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PLENARY TALK
From In—situ Host—Seeking data to continuous malaria modelling

Anna Shcherbacheva¹, Amadi Miracle², Heikki Haario²,*

¹ University of Helsinki, Finland
² Lappeenranta University of Technology. Finland

*Heikki.Haario@lut.fi

Abstract

Increasingly complex models have been developed to characterize the transmission dynamics of malaria. A well—known pitfall in this field is the lack of experimental real data, that would allow a proper calibration of the model parameters. On the other hand, the multiplicity of malaria transmission factors calls for a realistic modeling approach which incorporates various complex factors such as the effect of control measures, socio—economical variables, behavioral impacts of the parasites to the vector and interseasonal variability. We present an approach which combines in-situ data and the key parameters of continuous epidemiological model for malaria transmission. We stick to the classical Ross malaria model, but express the model parameters for biting rates and mortality as functions of the coverage of the population with LLINs. This is achieved by agent-based stochastic simulations, initially calibrated with hut-level experimental data. Subsequently, the results are generalized for community—level scenarios while employing regression analysis to fit response surfaces for the simulated contact and mortality rates. In addition to LLINs, complex phenomena such as change of behavior of the infected vector and the impact of different household sizes is included in the approach. The performance of the approach is tested against field data of Entomological Inoculation Rate values.
A Problem in Selecting between Human Mobility and Migration Model in Dengue Disease Transmission

Edy Soewono

Department of Mathematics, Institut Teknologi Bandung, Bandung, Indonesia

Abstract

The complexity of dengue transmission problem has been understood as a sophisticated phenomenon that is not fully understood. In reality not all phenomena which are contributing to the intensity of dengue infection can be accommodated perfectly in existing mathematical models. Among other sophisticated phenomena that cannot be satisfactorily adopted in the mathematical model is people’s mobility. It is very common that a person is infected with dengue in a location far from her/his home. The movement of people may vary from daily travel to offices, temporary visits to other places or even changing residences. The main question is how to measure the effect of mobility to the dengue incidences. For example, with the incoming large number of people from Jakarta to Bandung during weekends, what is the consequences to the dengue incidence in Bandung as well as in Jakarta. We consider here two cases of simplification, migrating people from one patch to other patch and mobility of people as part of the daily movement from one patch to another and returning to their homes. In general the (global) basic reproduction ratio of a system, if it is possible to construct, is not enough to measure the effect of mobility on each patch. Instead, the reproduction ratios which represent the endemic threshold in each patch are constructed analytically and analyzed.
Chaos Via Torus Destruction in Population Biology and Its Implications for Data Analysis

Nico Stollenwerk\textsuperscript{1,*}, Maíra Aguiar\textsuperscript{2}, Bob W. Kooi\textsuperscript{3}

\textsuperscript{1}CMAF—CIO, Lisbon University, Portugal
\textsuperscript{2}Centre for Mathematics and Applications, Faculty of Sciences and Technology, NOVA University of Lisbon, Portugal
\textsuperscript{3}Free University Amsterdam, The Netherlands

\textsuperscript{*}nico@ptmat.fc.ul.pt

Abstract

In the analysis of relatively simple models for dengue fever epidemiology, describing antibody dependent enhancement ADE and temporary cross—immunity, we encountered Hopf and torus bifurcations and, by increasing parameters slightly further, also the onset of deterministic chaos characterized by positive dominant Lyapunov exponents [1]. Such models describe well the large fluctuations observed in time series of dengue fever hospitalization cases. However the models are already high dimensional and any data analysis is difficult because of the chaotic behaviour and also the high number of initial conditions. We therefore search for simpler models in population biology with similar dynamical behaviour, one of the simplest originating from ecological models of Rosenzweig—MacArthur (R—MacA) type. The classical R—MacA model shows a Hopf bifurcation which under seasonal forcing turns into a torus bifurcation. By increasing the forcing further the onset of deterministic chaos was observed and e.g. described in [2], but lacking a further analysis of the onset of chaos as the tori break off. Via the analysis of two dimensional dominant Lyapunov exponent plots we revealed the chaotic regions to be inside Arnold tongues of the original tori [3]. This gives a first hint of further analysis of the original dengue fever models in which the interplay of different sub—systems can give rise to a similar scenario. Since the original dengue models are not seasonaly forced, the analysis of the autonomous systems place additional difficulties in identifying the interplaying frequencies. The full understanding of this dynamic scenario helps in the subsequent data analysis of empirical time series of dengue fever hospitalization cases, e.g. via iterated filtering, since it turns out that not a single model is describing the large fluctuations of the data but a dynamic scenario [4]. We will elaborate on this aspect of data analysis via quite new tools of model comparison as e.g. given by Bayes factor analysis. And again, the understanding of such models is vital for the understanding of any intervention measure, as e.g. the impact of the newly licensed dengue fever vaccine, which however turned out to be quite problematic exactly because of the subtle interplay between ADE and temporary cross—immunity [5, 6].

Keywords: (Dengue fever and chaos, Lyapunov exponents, Rosenzweig—MacArthur model, torus bifurcation, Arnold tongues)
References


Bioinformatics, Big Data and Precision Medicine

Mohammad Asif Khan
Centre for Bioinformatics, School of Data Sciences, Perdana University, Malaysia

asif@perdanauniversity.edu.my

Abstract

The turn of the 21st century has heralded unprecedented technological advancements in biomedical research. This has resulted in the high-throughput and highly automated quantification and digitization of biological data, driving the omics, big data revolution that allows for description of the molecular landscape of individuals, with astonishing depth and breadth. The translation of these advancements to improvement in clinical care, especially with respect to precision medicine, however, has been largely limited. Understanding complex diseases and translating the discoveries in a targeted fashion require significant cross-disciplinary collaboration. Bioinformatics is a transformative science that brings together this form of collaboration. Development of sophisticated bioinformatics tools, powered by Artificial Intelligence, among others, to map genetic variations to phenotypes accurately are enabling selective treatment approaches, targeting the root causes of diseases/disorders.
Developed by Sanofi Pasteur, a tetravalent dengue vaccine, Dengvaxia, was recently recommended by the World Health Organization (WHO) Strategic Advisory Group of Experts (SAGE) on Immunization, based partially on modeling results, to be used in countries with high dengue endemicity as evidenced by seroprevalence in the targeted age group of more than 50% (preferably 70%) [1]. Analyses of clinical trial data demonstrate that individuals who were seronegative (never infected with a dengue virus prior to vaccination) when vaccinated routinely develop non-protective dengue antibodies [2, 3]. Surprisingly, despite high rates of overt disease among vaccinated seronegative persons, mathematical models of populations with a seroprevalence of 70% have estimated an overall reduction of dengue hospitalizations on the order of 10–30% over a period of 30 years, with 80% vaccine coverage of 9 year-olds [1, 4]. It should be noted that accurate predictions in complex systems such as described in [4] can be only made for short periods of time. A 20–30–year prediction horizon puts in doubt the beneficial results of vaccine administration [5]. In this talk I will present an age structured model that was developed based on the WHO–SAGE recommendation to vaccinate persons age 9–45 years in dengue endemic countries. The model was used to explore the clinical burden of two vaccination strategies: 1) Vaccinate individuals, ages 9–45 years, seropositives and seronegatives, and 2) vaccinate individuals, ages 9–5 years, who are dengue immune only [6]. A sensitivity analysis of the proposed model will be discussed. Our mathematical model finds that significant reduction of hospitalizations can be only achieved when vaccine is directed exclusively to seropositive individuals [6]. When using a more recent data set by age and serostatus from the combined CYD14, CYD15, CYD57 trials, as reported in Table 1 in Martinez–Vega et al. [7], we confirm statistically the vaccine induced risk in seronegative individuals [8],[9].

**Keywords:** (Deterministic chaos, Positive Lyapunov exponents, Age structured models, Serostatus, Vaccine efficacy)
References


INVITED TALK
Global Stability of A Discrete SIR Epidemic Model with Saturated Incidence Rate

Agus Suryanto
Department of Mathematics Faculty of Mathematics and Natural Sciences, Brawijaya University, Jl. Veteran Malang 65145 INDONESIA
suryanto@ub.ac.id

Abstract

In this work a nonstandard finite difference scheme is implemented to discretize a SIR epidemic model with saturated incidence rate. The dynamical properties of the obtained discrete model are then analyzed. It is found analytically that the discrete model preserves all essential properties of the continuous model such as the positivity and boundedness of the solutions as well as the equilibrium points and their stability properties. The stability analysis here is performed locally via linearization of the discrete system around each equilibrium point and globally using discrete-time analogue of Lyapunov functions. Both local and global asymptotic stability of the equilibria are fully determined the basic reproduction number ($R_0$) irrespective of the time step size. We conclude that our discretized epidemic model is dynamically consistent with the corresponding continuous model. The analytical results are confirmed by numerical simulations.

Keywords: (Discrete epidemic model, Nonstandard finite Difference scheme, Dynamically consistent, Global stability, Lyapunov function)
A Comparison of Fuzzy Clustering Approaches for Gene Expression Profiling in Advanced Breast Cancer after Neoadjuvant Chemo-and Hormone Therapy

Setia Pramana1⇤, Syarifah Dewi2, Septelia Inawati Wanandi2, Ramadhan Karsono3

1 Center for Computational Statistics Studies, Politeknik Statistika STIS
2 Department of Biochemistry and Molecular Biology, Faculty of Medicine, Universitas Indonesia
3 Department of Oncology Surgery, Dharmais National Cancer Hospital

⇤setia.pramana@stis.ac.id

Abstract

Neoadjuvant chemo-and hormone therapy has been widely used for locally advanced breast cancer patients to reduce tumor size. However, the effect of both neoadjuvant therapy (NAT) on metastatic breast cancer remains unknown, particularly in association with apoptotic-pathway. Several studies have been carried out to investigate the expression of p53—apoptotic pathways genes in advanced breast cancer patients using standard approach such as the hierarchical clustering. Although this form of clustering shows basic cluster patterns, the accuracy of clusters need to be investigated further. In this study, we investigate of the gene expression profile in distinguishing breast cancer using advanced clustering approaches. We collected stage IIIb and IV breast cancer tissues from 46 patients before and after neoadjuvant chemo—(5−fluorouracil, anthracyclines, cyclophosphamides) and hormone (tamoxifen or aromatase inhibitor) therapy. Patients were treated for 6 months prior to tumor resection. The expression profile of p53—pathway genes was investigated using Next—Generation Sequencing and Targeted RNA expression p53 panel comprising of 52 genes (TruSeq®, Illumina). Several clustering methods, Fuzzy C—Means, Gustafsson Kessel FCM, Ensemble GK FCM methods are implemented and then compared using cluster validation indexes (Xie Benie, Partition Coefficient, Modified Partition Coefficient, Classification Entropy, Kwon, Tang, and Separation Indexes). The study reveals alteration of several p53—pathway gene expressions which indicate the effectiveness of both chemo- and hormone therapy to suppress tumor proliferation and induce apoptosis in advanced breast cancer prior to mammosurgery.

Keywords: (Next generation sequencing, Fuzzy clustering, Breast cancer, Gene expression)
From Data to Drug Decisions: How Precision Medicine Can Help Solve Real World Problems

Maulana Bachtiar

Yong Loo Lin School of Medicine, National University of Singapore (NUS), and the Data Analytics Lead of the Data Analytics Core at the Medical Sciences Cluster

*bachtiar.maulana@u.nus.edu

Abstract

Data is disrupting the way our society functions. While Go-Jek and Grab show how deep application of data analytics can facilitate a more efficient public transportation on the road, the healthcare industry is also going to benefit from human data utilization. But, real world application of traditional pharmacogenomics is challenging, partly due to the presence of population differences that are manifested in various levels in the clinics. As more data becomes available in healthcare, such as through greater adoption of electronic health record platform and lower cost of DNA sequencing, analytics would propel a faster adoption of ‘precision medicine’ in the clinics. Here, I will share how data analytics method can be applied in medical translational research, which can potentially lead to a faster adoption of precision medicine in healthcare in both developed and emerging economies.
Smart Probe for Intracellular Imaging: Lets Tame It!

Samira Husen Alamudi

Agency for Science, Technology and Research (A*STAR), Singapore

*samirahusenalamudi@gmail.com, samira.alamudi@sbic.a-star.edu.sg

Abstract

Fluorescence labelling of an intracellular biomolecule in native environment is a powerful strategy to achieve in-depth understanding of the biomolecules roles and functions. Besides being nontoxic and specific, desirable labelling probes should be highly cell permeable without nonspecific interactions with other cellular components. In this talk, I will discuss on the development of predictive model for designing such fluorescence probe by utilizing high-throughput screening in combination with cheminformatics. The results provide an efficient strategy for designing cell-permeable probes with no background interference. These probes, which are referred to as being tamed in character, provide novel tools for bioimaging applications in living condition.
Modelling Commuter Data for Dengue in Jakarta

Dipo Aldila\textsuperscript{1,*}, Nathania Audia \textsuperscript{1}, and Prama Setia Putra \textsuperscript{2}
\textsuperscript{1}Department of Mathematics, Universitas Indonesia
\textsuperscript{1}Department of Mathematics, Institut Teknologi Bandung
\textsuperscript{*}aldiladipo@sci.ui.ac.id

Abstract

A mathematical model of dengue spread will be discussed in this talk. A commuter of human in Jakarta which describes the daily mobility of human for working and school purposes is included into the model. Mathematical analysis of equilibrium point and their local stability were analyzed. Basic reproduction number as the spectral radius of the next-generation matrix conducted analytically. For a simple model which involve only two districts, the basic reproduction number is taken from the maximum of the local basic reproduction number for each district. Numerical sensitivity analysis of basic reproduction number respect to the mobility parameters is shown to give a better understanding of how mobility might impact the spread of dengue.

\textbf{Keywords}: (dengue, commuter, mobility, equilibrium, basic reproduction number)
Analysis of Mathematical Model of HIV−1 Infection in CD4+ T Cells Due to Cells to Cells Contact with Antiretroviral Treatment

Sutimin*, R. Heru Tjahjana, Sunarsih

Department of Mathematics, Diponegoro University, Semarang, Indonesia

*sutimin@undip.ac.id

Abstract

We modify a mathematical model that captures the spread of HIV−1 infection of CD4+ T cells by taking into account the contact from infected cells to healthy cells, the clearance of virus by healthy cells, and incorporating antiretroviral treatment. We analyze the model to describe the dynamics of HIV−1 infection and the effect of antiretroviral treatment in reducing the progression of HIV−1 infection. The basic reproduction number is derived from the next generation matrix of the model, then we analyze the stability of equilibria of the model. We analyze the stability of free disease equilibrium by using linearization, and the stability of endemic equilibrium by constructing Lyapunov function. If the basic reproduction number less than unity, free disease equilibrium is locally asymptotically stable, while endemic equilibrium is globally asymptotically stable when the basic reproduction number large than unity. The numerical results show that in the preventing of HIV−1 infection, the treatment of RTI drug may be more effective than that of PI drug.

Keywords: (HIV-1 infection, RTIs, PIs, CD4+T cells)

References


Indonesian Mangroves Extract Library: an Ideal Model towards Integration of Indonesian Biodiversity Information System

Kholis Abdurachim Audah¹,²
¹Academic Research and Community Services
²Department of Biomedical Engineering, Swiss German University, Prominence Tower, Alam Sutera, Tangerang 15143, Banten, Indonesia

* kholis.audah@sgu.ac.id

Abstract

Indonesia is home of approximately 30000 or about 10% of the worlds flowering plants and other biota both in land and marine with significant figures. This figure is of interesting facts regarding Indonesian biodiversity, which is considered as one of the most diverse in the world. The information can be more interesting and meaningful if details about particular biota is also known. Development of Indonesian Extract Library is very important as a small step towards the integration of the Indonesian Biodiversity Information System. The library should include but not limited to name and species, location, chemical composition and usage of a biota such as for foods, biomedical applications or other human needs. Additional information such as used methods or publications would be very useful as reference for further investigation. Among of many potential plants, Mangroves are very potential ones to be explored and used as an ideal model to develop an extract library. The library can be then expanded for any other organisms originated from Indonesian land or water. Implementation of barcoding system and integration of all data into a comprehensive information system is necessary. This can be utilized as a window of the Indonesian biodiversity as a whole and can be utilized for different purposes such as drug discovery and other noble causes for the betterment of human being.

Keywords: (Drug discovery, Extract library, Mangroves, Indonesian biodiversity, Information system)
Analysis of Multimodal Data using Fundus Images and Gene Expression Data to Diagnosis of Diabetic Retinopathy

A. Bustamam∗, D. Sarwinda, Gianinna Ardaneswari, Titin Siswantining
Department of Mathematics, Faculty of Mathematics and Natural Sciences, Universitas Indonesia

∗alhadi@sci.ui.ac.id

Abstract

Diabetic Retinopathy is a disease caused by long—term microvascular complications on diabetes mellitus patients. This research investigates texture feature capabilities from fundus images and gene expression data to detect diabetic retinopathy (DR). In our proposed method, we used two different methods for processing our data. In fundus images, we used improvement of local binary pattern (LBP) with calculation of LBP original value and magnitude value of fundus images. This method is compared with Local Line Binary Pattern (LLBP). In this study, two experiments (DR—Normal, Multiclass) were designed for two databases, DIARETDB0 database and STARE. Kernel PCA is choosed as feature selection method, and three classifiers are tested (Naive Bayes, SVM, and KNN). While, we implemented parallel Two-Phase Biclustering for gene expression data. For the first phase, we used parallel K—Means algorithm and the second phase using Cheng—Church Biclustering algorithm. The experimental results show that our proposed method has higher accuracy than LLBP, with accuracy of binary classification 100% for DRNormal and AMD-Normal. While, multiclass classification (DRAMD—Normal) achieves an accuracy 80–84%. Another results show that our proposed method give good performance in running time. These results suggest that our proposed method in this paper can be useful in a diagnosis aid system for diabetic retinopathy.

Keywords: (Diabetic retinopathy, Fundus images, LBP, Gene expression data, Biclustering, Parallel computing)
On Modified Logistic Growth Model

Windarto

Department of Mathematics, Faculty of Science and Technology, Universitas Airlangga

windarto@fst.unair.ac.id

Abstract

The mathematical model of growth has been extensively used to describe the dynamics of population growth, the spread of a rumor, the dynamics of chemical reactions and artificial neural network techniques. Population growth models can be classified into empirical growth models (e.g. Weibull model and Morgan-Mercer-Flodin model) and dynamic growth models (growth models derived from a differential equation). Most dynamic growth models are a modification of logistic growth models, including the Richards model and the Gompertz model. In this talk, we present a new modified logistic growth model as an alternative model to describe the growth of a population. We also compared the sensitivity of some population growth model due to trimmed data. We found that the empirical model more sensitive than the dynamic model.

Keywords: (Growth model, Modified logistic model, Empirical model, Trimmed data)
Having Fun with S—I—R Model
Nuning Nuraini*, Novriana Sumarti, Meta Kallista
Institut Teknologi Bandung, Indonesia

*nunnur4@gmail.com, novriana@math.itb.ac.id, meta.kallista@gmail.com

Abstract

From K—pop to U.S pop star, from movie series to blockbuster movie, mathematical modeling can help assess to describe the hits, prediction and some exciting aspect of that entertainment phenomena. Using only simple, well-known SIR model, we can have fun with this topic to ask students explore deeper and gain insight to do the research more applicable. We also deal with an open data source, define a problem, variables, parameters, and do the modeling cycle. We have a good result that makes us learn the dynamical analysis happily.

Keywords: (SIR model, Data source, Modeling cycle)
CONTRIBUTED TALK
Leptospirosis Disease Model: Seasonal Variation of Bacterial Population

Rudianto Artiono*, Budi Priyo Prawoto
Department of Mathematics, Universitas Negeri Surabaya

*ruddiantoartiono@unesa.ac.id

Abstract

Leptospirosis is a bacterial disease of worldwide importance. This disease can spread sporadically not only in the human population but also in the domestic animal population. The disease is transmitted by rats, which act as a reservoir for leptospira bacteria. It is well-known that high rainfall season can increase the number of human cases of leptospirosis. The survival rate of bacteria is known to change seasonally, mortality being lower in rainy season and higher in dry season. The aim of this study was to determine seasonal model of leptospirosis. Compartment model was used as a basis of model construction. Model had been built based on real phenomenon which involved human population, host animal population, vector animal population and leptospira bacteria. Seasonal effect had been considered in the growth of bacteria life cycle. Model analysis had been done through stability analysis of free endemic equilibrium and endemic equilibrium. Numerical simulation had been explored to figure out the behavior of seasonal model in the future. Some interpretations relate to the biology phenomenon had been summarized logically based on the model constructed.

Keywords: (Epidemiology, Leptospirosis, Seasonal model, Stability analysis)

References


Modelling The Number of New Pulmonary Tuberculosis Cases with Geographically Weighted Negative Binomial Regression Method

Tsuraya Mumtaz¹, Agung Priyo Utomo²
¹ Majoring in Statistics, Badan Pusat Statistik, Jakarta
² Majoring in Statistics, Politeknik Statistika STIS, Jakarta

13.7893@stis.ac.id , ² agung@stis.ac.id

Abstract

Tuberculosis (TB) is an infectious disease caused by Mycobacterium Tuberculosis. Until now, TB is still one of the main problems in many countries, especially developing countries. Indonesia ranked second as the country with the highest TB cases in the world in 2015. The number of new pulmonary TB cases in Indonesia continually increase by each year, where most cases were found in Java. This study was conducted to model the number of new pulmonary TB cases in Java by considering the spatial aspects and overdispersion using Geographically Weighted Negative Binomial Regression (GWNBR). As an evaluation, this study also compared the model resulted from GWNBR with the model generated from other commonly used methods such as negative binomial regression and Geographically Weighted Poisson Regression (GWPR). The result showed that the population density and percentage of healthy homes were not significantly influential in each region. While the number of health centers (Puskesmas), the percentage of smokers, the percentage of good PHBS, the percentage of diabetes mellitus, and the percentage of less BMI were significant in some regions only. In general, GWNBR model was better for modelling the number of new pulmonary TB cases than negative binomial regression and GWPR.

Keywords: (GWNBR, Spatial, Overdispersion, Pulmonary tuberculosis, Java)

References


Numerical Analysis of The Impact of Loss—sight and Undetected Cases in The Spread of TB

Dian Setyorini*, Bevina D. Handari, Dipo Aldila
Department of Mathematics, Universitas Indonesia, 16424 Depok, Indonesia
*diandeeice@gmail.com, bevina@sci.ui.ac.id, aldiladipo@sci.ui.ac.id

Abstract

TB disease until now is one of the world’s health problems. Loss-sight and undetected cases contribute to the high case in the spread of the TB. A deterministic model of TB including loss-sight and undetected cases with quarantine intervention is presented and analyzed in this talk. We employed a sensitivity analysis on the basic reproduction number ($R_0$) and identified the parameters that should be targeted by treatment strategies with quarantine intervention. Numerical simulations performed under various scenarios based on sensitivity analysis of $R_0$ will show how significant the role of treatment with quarantine to overcome the spread of TB. The more people infected with TB disease with loss-sight and undetected cases will be faster also the process of dissemination of TB disease that occurs. If this condition persists, then the effort to be done to overcome the spread of disease will take a long time, and the cost to be spent for the treatment of TB disease will be greater.

Keywords: (Dynamical system, Tuberculosis, Mathematical model, Quarantine, Basic reproduction number($R_0$))

References


Mathematical Analysis of a Tuberculosis (TB) Transmission Model with Vaccination in an Age Structured Population

Siti Laelatul Chasanah *, Dipo Aldila , Hengki Tasman
Department of Mathematics, Universitas Indonesia, 16424, Depok, Indonesia

*schasanah93@sci.ui.ac.id

Abstract

This study presents a mathematical model of Tuberculosis (TB) transmission considering BCG vaccination in an age-structured population to simulate the TB dynamic and evaluate the potential impact on active TB of several vaccination strategies. We developed a deterministic compartmental model where the population was distributed into seven compartments, i.e., susceptible individuals that can be vaccinated ($S_1$) and can’t be vaccinated ($S_2$), vaccinated ($V$), slow ($L$) and fast ($E$) exposed, infectious ($I$) and recovery ($R$). The mathematical model analysis was done by determining the equilibrium point of the system, analyze the stability of the equilibrium point and determine the Basic Reproduction Number ($R_0$). Some numeric interpretations were given by sensitivity analysis of parameters $u_1$, $u_2$ and $\xi$ to $R_0$ and autonomous model simulations. Numerical simulations of the model show that to reach a disease-free equilibrium point is not enough by maximizing one of the parameters $u_1$, $u_2$ or $\xi$. The vaccine is also more effective given to individuals under 30 years than the newborn.

Keywords: (Tuberculosis (TB), Vaccination, Age structured population)

References


Mathematical Models for The Dynamics of The HIV with Antiretroviral Treatment Interventions and The Effect of Apoptosis on T–Cells

Ahmad Rizal*, Dipo Aldila, Bevina D. Handari
Department of Mathematics, Faculty of Mathematics and Natural Sciences, University Indonesia, Depok 1624, Indonesia

*ahmadrizal@sci.ui.ac.id

Abstract

The development of HIV, when evaluated in vivo can be modeled into a system of ordinary differential equations using a deterministic approach. Until now, there is no medicine to cure HIV infection, but there is a treatment that can slow the progression of HIV in the body called Antiretroviral Treatment. In this paper, be formed a mathematical model for the dynamics of HIV in the body with the intervention of Antiretroviral Treatment and take into account the influence of Apoptosis on T–cells. The dynamic system analysis of the model uses the Routh–Hurwitz criterion and analyzes the Basic Reproduction Number ($R_0$) to determine the stability of the infectious free equilibrium point and the endemic equilibrium point. Numerical simulations are performed to analyze the effects of Antiretroviral Treatment intervention and the impact of Apoptosis on T–cells in inhibiting HIV progression.

Keywords: (HIV, Antiretroviral treatment (ART), Apoptosis, Equilibrium point, T–Cells)

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The Utilization of Optimal control on the HIV—1 Infection in CD4\(^+\) T Cells with RTI and PI Therapy

R. Heru Tjahjana*, Sutimin
Departement of Mathematics, Diponegoro University

*heru.math.undip@gmail.com

Abstract

The purpose of this paper is to expose the optimal strategy of controlling HIV—1 infection in CD4\(^+\) T cells with RTI and PI therapy. The scope of the paper includes a model of the dynamic system of HIV—1 infection in CD4 cells and a functional cost model that minimizes the population of free virus and therapeutical costs. From the dynamics system model and cost functional model are designed for optimal control for HIV—1 infection control. In this paper are obtained optimal control for RTI and PI therapies. The conclusions of this paper obtained are as follows, with the optimal control approach obtained infectious control strategy that minimizes the population of free virus and the cost of therapy. In other words, optimal control can be used as a good approach in determining infection control strategies that minimizes the population of free virus and the cost of therapy.

Keywords: (Optimal control, RTI therapy, PI therapy)

References


Symposium on Biomathematics 2018, Department of Mathematics, Universitas Indonesia.
The Importance of Social Interaction Factors on The Type 2 Diabetes Mellitus Prognosis Model

R.Ratianingsih*, Hajar, A.I.Jaya

Mathematics Study Program of Tadulako University

*ratianingsih@yahoo.com, hajar.200490@yahoo.com, jayaindraagus@gmail.com

Abstract

The preview work on diabetes mellitus (DM) model stated that obesity is the crucial phase of DM prognosis that consisted of several phases. The phases are susceptible ($S_N$), overweight ($S_O$), obesity ($O$), DM, metabolic syndrome ($MS$) and chronic ($C$), a condition indicated by such another coexist disease. This paper reconsiders the phase of $MS$ not only as a risk factor of $DM$ but also as a trigger factor of it. It means that the next phase of DM phase could be SM and the next phase of SM phase could be DM. Comparing to the preview model, the overweight-obesity transition rate ( ) and the successness of positive interaction between O and O S and or N S and between N S and N S , that is , are the important parameters to be considered for the existence of the critical point. The stability of the critical point of the nonlinear system is identified from the Jacobian matrix in form of six order factorized characteristic polynomial. The first-order provides a negative eigenvalue, while the second-order polynomial gives a discriminant value that identify the stability of the critical point. Such positive discriminant leads to a positive eigenvalue that comes to the unstable critical point becomes. When the discriminant is negative, the stability identification is extended to the third-order polynomial using the Routh Hurwitz criteria. Some requirements are needed to justify a stable critical point. The appearance of and parameters as the requirements of a stable critical point shows the importance of the social interaction in the DM prognosis. Finally, the discussion is completed by simulation that represents the dynamic of the DM prognosis process.

Keywords: (E)

References

Mathematical Model of the Effect of Bears on the Pacific Salmon Population in British Columbia

Jane Sahetapy-Engel, Azhary Ramadhanty, Eduardus Axel Wijaya, Dancent Sutanto, Ambar Winarni and Prama Setia Putra

Department of Mathematics,

Abstract

An interaction model for the Pacific salmon and bear population in British Columbia is discussed here. The phenomenon is shown during the salmons period of migration back to their birthplace river at the end of their life. During this returning home, large number of bears from the nearby state come and prey on them. This predation of salmon before spawning is suspected as the cause of the decline in Salmon production. Here a dynamical model involving a specific predator-prey type interaction between Salmon and Bears is constructed in the form of a non-autonomous dynamical system, in which the transition rate from the adult state of salmon to the spawning state is positive only in the month of migration. A dynamical analysis for stability of the coexistence equilibrium for the autonomous case is shown and a sensitivity analysis for the non-autonomous case is done numerically.

Keywords: (Predator-prey Equilibrium point Stability analysis)

References

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Real–Time Dengue Forecasting by the Method of Analogues

Afrina Andriani br Sebayang*, Mochamad Apri, Edy Soewono
Industrial and Financial Mathematics Group, Faculty of Mathematics and natural Sciences, Institut Teknologi Bandung, Bandung, 40132, Indonesia

*afrina.brsebayang@gmail.com

Abstract

The lack of preparedness in handling dengue cases is often caused by a deficiency or an inaccuracy in detecting real-time dengue surveillance data. Presently, with the ability to access historical data from dengue cases and with appropriate computational method, it is possible to develop an epidemiological forecasting method. Accurate forecasting method would markedly predict potential risk of dengue outbreak and improve the control and prevention of impending or ongoing epidemics. One of the biggest challenges in this area is how to generate real-time predictions and to assess the accuracy of the disease forecasting result. In this work, an Analogue method which is one of non-parametric forecasting method is proposed to predict the real-time future trend and prevalence for several weeks ahead of dengue incidence cases. Moreover, the forecasting accuracy will be addressed and tracked by calculating the correlation coefficient and root mean square between observed and forecasted data. As for the latter, the result yields long-term future trend prediction of dengue cases and estimates the limit of forecastability which provide a basic insight for future dengue monitoring and control strategies.

Keywords: (Epidemic forecasting, Error measure, Analogue method, Prediction)

References


Abstract

Bioinformatic is one of many aspect which is using classification methods. For example, it is used to determine phase level of a disease. This research will classify the phase of *Plasmodium falciparum* parasite which causes malaria. This disease is spread by an infected female *Anopheles* mosquito which contains *Plasmodium*. The result of this research could be used to determine *Plasmodium* parasite phase in infected peoples red blood cells. The purpose of this research is to discover the success rate of Multiclass Support Vector Machines method and analyze it in order to predict the parasite phase levels. The data of this study is image data of red blood cells which was infected by three kinds of *Plasmodium falciparum* parasite levels. In the process, this study will be using Canopy as Integration Development Environments of python programming language. From 112 trials, the highest number of accuracy is 87.5% for Multiclass Support Vector Machines one vs rest and one vs all methods which used the 4–fold cross validation with C=1 as parameter for both linear and RBF kernel with $\gamma = 0.0001$.

**Keywords:** (Malaria, *Plasmodium falciparum*, Classification, Multiclass support vector machines.)

References


A Stage—structure Predator—prey Model with Ratio—dependent Functional Response and Anti-predator

Adina Apriyani, Isnani Darti *, Agus Suryanto
University of Brawijaya

adina.apriyani94@gmail.com, * isnanidarti@ub.ac.id, suryanto@ub.ac.id

Abstract

This paper discusses a stage-structure predator-prey model with ratio-dependent functional response. The proposed mathematical model is a system of three nonlinear ordinary differential equations that describe the interactions between prey population, juvenile predator, and adult predator. It is assumed that only adult predators attack and consume the prey and have the ability to reproduce. Here, we also consider an anti-predator defense effects where prey can attack juvenile predator. However, it is also assume that adult predators help when juvenile predators are attacked by prey. The proposed model is analyzed dynamically, which includes the existence and local stability of equilibrium points. There are two equilibria, namely extinction of predator and the interior equilibrium point. The extinction of predator always exists and it is conditionally asymptotically stable. If the interior equilibrium exists, then it is asymptotically stable. Numerical solutions are carried out to illustrate the theoretical results.

Keywords: (Predator—prey model, Stage structure, Ratio-dependent response function, Anti-predator, Stability analysis)
Leslie—Gower Predator—Prey Model with Stage—Structure, Beddington—DeAngelis Functional Response, and Anti—Predator Behavior

Umu Salamah, Agus Suryanto*, Wuryansari Muharini Kusumawinahyu
Universitas Brawijaya

ummusalamah90.us@gmail.com, *suryanto@ub.ac.id, wmuharini@ub.ac.id

Abstract

In this paper, we concern with a Leslie-Gower predator-prey model with stage-structure on predator using the Beddington-DeAngelis functional response. The predator population is divided into two subpopulations, namely juvenile predator and adult predator. It is assumed that only adult predator which has ability to attack prey and to reproduce. Moreover, anti-predator behavior is also considered in this model, which is represented by the possibility of juvenile predator to be attacked by prey. Dynamical analysis on the model, including determination of equilibrium points, the existing condition, and the local stability of equilibrium point is performed. There are four equilibrium points, namely the extinction of all populations point, the extinction of prey point, the extinction of predator point, and the interior equilibrium point. The extinction of all populations point and the extinction of prey point always exist, while the predator extinction point and the interior point exist under some certain conditions. The extinction of all populations point is always unstable, while the other three equilibrium points are conditionally asymptotically stable. Some numerical simulations are performed to support the analytical results.

Keywords: (Predator—prey model, Stage—structure, Beddington—DeAngelis functional response, Anti—predator, Dynamical analysis)
Sensitivity and Stability Analysis of SEIR Epidemic Model with Information.

Robiatul Witari Wilda, Trisilowati*, Aruman Imron

University of Brawijaya

robiatulwitariwilda13@gmail.com, *trisilowati@ub.ac.id, maimr@ub.ac.id

Abstract

In this paper, the construction and analysis of SEIR epidemic model with information are discussed. This model contains information about how to prevent the spread of infectious diseases which is transmitted by infected individuals to susceptible individuals. Furthermore, the dynamical analysis of the model which includes determination of equilibrium points terms of existence, stability analysis of the equilibrium points and sensitivity analysis are observed. Local stability of the equilibrium point is determined by linearizing the system around the equilibrium point and checking for the eigen value sign of Jacobi matrix at each equilibrium point. Sensitivity analysis is performed by using sensitivity index to measure the relative change of $R_0$ on each parameter. Based on analysis result, there are two equilibrium points namely disease free-equilibrium point and endemic equilibrium points. The disease free-equilibrium point always exists and it is locally asymptotically stable if $R_0 < 1$. Moreover, the endemic equilibrium points exist and are locally asymptotically stable under certain conditions. From sensitivity analysis, it is found that disease transmission rate, recruitment rate and number of contacts rate of infected are the most sensitive parameters. Finally, numerical simulation is conducted to support the analysis result.

Keywords: (Sensitivity analysis, Stability analysis, SEIR epidemic, Information)
Evolutionary Dynamic of Insecticides Resistance in two—locus of Anopheles Mosquitoes

Dani Suandi*, Edy Soewono, Kuntjoro Adji Sidarto

Department of Mathematics, Institut Teknologi Bandung

*danisuandi@s.itb.ac.id

Abstract

The use of insecticides in various countries has long been done in malaria vector control. Unfortunately, continuous usage has been shown to reduce the effectiveness of insecticides, which is an indication of resistance. Consequently, the management of resistance needs to be improved such that the insecticides can be used effectively. Improvement is done by rotating different types of insecticides with different target sites, which is known as rotational techniques. However, irregular rotation techniques can also cause double resistance problem. In this paper, a mathematical model that describes the dynamic evolution of insecticide resistance is constructed based on different target insecticide sites. Existence and stability analysis is conducted to understand the factors that can accelerate resistance. Sensitivity analysis is also carried out to investigate the parameters that play essential roles in the evolutionary dynamic of insecticide resistance. Furthermore, numerical simulations are performed to show the effectiveness of rotational techniques in decreasing of the resistant mosquito population.

Keywords: (Evolutionary dynamic, Two-locus, Insecticides resistance, Existence and stability)

References


A Biclustering Procedure Using BicBin Algorithm for HIV–1 Human Protein Interaction Database in NCBI

Patuan Pangihutan Tampubolon*, Alhadi Bustamam
Mathematics Department, FMIPA, Universitas Indonesia, Kampus UI Depok, 16424, Indonesia

*ampubolon.patuan@sci.ui.ac.id

Abstract

The objective of establishing the HIV–1 Human Interaction Database in the NCBI is that to encourage the scientists to produce more publications. The database consists of two types of interactions that are collated from published reports—protein interactions and replication interactions. Biclustering is one of the data mining technique that may obtain insight from that database. This technique finds clusters by inspecting both rows and columns sets simultaneously. The BicBin algorithm is one of the biclustering method to a binary matrix. Therefore, it requires a systematic procedure to make biclusters from the database using this algorithm. We observe the database and select the HIV–1 proteins, the human proteins, and the interaction keywords. The interaction keywords are derived into three classes: regulating, regulated by, and bidirectional. The procedure consists of several steps. The first step is modeling the database into the bipartite graph. The second step is making a matrix which entry 1, 1, and $X$ represent the regulating, the regulated by, and the bidirectional interactions respectively. The entry 1 and then become the positive adjacency matrix and the entry 1 and become the negative adjacency matrix. The last step is inputting both of the binary matrix into the BicBin program

Keywords: (Protein Interactions, HIV–1, NCBI, Biclustering, BicBin)

References


Implementation of Factor Analysis for Bicluster Acquisition: Sparseness Projection (FABIAS) on Microarray of Alzheimers Gene Expression Data

Theresia B. P. Wutun*, Alhadi Bustamam, Titin Siswantining

Department of Mathematics, University of Indonesia, Depok, Indonesia

*theresia.bunga@sci.ui.ac.id

Abstract

Alzheimers is a chronic neurodegenerative disease that usually worsens over time, progressively destroys memory and other important mental functions. The number of people with Alzheimers is increased over these years. Treatment can help but this condition has no cure. Worldwide, approximately 44 millions people have Alzheimers, with care cost that is up to hundreds of billions every year. To face this alarming problem, we propose an implementation of Factor Analysis for Bicluster Acquisition : Sparseness Projection (FABIAS) to discover hidden patterns from microarray of Alzheimers gene expression data which include 54675 genes dan 161 samples. The development of microarray technology is used in data store of disease genetic expression. Usually, gene expression data is arranged in a data matrix, where gene corresponds to one row and each condition to one column. This research proposed FABIAS as one of biclustering method that is useful to discover some useful pattern or information from the data. From the experimental results, there are five, fifteen and fifty biclusters formed by Alzheimers gene expression data.

Keywords: (FABIA, FABIAS, bicluster, microarray, Alzheimer)

References


Dynamical Analysis of a Tumor Growth Model Involving Interferon Gamma

I.J.T.R.Tamsih, Trisilowati*, U. Habibah
Mathematics department, Faculty of Natural Science, University of Brawijaya, Indonesia
*trisilowati@ub.ac.id

Abstract

A tumor is cells that grow uncontrollably and become malignant, meanwhile our immune system turns out to have inhibitory factors in preventing the tumor development. This paper aims to construct and analyze a mathematical model of tumor and its interaction with some important immune system such as macrophages, activated CD8+ cytotoxic T-lymphocites(CTLs), and the immuno-stimulatory cytokine interferon gamma using a system of four coupled ordinary differential equations. It describes the effect of interferon gamma which activates macrophages in tumor decay process. The response of three different levels of macrophages strength are also investigated. Furthermore, dynamical analysis is conducted to investigate the existence and the stability of equilibrium points. Regarding to the result, the tumor free equilibrium point always exists and the interior equilibrium points exist if it satisfies cardans condition. The equilibrium points are stable under some circumstances. By using some estimated parameters from the literature, we present the numerical simulations which confirm to the analysis result.

Keywords: (Dynamical analysis, Interferon gamma, Macrophages, Tumor cells)

References


Effect of Host Mobility in Dengue Dynamical Model Inter—two cities

Heni Widayani*, Nuning Nurani
Department of Mathematics, Institut Teknologi Bandung

*heniwidayani@gmail.com

Abstract

Transmission of dengue disease has long been known as a complex phenomenon as indicated by unsuccessful prevention and control of dengue in many countries. This complication of transmission is caused among others by biological, climatological and human factors. The main problems with the human factor are mainly due to population mobility that is not easily modeled. In this study a simple model for analyzing the effect of human movement between two patches is constructed in the form of SIR—SI type with control terms in mosquito population. The mobilities of human are represented as linear terms with constant rates. The basic reproductive ratio and condition for coexistence equilibrium are obtained. Relation between mobility rates, control terms and reduction of the basic reproductive ratio is shown analytically. Interpretation for special cases are shown and the corresponding numerical simulation are presented.

Keywords: (Dengue, Mobility, Inter-two cities, Basic reproductive number)

References


Finding Correlated Bicluster from Gene Expression Data of Alzheimer Disease Using FABIA Biclustering Method

Nuning Setyaningrum*, Alhadi Bustamam, Titin Siswantining
Department of Mathematics, University of Indonesia, Depok, Indonesia

*nuning.setyaningrum@sci.ui.ac.id

Abstract

Alzheimer’s disease (AD) is a progressive, chronic neuro-degenerative interference of the human brain and the most common cause of dementia that causes problems with memory, thinking and behavior. Alzheimer’s disease data are gene expression found with microarray technique. The purpose of this research is to simultaneously find strong correlation bicluster among genes and samples gene expression data of AD available "Affymetrix Human Genome U133 Plus 2.0 Array” with 74 samples normal and 87 samples are affected AD in six different brain regions and each sample consisting of 54675 genes with an average age of ”79.8 ± 9.1” year. We apply the biclustering method, FABIA (Factor Analysis For Bicluster Acquisition) is a multiplicative biclustering model that assumes realistic non-Gaussian signal distributions with heavy tails. The FABIA model contains the product of Laplacian variables which is distributed by the Bessel function. FABIA utilizes well-understood model selection techniques like variational approaches and applies the Bayesian framework. The generative framework FABIA to determine the information content of each bicluster that having a high correlation between the genes and the samples, so the proposed method has great potential in the future of medical research.

Keywords: (Alzheimer, Biclustering, FABIA, Microarray)

References


Biclustering Protein Interactions between HIV–1 Protein and Human Protein Using LCM–MBS Algorithm

Olivia Swasti*, Alhadi Bustamam

Department of Mathematics, University of Indonesia, Depok, 16424, Indonesia

*olivia.swasti@sci.ui.ac.id

Abstract

Some of protein interactions are still unidentified. Thus, many research about protein interactions had been held. HIV–1 is a dangerous virus that has no medicine yet. The research about HIV–1 proteins and human proteins interactions leads into insight of drug target prediction. Biclustering technique is the beginning step before the prediction step. Biclustering is the process to cluster dataset through two perspectives. The result of biclustering can be applied to predict of unidentified protein interactions. Currently, this technique is more efficiently and effectively than experimental technique. The LCM–MBS is one of the biclustering algorithms to find biclusters from protein interactions dataset. This algorithm uses graph theory as the basic to obtain the maximal biclique. The algorithm can represent as enumeration tree. Every subtrees result the bicliques which are the biclusters. This algorithm performs quickly and efficiently in the term of memory consumptions. In this research, we apply the LCM–MBS algorithm for 13711 types of interactions between HIV–1 proteins and human proteins. We find 850 biclusters which the maximal bicluster has a size of 4 rows and 204 columns.

Keywords: (Protein interaction, Maximal biclique subgraphs, LCM–MBS algorithm)

References


A Dynamical Model of Invisible Wall in Mosquito Control

Mia Siti Khumaeroh *, Nuning Nuraini, Edy Soewono
Institute Teknologi Bandung, Indonesia
*miasitihumairoh@gmail.com

Abstract

Basically, mosquitoes have the opportunity to choose their blood meal from the available host in nature such as mammals, birds, reptiles, amphibians, fish as well as humans. In the blood-seeking process, the environmental conditions such as host availability and host abundance may form the characteristic in the mosquito to choose a particular host as compared to another host (preferences). The fact that some mosquitoes are the main vector causing various diseases in humans, has lead to investigate the importance of mosquitoes control by strategically changing their blood meal preference from humans to another host. Here we construct a model of preference alteration in mosquito involving larva, mosquito (anthropophilic, opportunistic, and zoophilic), human, and animal populations, using the control mechanism of repellent clothing usage and fumigation effect. The dynamical analysis and global sensitivity are analyzed to determine the dominant factor in mosquitoes preference alteration. Analysis result shows that repellent clothing usage increases the number of mosquitoes with zoophilic characteristic (animals as their blood resources preference), while the fumigation effect becomes the dominant factor that reduces the mosquito populations as a whole.

Keywords: (Mosquito preference, Invisible wall, Repellent, Anthropophilic, Opportunistic, Zoophilic )
Abstract

The emergence of new strains of the Ribonucleic acid (RNA) virus is still an important issue in the spread of influenza disease. The ability of RNA virus to mutate causes the immune system not to work properly. When the body is infected by a strain, immune memory cells will save the information about this strain. Memory cells will take action when the same strain strikes again so that the individual person is not re-infected. In secondary infection with different strains, memory cells can not necessarily function and the immune system may give wrong responses. This erroneous mechanism of response is called antibody-dependent enhancement (ADE). This ADE process results in a person who is infected with two different strains known as co-infection. The co-infection process will cause the virus to mutate and followed with the appearance of new strains. A SIRS (Susceptible—Infected—Recovered—Susceptible) model is constructed here to describe two-strain influenza transmission. Model analysis is conducted covering the condition of existence of coexistence equilibrium and its stability. A special case of co-infection is discussed thoroughly in which the two strains have the same characteristic. Parameter estimation is done with the use of incidence data for numerical simulation.

Keywords: (SIR model, Strain, Antibody dependent enhancement)

References


POLS Algorithm to Find a Local Optimum Bicluster on Interactions between HIV-1 and Human Proteins

Tesdiq Prigel Kaloka*, Alhadi Bustamam

Department of Mathematics, Faculty of Mathematics and Sciences, Universitas Indonesia, Depok, 16424

tesdiq@sci.ui.ac.id

Abstract

Protein is an important part of organism. Proteins must interact with other proteins to perform its functions properly. One of the interactions between proteins is the interactions between HIV–1 proteins and human proteins. Although HIV–1 and human proteins interact, we need to do depth analysis because some of HIV–1 proteins are not interact with human proteins. Bicluster is the method which used to observe this interaction. Bicluster can groups interactions by rows and columns, so we can analyze it easier. The local search framework based on pairs operation algorithm or called POLS algorithm. POLS algorithm is one of many algorithms to find a bicluster, it us a balanced biclique approach. The algorithm is good for binary data, because the initial step of the algorithm is to find optimum local value. The purpose of finding optimum local is to make sure whether a bicluster can be found or not. In this paper, we use POLS algorithm to find optimum local on data interactions between HIV–1 proteins and human proteins. We divided the data into two types. The first data is HIV positive and the second is HIV negative. In HIV positive, the optimum local of the interactions are asp, envelope surface glycoprotein gp120, BECN1, and IFNG. In HIV negative, we found the optimum local of the interactions are envelope surface glycoprotein gp120, envelope surface glycoprotein gp160 precursor, ICAM1, and ICAM3.

Keywords: (PPI, Bicluster, POLS Algorithm)

References


A Competition between Javan Rhinos (Rhinoceros Sondaicus) and Javan Bulls (Bos Javanicus) Model with Allee effect

Respati Mentari*, Eric Harjanto
Department of Mathematics,

*Respatimentari@gmail.com

Abstract

Allee effects on population growth are quite common for some spieces in nature. This effect reduces the rate of population growth when the population density is low. In this research, we consider a competition between Javan Rhinos (Rhinoceros Sondaicus) and Javan Bulls (Bos Javanicus) model. The phenomenon is shown in Ujung Kulon National Park in which the population of Rhinos did not increase for several decades. The Allee effect on this model occurs at the rate of Javan Rhino growth caused by inbreeding and sex-ration fluctuations. This model has five equilibrium points with possible coexistences. Dynamical analysis such as calculation of equilibrium points, condition of equilibrium existence and stability analysis of equilibria are shown analytically. Sensitivity analysis and biological interpretation for coexistence are thoroughly discussed.

Keywords: (Allee effects, Competition model, Rhinoceros Sondaicus, Bos Javanicus, Ujung Kulon National Park )
Gene Co—expression Network of Alzheimers Gene Expression

N.A. Wibawa*, Alhadi Bustamam, Titin Siswantining

Department of Mathematics, University of Indonesia, Depok, Indonesia

*nyoman.arda@sci.ui.ac.id

Abstract

Alzheimers is a dangerous disease that causes dementia. 60% – 70% cases of dementia are caused by this disease. Recovering gene co-expression network from Alzheimers gene expression data is essential to understand the information about Alzheimers. In this research, we use biclustering method to identify the latent structure among 54675 genes and 161 samples of Alzheimers gene expression data. BicMix is a new biclustering method to find gene expression network. This method has implemented on breast cancer, GTEx, tissue specific data. This method use Bayesian framework and models the data as result of multiplication of two sparse matrices, that are loading and factor matrix. The value of these matrices represent whether or not a gene or a condition included in a bicluster. Three Parameter Beta (TPB) distribution is used to induce the sparsity of these matrices. Caused by the largeness of gene expression data matrices that we process, this method use variational expectation maximization (VEM) to obtain all the parameters. Getting all the parameters means that we get the biclusters. Once we get the biclusters, the result can be used to build the gene co-expression network.

Keywords: (Alzheimer, Bicluster, BicMix, Gene expression)

References


On The Risk of Zika Virus Infection for Travelers

Mona Zevika*, Edy Soewono

Department of Mathematics, Institut Teknologi Bandung

monazevika@s.itb.ac.id

Abstract

It has been reported that the spread of Zika disease from an endemic country to other countries was originally distributed by tourists who were traveling and got infected in the endemic area and returned home with the Zika viruses (ZIKV). The potential threat of the disease from the returning tourists with the ZIKV infection has forced the health department to find proper precaution to avoid the wide spread of the disease. Here, a mathematical model constructed of SIR-SI type with mobility of people from one patch to an endemic patch is constructed. The force of infection is determined by considering the mosquito bite parameter and possibly obtaining the Zika virus from infected mosquitoes. Estimation of the risk of travelers to a Zika endemic patch is done by involving the force of infection or incidence rate, arrival time, and duration of stay in endemic areas.

Keywords: (Zika, Risk estimates, Force infection, Travelers.)

References


MARS and Bagging MARS in Stroke

Ria Dhea Layla Nur Karisma *, Sri Harini
Jalan Gajayana 50 Malang, Jawa Timur

riadhea@uin-malang.ac.id

Abstract

In 2010, World Health Organization (WHO) predicted cardiovascular cases caused of death amount of 73% total of a disorder of heart function in human. Stroke cause by disorganized blood circulation in human brain that increase of death in Estonia. Based on WHO data, Stroke suffered people that has age between 0 and 64 years old. The limitation of research is Ischemic and Hemorrhagic patients which are groups of Stroke in Medicum Clinic, Tallinn, Estonia. The aim in the research is to classify modified risk factors of Ischemic and Hemorrhagic whom are alcohol consumption, smokers, physical activity habit, body mass index (BMI), diet habit, and weight. Then, it applied both Multivariate Regression Spline (MARS) and Bagging MARS. Both are Machine Learning methods to overcome missing value and to increase accuracy. As result, the classification modified risks factor of Ischemic and Hemorrhagic patient using MARS and Bagging MARS are alcohol consumption, diet habit, smokers, physical activity, and BMI. Based on APER value (Apparently Error) both MARS and Bagging MARS have similar value that is 93,65% and 94,73%. In addition, MARS method is more stabilized model than Bagging MARS in the research.

Keywords: (Stroke, Ischemic, Hemorrhagic, Machine learning, MARS, Bagging MARS)

References

Epidemic Model of Co–infection of Dengue and Chikungunya

Edwin Setiawan Nugraha¹, Karunia Putra Wijaya², Thomas Götz², Nuning Nuraini¹, Edy Soewono*¹

¹Department of Mathematics, Institut Teknologi Bandung, 40132 Bandung, Indonesia
²Mathematical Institute, University Koblenz—Landau, 56070 Koblenz, Germany

*esoewono@math.itb.ac.id

Abstract

Health problems such as co–infection. Clinical conditions for co–infection are generally more severe than dengue or chikungunya infections. Information about long term behaviour of co–infection transmission is still limited and not much reported. Here, we propose an SIR–SI model of dengue and chikungunya epidemic in which co–infection occurs only in humans. In this model, co–infection occurs only through reinfection with chikungunya during the infection with dengue or though reinfection with dengue during the infection with chikungunya. The basic reproduction number is obtained analytically by using the next generation matrix. Stability of disease–free and single endemic equilibria are shown analytically. Further, complex behaviour of the co–existence equilibrium is shown numerically. The existence Hopf bifurcation, calculation of Lyapunov exponent and the corresponding limit cycle are also done numerically.

Keywords: (Dengue, Chikungunya, Co–infection, Mathematical modelling, Basic reproduction number.)

References


Abstract

Although dengue vaccine is available and it is efficacious among children who are seropositive, there remain questions about its effects on long-term. Given that the information around its long-term effects is not widely known, this may affect an individual's decision on the use of dengue vaccine. In this talk, we present the impact of individual vaccine decision—making behaviour on disease transmission dynamics. Based on game theory, we develop a mathematical model and theoretically assess the impact of an individual's decision on the use of dengue vaccine on dengue transmission dynamics.

Keywords: (Dengue, Vaccine, Imitation dynamics)
Exploration on Virus Transmission using Complex Networks: Pandemic Flu in Los Angeles

Andreas M.M., Ari Juanda, Febi Andhika, Haris Bhakti Permana, Prama Setia Putra*, Nuning Nuraini

Department of Mathematics, Institut Teknologi Bandung, 40132 Indonesia

Abstract

Virus is a parasite which can spread through human interactions. This thing can be very dangerous to human life because it causes many diseases. There was a science-fiction film which depicted the propagation of deadly virus known as Pandemic Flu or Spanish Flu in Los Angeles. This film exhibited the spread of virus between some regions in Los Angeles and the source of infection was identified in the end of the film. On different way to the film plot, the objectives of this modelling are to perform the simulation of virus spread on 30 locations in Los Angeles and to analyze the effect of network selection towards virus spreading on those 30 locations. There are two networks approaches to perform the modelling of virus spreading which are distance-based network and scale-free network. Scale-free network structure shows faster time to spread the virus among different locations than distance-based network. Time of virus spread is determined through two patches SIS model.

Keywords: (Virus, Pandemic flu, SIS model, Distance-Based network, Scale-Free network)

*setiaputra@math.itb.ac.id
Optimal Fish Harvesting Strategy using Forward–Backward Sweep Method

Nailul Izzati*, Imamatul Ummah
Faculty of Engineering, Hasyim Asyari University

*nailulizzati@unhasy.ac.id

Abstract

Overfishing are one of worldwide environmental issues. Indonesia, as maritime country, is facing the same problem. In 2015, according to Division Head of Capture Fisheries of Marine and Fisheries Office of East Java, Eryono, the exploitation that occurs in Java Sea reached 95% of its total potential [1]. To overcome this situation, Ministry of Maritime Affairs and Fisheries Republic of Indonesia decide to announce Ministrial Regulations MMAF No. 2 Year 2015 that forbid non-eco-friendly catching tools, and recommend the friendly one [2]. But up until 2018, this regulation is rejected by most of the fishermen that operate in Java Sea, because it need a huge fund to switch their catching tool to another one, and the revenue they yielded by using the recommended one is not profitable. So that, it is required to have another strategy to deal with this problem. In this study, we propose a harvesting strategy to achieve sustainable fishing in Indonesia. The aim of this study is to obtain an optimal harvesting strategy by considering fish harvesting restriction and taxation as control variables, with objective to maintain the optimality of fish population and the fishermen income. We purpose Pontryagin Maximum Principle [3] to get the characteristic of optimal control problem solution analytically. The characteristic obtained are numerically simulated by Forward–Backward Sweep Method [4]. Using Pontryagin Maximum Principle in the optimal control problem, we obtain the optimal fish harvesting strategy which is characterized by bang-bang and singular control, and its switching function. Numerical simulation showed that the optimal fish harvesting strategy obtained could optimize the fish population and net revenue of the fishermen.

Keywords: (Bang–bang control, Fish harvesting mathematical model, Forward–Backward sweep method, Pontryagin maximum principle, Switching function.)

References


Mathematical Model of PI3K/AKT Pathway in The Absence of Protein Phosphatase in AML

Y. A. Adi\textsuperscript{1,2,*}, L. Aryati\textsuperscript{2}, F. Adi Kusumo\textsuperscript{2}, and M. S. Hardianti\textsuperscript{3}

\textsuperscript{1}Departement of Mathematics, Universitas Ahmad Dahlan, Indonesia
\textsuperscript{2}Departement of Mathematics, Universitas Gadjah Mada, Indonesia
\textsuperscript{3}Department of Internal Medicine, Universitas Gadjah Mada, Indonesia

\textsuperscript{*}yudi.adi@math.uad.ac.id

Abstract

A model for PI3K/AKT pathway in Acute Myeloid Leukemia (AML) is described. We analyze a mathematical model for the study of the interaction between PIP3, AKT, and FOXO3a in the PI3K/AKT pathway. We assume that the biochemical reaction in this pathway following the Hills equation. To conduct the mathematical analysis, we consider the case that the mechanism of dephosphorylation protein does not work properly. Then, we analyze the model using the stability theory of differential equations. Firstly, the existence of steady states and their stability are discussed. Secondly, numerical simulations are given to the influence of the key parameters on the spread of AML disease, to support the analytical results of the model. Our results show how target therapy can be performed on the PI3K/AKT pathway for the treatment of AML.

Keywords: (PI3K/AKT pathway, Mathematical model, Stability)

References


Performance Comparison of the Convolutional Neural Network Optimizer for Photosynthetic Pigments Prediction on Plant Digital Image

K.R. Prilianti\textsuperscript{1,3,*}, T.H.P. Brotosudarmo\textsuperscript{2}, S. Anam\textsuperscript{3}, A. Suryanto\textsuperscript{3}

\textsuperscript{1}Department of Informatics Engineering, Ma Chung University, Indonesia
\textsuperscript{2}Ma Chung Research Center for Photosynthetic Pigments, Indonesia
\textsuperscript{3}Department of Mathematics, Brawijaya University, Indonesia

\textsuperscript{*}kestrilia.rega@machung.ac.id

Abstract

Determination of photosynthetic pigments in intact leaves is an essential step in the plant analysis. Along with the rapid development of digital imaging technology and artificial intelligence, determination of plant pigments can now be done in a non-destructive and real-time manner. In previous research, a prototype of the non-destructive and real-time system has been developed by utilizing the Convolutional Neural Network (CNN) model to produce predictions of three main photosynthetic pigments, i.e., chlorophyll, carotenoid, and anthocyanin. The CNN model was chosen due to its ability to handle raw digital image data without prior feature extraction. In the near future, this ability will be useful for developing analytical portable devices. Input of the system is plant digital image (in RGB format), and the output are predicted pigment concentration. Convolutional Neural Network performance depends on several factors, among them are data quality, algorithm tuning (weight initialization, learning rate, activation function, network topology, batches and epochs, optimization and loss) and models combination. The focus of this research is to improve the accuracy of CNN model by optimizing the selection for updating CNN architecture parameters which are optimization method and the loss function. As it is already known, there is no single optimizer can outperform for all cases. The selection for the optimizer should be made by considering the variability of the data and the nonlinearity level of the relationship patterns that exist in the data. Because the theoretical calculation is not enough to determine the best optimizer, an experiment is needed to see at firsthand the performance of optimizers that allegedly matches the characteristics of the data being analyzed. Gradient descent optimization method is well known for its ease of computing and speed of convergence on large datasets. Here, 7 gradient descent—based optimizers were compared, i.e., Stochastic Gradient Descent (SGD), Root Mean Square Propagation (RMSProp), Adaptive Gradient (Adagrad), Adaptive Delta (Adadelta), Adaptive Max Pooling (Adamax), Adaptive Momentum (Adam), and Nesterov Adaptive Momentum (Nadam). We proved that Adamax and Adam was the best optimizer to improve CNN ability in handling a digital image-pigments content relationship.
Keywords: (Convolutional neural network, Digital image, Gradient descent optimizer, Photosynthetic pigments)

References


Mathematical Model of Dengue Transmission with Mobility Aspect

Muhammad Fakhruddin*, Nuning Nuraini, Edy Soewono
Department of Mathematics, Institut Teknologi Bandung, 40132 Bandung, Indonesia

*mfakhruddin@s.itb.ac.id

Abstract

Dengue is one of the most viral vector-borne diseases in the world. One of the driving factors of dengue transmission is human mobility either on a local or global scale. Mobility of people at a large scale could transmit dengue viruses from an endemic area to a non-endemic area and possibly increase the endemicity in both areas. In this study, we investigate the role of human mobility in the dynamics of dengue transmission with an SIR—SI type model. Two options in reducing the model are presented to reduce unobserved parameters. We do parameter estimation based on dengue incident data. Furthermore basic reproduction ratio, stability of coexistence equilibrium, and sensitivity analysis are presented with respect to mobility rates.

Keywords: (Dengue transmission, Mobility, Parameter estimation)

References


The Helicoverpa Armigera Spread Controlling Model on The Glycine Max Growth using Zea Mays L

S. I. Lestari, J. W. Puspita*, R. Ratianingsih*
Mathematics Study Program Tadulako University

*juni.wpuspita@yahoo.com, ratianingsih@yahoo.com

Abstract

This paper discusses the pest spread problem founded in the growth of Glycine Max that disturbed by Helicoverpa attack. To divert the pest, Zea Mays L is proposed to protect the Glycine Max growth. An interaction scheme is constructed by consider the life cycle of Helicoverpa Armigera, Glycine Max and Zea Mays. The scheme is used as the basis of a mathematical model that describe the interaction among the related subpopulation. The stability of the the model is analysed by linearization method at the endemic critical point. An asymptotic stable critical point shows that the zea mays successes to overcome the pest attack.

Keywords: (Glycine max, Helicoverpa armigera, Linearization method, Mathematical model, Zea Mays L)

References


SIR—SI Model for Malaria Disease with Treatment and Vector Control

Kemal Adam Roisy*, Dr. Dipo Aldila
Department of Mathematics, Universitas Indonesia

Abstract

In this talk, a mathematical model of malaria with intervention of fumigation ($u_1$) and medical treatment ($u_1$) will be discussed. Equilibrium points and their stability are analyzed analytically and numerically. Basic reproduction number ($R_0$) of the model has been determined with Next Generation Matrix approximation. We found that if $R_0 > 1$, then we have an endemic equilibrium. While if $R_0 > R^*$, we only have a disease free equilibrium, where $R^*$ is the threshold of the backward bifurcation. A backward bifurcation appears when $R^* < R_0 < 1$, which arise two endemic equilibrium points. Some numerical simulations for the bifurcation and the autonomous model is given in the end of the talk.

Keywords: (Malaria, Backward bifurcation, Fumigation, Medical treatment, SIR—SI model)

References


Modeling of Rabies Transmission Dynamic between Human and Dogs with the Effect of Immunocontraceptive Vaccine

Eti D. Wiraningsih¹*, Asep K. Supriatna²

¹Department of Mathematics, Faculty of Mathematics and Natural Sciences, State University of Jakarta, DKI-Jakarta, Indonesia address
²Department of Mathematics, Faculty of Mathematics and Natural Sciences, University of Padjadjaran, Bandung-West Java, Indonesia

etdwi@gmail.com

Abstract

We formulated a deterministic model for the transmission dynamics of rabies virus in the dogs-human zoonotic cycle. The effect of immunocontraceptive vaccine in dogs is considered on the model, then the stability was analysed to get basic reproduction number. We use the next generation matrix method to analyze the stability of the Disease Free Equilibrium of this model.

Keywords: (Stability analysis, Rabies model, Immunocontraceptive vaccine.)

References


Mathematical Model of Zika Virus Transmission with Saturated Incidence Rate

Puji Andayani¹*, Lisa Risfana Sari¹, Agus Suryanto², Isnani Darti²

¹Universitas Internasional Semen Indonesia
²Department of Mathematics, Brawijaya University

puji.andayani@uisi.ac.id

Abstract

Zika virus is a type of virus lead by Aides Aegypti mosquitoes. This virus is potentially spread in the tropics area. Long-term effects of the Zika virus are quite harmful, including of hydrocephaly and GBs. Mathematical models have a very important role in the case of disease spread. In this paper, we propose and analyze the model of Zika virus transmission with saturated incidence rate. This model consists of five nonlinear ordinary differential equations which are reducing to be three nonlinear equations. The mathematical model obtained will be analyzed dynamically. Analytically in disease free condition, it is persuaded mortality which is shown that the disease free equilibrium is locally asymptotically stable when the reproduction number is less than unity. Otherwise, the endemic equilibrium stable. Further, the numerical simulation used to explore the behavior of equilibrium of the system.

Keywords: (Zika transmission, Saturated incidence rate, Reproduction number)

References


Modeling The Spread of Bacterial Resistance in Hospital

Nela Rizka, Mochamad Apri, Pratiwi Wikaningtyas
Bandung Institute of Technology, Indonesia

*nelafaruq79@gmail.com, m.apri@math.itb.ac.id, pratiwi@fa.itb.ac.id

Abstract

Antibiotic resistance is the ability of bacteria to avoid or inhibit attacks from antibiotics. The phenomenon of the spread antibiotic resistance has increased significantly, especially in hospitals. The negative impacts arising from these phenomena include the high treatment cost and high mortality rates of patients due to infectious disease. In response to these problems, this work proposed a model of spread bacterial resistance in hospitals. From analysis of model, we obtained that the spread of bacterial resistance in the hospital, at the end, still occur even though the patient get antibiotics therapy. Meanwhile, if the patient’s level of awareness to keep themselves from resistant bacterial contamination is considered, then the spread of resistance in the hospital can be controlled. The higher the level of patient awareness the smaller the spread of resistance occurs.

Keywords: (Ordinary differential equations systems, The spread of bacterial resistance, Antibiotics)
Blighted Ovum Detection Using Deep Convolution Neural Network Method

Feni Andriani*, Iffatul Mardhiyah
Gunadarma University

*feni.andriani@staff.gunadarma.ac.id

Abstract

Blighted Ovum is a state of conception that contains no fetus. Early detection of Blighted Ovum may reduce the risk of miscarriage. One tool that can be used in the detection of Blighted Ovum is by using ultrasonography. However, the detection of Blighted Ovum through ultrasound image is still difficult, because it is still very dependent on the level of knowledge and subjectivity of medical experts. One of the most successful ultrasound image detection or classification methods is Deep Learning. Deep learning is growing rapidly due to the development of Graphical Processing Unit (GPU). One of the best machine learning methods in terms of image classification by utilizing GPU is called Deep Convolutional Neural Network method. This method consists of three stages. The first stage is the feature extraction of ultrasound image data. The second stage of the learning phase or training by using feedforward and backpropagation methods. The third stage is the phase of image classification using feedforward method. This research will develop an automatic classification algorithm on the ultrasound examination result using Deep Convolutional Neural Network in Blighted Ovum detection. This study is also expected to assist medical experts in providing quick and accurate decisions on whether or not Blighted Ovum is present, so fetal rescue is not too late. the accuracy of the algorithm implementation is 80%.

Keywords: (Blighted ovum, Deep learning, Graphical processing unit miscarriage, Ultrasound)

References


Mathematical Model for Rise and Fall Army Population

Anita Triska*, Heni Widayani, Nuning Nuraini

*Industrial and Financial Mathematics Research Group, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung.

anit.triska@gmail.com

Abstract

An armed force is a professional organization formally authorized by a sovereign state to use deadly force and weapons to support sovereignty of the state. It typically consists of Army, Navy, Air Force, and Marines. One of their main tasks is assigned in war either to defend their state independence or just for political reason. Recruitment rate of military member is an important to ensure the sustainability of this military system. This study construct mathematical model which give the dynamics of citizen and army population. The first model involves systems of time-dependent ordinary differential equation. Dynamical analysis such as existence and stability of equilibrium point are obtained. Threshold value for stability of each equilibrium point can be biologically interpreted. The model was developed into a partial differential equation which is time and space-dependent. The second model is represented with reaction-diffusion model with self and cross diffusion. Two different boundary conditions are implemented for the army population which will be illustrated in numerical simulation.

Keywords: (Army, War, Dynamical population model)

References


Stability of Hepatitis B Virus Model with Cure and Absorption Effect

Lisa Risfana Sari*, Puji Andayani

*Universitas Internasional Semen Indonesia

Abstract

Considering hepatitis B as one of challenge to public health, we introduce a modified mathematical model of hepatitis B infection with cure and absorption effect. There are two equilibria, virus free equilibrium and endemic equilibrium. Numerical simulations indicate that the basic reproductive ratio is related to the existence condition of endemic equilibrium. If the basic reproductive ratio is less than one then virus free equilibrium is established, while if the basic reproductive ratio is greater than one then endemic equilibrium is established. Numerical simulations suggest that immune response have a role to control the infection.

Keywords: (Absorption effect, Cure, Hepatitis B virus, Reproduction number.)

References


**Optimal Control of Innate Immune Response in Infected Lung—Macrophages by *Streptococcus Pneumoniae***

Usman Pagalay*, Dewi Zumrotul Nafisa, Heni Widayani  
*Department of Mathematics, Mathematics State Islamic University Maulana Malik Ibrahim Malang*  
*usmanpagalay@yahoo.co.id*

**Abstract**

Innate immune response in lung macrophages can be modeled as a system of first order nonlinear differential equations. This model consists of bacterial *Streptococcus Pneumoniae* populations, inactive macrophages, and active macrophages. We performed optimal control using Pontryagin Minimum Principle and simulated using finite difference and Runge Kutta fourth order. The results show either bacterial growth using control or not. This growth is suppressed by proinflammatory cytokines. If an individual has a good immune system then growth time of bacteria *streptococcus pneumoniae* becomes slower. Further, if an individual has a bad immune system, then growth time becomes faster.

**Keywords**: (Innate immune, Lung macrophages, Streptococcus Pneumoniae, Optimal control)

**References**


Muhammad Ahsar Karim 1,2,*, Agus Yodi Gunawan1, Mochamad Apri1, and Kuntjoro Adj Sidarto1

1Department of Mathematics, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Jl. Ganesha 10 Bandung, Indonesia
2Permanent Address: Program of Mathematics, Faculty of Mathematics and Natural Sciences, Universitas Lambung Mangkurat, Jl. A. Yani Km. 36 Banjarbaru, Indonesia

*m.ahsar@ulm.ac.id

Abstract

In general, most of systems biology may contain uncertainties, either on structures or parameters. These uncertainties are possibly either due to limitations of available data, complexity of the systems, or environmental or demographic changes. One of typical behavior that commonly appears in the systems biology is a periodic behavior. Mathematical model of the system with periodic behavior often exhibit complex dynamic behaviors, depending on the initial values and parameters. By accommodating uncertainties in the model, it certainly requires an intensive study in terms of mathematical structures descriptions, methodologies for determining solutions and procedures for parameter estimations. One of the mathematical models that describes periodic behavior is External Forced Oscillation of Fuzzy Duffing Equation. In this work, the model will be considered as our subjects by assuming that the initial values have uncertainties in terms of Fuzzy Numbers. The resulted fuzzy models will be studied by two fuzzy differential approaches, namely Hukuhara Differential and Fuzzy Differential Inclusions. Applications of Fuzzy Arithmetic to the model leads us into Alpha-Cut Deterministic Systems, with some additional equations. These systems are then solved by Extended Runge-Kutta Method. In contrast to the standard Runge-Kutta Method, the extended Runge-Kutta method utilizes new parameters in order to enhance the order of accuracy of the solutions by including both function and its first derivative values in the calculations. Among those fuzzy approaches, Fuzzy Differential Inclusions is the most appropriate approach to capture periodic behaviors of the model, using extended Runge-Kutta method. Finally, we demonstrate how to estimate parameters using Fuzzy Differential Inclusions to our generated fuzzy simulation data.

Keywords: (External forced oscillation of fuzzy duffing equation, Hukuhara differential, Fuzzy differential inclusions, Extended Runge–Kutta method, Parameter estimation)

References


Lina Aryati 1, Tri Sri Noor Asih2, Fajar Adi—Kusumo1,*, Mardiah Suci Hardianti4
1Department of Mathematics Faculty of Mathematics and Natural Sciences Universitas Gadjah Mada Indonesia
2Department of Mathematics Faculty of Mathematics and Natural Sciences Semarang State University Indonesia
4Faculty of Medicine Universitas Gadjah Mada Indonesia

*fadikusumo@ugm.ac.id

Abstract

We consider a cervical cancer model with a treatment focusing on the precancerous cells. As one of the objectives of treatment is dealings with recovery, in this paper, we give the sufficient conditions for the disease free equilibrium to be globally asymptotically stable. These conditions hopefully could guide us in the effort of healing. We also give numerical simulation to illustrate the dynamic of recovery process.

Keywords: (Cervical cancer, Disease free equilibrium, Global stability.)

References


Minimizing Parameter and Dynamical Uncertainties in Biological Models

Levina Michella *, Mochammad Apri
Institut Teknologi Bandung
levinamichella@gmail.com

Abstract

Mathematical model of a biological phenomenon contains parameters related to the interactions in the biological systems. Some of these parameters may have to be estimated from experimental data. However, due to some constraints, data that can be obtained from experiments are limited. Thus, if the data is not informative, this limitation leads to large parameter and dynamical uncertainties in biological models. Consequently, the behavior of the model will be elusive. Here we propose several strategies to perform informative experiments to reduce the uncertainties. Given a few experimental data, in our work, parameter estimation is carried out numerically by Controlled Random Search method. This yields an ensemble of parameter estimates. Based on this estimates, the times that give the highest dynamical uncertainty are chosen to indicate the time at which measurements have to be done. In addition, we also look for some experimental conditions that can falsify the obtained estimates. This is conducted by finding the conditions that give the highest dynamical uncertainty. In this way, the parameter and dynamical uncertainties of the model can be reduced efficiently.

Keywords: (Biological model, Parameter estimation, Controlled random search, Parameter uncertainty, dynamical uncertainty)

References


A Fuzzy Basic Reproduction Number for A Fuzzy Smoker Growth Model

Herlinda Nurafwa Sofhya*, Agus Yodi Gunawan
Institut Teknologi Bandung, Indonesia

*herlindanurafwa15@gmail.com

Abstract

Consumption of a large amount of cigarettes in a public society is one of the main concerns in every countries since cigarettes may become the source of all dangerous diseases, like TBC, Cancer and many other health and social problems. Many programs have been simulated by government to overcome smoking problems. One of important things for the governement is to predict smokers growth population. In this paper, we derive a smoker growth model in which the population is classified by three sub populations: a potential smoker, an active smoker, and a quitted smoker. Commonly, the transmission rate in the classical model is assumed to be constant. However, in reality the transmission among them may depend on age of smoker. To get insight into this, the transmission rate will here be relaxed to be dependence of ages and contain uncertainty that is considered as a triangular fuzzy number. Our main focus will be paid into determination of fuzzy basic reproduction number through fuzzy expected value concept. Using the resulted fuzzy basic reproduction number, we calculate the critical age smoker above which the endemic case takes place. It turns out this critical age is less than that of resulted from the classical (non-fuzzy) basic reproduction number. It means that fuzzy smoker growth model may be considered as an early warning model for the endemic case.

Keywords: (Smoker growth model, Fuzzy number fuzzy, Expected value, Basic reproduction number, Endemic )
Protein Sequence Analysis of The Zika Virus and The Dengue Virus Using Smith Waterman Algorithm

Mohammad Syaiful Pradana*, Siti Amiroch
Department of Mathematics, Faculty of Mathematics and Natural Sciences Universitas Islam Darul 'Ulum Lamongan, Indonesia

*Syaifulp@unisda.ac.id

Abstract

Zika virus that had a warm conversation in the media last year is very interesting to study, especially because the Zika virus caused symptoms similar to dengue fever. The virus is transmitted to humans by mosquitoes of the genus Aedes, principally Aedes aegypti mosquitoes in tropical regions is the same that transmits dengue, chikungunya and yellow fever.

In Brazil, local health authorities have observed an increase syndrome Zika virus infection in the community, as well as an increase in babies born with microcephaly (enlarged head) in northeast Brazil. In addition, more than 13 countries in the Americas have reported sporadic Zika virus infection that show very rapid geographic expansion. While in Indonesia, the euphoria is also increasingly prevalent virus discussed especially after the discovery of Jambi positive patients infected with the virus Zika on January 26, 2016 last.

Moving on from this, the authors wanted to know how the sequences protein zika virus when compared with the dengue virus, the percentage of identical as well as the calculation of local alignment its using the Smith Waterman algorithm. In addition it will also be known genetic mutations that occur in zika virus from its origin until zika virus into Indonesia and phylogenetic tree spread of the virus to get to Jambi.

By using matlab programming, systems designed user interface that is used for sequence alignment using the Smith Waterman algorithm, as well as link to the system comes with the browser as an option for online data retrieval. From the results obtained in matlab alignment between sequences identical values of precision turned out higher than with BLAST. Likewise, the time duration shorter Matlab simulation results compared with the output of BLAST

Keywords: (Sequence Analysis, Zika virus, Dengue virus, Smith Waterman algorithm)

References


Mathematical Modeling of Panama Disease Infection inside Banana Leaves

Mochamad Apri*, Husna Nugrahpraja, Mudita Gunawan, Gandhiano Putera, Monica Reynata Sulaeman, Marcelino Wijaya, Joanne Immanuela Rachman

Department of Mathematics, Institut Teknologi Bandung

*m.apri@math.itb.ac.id

Abstract

Panama disease is lethal fungal disease that attacks the root and leaves of Banana plant. It is caused by Fusarium Oxysporum f.sp. Cubense which infects and inhibits the plant from getting enough nutrients. As a result, the old leaves become yellow, wilt, and collapse, which eventually leads to the death of the plant. To understand the mechanisms of the infection, in this work we develop a mathematical model that describes the interactions between the fungus and proteins that play role in the leaves growth during the infection. The model consists of a set of nonlinear differential equations. The equilibrium points and their stability are analyzed and a numerical simulation will be presented.

Keywords: (Panama disease, Banana leaf, Mathematical model, Differential equation)