

**EN-625.664.81.SP21 COMPUTATIONAL STATISTICS**

**COURSE PROJECT**

# **SIR Epidemiology Model in a Homogeneous Population by Adaptive Markov Chain Monte Carlo (MCMC)**

**By Ricca Callis**

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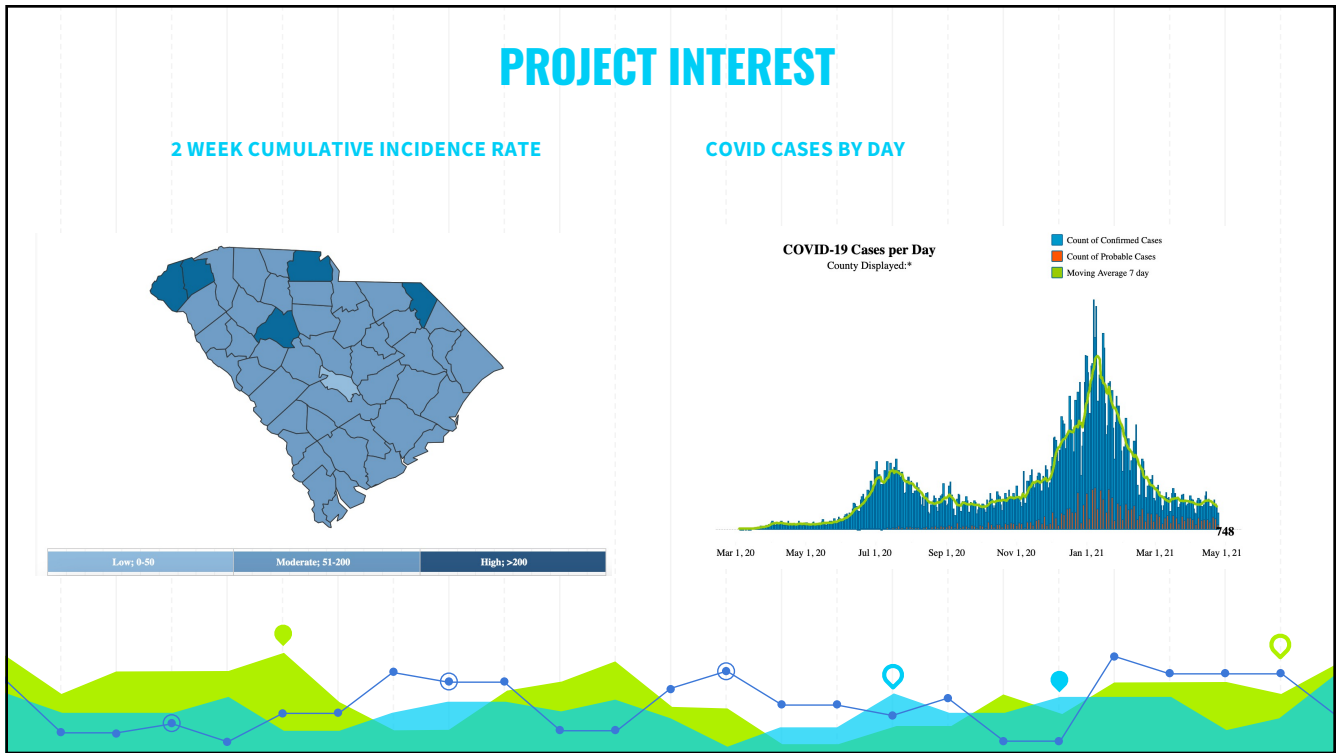
# **HELLO!**



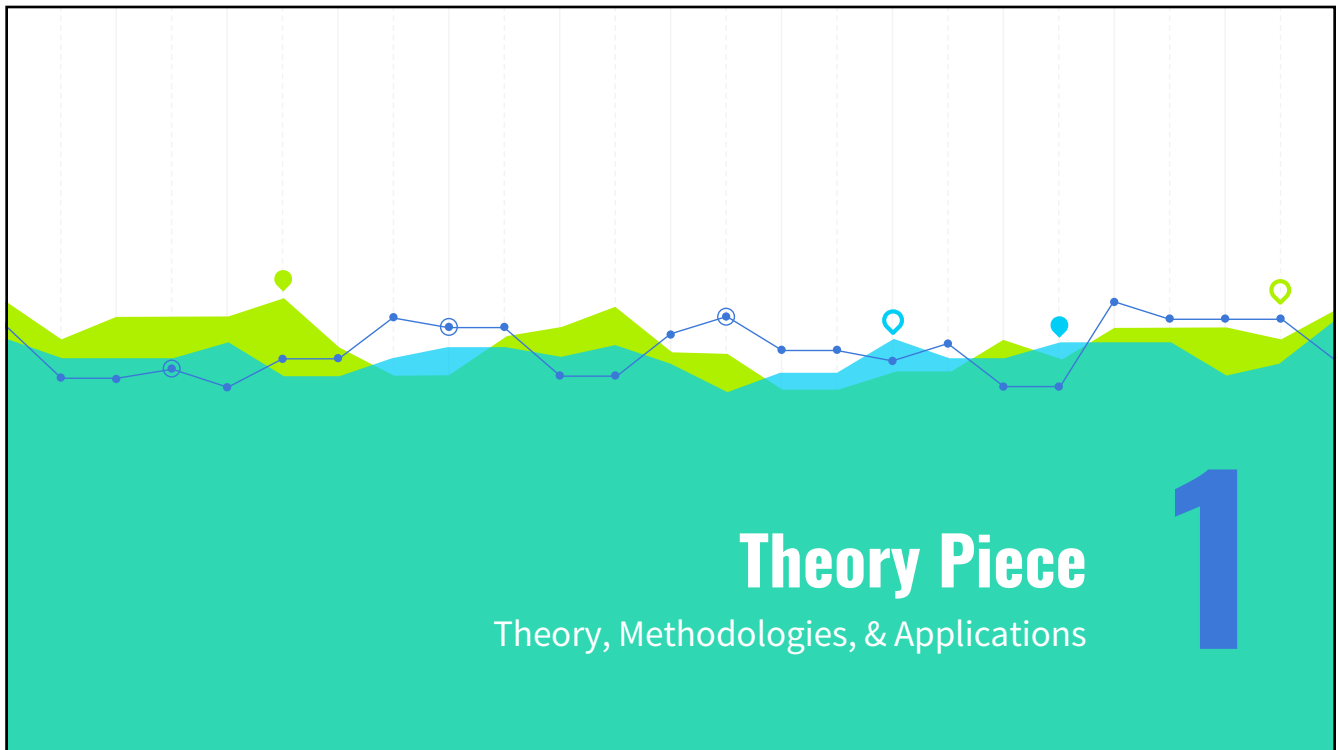
## **I am Ricca Callis**

Managing BMH COVID-19 Vaccine Clinic & Mobile Testing Unit  
has inspired this course project

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## COMPARTMENTAL MODEL FRAMEWORK

- **Model:** Differential equations of dynamic systems
- **Compartment:**
  - Abstract entity representing the quality of interest
  - Equivalent to a system state
  - Visually conceptualized as a box
  - Internally homogeneous
- **Compartment Interactions:** Through a set of rate equations
  - Visually conceptualized by arrows between compartments
- **Net Flow Into a Compartment:** A set of first order linear or nonlinear equations

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## COMPARTMENTAL MODEL FRAMEWORK

For an  $n$  compartment system,

- **Compartment/state variables**  $\mathbf{x}(t) = [x_1(t), \dots, x_n(t)]^T$
- **State-space model:**

$$\dot{\mathbf{x}}(t) = \mathbf{f}(\mathbf{x}(t), \mathbf{w}(t); \boldsymbol{\theta}(t), t)$$

$$\mathbf{y}(t) = \mathbf{g}(\mathbf{x}(t); \boldsymbol{\theta}(t), t) + \mathbf{v}(t)$$

- where,

$\mathbf{f}(\cdot)$  is the state dynamics function corresponding to the compartmental model

$\mathbf{w}(t) = [w_1(t), \dots, w_1(t)]^T$  is the external system inputs

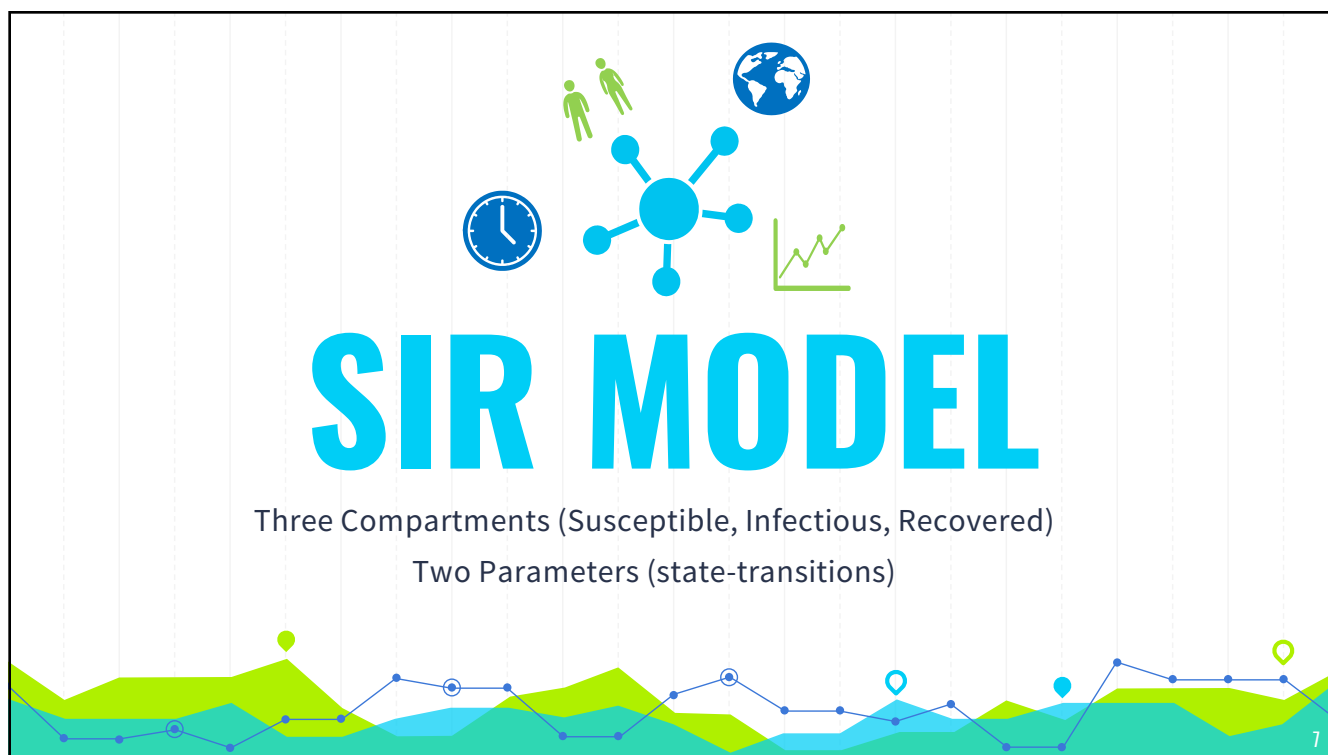
$\mathbf{y}(t) = [y_1(t), \dots, y_m(t)]^T$  is the vector of observable model invariables (i.e., outputs)

$\mathbf{g}(\cdot)$  is the function that maps state variables to observations (measurements)

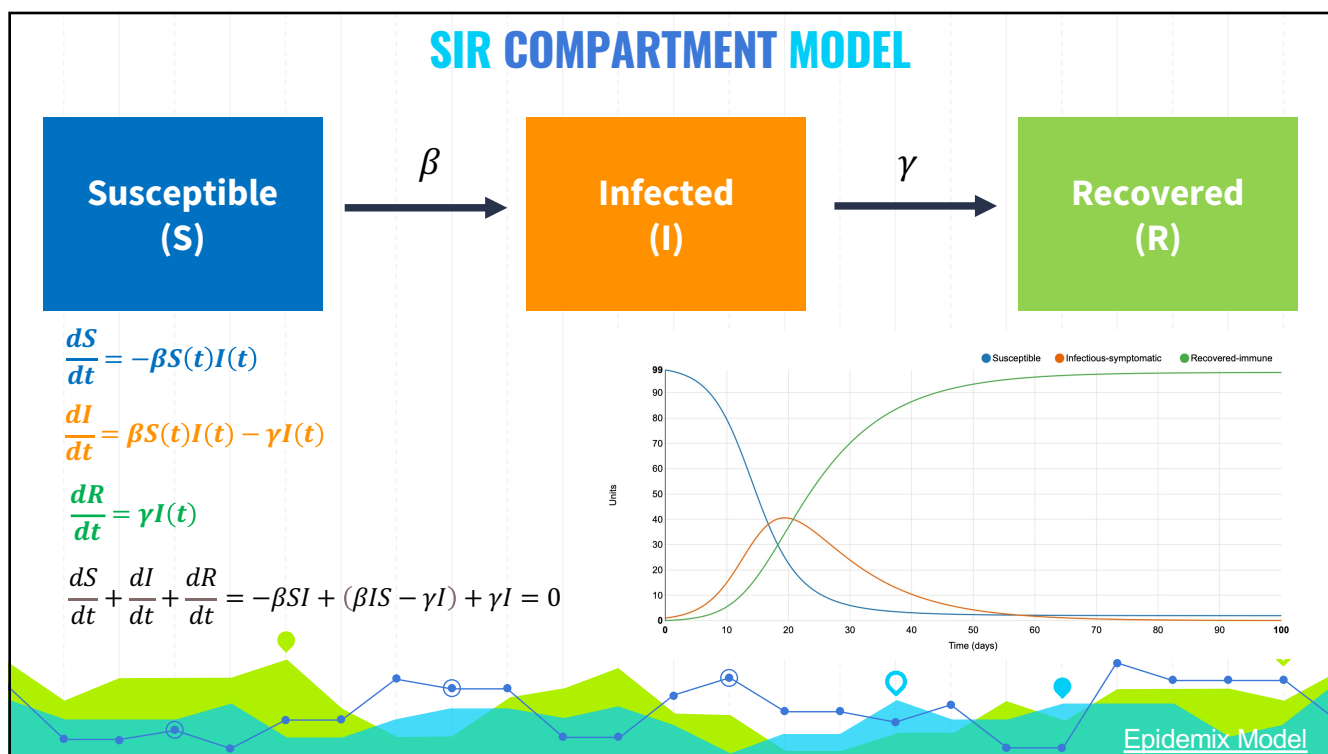
$\mathbf{v}(t) = [v_1(t), \dots, v_m(t)]^T$  is the vector of measurement error

$\boldsymbol{\theta}(t) = [\theta_1(t), \dots, \theta_p(t)]^T$  is the vector of model parameters to be set or identified

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## SIR MODEL PARAMETERS

### ● $\beta$ : Transmission parameter

- Depends on effective contact per unit of time
- Most important parameter, but difficult to estimate directly
- Can be estimated if we assume individuals mix randomly:  $\beta = \frac{R_0}{ND}$  (where  $D$  is duration of infectiousness)

### ● $R_0$ : Reproductive number

- A measure of how infectious the disease is
- The average number of new infected individuals caused by one infectious individual.
- Can be estimated by fitting model predictions to observed data:  $R_0 = \frac{\beta S_0}{\gamma}$  (where  $S_0$  is the initial number of susceptible individuals)



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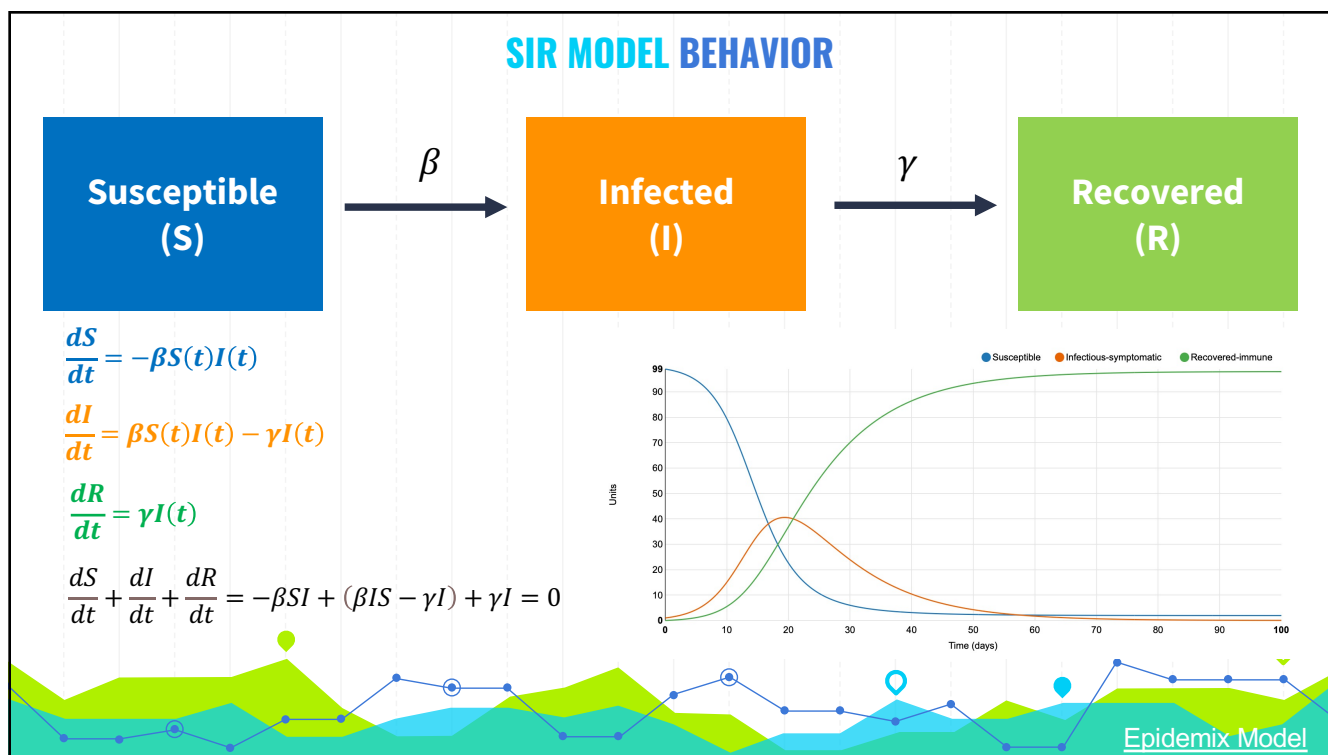
## SIR MODEL BEHAVIOR

### ● $R_0$ : Reproductive number

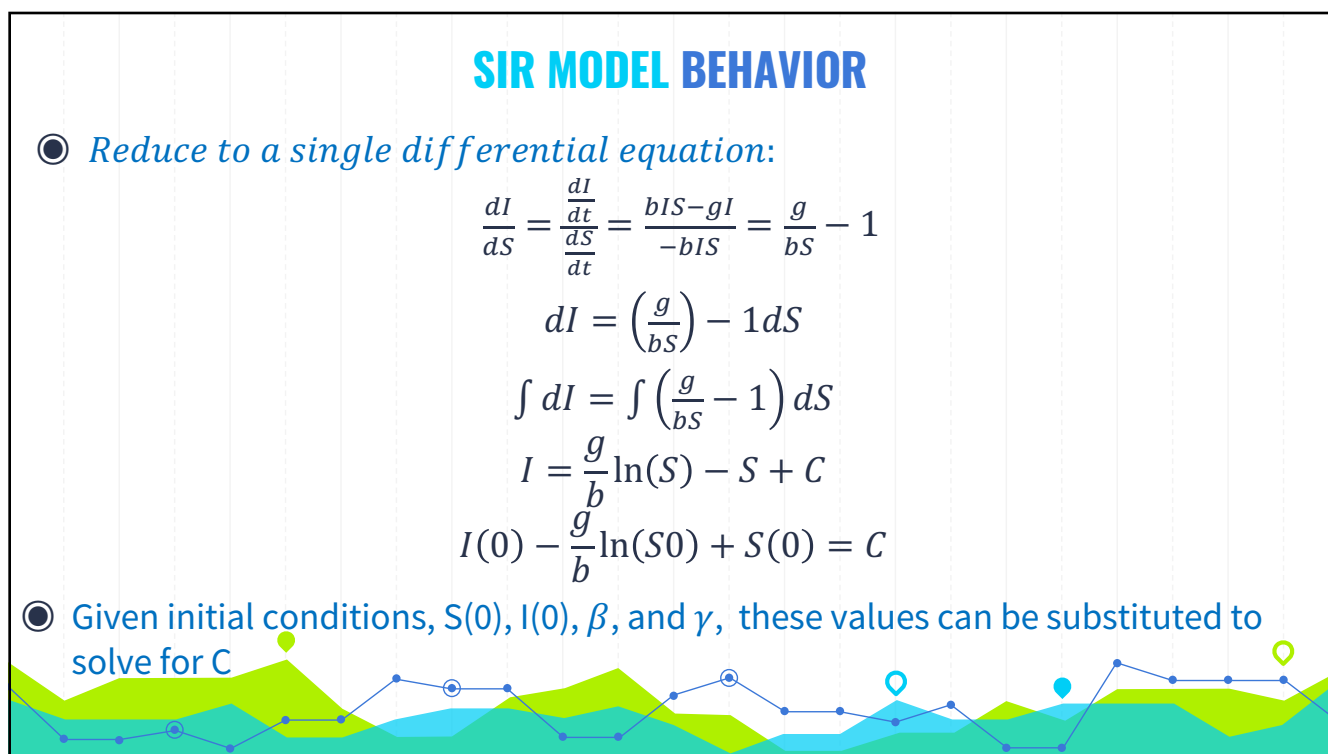
- clearly affected by both transmission ( $\beta$ ) and recovery ( $\gamma$ ) rates.
- When  $R_0 > 1$ , the occurrence of the disease will increase.
  - Here,  $I(t)$  increases, reaches a maximum, and then decreases to zero as  $t \rightarrow \infty$ .
- When  $R_0 < 1$ , the occurrence of the disease will decrease and eventually die out.
  - Here,  $I(t)$  decreases monotonically to zero as  $t \rightarrow \infty$ .
- However, when  $R_0 = 1$ , the disease occurrence will remain constant.
- We can see that values of  $R_0$  close to 1 produce very slow-growing epidemics, while values of  $R_0$  much greater than one produce fast, explosive epidemics.



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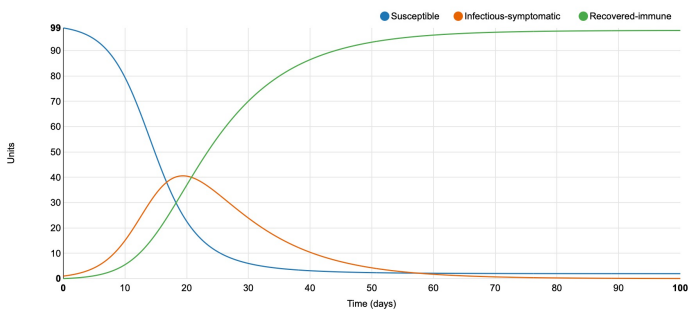


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## SIR MODEL BEHAVIOR

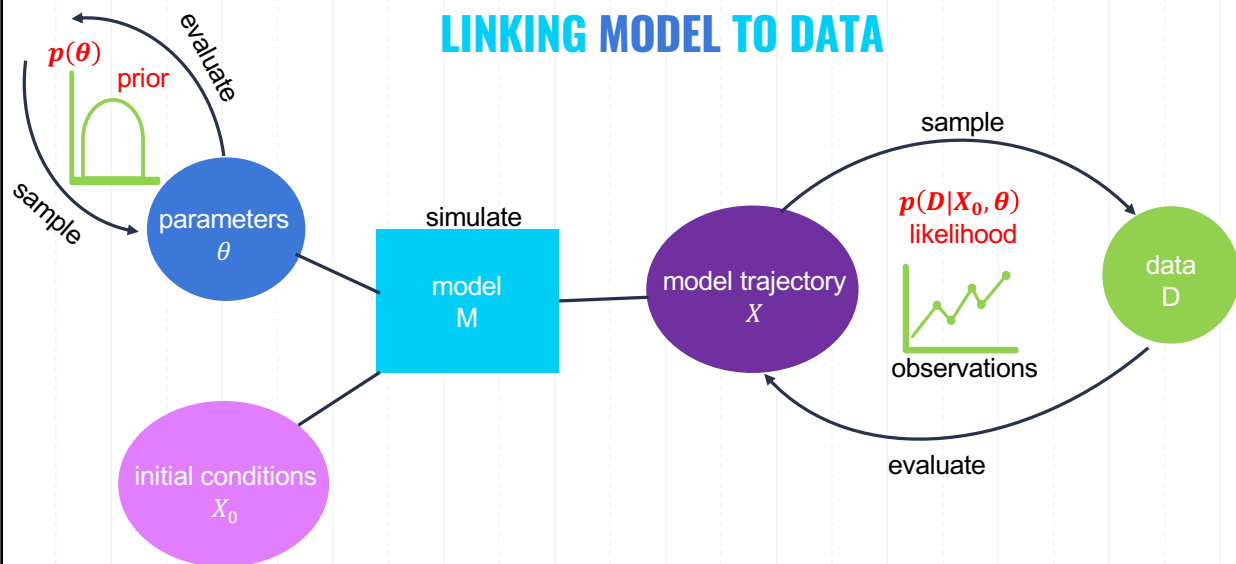
### How the compartmentalized groups will act as $t \rightarrow \infty$

- Susceptible group will decrease over time and approach 0
- Recovered group will increase and approach population size (N)
- The rate of change for the infected group depends on  $\beta$ ,  $\gamma$ , and  $S(t)$ .
  - When  $\beta S(t)$  is less than  $\gamma$ : the rate of change for the infected group is negative.
  - When  $\beta S(t)$  is greater than  $\gamma$ : the rate of change for the infected group is positive.
  - When  $\beta S(t)$  is equal to  $\gamma$ : the rate of change for the infected/infectious group is zero.
- The disease always dies out



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## LINKING MODEL TO DATA



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## BAYESIAN INFERENCE

- Calculate the posterior  $p(\theta|data)$ 
  - Inherent uncertainty in parameters
  - Posterior is the probability distribution of a random variable  $\theta$
- Bayes' Rule  $p(\theta|data) = \frac{p(data|\theta)p(\theta)}{p(data)}$ 
  - $p(\theta|data)$  is the posterior
  - $p(data|\theta)$  is the likelihood
  - $p(\theta)$  is the prior
  - $p(data)$  is the normalization constant
- i.e.,  $(posterior) \propto (normalization\ likelihood) \cdot (prior)$

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## BAYESIAN INFERENCE

- Expectation Values
  - Parameter(s)  $\theta$  are interpreted as a random variable, distributed according to the posterior:  $p(\theta|data) \propto p(data|\theta)p(\theta)$
  - We want to generate **samples** of  $\theta$  from this distribution
  - To calculate the expected value of any quantity, given the data, we integrate over  $p(\theta)$ :  $E[A] = \int p(\theta|data)X(\theta)d\theta$
  - E.g., for SIR model, if we know  $p(\beta, \gamma)$ , we can calculate the expected value of  $R_0$ :  $E[R_0] = \int p(\beta, \gamma|data) \frac{\beta}{\gamma} d\beta d\gamma$

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## BAYESIAN INFERENCE

### ● Sample Approximation

- How do we find an expression for  $p(\beta, \gamma | \text{data})$ ?
- Monte-Carlo approximation:

$$\int f(x)p(x)dx \approx \sum_x p(x)f(x)$$

- Or, draw N samples from  $p(x)$  and calculate

$$\int f(x)p(x)dx \approx \frac{1}{N} \sum_{x \sim p(x)} f(x)$$

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## MARKOV CHAIN MONTE CARLO

A chain of samples where each proposed  $\theta^*$  depends on the previous one

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## MARKOV CHAIN MONTE CARLO (MCMC)

- **Markov chain:** stochastic sequence of states in which the next state depends only upon the current state  $\theta_{t+1} \sim \mathbb{D}(\theta_t)$
- **Algorithms generates a sequence of parameter values**  $\theta_1, \theta_2, \dots$ , whose empirical distribution, approaches the posterior distribution.
- The generation of the vectors in the **chain**, is done by random numbers (Monte Carlo) in such way that each new point may only depend on the previous point (Markov chain).
  - The chain is used as if it is a sample from the posterior.
- **Metropolis-Hastings Algorithm:** a particular way of using MCMC to sample from a distribution

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## METROPOLIS-HASTINGS ALGORITHM

- Generate a Markov chain with a transition density

$$p(\theta, \theta^*) = q(\theta, \theta^*)\alpha(\theta, \theta^*), \theta \neq \theta^*$$

$$p(\theta, \theta) = 1 - \int q(\theta, \theta^*)\alpha(\theta, \theta^*)d\theta$$

For some proposal density  $q$  and for acceptance probability  $\alpha$

- The chain is reversible IFF

$$f(\theta)q(\theta, \theta^*)\alpha(\theta, \theta^*) = f(\theta^*)q(\theta^*, \theta)\alpha(\theta^*, \theta)$$

- Thus, we choose  $\alpha$  as

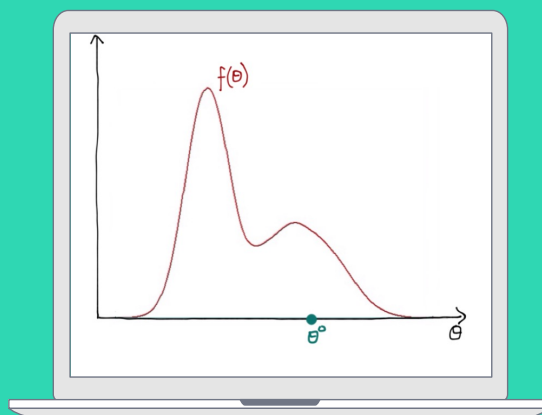
$$\alpha(\theta, \theta^*) = \min \left\{ 1, \frac{f(\theta^*)q(\theta^*, \theta)}{f(\theta)q(\theta, \theta^*)} \right\}$$

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## METROPOLIS-HASTINGS ALGORITHM

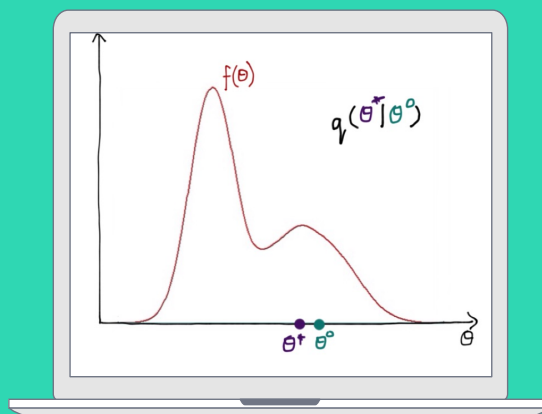
1. Initialize  $\theta^0$  and proposal density  $q$ , set  $\theta = \theta^0$



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## METROPOLIS-HASTINGS ALGORITHM

1. Initialize  $\theta^0$  and proposal density  $q$ , set  $\theta = \theta^0$
2. Sample  $\theta^* \sim q(\theta^* | \theta)$



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## METROPOLIS-HASTINGS ALGORITHM

1. Initialize  $\theta^0$  and proposal density  $q$ , set  $\theta = \theta^0$

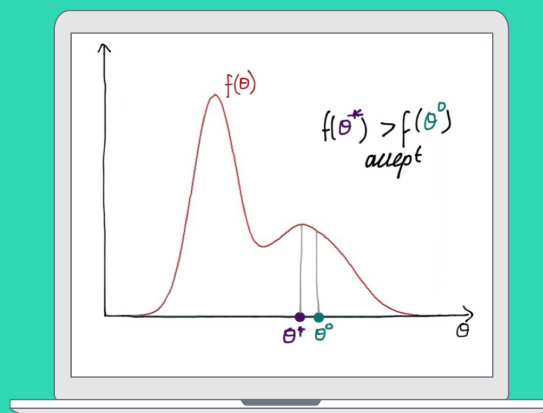
2. Sample  $\theta^* \sim q(\theta^*|\theta)$

3. Compute acceptance probability,  $r$

### ACCEPTANCE

- If  $q(\theta^*|\theta)$  symmetric, then  

$$r = \min\left(1, \frac{f(\theta^*)}{f(\theta)}\right)$$
- Move to  $\theta^*$  if more probable than  $\theta$



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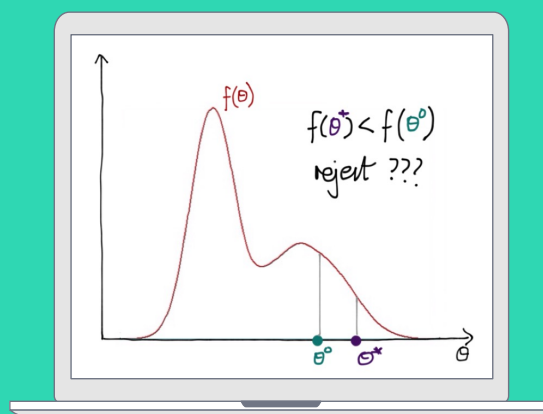
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- If  $q(\theta^*|\theta)$  asymmetric, then  

$$r = \min\left(1, \frac{f(\theta^*)q(\theta|\theta^*)}{f(\theta)q(\theta^*|\theta)}\right)$$



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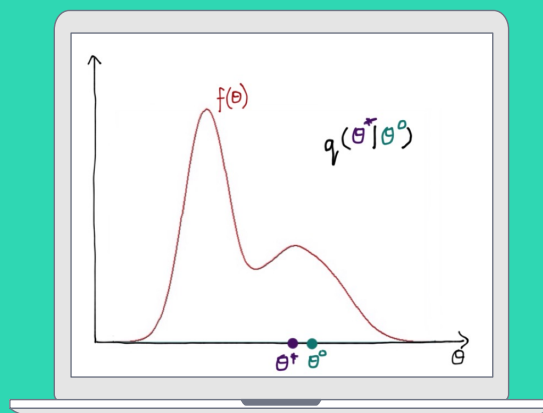
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4. Draw  $u \sim \text{Uniform}[0,1]$



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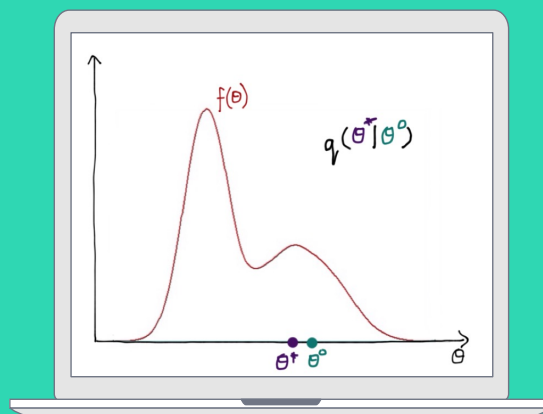
$$r = \min\left(1, \frac{f(\theta^*)q(\theta | \theta^*)}{f(\theta)q(\theta^* | \theta)}\right)$$

4. Draw  $u \sim \text{Uniform}[0,1]$

5. Set new sample to

$$\theta_{i+1} = \begin{cases} \theta^*, & \text{if } u < r \\ \theta_i, & \text{if } u \geq r \end{cases}$$

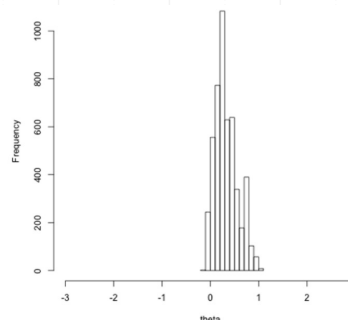
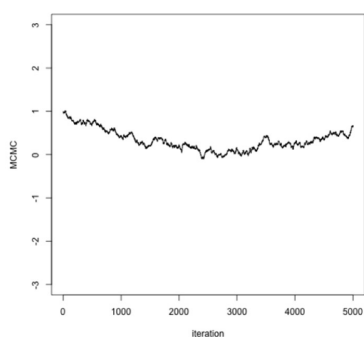
6. Repeat sets 2-5



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## CHOOSING A PROPOSAL DISTRIBUTION : "GOLDIE LOCKS"

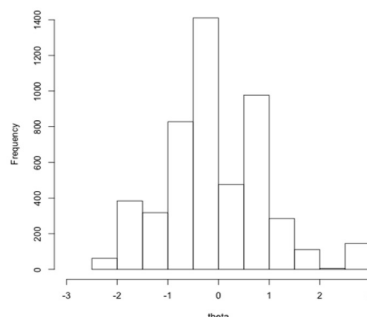
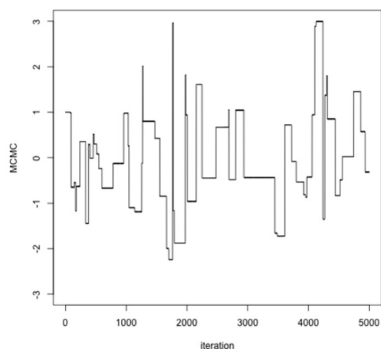
- If **variance is too small**, the chain will be slow to reach the target distribution



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## CHOOSING A PROPOSAL DISTRIBUTION: "GOLDIE LOCKS"

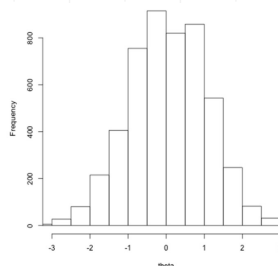
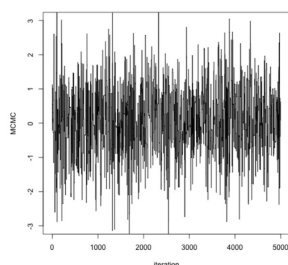
- If **variance is too high**, many proposed values will be rejected and the chain will stick in one place for many steps



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## CHOOSING A PROPOSAL DISTRIBUTION: “GOLDIE LOCKS”

- If **variance is just right**, the chain will efficiently explore the full shape of the target distribution



- We can either:
  - **Trial and Error**: Try several different proposal distributions (pilot runs) , aiming for acceptance rate of 24-40%
  - Use **Adaptive MCMC**

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## ADAPTIVE MCMC

- New point depends on previous point AND on earlier history of the chain
- **The adaptation** is based on an increasing part of the chain
- Uses a **Gaussian proposal with covariance**  $C_n$  that depends on the chain generated so far:

$$C_n = \begin{cases} C_0, & n \leq n_0 \\ s_d \text{cov}(\theta_1, \dots, \theta_n) + s_d \varepsilon I_d, & n > n_0 \end{cases}$$

- Where
  - $s_d$  is a parameter that depends only on the dimension  $d$  of the sample space (usually  $s_d = 2.4^2/d$ )
  - $\varepsilon > 0$  is a constant we keep very small
  - $n_0 > 0$  is the length of the initial nonadaptive period

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## SUMMARY POINTS

- SIR Compartmental Model
- Likelihood as  $p(\text{data}|\theta)$  to express closeness of model to data
- Bayesian inference:  $(\text{posterior}) \propto (\text{normalized likelihood}) \cdot (\text{prior})$
- To estimate quantities or project into the future, need to calculate.  

$$E[A] = \int p(\theta|\text{data})X(\theta)d\theta$$
- Monte Carlo sampling as a method to calculate this
- Use Metropolis-Hastings Markov-Chain Monte Carlo Method
- Adaptive MCMC

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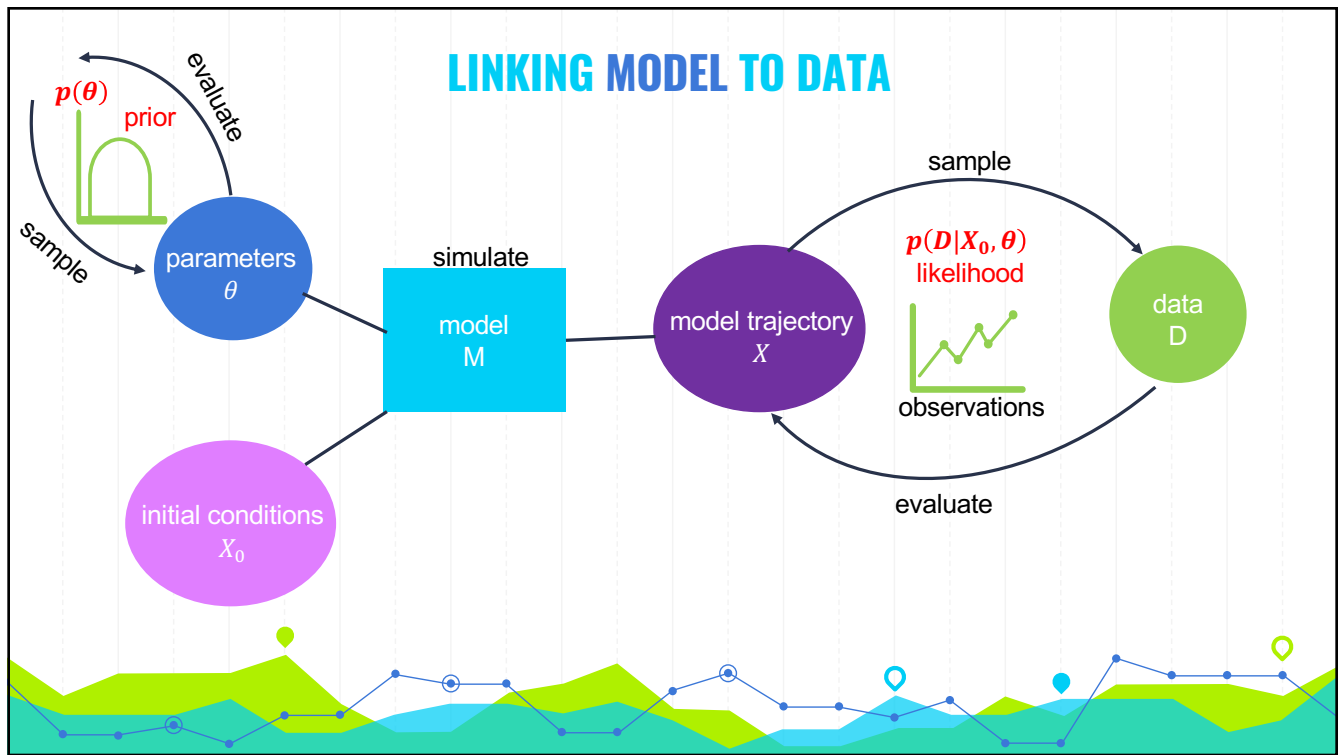
## Computational Piece

Programmed Computational Example (Code, Output, & Graphs)

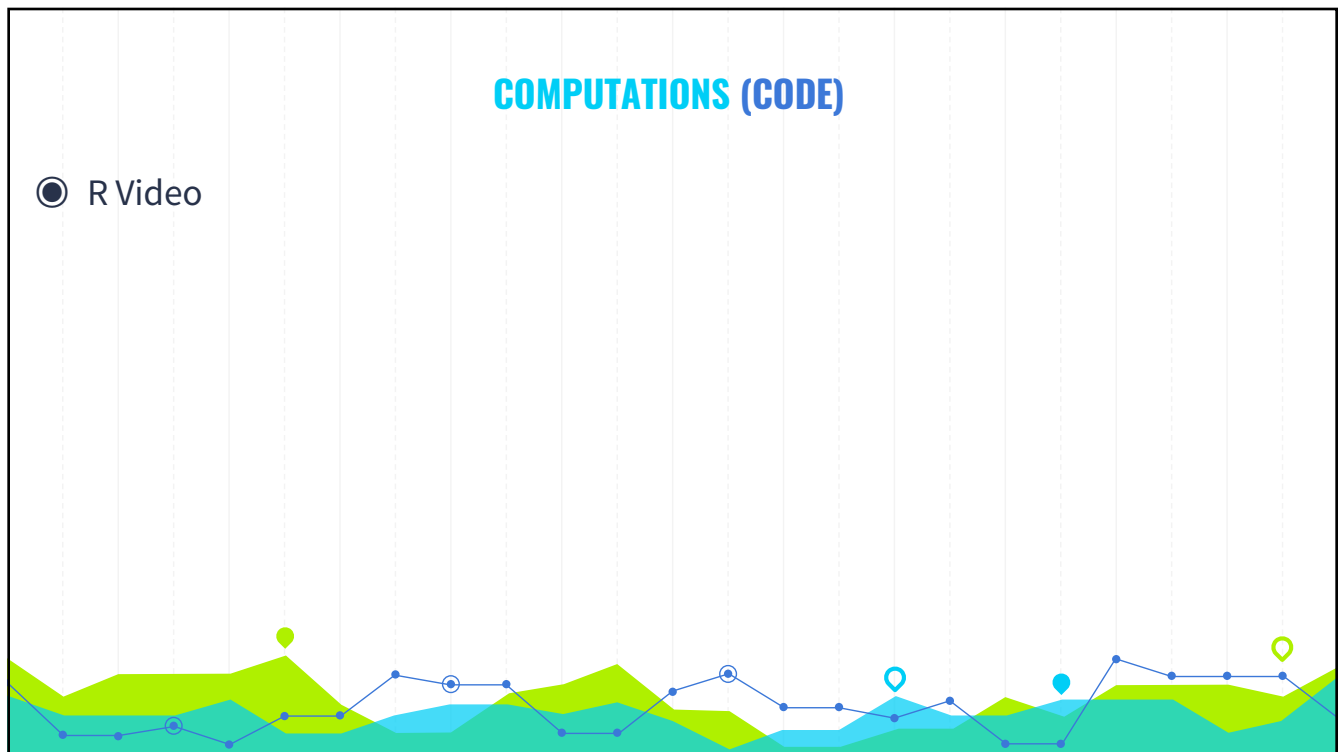
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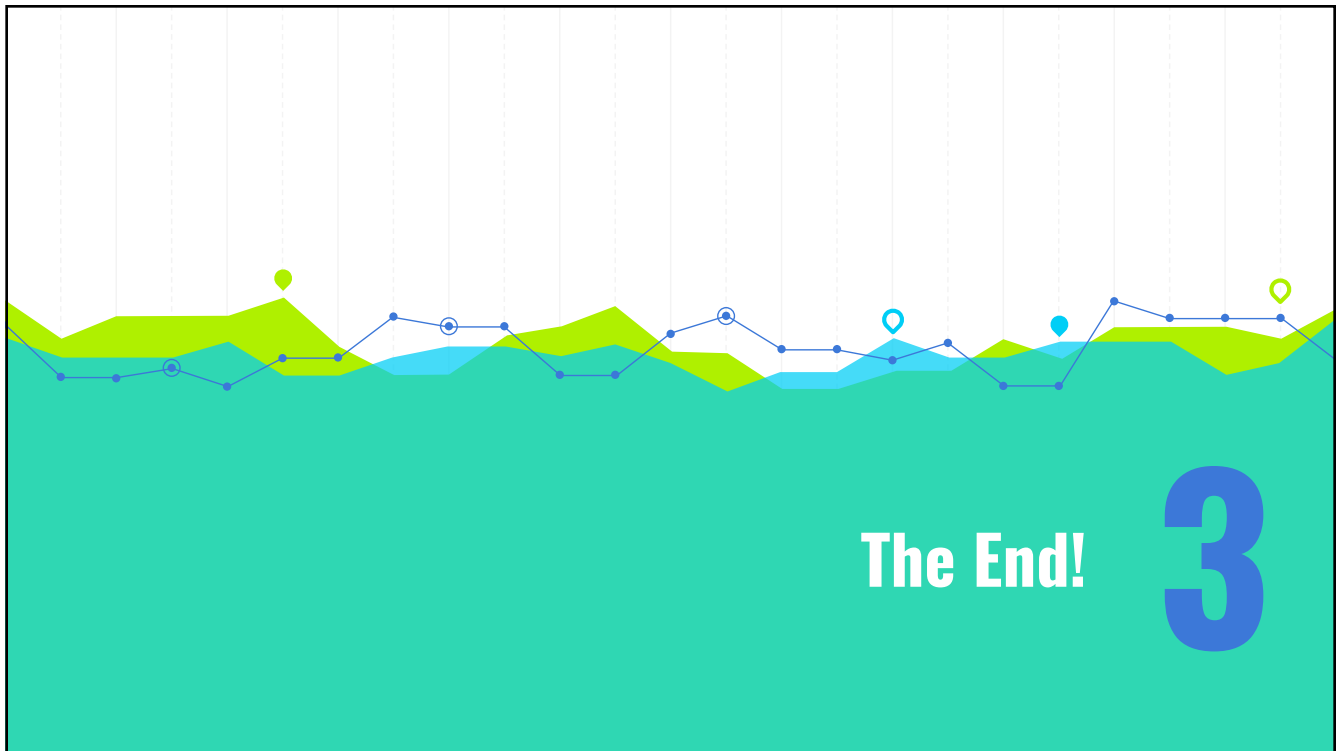




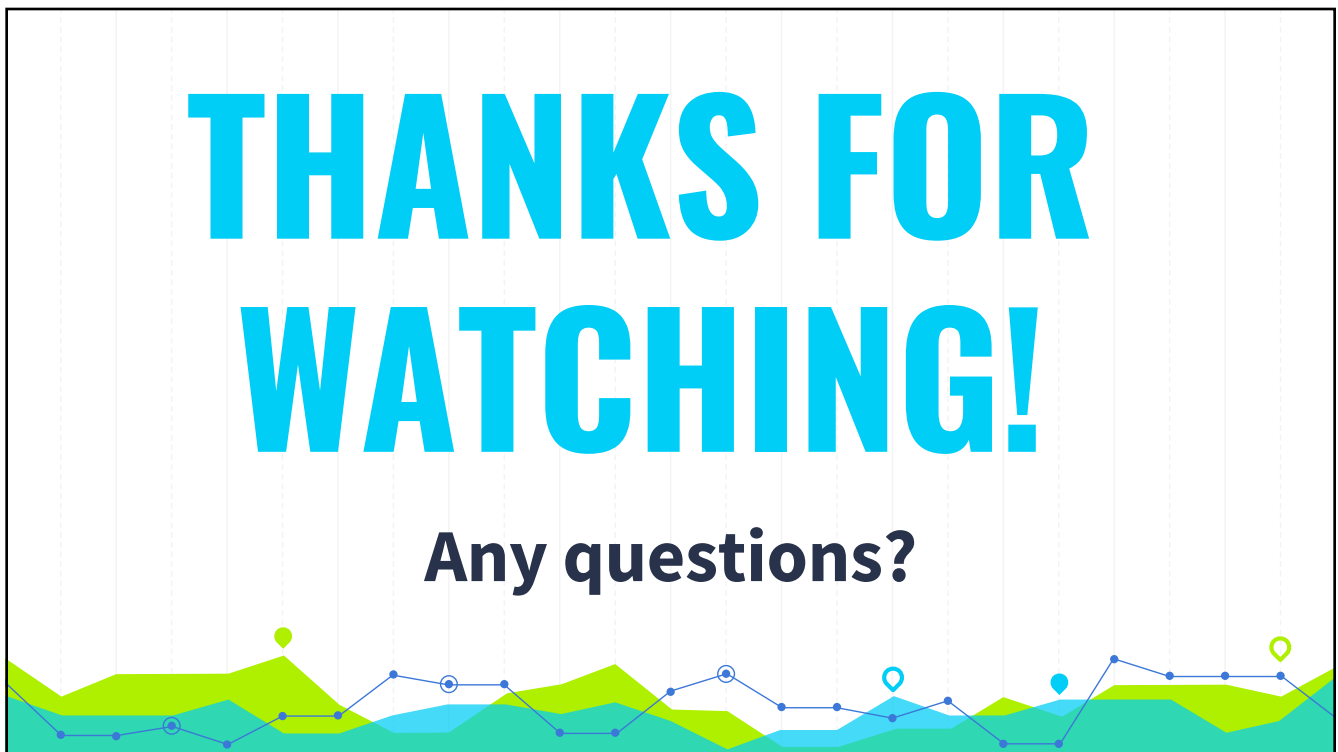
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## REFERENCES

- Allen, L. J. S. (2017). A primer on stochastic epidemic models: Formulation, numerical simulation, and analysis. *Infectious Disease Modeling*, 2, 128-142.
- Angulo, J. M., et al. (2012). Modeling of space-time infectious disease spread under conditions of uncertainty. *International Journal of Geographical Information Science*, 26(10), 1751-1772.
- Artalejo, J. R., Economou, A., & Lopez-Herrero, M. J. (2015). The stochastic SEIR model before extinction: Computational approaches. *Applied Mathematics and Computation*, 265, 1026-1043.

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## REFERENCES

- Bai, Y. (2009). "An Adaptive Directional Metropolis-within-Gibbs Algorithm." Technical Report in Department of Statistics at the University of Toronto.
- Baker, M. J. (2014). Adaptive Markov Chain Monte Carlo Sampling and Estimation in Mata. *The Stata Journal*, 14(3), 623-661.
- Ball, F. & Neal, P. (2002). A General Model for Stochastic SIR Epidemics with Two Levels of Mixing. *Mathematical Biosciences*, 180, 73-102.
- Becker, A. D., & Grenfell, B. T. (2017). tsiR: An R Package for Time-Series Susceptible-Infected-Recovered Models of Epidemics. *PLOS One*, 12(9), e0185528.

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## REFERENCES

- Brauer, F., Castillo-Chavez, C., & Feng, Z. (2019). *Mathematical Models in Epidemiology*. Springer. New York, NY.
- Britton, T., & Pardoux, E. (2019). *Stochastic Epidemic Models with Inference*. Springer. Cham, Switzerland
- Capistran, M. A., Christen, J. A., & Velasco-Hernandez, J. X. (2012). Towards Uncertainty Quantification and Inference in the Stochastic SIR Epidemic Model. *Mathematical Biosciences*, 240, 250-259.
- Chowell, G., Hyman, J. M., Bettencourt, L. M. A., Castillo-Chavez, C. (2009). *Mathematical and Statistical Approaches in Epidemiology*. Springer. New York, NY.


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## REFERENCES

- Coelho, F. C., Codeco, C. T., & Gomes, M. G. M. (2011). A Bayesian Framework for Parameter Estimation in Dynamical Models. *PLOS One*, 6(5), e19616.
- Costa, P. J. (2017). *Applied Mathematics for the Analysis of Biomedical Data*. Wiley. Hoboken, NJ.
- Costa, P. J., Dunyak, J. P., & Mohtashemi, M. (2005). Models, Prediction, and Estimation of Outbreaks of Infectious Disease, *Proceedings, IEEE Southeast Conference*, Ft. Lauderdale, FL, USA, 174-178.
- Earn, D. J. D., Rohani, P., Bolker, B. M., & Grenfell, B. T. (2000). A Simple Model for Complex Dynamical Transitions in Epidemics. *Science*, 287(28), 667-287.

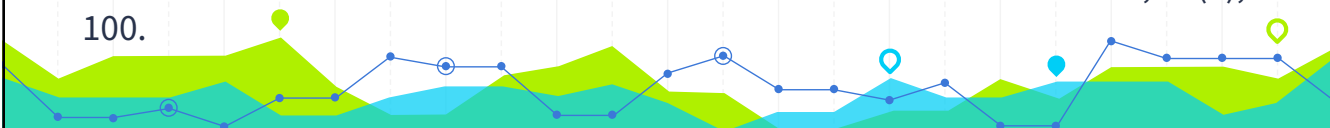
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## REFERENCES

- Gilks, W., & Roberts, G. (1996). "Strategies for Improving MCMC." In Gilks, W., Richardson, S., Spiegelhalter, D. (Eds.), Markov Chain Monte Carlo in Practice, p. 89-114. Chapman & Hall, Boca Raton, FL.
  - Greenwood, P. E., & Gordillo, L. F. (2009) Stochastic Epidemic Modeling. In: Chowell G., Hyman J.M., Bettencourt L.M.A., Castillo-Chavez C. (Eds) Mathematical and Statistical Estimation Approaches in Epidemiology. Springer, Dordrecht.
  - Haario, H., Saksman, E., & Tamminen, J. (2001). "An Adaptive Metropolis Algorithm." Bernoulli, 7(2), 223-242.
  - Haario, H., Laine, M., Mira, A., & Saksman, E. (2006). Dram: efficient adaptive mcmc. Statistics and Computing, 16(4):339-354.
- 

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## REFERENCES

- Hastings, W. (1970). "Monte Carlo Sampling Methods Using Markov Chains and Their Applications." Biometrika, 57(1), 97-109.
  - Jenness, S. M., Goodreau, S. M., & Morris, M. (2018). EpiModel: An R Package for Mathematical Modeling of Infectious Disease Over Networks. Journal of Statistical Software, 84(8).
  - Johnson, L. T., & Geyer, C. J. (2011). Variable Transformation to Obtain Geometric Ergodicity in the Random-Walk Metropolis Algorithm. Annals of Statistics, 40(6), 3050-3076.
  - Kass, R. E., Carlin, B. P., Gelman, A., & Neal, R. M. (1997). Markov Chain Monte Carlo in Practice: A Roundtable Discussion. The American Statistician, 52(2), 93-100.
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## REFERENCES

- Kennedy, W. G., Agarwal, N., & Yang, S. J. (2014). Social Computing, Behavioral-Cultural Modeling, and Prediction. 6<sup>th</sup> International Conference, SBP. Springer. Washington, DC.
- Kermack, W. O., & McKendrick, A. G. (1927). A Contribution to the Mathematical Theory of Epidemics. *Proceedings of the Royal Society London*, 115, 700-721.
- Laine, M., et al. (2008). Adaptive MCMC methods with applications in environmental and geophysical models. Finnish Meteorological Institute.
- Metropolis, N., Rosenbluth, A., MN, R., & Teller, E. (1953). "Equation of State Calculations by Fast Computing Machines." *Journal of Chemical Physics*, 21, 1087-1092.

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## REFERENCES

- Merl, D., Johnson, L. R., Gramacy, R. B., & Mangel, M. (2009). A Statistical Framework for the Adaptive Management of Epidemiological Interventions. *PLOS One*, 4(6), e5807.
- Muellner, U. et al. (2018). Epidemix – An Interactive Multi-model Application for Teaching and Visualizing Infectious Disease Transmission. *Epidemics*, 23, 49-54.
- Ndanguza, D., Mbalawata, I.S., & Nsabimana, J. P. (2016). Analysis of SDEs Applied to SEIR Epidemic Models by Extended Kalman Filter Method. *Applied Mathematics*, 7, 2195-2211.
- Nguyen, D., de Valpine, P., Atchade, Y., Turek, D., Michaud, N., & Paciorek, C. (2018). Automatic Adaptation of MCMC Algorithms. arXiv preprint arXiv:1802.08798.

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## REFERENCES

- Roberts, G., & Rosenthal, J. (2007). "Coupling and Ergodicity of Adaptive Markov Chain Monte Carlo Algorithms." *Journal of Applied Probability*, 44, 458-475.
- Roberts, G., & Rosenthal, J. (2009). "Examples of Adaptive MCMC." *Computational Statistics and Data Analysis*, 18, 349-367.
- Rosenthal, J. S., & Yang, J. (2018). Ergodicity of Combocontinuous Adaptive MCMC Algorithms. *Methodology and Computing in Applied Probability*, 20, 535-551.
- Sameni, R. (2020). Mathematical Modeling of Epidemic Diseases; A Case Study of the COVID-19 Coronavirus, *arXiv:2003.11371 [q-bio.PE]*.
- Smith, R.C. (2013). Uncertainty quantification: theory, implementation, and applications, volume 12. Siam.

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## REFERENCES

- Taghizadeh, L., Karimi, A., & Heitzinger, C. (2020). Uncertainty Quantification in Epidemiological Models for the COVID-19 Pandemic. *Computers in Biology and Medicine*, 125, 104011.
- Talawar, A. S., & Aundhakar, U. R. (2016). Parameter Estimation of SIR Epidemic Model Using MCMC Methods. *Global Journal of Pure and Applied Mathematics*, 12(2), 1299-1306.
- Texier, G., Jackson, M. L., Siwe, L., Meynard, J-B, Deparis, X., & Chaudet, H. (2016). Building Test Data from Real Outbreaks for Evaluating Detection Algorithms. *PLOS One*, 12(9), e0183992.

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