University of Khartoum
Faculty of Mathematical Sciences
Department of Applied Mathematics
Industrial and Computational master program

1- Introduction to Next Generation Matrix (NGM)

The basic reproduction number R_0 is a central threshold parameter for characterizing the dynamics of an epidemiological model described by system of ordinary differential equations. Its know that if $R_0 < 1$ then the epidemic free equilibrium is locally asymptotically stable, and if $R_0 > 1$ the system is unstable and the epidemic continues to spread.

In this project the student will learn the fundamentals of building and analyzing compartmental model and derive its R_0 formula using next generation matrix approach. Then he/she will apply it to the dynamics of COVID-19 pandemic as a case study.

Selected references:

1. P. *van den Driessche and James Watmough (2001). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences 180 (2002) 29–48.*
2. *O. Diekmann, J. A. P. Heesterbeek and M. G. Roberts (2010). The construction of next-generation matrices for compartmental epidemic models. J. R. Soc. Interface (2010) 7, 873–885.*
3. *Milligan GN, Barrett AD (2015). Vaccinology: an essential guide*. Chichester, West Sussex: Wiley Blackwell.
4. *Becker NG, Glass K, Barnes B, Caley P, Philp D, McCaw JM, et al. (April 2006).The reproduction number".Using Mathematical Models to Assess Responses to an Outbreak of an Emerged Viral Respiratory Disease. National Centre for Epidemiology and Population Health.*

2- Bayesian Inference for dynamical Models

Increasingly many applications in engineering, biology and physics are modeled as dynamical systems in form of ordinary differential equations. Usually these models are governed by set of parameters, which their exact values are not known in advance and has to be estimated from observable data. Bayesian inference offers a concise approach for parameters estimations that enables to account for inherent systematic errors and large statistical biases, and incorporation of previous existing knowledge about the phenomena of interest by means of priors.

This project aims at introducing the student to Bayesian approach for parameters inference, using Metropolis-Hastings algorithm, which provides a method of constructing a Markov Chain whose stationary distribution is the desired solution. The Lotka-Volterra model will be used as an example.

Selected references:

1. Bayesian Inference for Epidemic Models Features of Epidemic Data.
2. Edward S Knock *and* Philip D O'Neill *(2014)Bayesian model choice for epidemic models with two levels of mixing. Biostatistics 15(1),45-49.*

3. [Li Yuting I](#) et al (2021) Efficient Bayesian inference of fully stochastic epidemiological models with applications to COVID-19 *R. Soc. open sci.* **8** 211065 211065.

4. Theodore Kypraios, Peter Neal, Dennis Prangle (2017) A tutorial introduction to Bayesian inference for stochastic epidemic models using Approximate Bayesian Computation. Mathematical Biosciences, Volume 287, 42-53.

5. The Metropolis Hastings algorithm: https://stephens999.github.io/fiveMinuteStats/MH_intro.html.

6. The Metropolis–Hastings algorithm C.P. Robert1,2,3 1Universit´e Paris-Dauphine, University of Warwick, and 3 CREST.

7. Bayesian Estimation of Epidemiological Models: Methods, Causality, and Policy Trade-Offs. Jonas E. Arias, Jes´us Fern´andez-Villaverde Juan F. Rubio-Ram´ırez, Minchul Shin. April 16, 2021

3- Group Testing via Binary Matrices.

Rapid detection of individuals infected by a virus like COVID-19 is vital in controlling spread of disease. The traditional individual testing approach, like RT-PCR test per one sample of COVID-19, is expensive, time-consuming, and requires large laboratory capacities and capabilities. Group testing approach, which combine multiple samples together in one test, is an alternative to overcome these challenges, and finding and efficient mathematical construct is an active research area of this field. This project is about designing an efficient single-round and non-adaptive group testing method using sparse binary matrices with implementation in Python/R/Julia or Matlab.

Selected references:
1. Robert Dorfman. The Detection of Defective Members of Large Populations. The Annals of Mathematical Statistics, 14(4):436 – 440, 1943. doi: 10.1214/aoms/1177731363.

2. Ndishimye P. Butera Y. et al. Mutesa, L. A pooled testing strategy for identifying SARS-CoV-2 at low prevalence. Nature, 589:276–280, 10 2020. doi: 10.1038/s41586-020-2885-5.

3. Shental et al. Efficient high-throughput sars-cov-2 testing to detect asymptomatic carriers. Science Advances, 6(37), 2020. doi: 10.1126/sciadv.abc5961.

4. Yining Liu, Sachin Kadyan, and Itsik Pe'er. A recovery algorithm and pooling designs for one-stage noisy group testing under the probabilistic framework. medRxiv, 2021. doi: 10.1101/2021. 03.09.21253193.

5. Simon Foucart and Holger Rauhut. A Mathematical Introduction to Compressive Sensing. 2013. ISBN 978-0-8176-4947-0. doi: 10.1007/978-0-8176-4948-7.