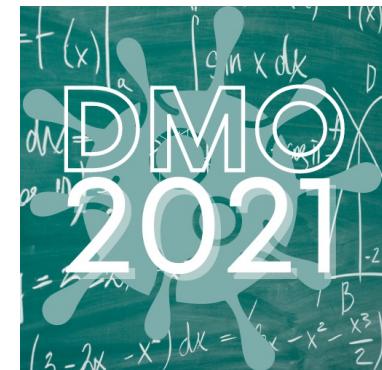
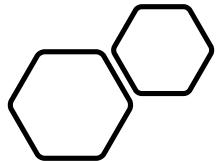


Workshop Programme



Time	27 th July 2021, Tuesday Introduction to Disease Models and R	28 th July 2021, Wednesday Basic R	29 th July 2021, Thursday Disease Modeling	TBA
0830	<i>Webex Platform Open</i>	<i>Webex Platform Open</i>	<i>Webex Platform Open</i>	<i>Webex Platform Open</i>
0830-0900	<i>Attendance Sign-in</i>	<i>Attendance Sign-in</i>	<i>Attendance Sign-in</i>	<i>Attendance Sign-in</i>
0900-1015	Introduction to Disease Models	Functions	SIR Models	Invited Lecture I
1015-1030	Short break	Short break	Short break	Short break
1030 - 1230	Fundamentals of <i>R</i>	Graphs	Build an epidemiological model in <i>R</i>	Group Project Presentation
1230 -1400	Lunch break	Lunch break	Lunch break	Lunch break
1400-1530	Basic Data Processing in <i>R</i>	Packages	Model Analysis I	Group Project Presentation
1530-1545	Short break	Short break	Short break	Short break
1545-1700	Basic Data Manipulation in <i>R</i>	Scripting	Model Analysis II	Group Project Presentation & Workshop Ends



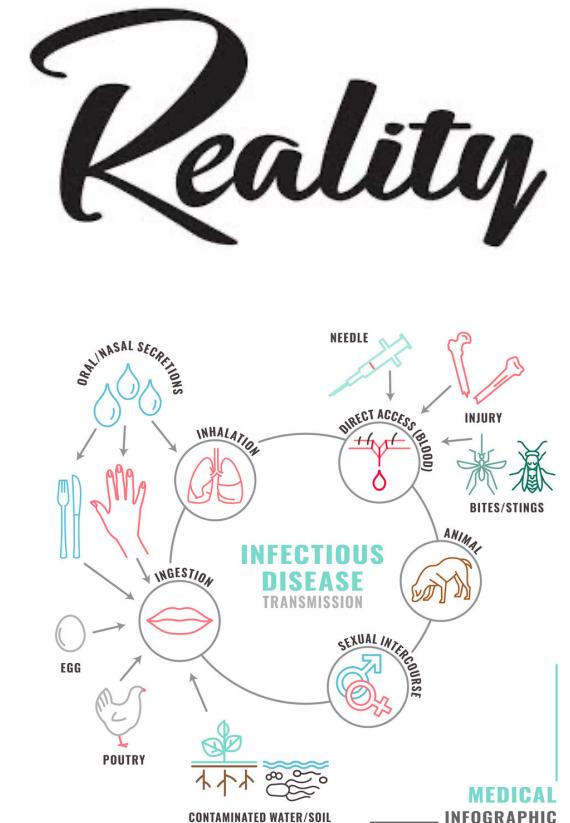
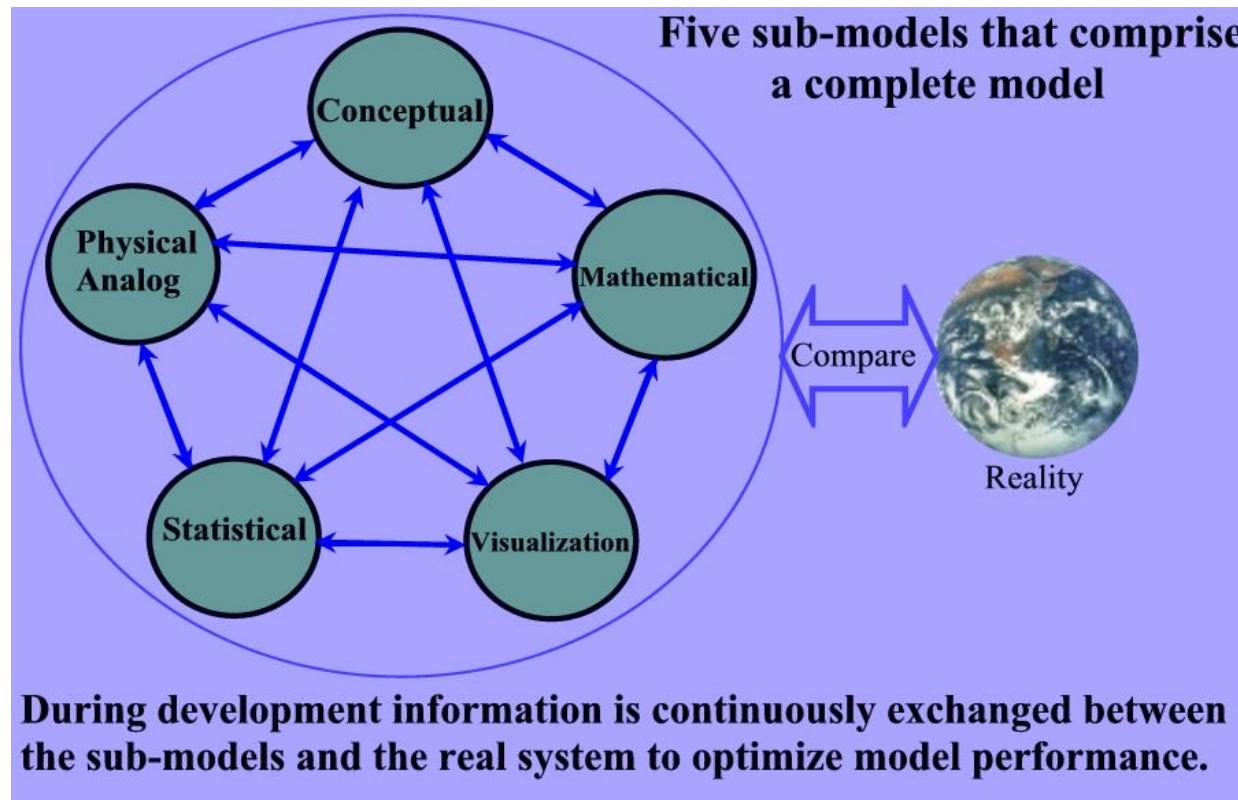
Introduction to Disease Models

Associate Professor Dr Jane Labadin

Faculty of Computer Science and Information Technology

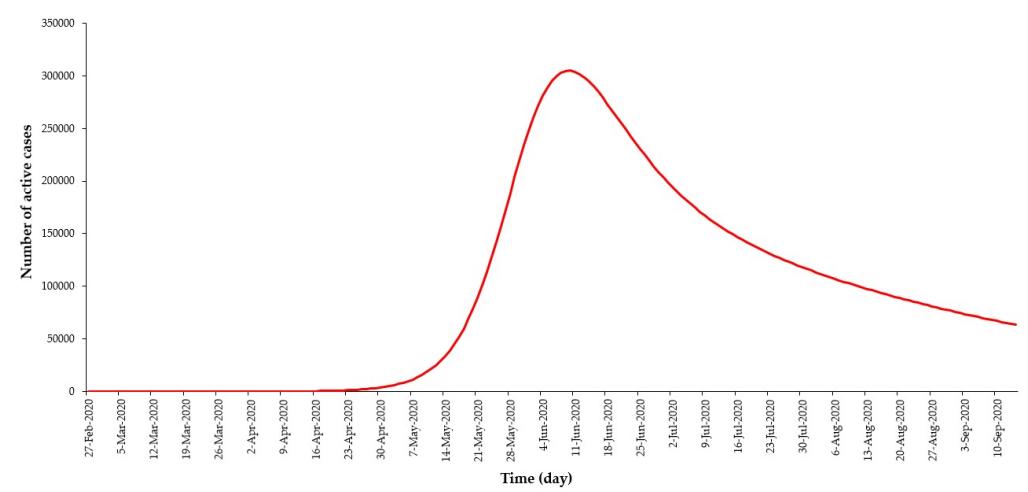
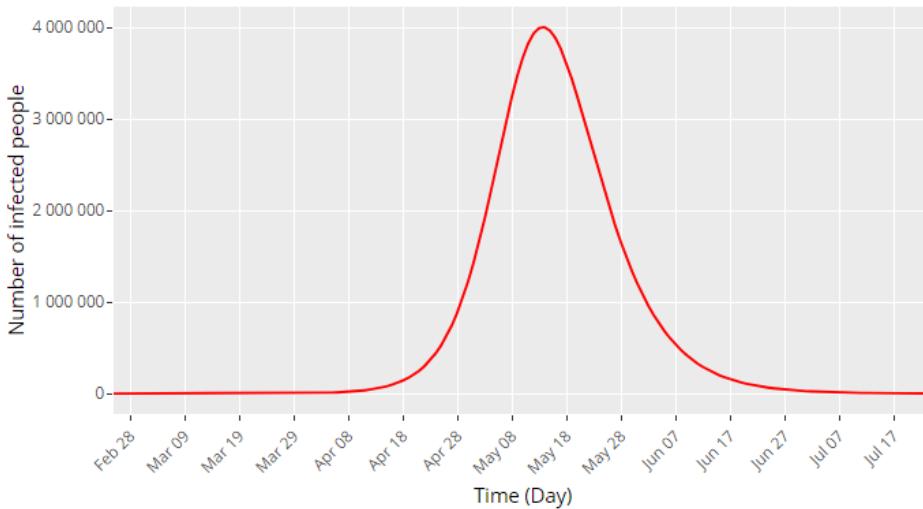
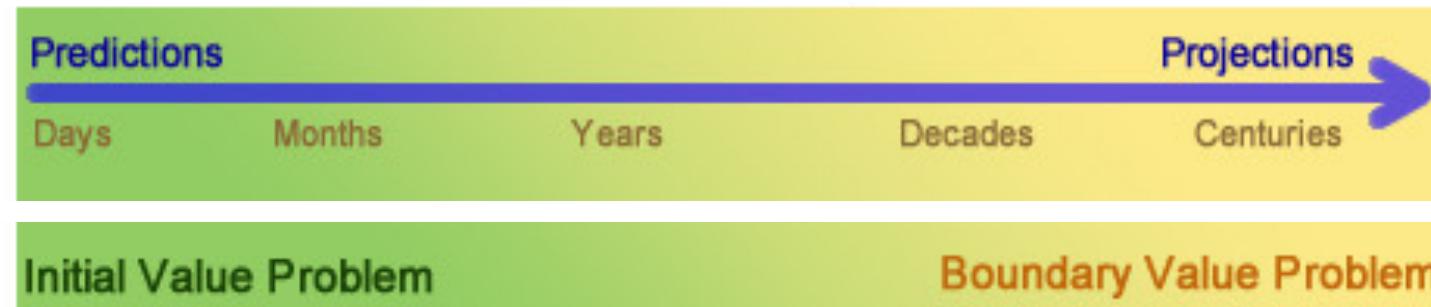
Universiti Malaysia Sarawak

What is a Disease Model?



Why?

Prediction vs Projection



Understanding the Problem

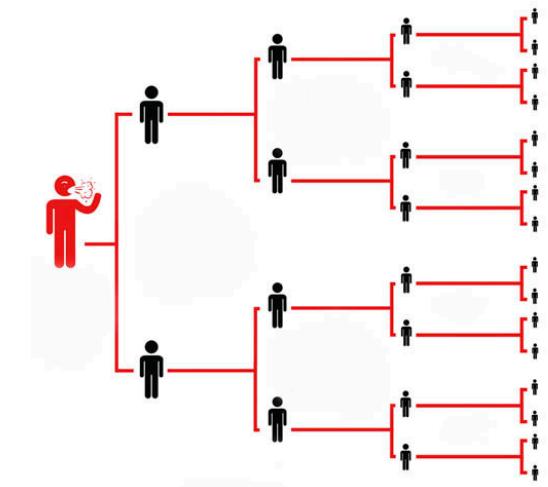
R_0 (Basic Reproduction Number)

The average number of people infected by one infected person in a fully susceptible population

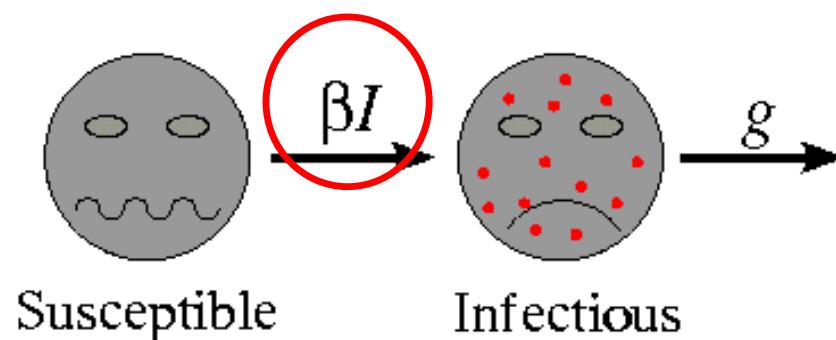
$R_0 > 1$, Infection take off

$R_0 < 1$, Infection die out

Disease	R_0
Measles	14
Rubella	6
Ebola	1.5 - 1.9
COVID-19	3.3 - 5.7



What makes people get infected?





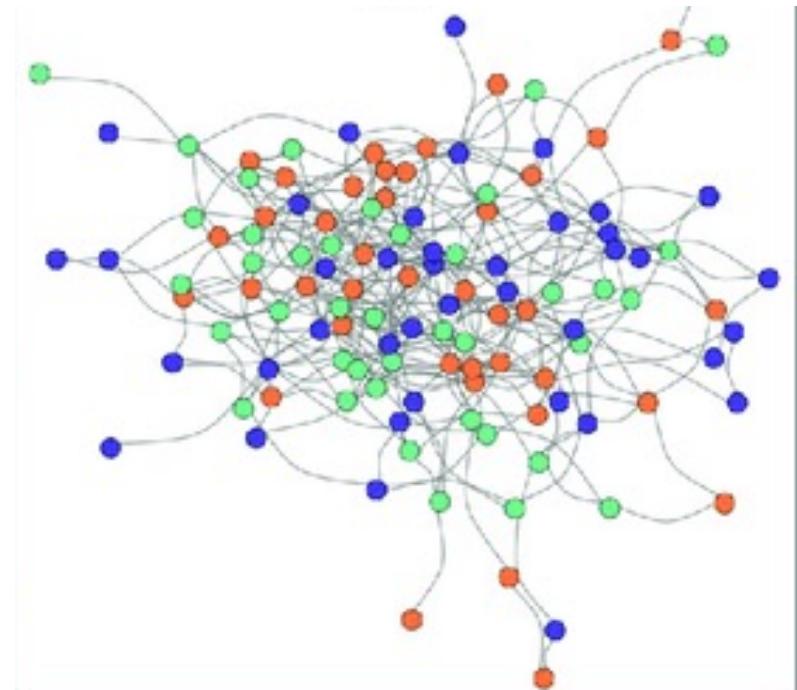
Homogeneous

- The population is assumed well-mixed
- Shared same contact and risk for whole population
- ODEs

Heterogeneous

- Considered the heterogeneity for each individual (age, occupation, gender)
- PDEs, Agent-based model, Network model

Characterizing the Problem



Formulating the model

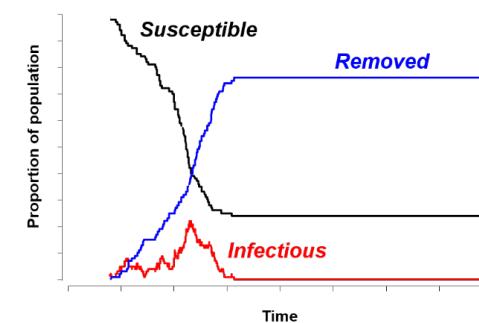
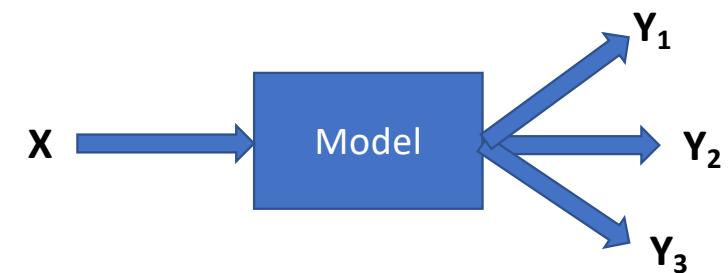
Deterministic

- Depend on initial conditions and parameters value
- No variation in output by given same model structure, initial conditions and parameters value

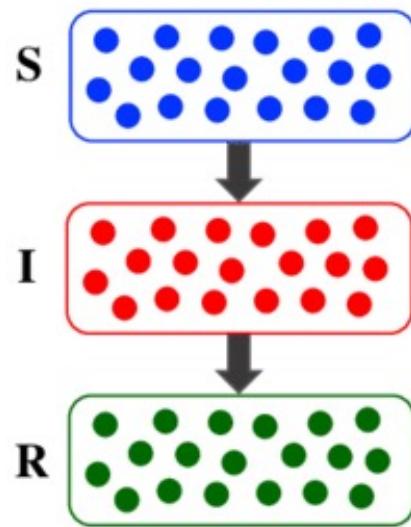


Stochastic

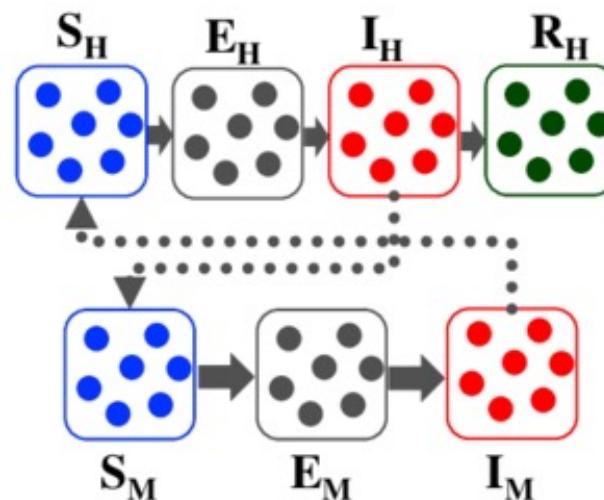
- The probability are incorporated in model
- Different output for each simulation
- Stochastic effect is introduced in model (demographic, environmental)
- Important when the number of cases are small



A. Compartmental model



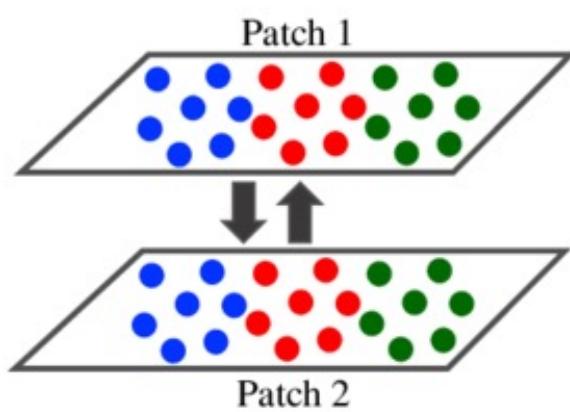
B. Vector-borne
compartmental model



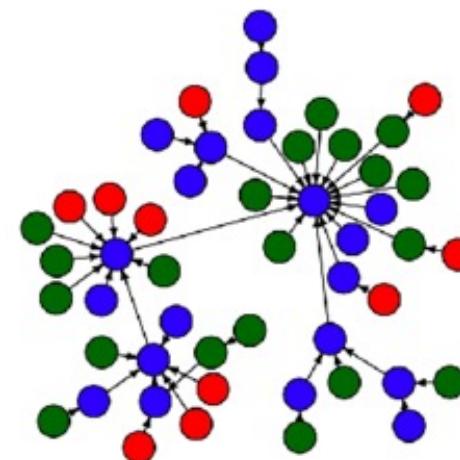
C. Spatial model



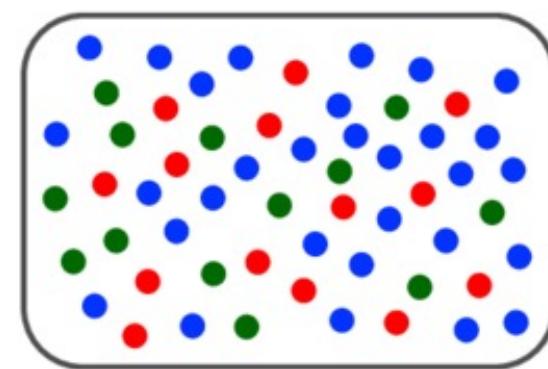
D. Metapopulation model



E. Network model



F. Individual-based model





Article

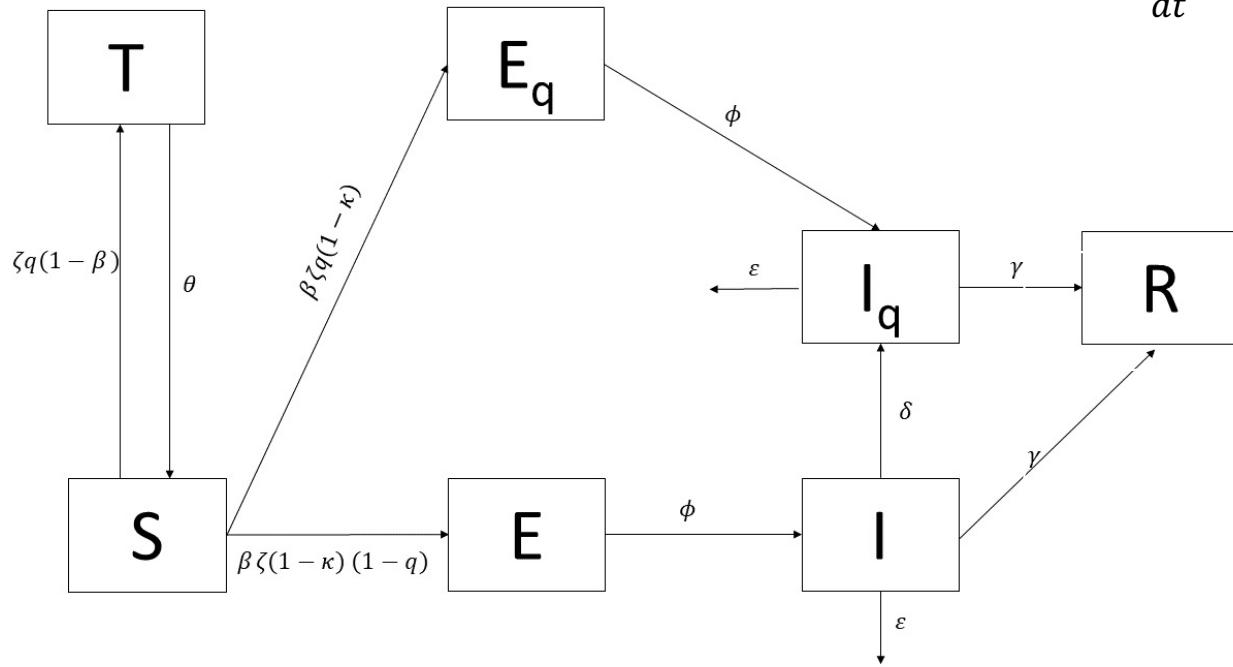
Modelling the Effectiveness of Epidemic Control Measures in Preventing the Transmission of COVID-19 in Malaysia

Balvinder Singh Gill ¹, Vivek Jason Jayaraj ^{2,3}, Sarbhan Singh ¹, Sumarni Mohd Ghazali ¹, Yoon Ling Cheong ¹, Nuur Hafizah Md Iderus ¹, Bala Murali Sundram ¹, Tahir Bin Aris ¹, Hishamshah Mohd Ibrahim ³, Boon Hao Hong ⁴ and Jane Labadin ^{4,*}

T : Traced Negative

E_q : Traced Positive

I_q : Isolated Infectious



$$\frac{dS}{dt} = \theta T - \frac{\beta \zeta q(1 - \kappa)SI}{N} - \frac{\beta \zeta(1 - q)(1 - \kappa)SI}{N} - \frac{\zeta q(1 - \beta)SI}{N},$$

$$\frac{dT}{dt} = \frac{\zeta q(1 - \beta)SI}{N} - \theta T,$$

$$\frac{dE}{dt} = \frac{\beta \zeta(1 - q)(1 - \kappa)SI}{N} - \phi E,$$

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

$$\frac{dE_q}{dt} = \frac{\beta \zeta q(1 - \kappa)SI}{N} - \phi E_q,$$

$$\frac{dI_q}{dt} = \phi E_q + \delta I - \gamma I_q - \epsilon I_q,$$

$$\frac{dR}{dt} = \gamma(I + I_q).$$

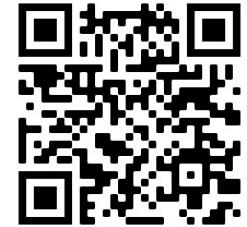
$$R_0 = \frac{\beta(1-q)(1-\kappa)\zeta}{\delta + \gamma + \epsilon}.$$

 International Journal of
Environmental Research
and Public Health



Article
Modelling the Effectiveness of Epidemic Control Measures in Preventing the Transmission of COVID-19 in Malaysia

Balvinder Singh Gill ¹, Vivek Jason Jayaraj ^{2,3} , Sarbhan Singh ¹ , Sumarni Mohd Ghazali ¹, Yoon Ling Cheong ¹ , Nuur Hafizah Md Iderus ¹, Bala Murali Sundram ¹, Tahir Bin Aris ¹, Hishamshah Mohd Ibrahim ³ , Boon Hao Hong ^{4,*}  and Jane Labadin ^{4,*} 



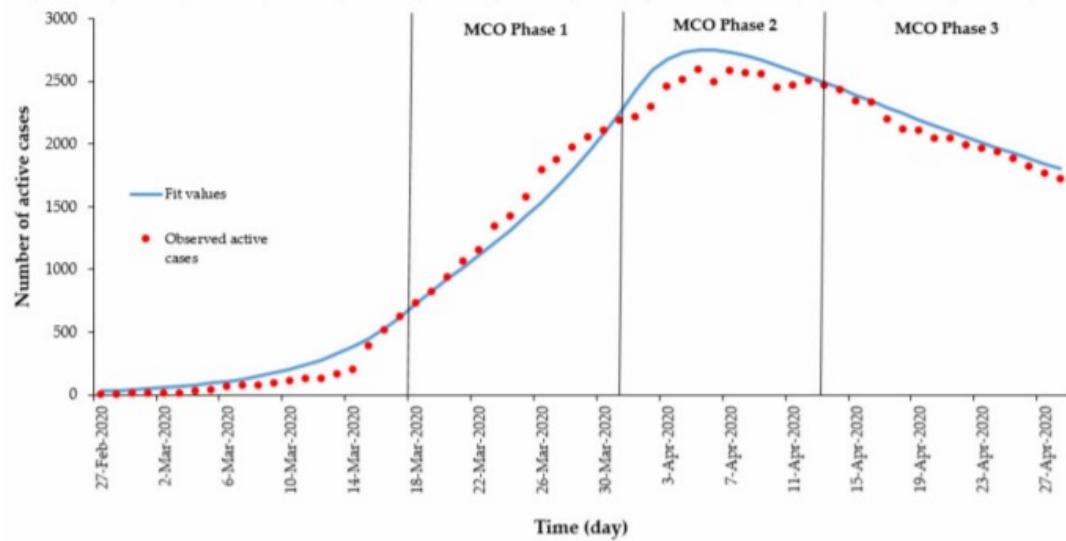
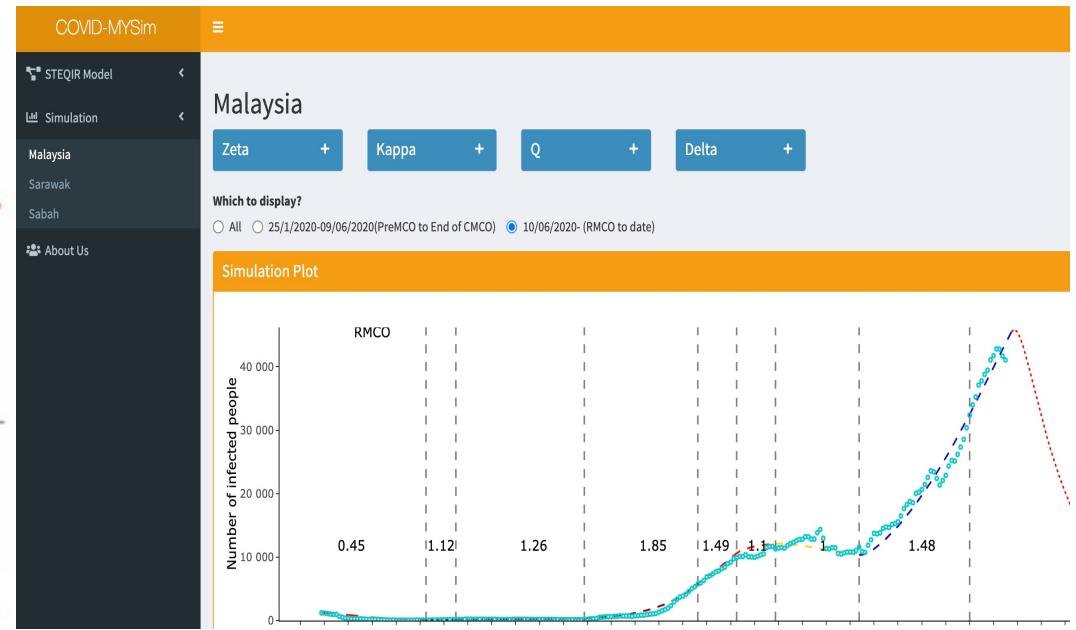


Figure 5. Observed number of COVID-19 active cases and models fit by day at different MCO phases, February to April 2020, Malaysia.



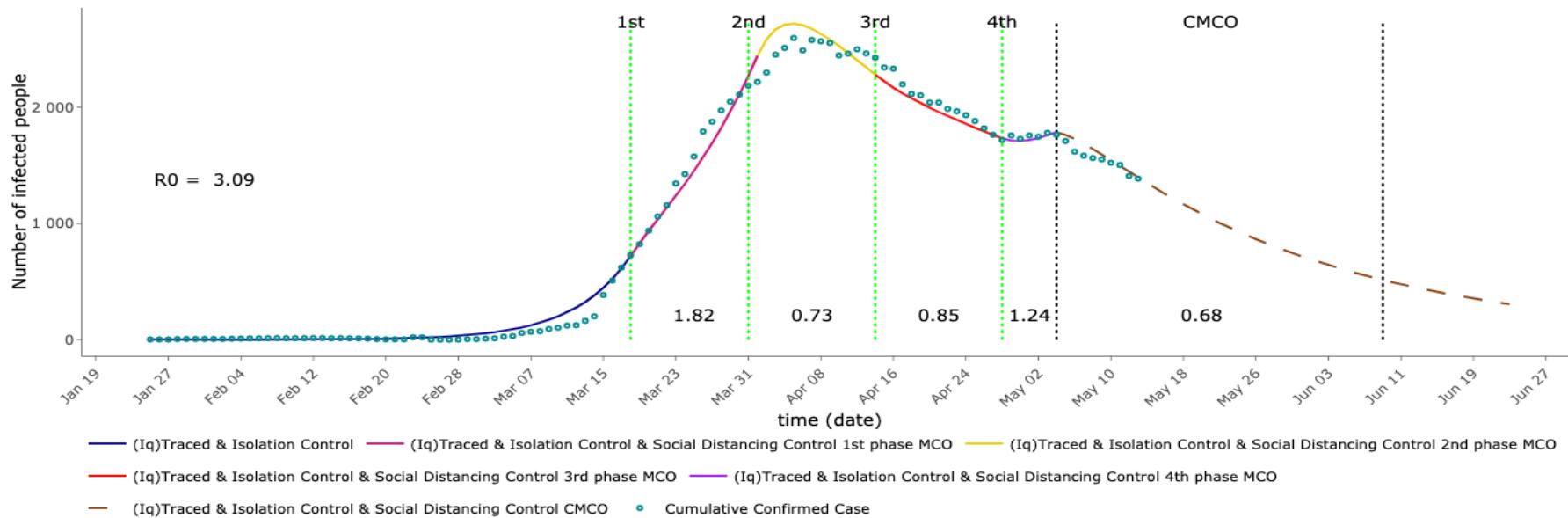


Figure 1: The visual output of the tool on Malaysia daily total active cases from the beginning of the outbreak to the point of writing

Parameter	Pre-MCO	MCO Phase 1	MCO Phase 2	MCO Phase 3	MCO Phase 4	CMCO (to date)
ζ	25	15	6	7	15	20
κ	0.05	0.05	0.05	0.05	0.35	0.8
R_0	3.09	1.82	0.73	0.85	1.24	0.68

J. Labadin & B.H. Hong, “The Estimated Compliance of the Public towards the Movement Control Order” 4th Report to MoH

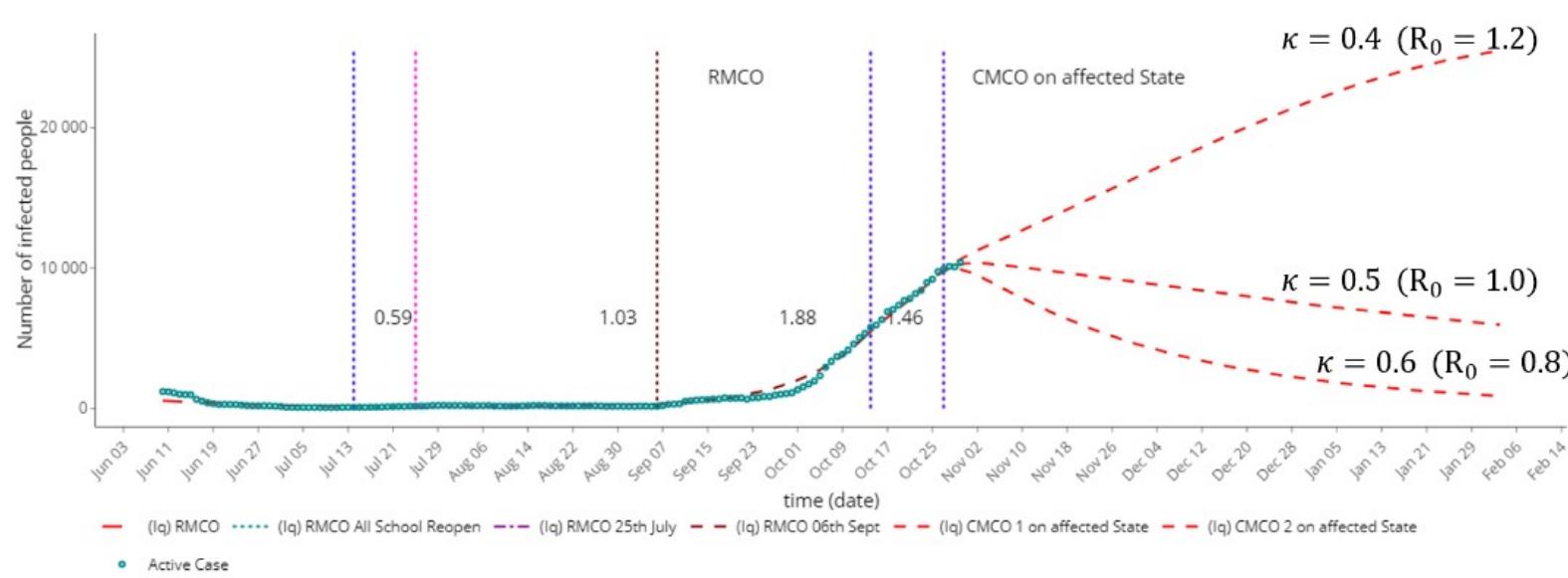


Figure 1: The visual output of the COVID-MYSim tool beginning at the start of the Recovery Movement Control Order (RMCO) to the point of writing

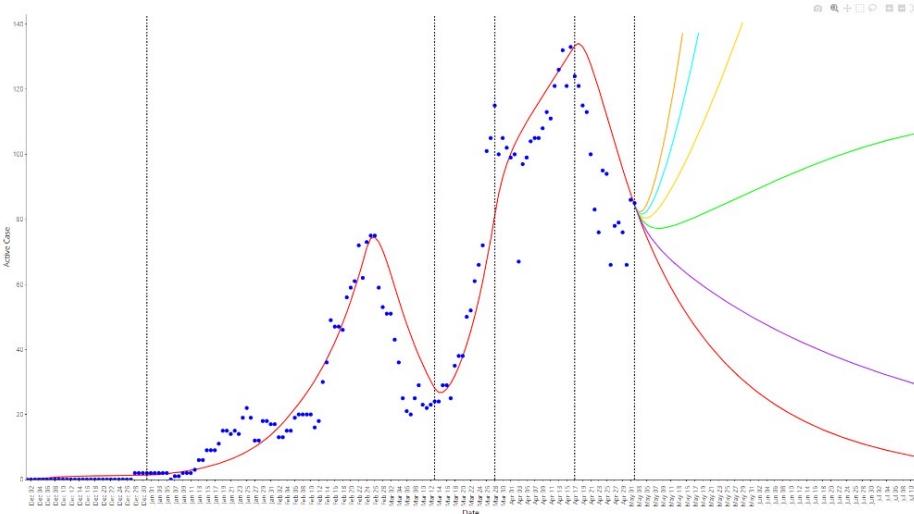
Parameter	CMCO	RMCO 1	RMCO 2	RMCO 3	RMCO 4	CMCO 1
ζ	20	20	25	25	25	23
κ	0.71	0.75	0.65	0.55	0.36	0.46
R_0	0.68	0.59	1.03	1.88	1.46	

J. Labadin & B.H. Hong, "Malaysia's Third Wave of the COVID-19 Outbreak – are we at the peak yet?" 5th Report to MoH

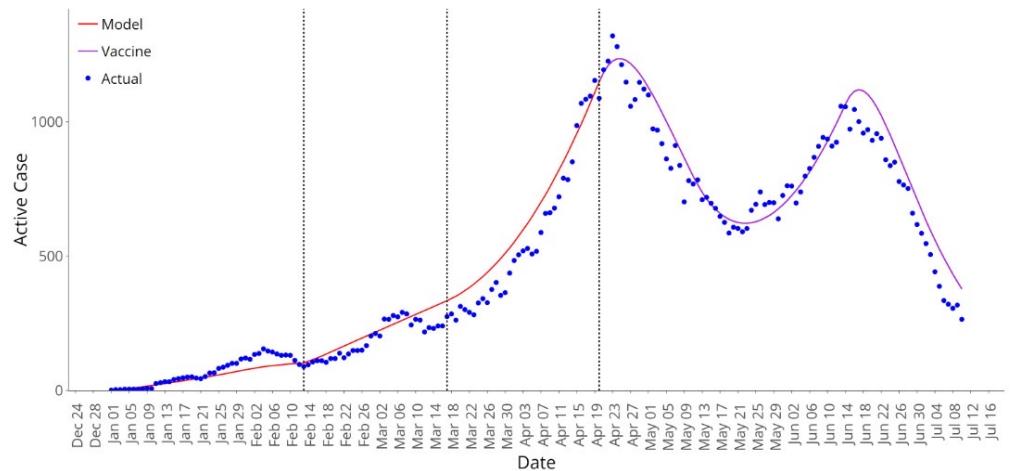


Experience COVID-MYSim

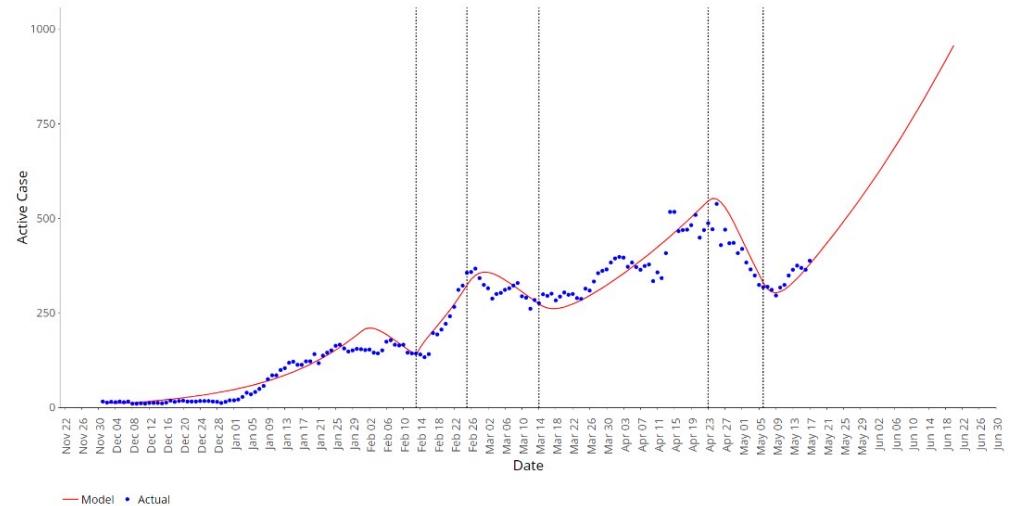
Samarahan



Bintulu



Kuching



Model Simulation for the Spread of Rabies in Sarawak, Malaysia

Nur Asheila Abdul Taib[#], Jane Labadin[#], Phang Piau[#]

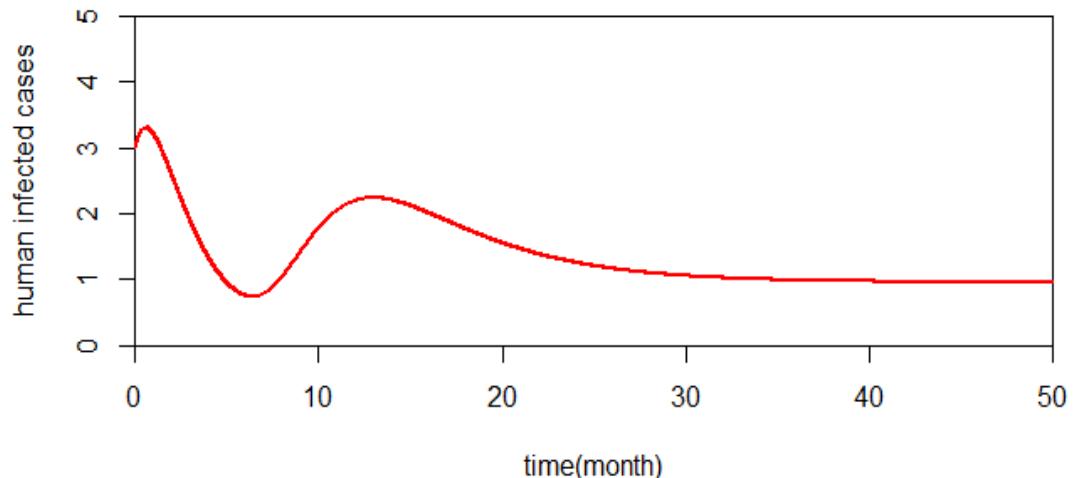
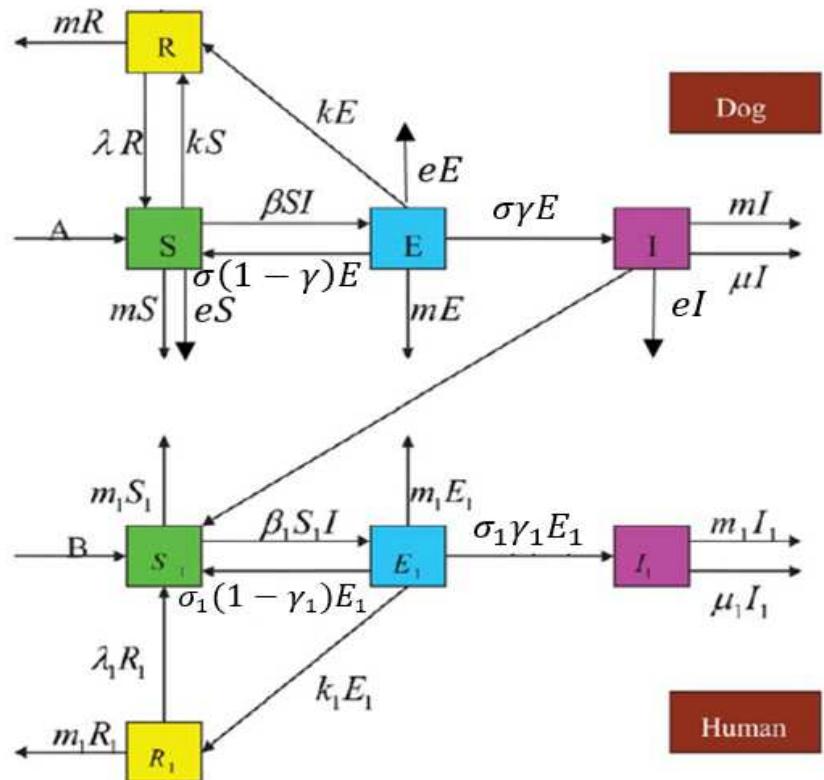
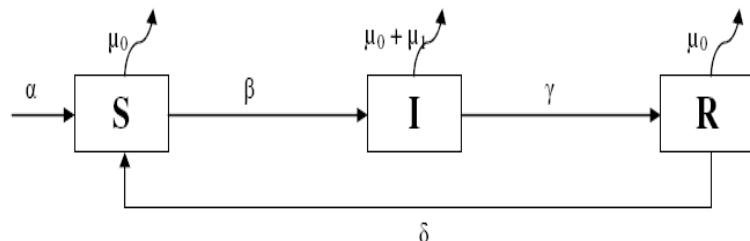
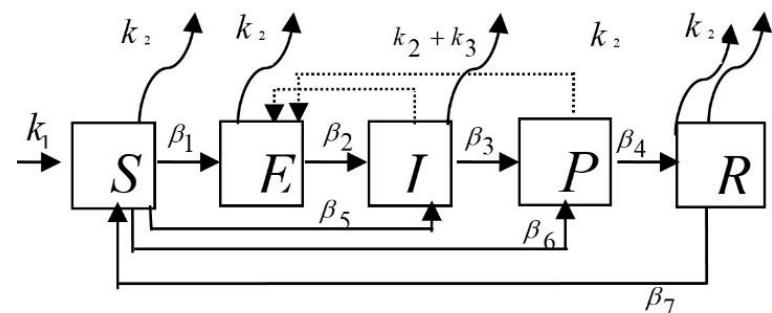


Fig. 3 Simulated number of infected human rabies cases for 51 months from month-0 (June 2017) to month-50 (August 2021).

Hand, Foot and Mouth Disease

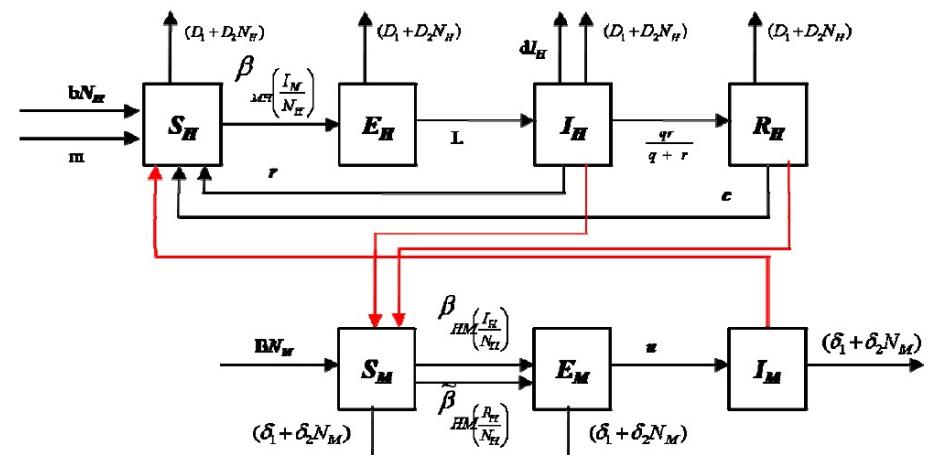


Chuo, F., Tiing, S., & Labadin, J. (2008, May). A simple deterministic model for the spread of hand, foot and mouth disease (HFMD) in Sarawak. In *2008 Second Asia International Conference on Modelling & Simulation (AMS)* (pp. 947-952). IEEE.



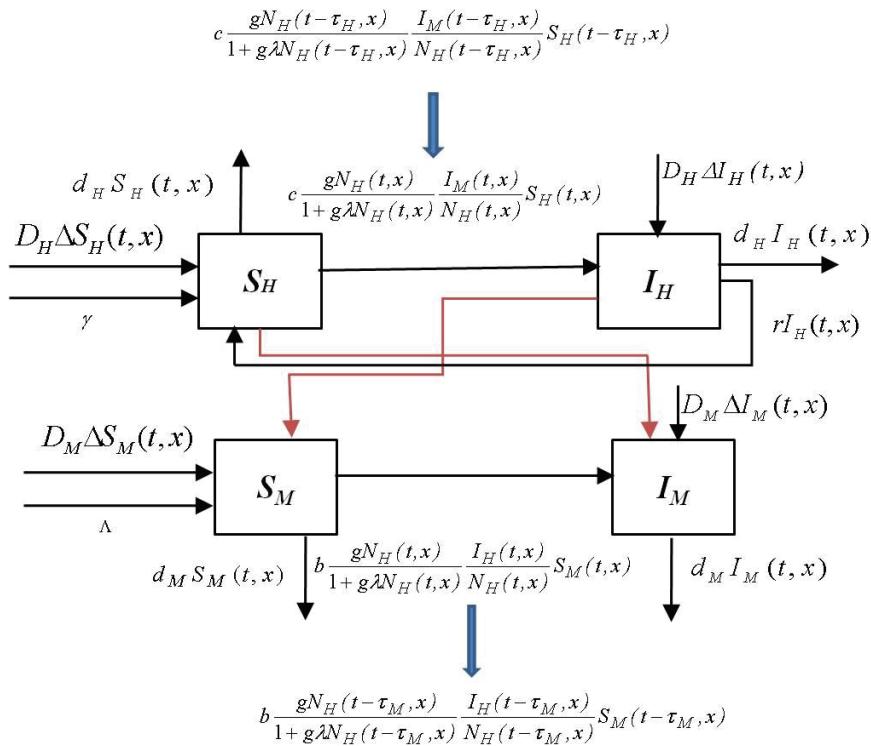
Chan, S. J., Labadin, J., & Podin, Y. (2017). A dynamic SEIPR model for the spread of hand, foot and mouth disease in Sarawak. *Journal of Telecommunication, Electronic and Computer Engineering (JTEC)*, 9(3-10), 125-129.

Malaria

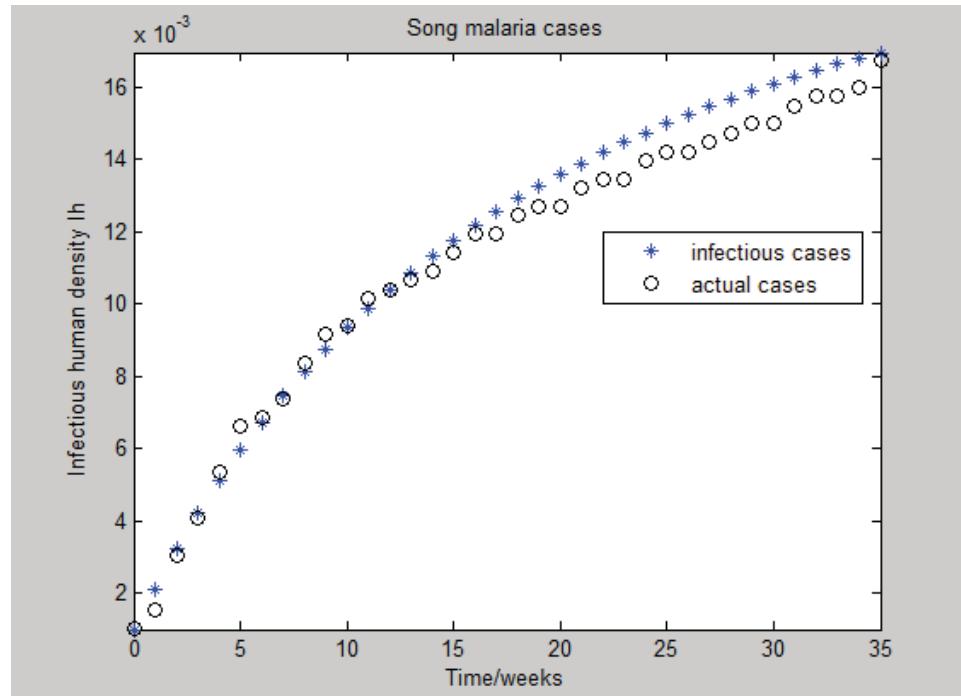


Labadin, J., Kon, C. M. L., & Juan, S. F. S. (2009, October). Deterministic malaria transmission model with acquired immunity. In *Proceedings of the world congress on engineering and computer science* (Vol. 2, pp. 20-22).

Mosquito Borne Disease (Zika, Dengue, Malaria)



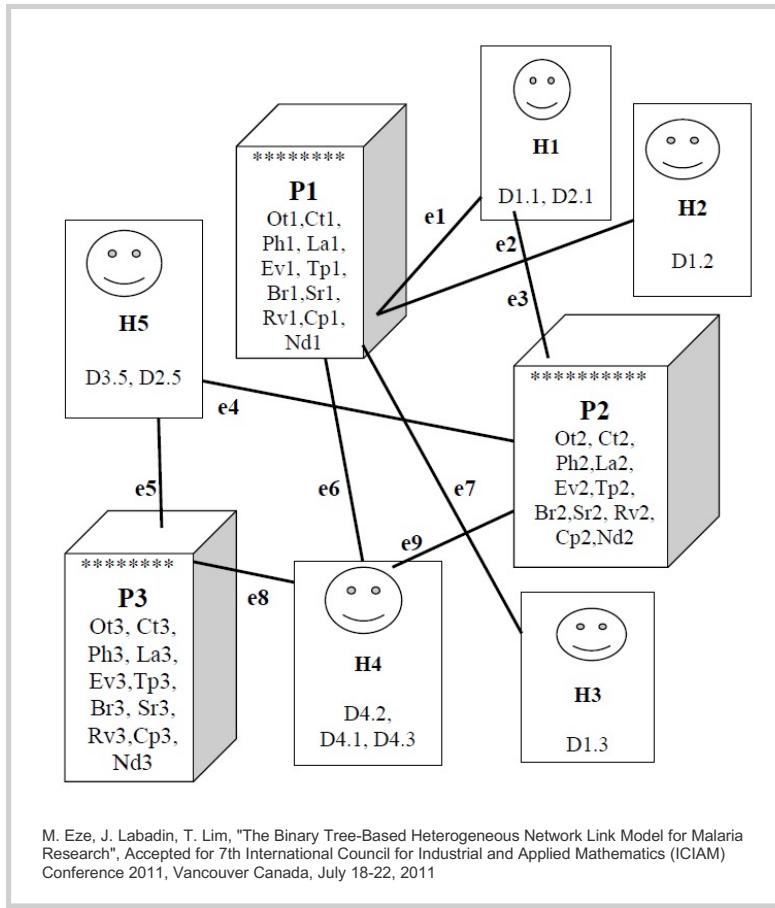
Kon, C. M. L., & Labadin, J. (2015, May). Spatial model for transmission of mosquito-borne diseases. In AIP Conference Proceedings (Vol. 1660, No. 1, p. 050023). AIP Publishing LLC.



Kon, C. M. L., & Labadin, J. (2019). Simulating Dengue: Comparison of Observed and Predicted Cases from Generic Reaction-Diffusion Model for Transmission of Mosquito-Borne Diseases. *MATEMATIKA: Malaysian Journal of Industrial and Applied Mathematics*, 35(3).

Experience work models

Malaria



M. Eze, J. Labadin, T. Lirm, "The Binary Tree-Based Heterogeneous Network Link Model for Malaria Research", Accepted for 7th International Council for Industrial and Applied Mathematics (ICIAM) Conference 2011, Vancouver Canada, July 18-22, 2011

Dengue



MOZZHUB : Dengue Hotspots Detection Tool Incorporating BNM

Dashboard New Case Case Record

Dengue Hotspot List

- #1 Jalan Mendu, Kuching, 93300 Bahagian Kuching, Sarawak
- #2 Serian, 94700 Bahagian Samarahan, Sarawak
- #3 Jalan Lumba Kuda, Kuching, 93450 Bahagian Kuching, Sarawak
- #4 Lorong Tun Ahmad Zaidi Adruce 20
- #5 Jalan Tapah 1, Kuching, 93250 Bahagian Kuching, Sarawak
- #6 Jalan Datuk Muhammad Musa, Samarahan, 94300 Bahagian Samarahan, Sarawak
- #7 Kuching, 93050 Bahagian Kuching, Sarawak
- #8 Kuching, 93050 Bahagian Kuching, Sarawak
- #9 Jalan Borneo Heights, Kuching, 93250 Bahagian Kuching, Sarawak
- #10 Jalan Matang, Kuching, 93050 Bahagian Kuching, Sarawak

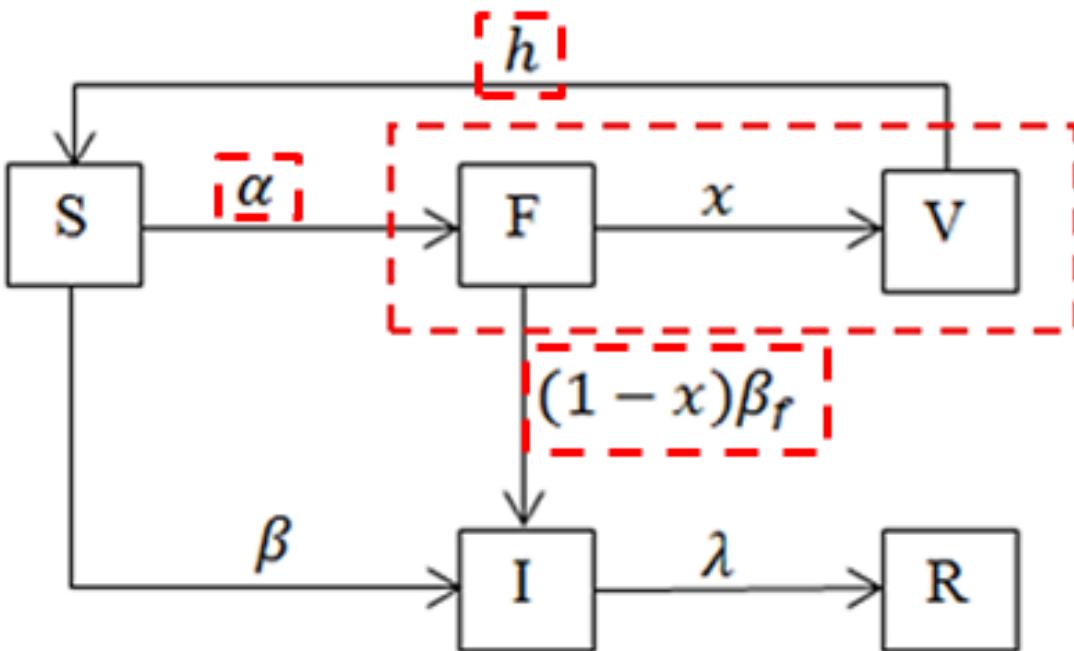
Dengue Hotspot Distribution Heatmap

Leaflet | © OpenStreetMap contributors

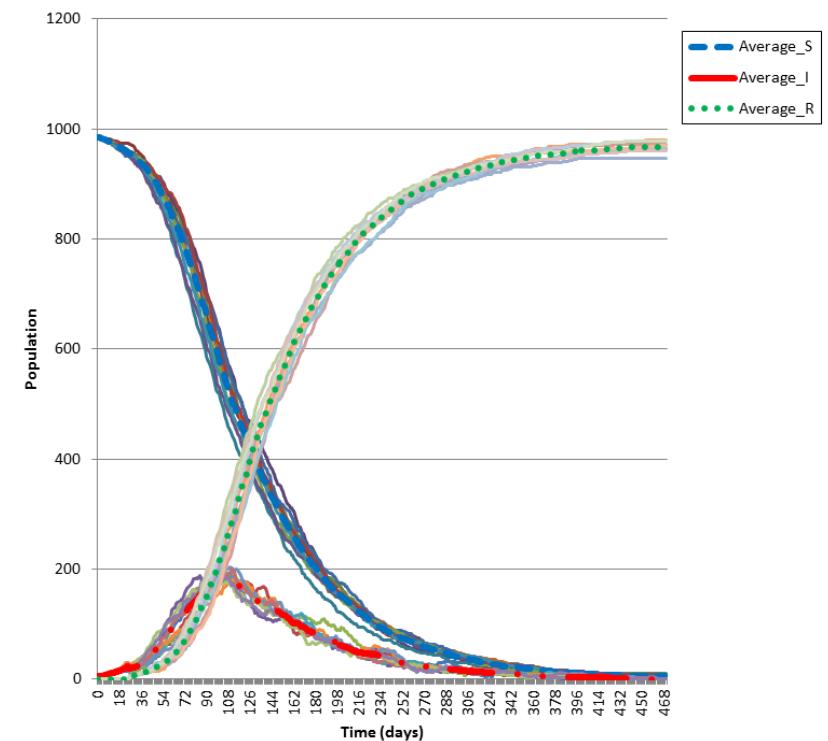
Case Statistic

Category	Case Number
1	10
2	5
3	4
4	2

Vaccination Preventable Disease



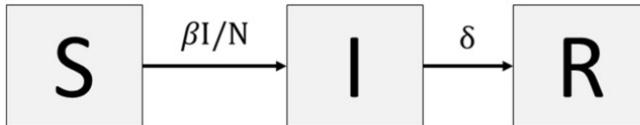
Li, T. S., Labadin, J., Piau, P., Tyng, L. Y., & Abd Rahman, S. (2015). Human behavioral changes and its impact in disease modeling. *Jurnal Teknologi*, 77(33).



Tracking the early depleting transmission dynamics of COVID-19 with a time-varying SIR model

Kian Boon Law¹, Kalaiarasu M. Peariasamy¹, Balvinder Singh Gill², Sarbhan Singh², Bala Murali Sundram², Kamesh Rajendran², Sarat Chandra Dass³, Yi Lin Lee¹, Pik Pin Goh¹, Hishamshah Ibrahim⁴ & Noor Hisham Abdullah⁴

A. Classical SIR model



Equation

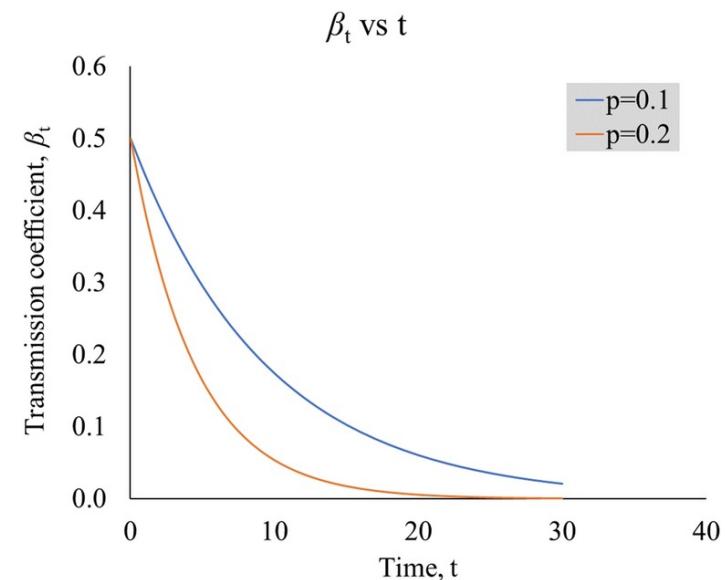
$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta IS}{N} \\ \frac{dI}{dt} &= \frac{\beta IS}{N} - \delta I \\ \frac{dR}{dt} &= \delta I\end{aligned}$$

B. Modified SIR model

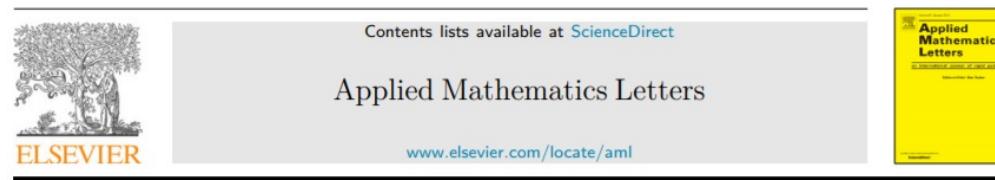


Equation

$$\begin{aligned}\frac{dS}{dt} &= -\frac{z\beta_t IS}{N} \\ \frac{dI}{dt} &= \frac{z\beta_t IS}{N} - \delta I \\ \frac{dR}{dt} &= \delta I\end{aligned}$$

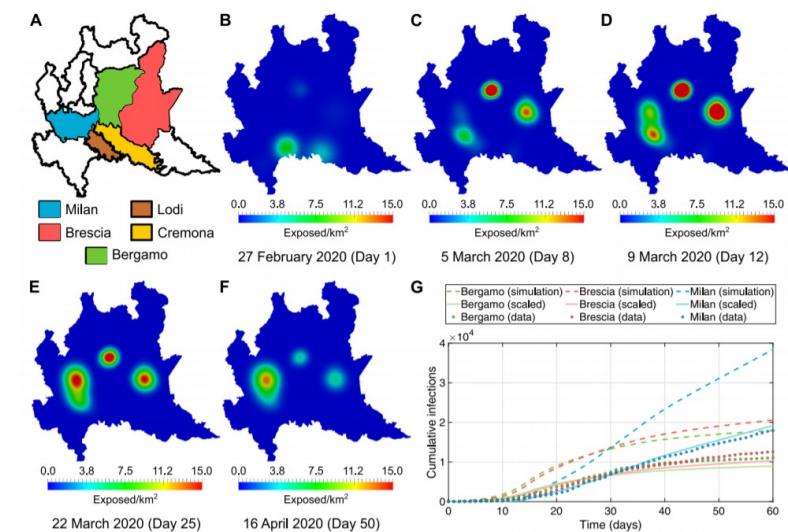
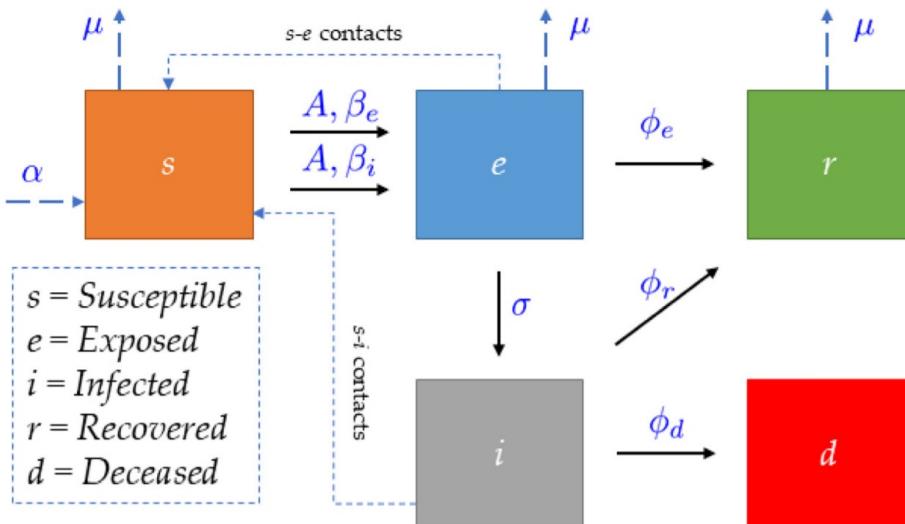


Compartmental Modeling Spatiotemporal Model



Simulating the spread of COVID-19 via a spatially-resolved susceptible–exposed–infected–recovered–deceased (SEIRD) model with heterogeneous diffusion

Alex Viguerie^a, Guillermo Lorenzo^e, Ferdinando Auricchio^a, Davide Baroli^f, Thomas J.R. Hughes^e, Alessia Patton^a, Alessandro Reali^a, Thomas E. Yankeelov^{d,e}, Alessandro Veneziani^{b,c,*}



Coronavirus Pandemic

Forecasting daily confirmed COVID-19 cases in Malaysia using ARIMA models

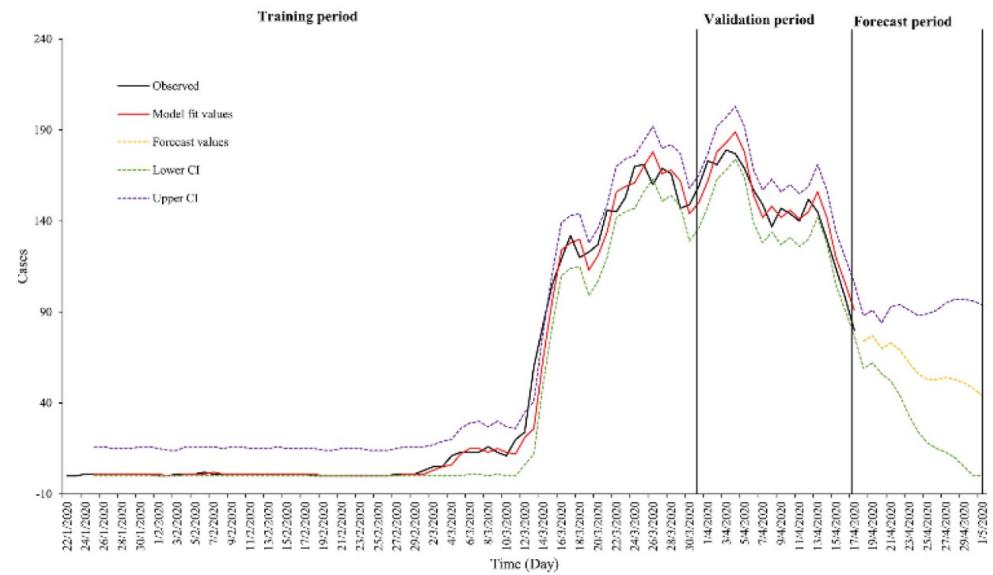
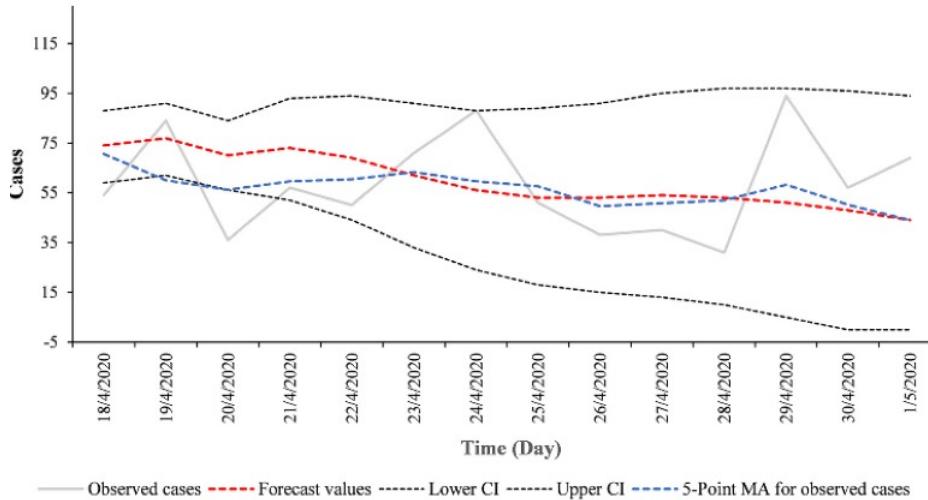
Sarban Singh¹, Bala Murali Sundram¹, Kamesh Rajendran¹, Kian Boon Law², Tahir Aris¹, Hishamshah Ibrahim³, Sarat Chandra Dass⁴, Balvinder Singh Gill¹

¹ Institute for Medical Research (IMR), Ministry of Health, Kuala Lumpur, Malaysia

² Institute for Clinical Research (ICR), Ministry of Health, Shah Alam, Malaysia

³ Ministry of Health, Putrajaya, Malaysia

⁴ Heriot-Watt University, Putrajaya, Malaysia



Statistical Modeling Linear Regression Model



Diabetes & Metabolic Syndrome: Clinical
Research & Reviews



Volume 14, Issue 5, September–October 2020, Pages 1467-1474

Prediction of new active cases of coronavirus disease (COVID-19) pandemic using multiple linear regression model

Smita Rath ^a✉, Alakananda Tripathy ^a, Alok Ranjan Tripathy ^b

Table 1 Correlation Table of Odisha Daily Covid-19 Cases

	Positive	Active	Recovered	Deceased
Positive	1			
Active	0.997739	1		
Recovered	0.977684	0.964648	1	
Deceased	0.979267	0.978835	0.957287	1

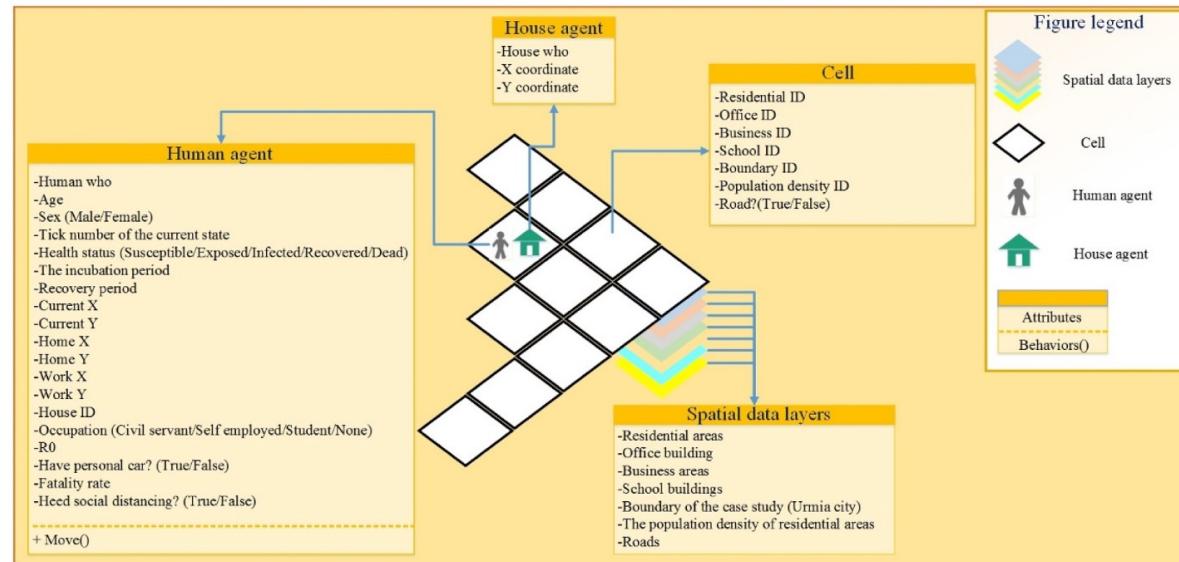
	Coefficients	Standard Error	t Stat	P-value	Lower 95%	Upper 95%	Lower 95.0%	Upper 95.0%
Intercept	2E-09	4.12E-10	4.164241	0.6734	9.02616E-10	2.53E-09	9.02616E-10	2.53164E-09
Positive	1	2.52E-15	3.97E+14	0.6633	1	1	1	1
Recovered	-1	2.56E-15	-3.9E+14	0.6533	-1	-1	-1	-1
Deceased	1	2.41E-14	4.16E+13	0.6753	1	1	1	1

Agent-Based Modeling



Spatio-temporal simulation of the novel coronavirus (COVID-19) outbreak using the agent-based modeling approach (case study: Urmia, Iran)

Navid Mahdizadeh Gharakhanlou ^a, Navid Hooshangi ^{b,*}





COVID-19 Scenarios About FAQ Updates Team

<https://covid19-scenarios.org/>

Web-based Tools



<https://como.bmj.com/>

squire 0.6.3  Parameters Reference News

squire

<https://mrc-ide.github.io/squire/>

IHME | GHDx | GBD Compare Search

 IHME Measuring what matters

<http://www.healthdata.org/covid>

Home Results News & Events Projects Get Involved About

COVID-19 resources

Covid-19 resources

 centre for mathematical modelling of infectious diseases

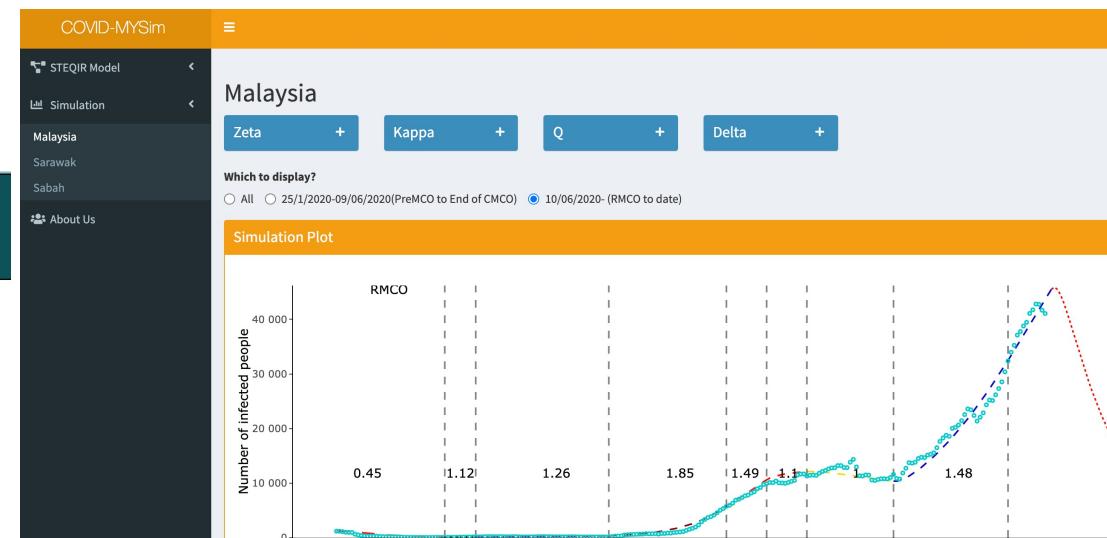
CMMID Repository Home Covid-19 Apps R and Nowcasts About

<https://cmmid.github.io/topics/covid19/>

 IDM Covasim

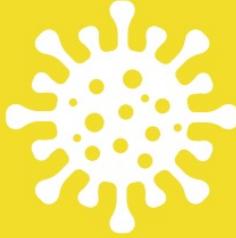
Configuration <https://app.covasim.org/>

General options ^



https://wenhao0117.shinyapps.io/covid-19_mal/

COVID-19 Multi-Model Comparison Collaboration (CMCC)



<https://decidehealth.world/en/cmcc>



Models Impact

CMCC). The Technical Group was chaired by Prof. Marc Brisson (Laval University, Canada) and comprised Mr. Nigel Gay (Independent consultant, UK), Dr. Jane Labadin (Universiti Malaysia Sarawak, Malaysia), Prof. Jodie McVernon (The Peter Doherty Institute for Infection and Immunity, Australia), Dr. Paula Mendes Luz (Oswaldo Cruz Foundation, Brasil), Prof. Wilfred Ndifon (African Institute of Mathematical Sciences, Rwanda), Dr. Brooke Nichols (Boston University/Wits Health Consortium, South Africa), Dr. Shankar Prinja (Postgraduate Institute of Medical Education and Research, India), Prof. Joshua Salomon (Stanford University, USA), and Dr. Akhona Tshangela (Africa CDC, Ethiopia). The Secretariat of the Technical Group comprised Dr. Hannah Clapham (National University of Singapore, Singapore), Dr. Mohamed Gad (Imperial College London, UK), Dr. Adrian Gheorghe (Imperial College London, UK), Dr. Raymond Hutubessy (World Health Organization, Geneva), Dr. Itamar Megiddo (University of Strathclyde, UK), Mr. Christopher Painter (HITAP, Thailand), and Mr. Francis Ruiz (Imperial College London, UK).

*Thank
you !*



Contact me for further enquiries:
ljane@unimas.my