NY Epidemic

GB- Total Cases/Day



Daily Increase

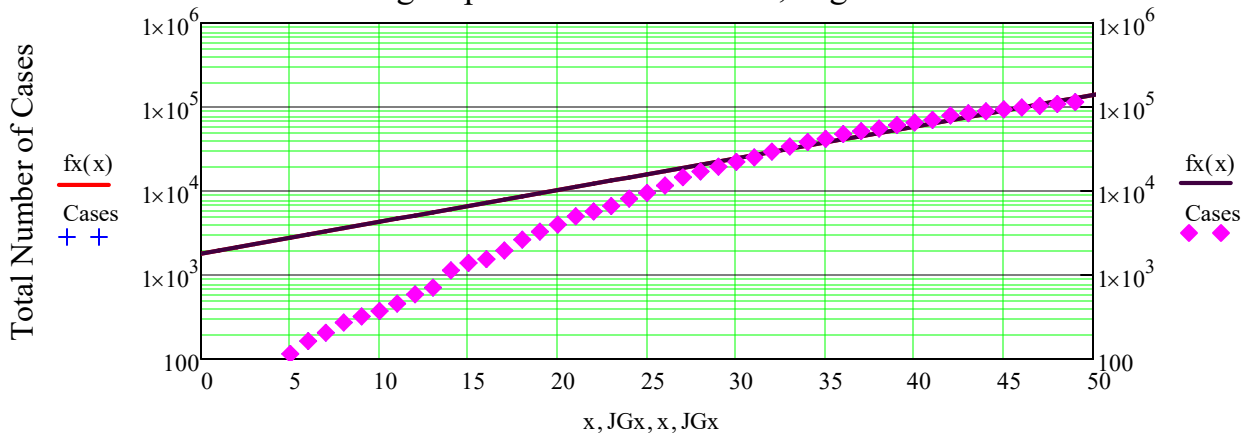


## GB Reproductive Ratio R\_{0L}:

```
LM := log(Cases)
slope(JGx, LM) = 0.075
```

R\_{0L}(0.106, 10) = 2.06

## GB: Left Log Exponential Fit & Cases, Right Linear Cases



Number of Days from Initial 100 Cases

# SEIRM Methodology: Estimate Outcome of the UK Epidemic

Our methodology is similar to most papers, the major difference is we use Mathcad's Error Minimization function Minerr, not Python, R, or MATLAB's Minimization Tool.

$$S_{0,x} := 66.4 \cdot 10^6 \cdot 0.8$$

**SEIRM Model**  $Mdl(\beta, \beta_m, t_e, N) := SEIRM\left(S_0, 23, \beta, \beta_m, t_e, 2, \frac{1}{6.8}, N\right)$   $Mod(\beta, \beta_m, t_e) := Mdl(\beta, \beta_m, t_e, 48)^{\langle 1 \rangle}$

$L := \frac{1}{6.8}$  **Initial Guess (SIRD Params):**  $(\beta, \beta_m, t_e) := (0.19, 0.063, 20)$

## Use Levenberg-Marquardt Method: Minimize Least Squares Error to Residual

Define a Residual to be the difference between the current data points HInf, HRec, HDed and SIRDModel

$$Residual(\beta, \beta_m, t_e) := JGy - Mod(\beta, \beta_m, t_e) \quad Rc = 50 \quad n := 0..Rc - 1 \quad rows(Mod(\beta, \beta_m, t_e)) = 50$$

### Condition to Minimize the Residual Least Squares Fit Error Using L-V Minerr Method

Given  $0 = Residual(\beta, \beta_m, t_e)$   $(b, \beta_m, t_e) := Minerr(\beta, \beta_m, t_e)^T$   $(b, \beta_m, t_e) = (0.734, 0.273, 26.176)$

$$\frac{ERR}{R} = 1109.846$$

$$R_{0,x} := \frac{b}{L} = 4.989$$

$$R_{0,x} := \frac{\beta_m}{L} = 1.857$$

## Extracted Parameters of GB COVID-19 Epidemic

### Imax, Calculate Days to Double, D2X and Fit Power Function to USA JH Data

$$ex := 1.4 \quad FitPwr(ex, t) := JGy_0 \cdot ex^t$$

ResidJG<sub>2</sub>(ex) := JGy - FitPwr(ex, JGx) **Given**  $0 = ResidJG_2(ex)$   $Ex := Minerr(ex)$   $Ex = 1.198$

### Fit JHy with a Power Function, PWR(t):

$$Pwr(t) := JGy_0 \cdot Ex^t$$

$$D2X(Ex) := \frac{\ln(2)}{\ln(Ex)}$$

$$D2X(Ex) = 3.843$$

$$Dbl\_Days(9415, 100, 15, 0) = 2.288$$

$$100 \cdot 2^{\frac{16}{2.309}} = 12188.753$$

The number of days it takes infections to double,  $t_{2x}$

$$t_{2x} := \frac{1}{b} \quad t_{2x} = 1.363$$

$$b = 0.734$$

The number of days it takes to recover,  $t_{rec}$

$$\gamma = 0.063 \quad t_{rec} := \frac{1}{L} \quad t_{rec} = 6.8$$

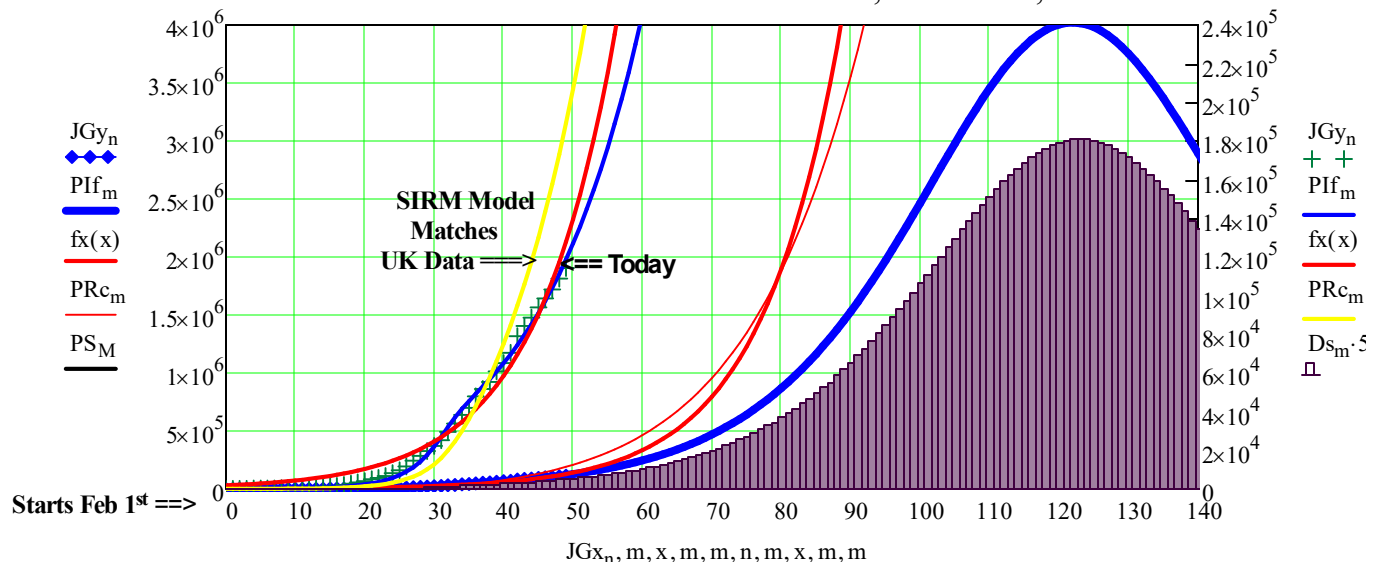
$$R_{0,x} := \frac{b}{L + \delta} = 4.825$$

Proj := Mdl(b,  $\beta_m$ ,  $t_e$ , 140)  $Pif := Proj^{\langle 1 \rangle}$   $PRc := Proj^{\langle 2 \rangle}$   $PS := Proj^{\langle 0 \rangle}$   $Ds := Proj^{\langle 3 \rangle}$   $max(Ds) = 36178.301$

$R_{0,x} := rows(Pif) = 142$   $m := 0..R_p - 1$   $Tot\_Deaths := \sum Ds$   $Tot\_Deaths = 1.681 \times 10^6$   $max(Pif) = 4.02 \times 10^6$

## SEIRM Mitigation Scenario: Reasonably Good Match to UK Cases to Date

UK: Infection Cases vs. SEIRM Model Sus, Infections, and Rec



# Italy COVID19 Cases

## Growth Data and Curve Fit for WHO COVID-19: Total Cases in Italy

Source: CDC Data for Total Number of World Cases Reported to WHO (Virus is called (SARS-CoV-2))

[https://en.wikipedia.org/wiki/Template:2019%E2%80%9320\\_coronavirus\\_outbreak\\_data/WHO\\_situation\\_reports](https://en.wikipedia.org/wiki/Template:2019%E2%80%9320_coronavirus_outbreak_data/WHO_situation_reports)

<https://www.statista.com/statistics/1101680/coronavirus-cases-development-italy/>

Read Data File: WCases := READPRN("Italy COVID-19 Feb 21 to April 11 2020 Totals.txt") JIy := WCases

Rc := rows(WCases) Rc = 52 i := 1..Rc - 1 k := 0..Rc - 1 days<sub>i</sub> := i rows(WCases) = 52 rows(days) = 58

WCases<sub>Rc-1</sub> = 1.523 × 10<sup>5</sup> Calculate the Rate of Growth of Cases and Find Average WCases<sub>0</sub> = 3  
 NCs<sub>i</sub> := WCases<sub>i</sub> - WCases<sub>i-1</sub> New\_Cases := NCs

rate<sub>i</sub> := 100 \* (NCs<sub>i</sub> / WCases<sub>i-1</sub>) WCases<sub>Rc-1</sub> = 1.523 × 10<sup>5</sup> rate := rate + 1 rate<sub>avg</sub> := mean(rate) = 14.861

Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{\text{rate}_{avg}}{100}\right)}$$

Days to Double: Dbl = 5.003

Using Exp Dble Fn Method:

$$F_n = N_0 \cdot e^{t} \quad \text{Days}_{double} = \bullet$$

Exponential Growth ==> Italy Epidemic

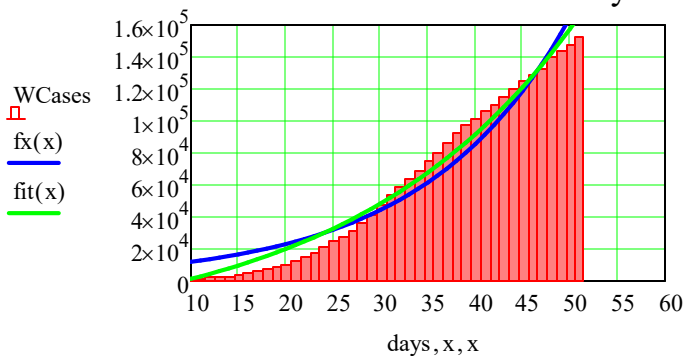
k := 0..Rc - 1 Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

dz<sub>k</sub> := k gx := (100 0.3)<sup>T</sup> F(x, v, m) := v · e<sup>m·x</sup> (v m) := genfit(dz, WCases, gx, F)<sup>T</sup> fx(d) := v · e<sup>m·d</sup>

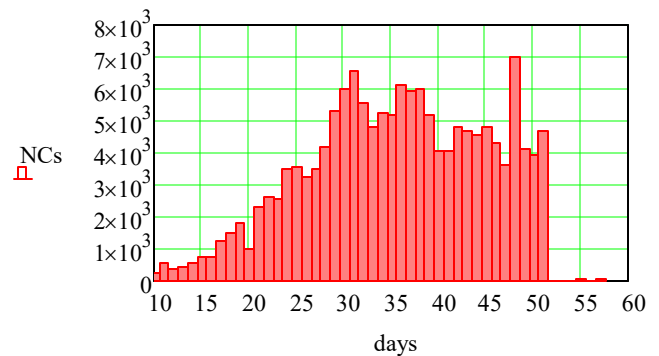
(a k c) := expfit(dz, WCases, guess)<sup>T</sup> (a k c) = (23369.425 0.042 -34277.269) fit(x) := a e<sup>k·x</sup> + c

Note: the large increase day 25 is because of a change in reporting from laboratory confirmed to all confirmed.

Total Number of Cases/Day

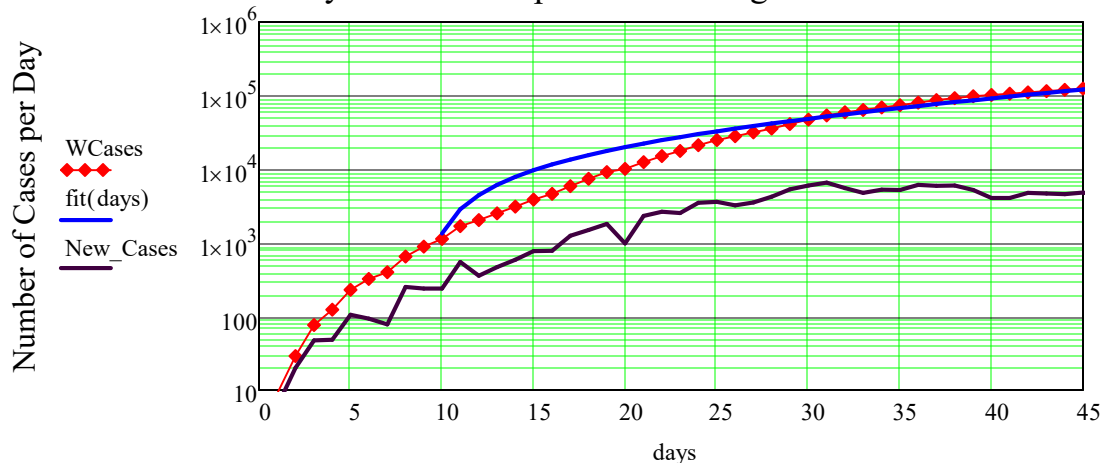


New Cases



Italy- Cases & Exp Fit - Lin&Log Scale & New Cases

$$R_{0m} := m \cdot 10 - 1 = -0.344$$



$$Dbl\_Days(JIy_{Rc-1}, JIy_0, Rc, 0) = 3.327$$

Italy Reproductive Ratio  $R_{0L}$ :

$$LW := \log(WCases)$$

slope(days, LW) = ■

$$R_{0L}(0.04, 10) = 1.4$$

# Spain COVID19 Cases and Deaths

## Growth Data and Curve Fit for WHO COVID-19: Total Cases in Spain

Source: CDC Data for Total Number of World Cases Reported to WHO (Virus is called (SARS-CoV-2))

Read Data File: <https://ourworldindata.org/coronavirus-source-data>

$WCases := READPRN("Spain COVID-19 Feb 26 to April 23 CasesTotNew Deaths TN.txt")$        $JSy := WCases$  <sup>(0)</sup>  
 $Rc := rows(WCases)$      $Rc = 58$      $i := 1..Rc - 1$      $k := 0..Rc - 1$      $dz_k := k$      $rows(JSy) = 58$      $WC := JSy$      $daqs_k := k$   
 $JSy_{Rc-1} = 2.084 \times 10^5$       **Calculate the Rate of Growth of Cases and Find Average**       $rows(daqs) = 58$

$New\_Cases_i := WC_i - WC_{i-1}$        $NCs := New\_Cases$   
 $rate_i := 100 \frac{New\_Cases_i}{WC_{i-1}}$        $WC_{Rc-1} = 2.084 \times 10^5$        $rate := rate + 1$        $rate_{avg} := mean(rate) = 13.605$

**Calculate the Number of Days for Cases to Double - Dbl:**

$Dbl\_Days(JSy_{Rc-1}, JSy_0, Rc, 0) = 3.903$

$$Dbl := \frac{\ln(2)}{\ln\left(1 + \frac{rate_{avg}}{100}\right)}$$

**Rate Days to Double:**       $Dbl = 5.434$

**Using Exp Dble Fn Method:**

$$Fn = N_0 \cdot e^t \quad \text{Days}_{double} = \blacksquare$$

### Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

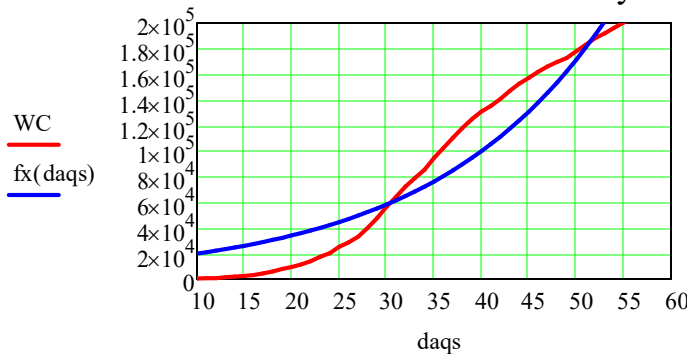
$gx := (100 \ 0.3)^T$      $F(x, v, m) := v \cdot e^{m \cdot x}$      $(v \ m) := genfit(dz, WC, gx, F)^T$      $(v \ m) = (11516.074 \ 0.05)$      $fx(t) := v \cdot e^{m \cdot t}$   
 $(a \ k \ c) := expfit(dz, WC, guess)^T$      $(a \ k \ c) = (63344.264 \ 0.028 \ -84304.2)$      $fit(x) := a e^{k \cdot x} + c$

### Exponential Growth ==> Spain Epidemic

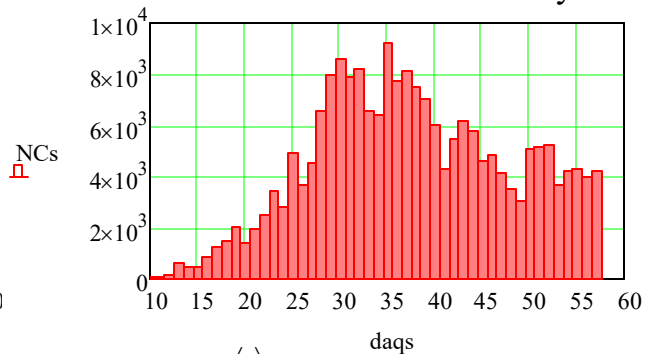
$$R_{0max} := m \cdot 10 - 1 = -0.46$$

Note: the large increase day 25 is because of a change in reporting from laboratory confirmed to all confirmed.

Total Number of Cases/Day

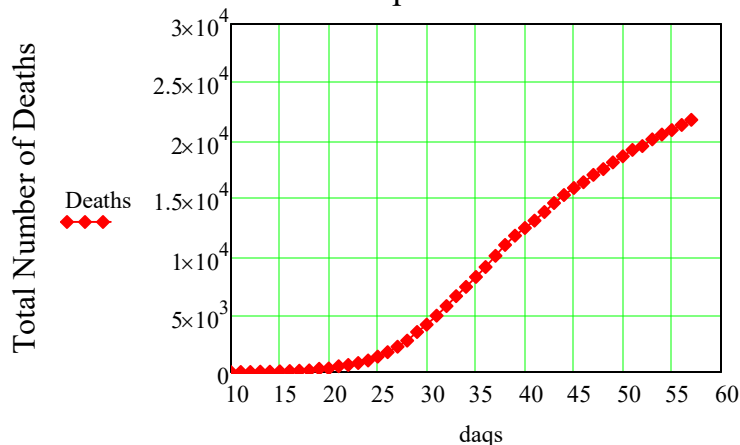


Number New Cases Daily



Deaths := WCases <sup>(2)</sup>

Spain- Deaths



**Spain Reproductive Ratio  $R_{0L}$ :**

$$LW := \log(WC)$$

$slope(daqs, LW) = 0.072$

$$R_{0L}(0.04, 10) = 1.4$$

# S Korea J. Hopkins Feb 20 - April 7: Quenched

```
JH_SK := READPRN("JHU S Korea Inf 2-20 to 4-7 - Cols.txt")  JHy := JH_SK
Cases := JHy  Rj := rows(Cases) = 48  p := 0..Rj - 1  Rc := rows(Cases)  Rc = 48  i := 1..Rc - 1
New_Cases_i := Cases_i - Cases_{i-1}  JKx_p := p  days_i := i  rows(Cases) = 48  rows(days) = 58
```

## Calculate the Rate of Growth of Cases, Find Average Rate, and Days to Double from Avg. Rate

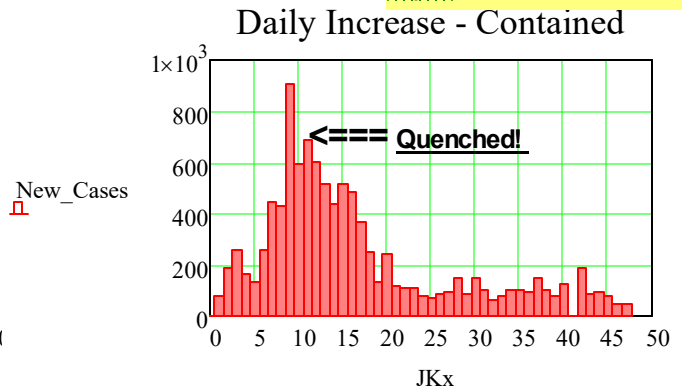
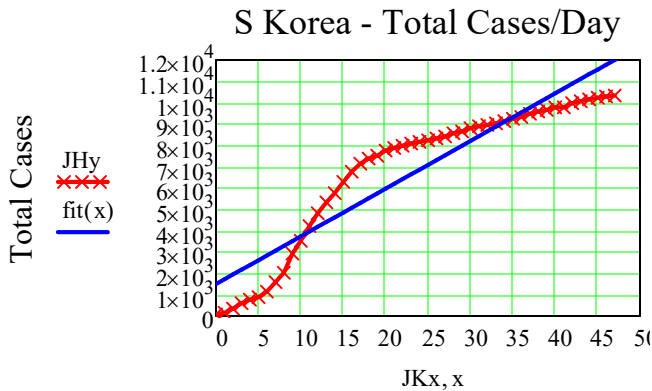
```
rate := 100 * (New_Cases_1 / Cases_{1-1})  Cases_{Rc-1} = 10331  JHy_0 = 80  rate := rate + 1  rate_avg := mean(rate) = 9.803
```

## Calculate the Number of Days for Cases to Double - Dbl:

```
Dbl := ln(2) / ln(1 + rate_avg / 100)  Days to Double: Dbl = 7.412
Dbl_Days(JHy_{Rc-1}, JHy_0, Rc, 0) = 6.845
```

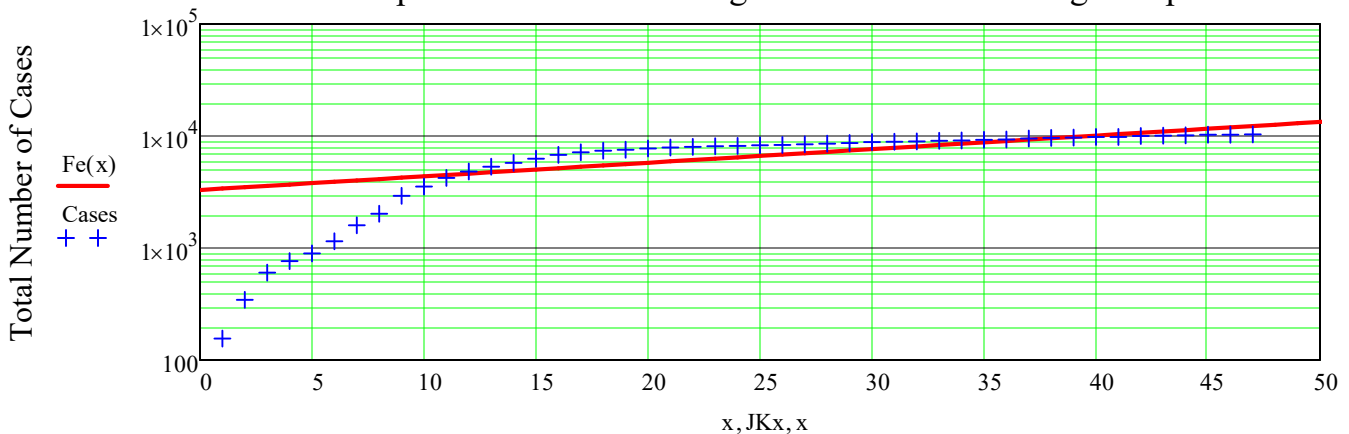
## Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

```
a := 1  k := 0.01  c := 1  guess := (a k c)^T  gx := (100 0.3)^T  Fe(x, v, m) := v * e^{m * x}  (v, m) := genfit(JKx, JHy, gx, Fe)^T
(a k c) := expfit(JKx, JHy, guess)^T  (a k c) = (2.99 * 10^9 7.477 * 10^{-1} Fe(x) := v * e^{m * x}
fit(x) := a * e^{k * x} + c  v = 3298.003  Pop of S Korea: 51.5 Million  dv(N) := ln(N/v) / m
R_0 := m * 10 - 1 = -0.72
```



```
SK Reproductive Ratio R_0L: LM := log(Cases)  slope(JKx, LM) = 0.028  R_0L(0.053, 10) = 1.53
```

## S. Korea - Epidemic Contained: Log shows this is NO Longer Exponential





# Methodology to Extract Mitigation Parameters for S. Korea

S. Korea Applied Mitigation to Contain their COVID -19 Epidemic. Model their Mitigation.

**SEIRM Model**  $Mdl(\beta, \beta_m, N) := SEIRM\left(52 \cdot 10^6, 80, \beta, \beta_m, 3, 3.8, \frac{1}{7}, N\right)$   $Mod(\beta, \beta_m) := Mdl(\beta, \beta_m, 46)^{\langle 1 \rangle}$

**Initial Guess (SIRD Params):**  $(\beta, \beta_m) := (0.4, 0.3)$   $S\gamma M(S_0, I_0, \beta, \beta_{mit}, t_{el}, z, \gamma, N)$

## Use Quasi-Newton Method: Minimize Least Squares Error

$$LSQFit = \sqrt{\sum (JHy - Model(\beta, \gamma))^2}$$

## Use Levenberg-Marquardt Method: Minimize Least Squares Error to Residual

Define a Residual to be the difference between the current data points JHy and SIRM Model

$$Residual(\beta, \beta_m) := JHy - Mod(\beta, \beta_m) \quad R := rows(JHy) \quad R = 48$$

### Condition to Minimize the Residual Least Squares Fit Error Using L-V Minerr Method

Given  $0 = Residual(\beta, \beta_m) \quad 0.1 \leq \beta \leq 0.4 \quad 0.01 \leq \beta_m \leq 0.3$

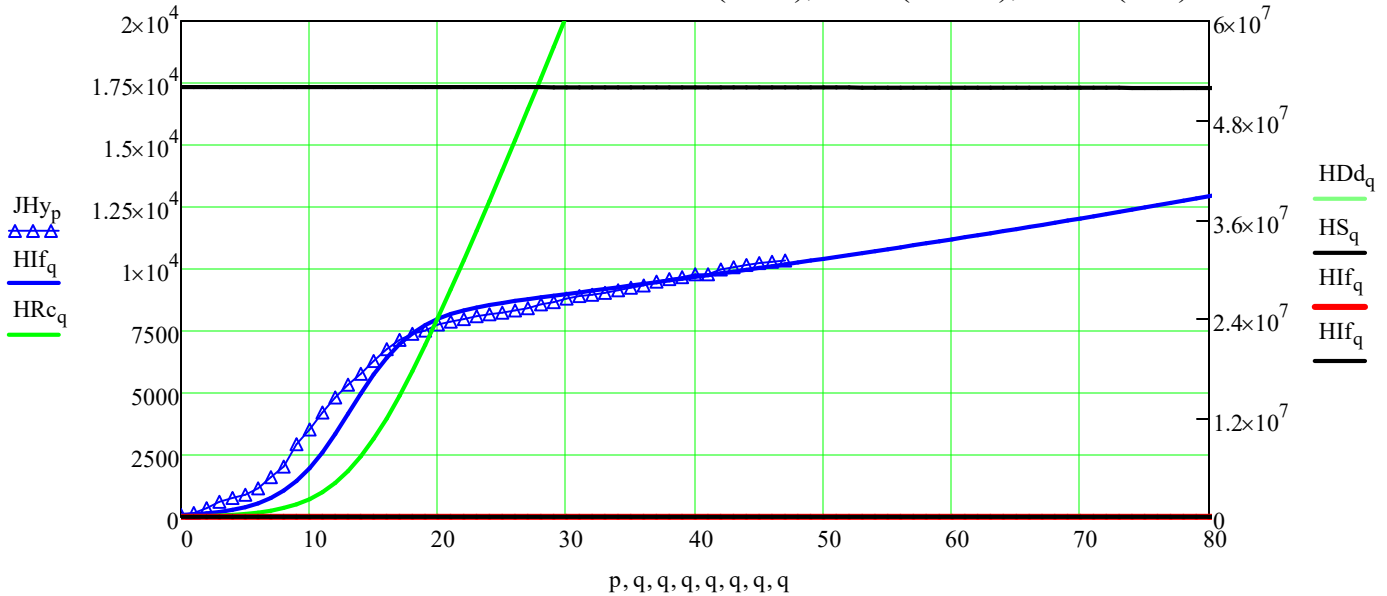
**Use Minerr to Extract Optimal Parameters:**  $(b, \beta_m) := Minerr(\beta, \beta_m)^T \quad (b, \beta_m) = (1.248, 0.163)$

Infected  $Hif := Mdl(b, \beta_m, 140)^{\langle 1 \rangle} \quad HRc := Mdl(b, \beta_m, 140)^{\langle 2 \rangle} \quad HD := Mdl(b, \beta_m, 140)^{\langle 3 \rangle} \quad \frac{ERR}{R} = 83.623$

$HS := Mdl(b, \beta_m, 140)^{\langle 0 \rangle} \quad R_{ppv} := rows(Hif) = 142 \quad \max(HD) = 177.473$

## Good Match of SEIRM Mitigation Model (Symbols) to Data (Dots)

Model vs Data - S. Korea: Infected (Blue), Rec. (Green), Dead (Blk)



## Extracted Parameters of South Korea COVID-19 Epidemic

The number of days it takes infections to double,  $t_{2x}$   $t_{2x} := \frac{1}{b}$   $t_{2x} = 0.801$   $\delta := 0.005$

The number of days it takes to recover,  $t_{rec}$   $t_{rec} := \frac{1}{L}$   $t_{rec} = 6.8$

Basic Reproductive Ratio before and after Intervention:  $R_0 := \frac{b}{L + \gamma}$   $R_{0\delta} := \frac{b}{L + \gamma}$   $R_0 = 5.94$   $R_{0\delta} = 5.94$

# World COVID19 Cases

## Growth Data and Curve Fit for WHO COVID-19: Total Cases in World

Source: CDC Data for Total Number of World Cases Reported to WHO (Virus is called (SARS-CoV-2))

[https://en.wikipedia.org/wiki/Template:2019%E2%80%9320\\_coronavirus\\_outbreak\\_data/WHO\\_situation\\_reports](https://en.wikipedia.org/wiki/Template:2019%E2%80%9320_coronavirus_outbreak_data/WHO_situation_reports)

Read Data File:  $WCases := READPRN("World COVID-19 Feb 1 to April 7 2020 Totals.txt")$  JWY := WCases

$Rc := rows(WCases)$   $Rc = 67$   $i := 1..Rc - 1$   $days_i := i$   $rows(WCases) = 67$   $rows(days) = 67$

### Calculate the Rate of Growth of Cases and Find Average and Days to Double from Average Rate

$WC := WCases$   $WC_{Rc-1} = 1.317 \times 10^6$   $New\_Cases_i := WCases_i - WCases_{i-1}$   $NewC := New\_Cases$   
 $rate := 100 \frac{New\_Cases_i}{WCases_{i-1}}$   $WCases_{51} = 3.381 \times 10^5$   $rate := rate + 1$   $rate_{avg} := mean(rate) = 8.83$

### Calculate the Number of Days for Cases to Double - Dbl:

$$Dbl := \ln(2) \cdot \left( \ln \left( 1 + \frac{rate_{avg}}{100} \right) \right)^{-1}$$

Days to Double: Dbl = 7.412

$$Dbl\_Days(JWY_{Rc-1}, JWY_0, Rc, 0) = 9.875$$

### Calculate Number of Days to Double (D2X) and Fit Power Function to World Data

$FPr(ex, t) := WC_0 \cdot ex^t$   $ResW(ex) := WC - FPr(ex, days)$  Given  $0 = ResW(ex)$   $Ex := Minerr(ex)$   $D2X(Ex) = 9.825$

### Exponential Growth ==> World Epidemic

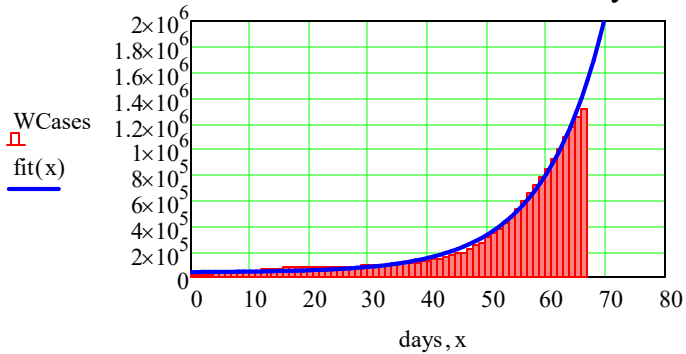
$$R_0 := Ex \cdot 10 - 1 = 9.731$$

### Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

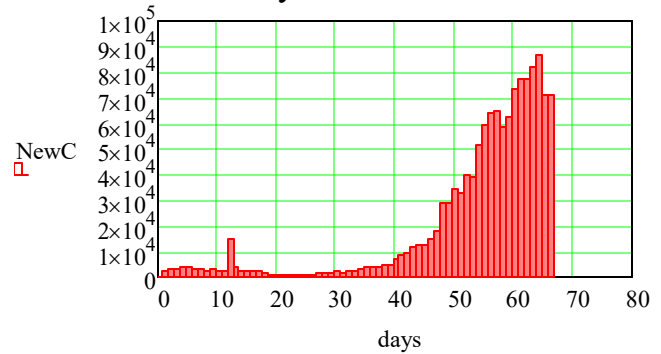
$(a \ k \ c) := \text{expfit}(days, WCases, guess)^T$   $(a \ k \ c) = (2420.678 \ 0.096 \ 36065.512)$   $fit(x) := a e^{k \cdot x} + c$

Note: the large increase day 25 is because of a change in reporting from laboratory confirmed to all confirmed.

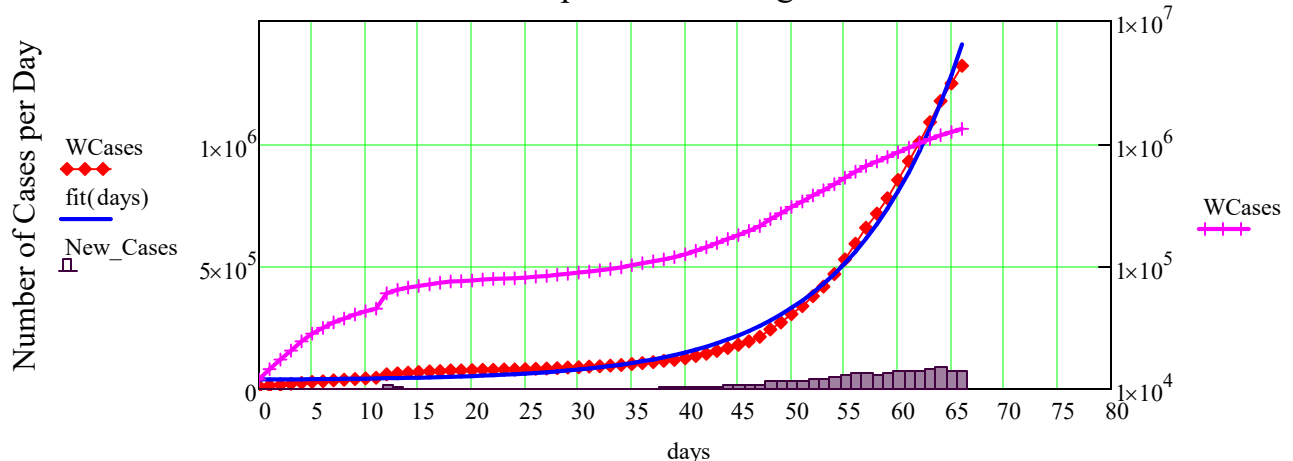
Total Number of Cases/Day



Daily % Rate of Growth



World- Cases & Exp Fit - Lin&Log Scale & New Cases



### World Reproductive Ratio $R_{0L}$ :

$$LW := \log(WCases)$$

$$\text{slope}(days, LW) = 0.025$$

$$R_{0L}(0.04, 10) = 1.4$$

# Deaths: World, Fr, Ge, It, South Korea, Sp, Sw, UK, USA

## Compare Deaths per Capita: USA Lower than Europe

Source: <https://ourworldindata.org/coronavirus-source-data>

**Order of Data:** World France Germany Italy South Korea Spain Sweden United Kingdom USA

Deaths := READPRN("Deaths World FR GE IT SK Sp UK US SW Feb 22 to April 19.txt")

Pop\_Millions := (7580 66.9 83.7 60.4 52 46.728 10.2 66.48 327)<sup>T</sup> w := 0..8

$R_c := \text{rows}(\text{Deaths}) \quad R_c = 58 \quad i := 1..R_c - 1$   $\text{Total\_Deaths}^{(w)} := \sum \text{Deaths}^{(w)}$

Total\_Deaths =  $(2.2 \times 10^6 \quad 2.398 \times 10^5 \quad 47386 \quad 4.488 \times 10^5 \quad 6542 \quad 3.247 \times 10^5 \quad 15129 \quad 1.636 \times 10^5 \quad 3.627 \times 10^5)$

**Deaths per Million, DpM:**  $\text{DpM}^{(w)} := \frac{\text{Deaths}^{(w)}}{\text{Pop\_Millions}_w}$

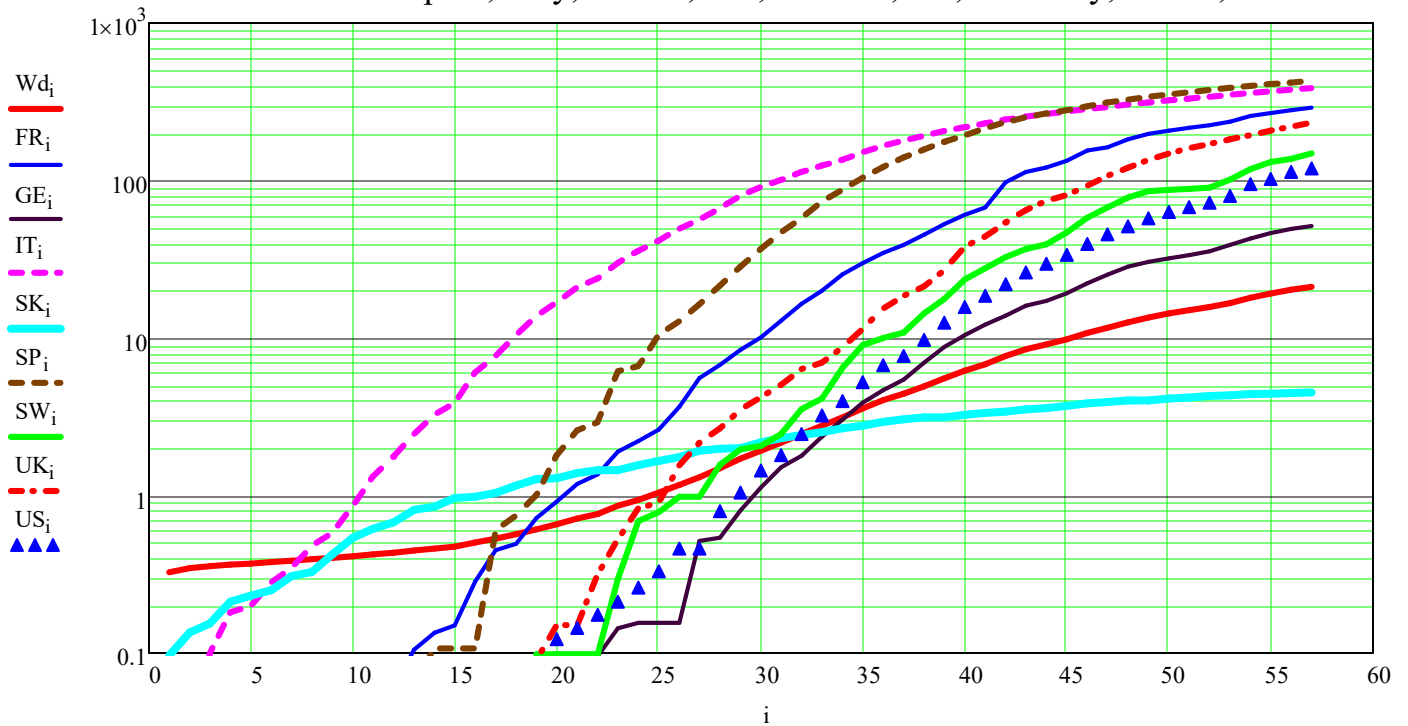
Wd := DpM<sup>(0)</sup> FR := DpM<sup>(1)</sup> GE := DpM<sup>(2)</sup> IT := DpM<sup>(3)</sup> SK := DpM<sup>(4)</sup>

SP := DpM<sup>(5)</sup> SW := DpM<sup>(6)</sup> UK := DpM<sup>(7)</sup> US := DpM<sup>(8)</sup>

## Deaths per Million in Order of Largest to Smallest

Spain, Italy, France, UK, Sweden, US, Germany, World, S. Korea

Deaths/Million: Spain, Italy, France, UK, Sweden, US, Germany, World, S.Korea



Number of Days from February 22

**The Order of the First Appearance of Deaths:** World, South Korea, Italy, France, Spain, UK, US, SW, GE

# World COVID19 Deaths

WD := READPRN("World Deaths OWD Feb 1 to April 30.txt")      R<sub>c</sub> := rows(WD)      i := 1..R<sub>c</sub> - 1

NewD<sub>i</sub> := WD<sub>i</sub> - WD<sub>i-1</sub>      **WD<sub>R<sub>c</sub>-1</sub> = 2.271 × 10<sup>5</sup>**      WCases := WD      JW<sub>y</sub> := WCases      days<sub>i</sub> := i

## Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

(a k c) := expfit(days, WD, guess)<sup>T</sup>      (a k c) = (2970.068 0.05 -10282.265)      fit(x) := a e<sup>k·x</sup> + c

## Calculate the Rate of Growth of Cases and Find Average and Days to Double from Average Rate

WC := WCases      New\_Cases<sub>i</sub> := WCases<sub>i</sub> - WCases<sub>i-1</sub>      NewC := New\_Cases  
 rate := 100  $\frac{\text{New\_Cases}_i}{\text{WCases}_{i-1}}$       WCases<sub>51</sub> = 14603      rate := rate + 1      rate<sub>avg</sub> := mean(rate) = 9.527

## Calculate the Number of Days for Cases to Double - Dbl:

Dbl := ln(2) ·  $\left( \ln \left( 1 + \frac{\text{rate}_{\text{avg}}}{100} \right) \right)^{-1}$       **Days to Double: Dbl = 8.192**  
 Dbl\_Days(JW<sub>y<sub>R<sub>c</sub>-1</sub></sub>, JW<sub>y<sub>0</sub></sub>, R<sub>c</sub>, 0) = 9.206

## Calculate Number of Days to Double (D2X) and Fit Power Function to World Data

FPr(ex, t) := WC<sub>0</sub> · ex<sup>t</sup>      ResW(ex) := WC - FPr(ex, days)      Given 0 = ResW(ex)      Ex := Minerr(ex)      **D2X(Ex) = 8.781**

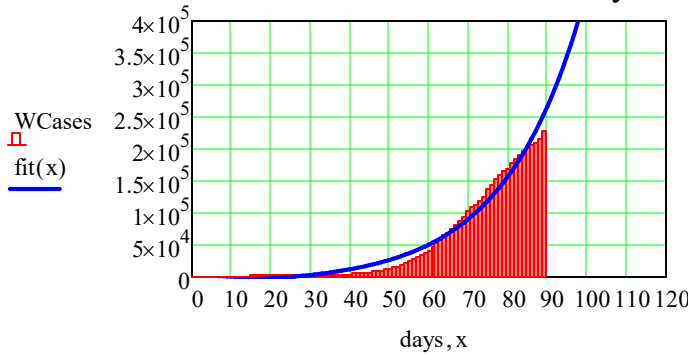
## Exponential Growth ==> World Epidemic

**R<sub>0</sub> := Ex · 10 - 1 = 9.821**

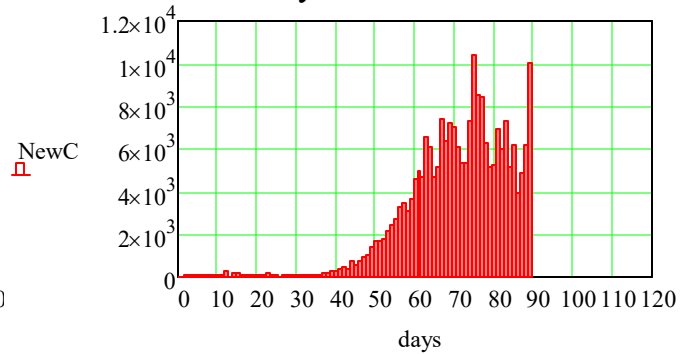
## Calculate Parameters for Exponential Fit, fit(x), to Total Number of Cases

(a k c) := expfit(days, WCases, guess)<sup>T</sup>      (a k c) = (2970.068 0.05 -10282.265)      fit(x) := a e<sup>k·x</sup> + c

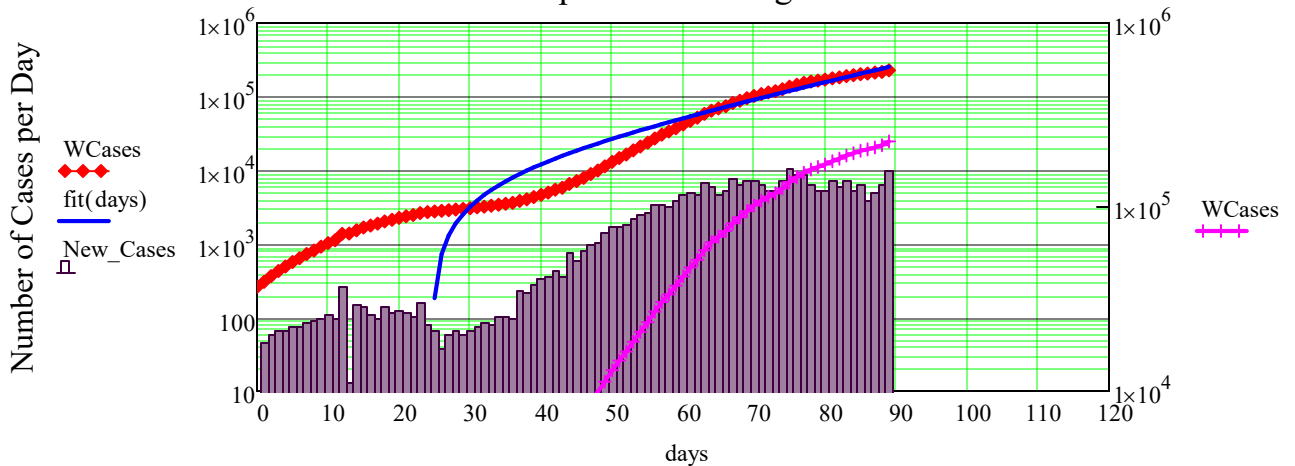
Total Number of Cases/Day



Daily % Rate of Growth



World- Cases & Exp Fit - Lin&Log Scale & New Cases



# Computational Tools - Computer Algebra Systems

This work started with the goal of understanding and predicting the dynamics of the COVID-19 disease. Implementing this goal has required use of some foundational concepts and Mathematical Tools.

## Foundational Concepts and Mathematical Tools

- ◆ Goal: Model Biological Transmission, Immune System, and Compartmental Population Dynamics
- ◆ Analyzing Dynamics Requires Non Linear Differential Equations, NLDE
- ◆ Delayed Differential Equations, DDE, are a great model for COVID-19's incubation and latent properties
- ◆ Recently, the Mathematics of Neural Networks to expands understanding Emergent Properties of Systems
- ◆ Classical (Newtonian) Analytic Methods work well only for idealized systems, e.g. Planetary Motion
- ◆ Most curves/dynamics are not analytic and thus not tractable with Analytic Ordinary Differential Equations
- ◆ Population Dynamics for infectious disease transmission are fundamentally Statistical/Stochastic processes
- ◆ Analysis of these systems requires a Twentieth-Century Math Approach, TCMA
- ◆ Twentieth-Century Approach employs Numeric Computer Solution Methods, such as Euler's Method
- ◆ Software is the foundational component in Computer Methods
- ◆ I started this work with the Engineering Computational Algebra Software, **Mathcad, as the Modeling Tool**
- ◆ Mathcad could not implement Delayed Differential Equations or some of the Stochastic Methods
- ◆ Had to investigate other tools: Mathematica, MatLab, R, Python, Maple
- ◆ Mathematica is Symbolic and has great horsepower, but it is a little too temperamental for my taste
- ◆ MatLab is more of an Engineering Matrix Approach and could require expensive additional Math Packages
- ◆ R has the statistical packages, but its front end and graphing are limited.
- ◆ Python is a programming/text language, not primarily Symbolic or Mathematical. Attention to details is tedious.
- ◆ Maple, while not ideal for my purposes, has the required horsepower, such as DDE Solving Capability.
- ◆ Maple's Computation Engine uses more of a Mathematical, Symbolic Programming approach than Mathcad.

## Retooling at Mid-Course

This work was started with, and is documented with Mathcad.

However, some of the later computational work, such as DDEs were done with Maple 2020. After solving DDE models in Maple, the form of the Mathematical Model and results of the calculations were then transferred to Mathcad for plot presentation and documentation.

## Limitations of Least Squares Parameter Extraction Method

Does not assume any error distribution

Assumes that parameter extraction does not depend on the order of infections

Assumes positive and negative deviations are equivalent

Number of new cases at different times is probably not independent

Cannot give any statistical information

It is better to use a Statistical Maximum Log-Likelihood Method

## Calculate R0

Number of secondary infectives per primary infective **per generation**  $1/\gamma$ .

$$R_0 = \frac{\beta N}{\gamma}$$

## Notes

*Discrete epidemic models with arbitrary stage distributions and applications to disease control.*

GDM: SEQIHR Model - Q: Quarateened, Not Inf, H=Isolated

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