2021 한국수리생물학회 연례 학술대회

2021 Annual Conference of
Korean Society for Mathematical Biology (KSMB '21)

초 록 집

Program & Abstracts

일시 _ 2021년 8월 26일(목) ~ 8월 28일(토)

장소 _ 제주시 소노벨제주리조트

| 주최 | 한국수리생물학회
| 주관 | 국가수리과학연구소
부산대학교 산업수학센터
한국수리생물학회
| 후원 | 국가수리과학연구소, 부산대학교 산업수학센터

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주최: 한국수리생물학회

주관: 국가수리과학연구소

부산대학교 산업수학센터

한국수리생물학회

후원: 국가수리과학연구소, 부산대학교 산업수학센터

2021 한국수리생물학회 학술대회 조직위원회

조직위원장	김용국	경북대학교
	김상일	부산대학교
	조도상	국가수리과학연구소
조직위원	정일효	부산대학교
	이창형	UNIST
	김양진	건국대학교
	정석근	제주대학교

2021 한국수리생물학회 학술대회 일정표

8월 26일-28일
소노벨제주리조트

날짜	시간	일정	강연장			
8월 26일(목)			세미나룸 1	세미나룸 2	세미나룸 3	Lobby
	15:00 ~	Registration				Registration
	16:00-17:40	Session	General Session A1 Infectious Disease modeling I (발표자: 고영석, 서지연, 이종민, 김보연)	General Session A2 Mathematical Modeling of Biological Systems (발표자: 김광중, 채석주, 이태용)	Genral Session A3 Modeling and Data Analysis in Medical Science (발표자: 이준호, 이동구, 이태린, 조혜령)	
8월 27일(금)			세미나룸 1	세미나룸 2	세미나룸 3	Lobby
	08:30 ~	Registration				Registration
	09:00-10:40	Parallel Sessions	Special Session B1 Medical Mathematics in Data Science and Applications (좌장: 이효정)	Special Session B2 Mathematical Modeling in Medicine (좌장: 이완호)	Special Session B3 Analysis and Modeling of PDEs in Biological Systems (좌장:배한택, 최규동)	
	10:40-10:50	Break				Break
	10:50-11:00	Opening Ceremony	Opening Remarks			
	11:00-11:50	Plenary Lecture	Plenary Lecture I Application of Artificial Intelligence in Medical Field (Speaker: 강도영)			
	12:00-13:30			코로나19 수리모델링 TF 미팅		
	13:30-15:10	Parallel Sessions	Speical Session C1 Mathematical Analysis and Methods in the Dynamics of Biological System: Cancers and Circadian Clock I (좌장: 김양진)	Special Session C2 Population Model (좌장: 전태수, 박영석)	Speical Session C3 Pharmacokinetic and Pharmacodynamic Model (PKPD) (좌장: 정일효)	
	15:10-15:20	Break				Break
	15:20-17:00	Parallel Sessions	Special Session D1 Mathematical Analysis and Methods in the Dynamics of Biological System: Cancers and Circadian Clock II (좌장: 김재경)	Speical Session D2 정수생태계 변화 예측모델 (좌장:박영석)	Speical Session D3 의생명에 활용되는 데이터분석 (좌장: 윤강준)	
	17:00-17:10	Break				Break
	17:10-18:00	Plenary Lecture	Plenary Lecture II Mathematical AI and COVID-19 (Speaker: 황형주)			
8월 28일(토)			세미나룸 1	세미나룸 2	세미나룸 3	Lobby
	09:30 ~	Registration				Registration
	10:00-11:40	Parallel Sessions	Special Session E1 Mathematical Modeling of COVID-19 and Beyond (좌장: 이선미)	General Session E2 Infectious Disease Modeling II (발표자: 심은하, 최용인, 문무경, 김슬기)	General Session E3 Modeling in Ecology and Fisheries (발표자: 정동원, 장영석, 위윤주, 오규진)	
	11:40	Closing				

2021 KSMB 학술대회 일정

8월 26일 (목)

16:00-17:40 General Session A1: Infectious Disease Modeling I

① Mathematical modeling of COVID-19 epidemic in the Republic of Korea considering heterogeneous transmission (Youngsuk Ko)

② Modeling the Impact of Rapid Diagnostic Tests and Tafenoquine on the Plasmodium Vivax Malaria Burden in North Korea (Jiyeon Suh)

③ Mathematical modeling of COVID-19 in the Republic of Korea and scenario-based-study for the estimation of herb immunity achievement (Jongmin Lee)

④ The impact of the Covid-19 on Tuberculosis in South Korea (Boyeon Kim)

16:00-17:40 General Session A2: Mathematical Modeling of Biological Systems

① Reaction-advection-diffusion competition models under lethal boundary conditions (Kwangjoong Kim)

② First passage time approach reveals sources of noise in the timing of intracellular events (Seokjoo Chae)

③ Optimal Control for Oncolytic Virus Treatment (Taeyong Lee)

16:00-17:40 General Session A3: Modeling and Data Analysis in Medical Science

① Atorvastatin-mediated rescue of cancer-related cognitive changes in combined anticancer therapies (Junho Lee)

② Mathematical model of STAT signaling pathway in cancer development and optimal control approaches (Donggu Lee)

③ Data analysis of patient-specific lifelogging obtained from wearable devices (Tae-Rin Lee)

④ Computer simulation of blood flow in the cerebrovascular structure of brain (Hyeryoung Cho)

8월 27일 (금)

09:00-10:40	**Special Session B1: Medical Mathematics in Data Science and Applications (Organizer: Hyojung Lee)**

① Modeling for Mathematical Biology Potential epidemiologic indicators in the infectious disease control and their future use (Changhoon Kim)
② Recent works in Division of Medical Mathematics at NIMS (Hyoung Suk Park)
③ Approach to solve the mathematical problems using medical data (Hyoung Lee)
④ Application of a Virtual Alignment Method to the dental prostheses and diagnosis (Kyoungtaek Jun)

09:00-10:40	**Special Session B2: Mathematical Modeling in Medicine** **(Organizer: Wanho Lee)**

① Computational simulation of guidewire motion in a blood vessel (Wanho Lee)
② Axial Green function Method for viscous fluids and its applications (Junhong Jo)
③ Global Well-Posedness of Nutrient-Taxis Systems Derived by a Food Metric (Minha Yoo)
④ Modelling for Functions of Anatomical Structures (Seunggyu Lee)

09:00-10:40	**Special Session B3: Analysis and Modeling of PDEs in Biological Systems (Organizer: Hantaek Bae, Kyudong Choi)**

① Chemotaxis system derived by food metric (Sun-Ho Choi)
② A system arises from plasticity and chemotaxis: result in stable regime (Min-Gi Lee)
③ Spatial Segregation in Homogeneous Environment (Ohsang Kwon)
④ Modeling for Mathematical Biology (Myeongju Chae)

10:40-10:50	**Break**
10:50-11:00	**Opening Remarks** **(KSMB 회장)**

11:00-11:50 **Plenary Lecture I: Appplication of Artificial Intelligence in Medical Field (Speaker: Do-Young Kang)**

12:00-13:30 **Break**

13:30-15:10 **Special Session C1: Mathematical Analysis and Methods in the Dynamics of Biological System: Cancers and Circadian Clock I**

(Organizer: Yangjin Kim)

① **Mathematical and computational modeling for cancer treatment (Eunjung Kim)**
② **Oscillatory timeseries data sheds light on molecular mechanisms (Jae Kyoung Kim)**
③ **Mathematical modeling and computational simulation of a cytokine shield formation of senescent tumor cells (Chaeyoung Lee)**
④ **Reducing the risk of accumulating mutations via cell competitions in a hierarchical tissue (Hye Jin Park)**

13:30-15:10 **Special Session C2: Population Model**

(Organizer: Tae-Soo Chon, Young-Seuk Park)

① **Recent Trends of Data-Driven Models in Ecology (Young-Seuk Park)**
② **A spatially explicit model applied to nutria (Myocastor coypus) population dispersal in field conditions in Korea (Nam Jung)**
③ **Predicting dispersal of invasive sika deer (Cervus nippon) in a novel group-based model (KyoungEun Lee)**
④ **Individual-based simulation for wild boar (Sus scrofa) dispersal and disease transmission in linking with behaviour states defined by hidden Markov model (Thakur Dhakal)**
⑤ **Hidden Markov model applied to behavioural states in wild boar (Sus scrofa) movements in linking with self-organizing map (Tae-Soo Chon)**

13:30-15:10 **Special Session C3: Pharmacokinetic and Pharmacodynamic Model (PKPD) (Organizer: Il Hyo Jung)**

① **Development of physiologically based pharmacokinetic model of entrectinib in rats and humans (In-Soo Yoon)**
② **A transit and fractional order derivative model of lapatinib (Jong Hyuk Byun)**
③ **Can you tell how effective a COVID-19 prevention strategy is at elementary**

schools? (Yong-Jung Kim)

④ Accurate Prediction of Drug Clearance in Liver (Yun Min Song)

15:10-15:20 **Break**

15:20-17:00 **Special Session D1: Mathematical Analysis and Methods in the Dynamics of Biological System: Cancers and Circadian Clock II**

(Organizer: Jae Kyoung Kim)

① PET tracing of biodistribution for orally administered 64Cu-labeled polystyrene in mice (Jin Su Kim)

② Mathematical Modeling for Pacemaker-neuron-dependent Molecular Rhythm Alteration by Drosophila Clock Mutant (Eui Min Jeong)

③ Spatial Heterogeneity Mediated Treatment Response (Masud M A)

④ Inference of stochastic dynamics in biochemical reaction networks by exploiting deterministic dynamics (Hyukpyo Hong)

15:20-17:00 **Special Session D2: 정수생태계 변화 예측모델**

(Organizer: Young-Seuk Park)

① 생물 모니터링 자료를 이용한 담수생태계의 먹이망 구축 (이다영)

② 국내 담수 어류의 45종과 멸종위기 어류 20종의 먹이원 분석 (지창우)

③ 한강 수계 내 호소에서 저서성 대형무척추동물 및 수질에 대한 어류 군집 구성 변화 예측 (이대성)

④ 해석가능한 기계학습 기법을 활용한 녹조현상의 예측 (신지훈)

⑤ Delf3D 모델을 활용한 주암호 물순환 및 수질변동 특성 분석 (이정현)

15:20-17:00 **Special Session D3: 의생명에 활용되는 데이터분석**

(Organizer: Gangjoon Yoon)

① Computational approach to simulate microswimmers propelled by bacterial flagella (Wanho Lee)

② Machine learning approach using routine immediate postoperative laboratory values for predicting postoperative mortality (Yongkeun Park)

③ Deep learning model for the prediction of EBV status in gastric cancer (Sangjeong Ahn)

	④ False promise of ending COVID-19 by vaccination without treatment (YongKuk Kim)
17:00-17:10	**Break**
17:10-18:00	**Plenary Lecture II: Mathematical AI and COVID-19** **(Speaker: Hyung Ju Hwang)**

8월 28일 (토)

10:00-11:40 **Special Session E1: Mathematical Modeling of COVID-19 and Beyond (Organizer: Sunmi Lee)**

① Collateral health effects of COVID-19 (Hee-Sung Kim)

② The effects of vaccination and Non-Pharmaceutical Interventions I on COVID-19 transmission dynamics in Korea (Jung Eun Kim)

③ Estimating the Basic Reproduction Number of COVID-19 on heterogeneous network (Sungchan Kim)

④ A Model-informed Reopening Strategy based on a Case Study of Ontario, Canada (Kyeongah Nah)

10:00-11:40 **General Session E2: Infectious Disease Modeling II**

① Impact of COVID-19 variants on the vaccination program in South Korea (Eunha Shim)

② Effects of social distancing on COVID-19 control in Korea based on age-structured modeling (Yongin Choi)

③ Risk assessment of HPAI on poultry farms in relation to migratory birds using a Maxent model (Mugyeom Moon)

④ Exploring the roles of vehicle transmission in inter-farm modelling for Foot-and-Mouth Disease (Slghee Kim)

10:00-11:40 **General Session E3: Modeling in Ecology and Fisheries**

① 자료가 제한된 상황에서 한국 남동해역 멸치(Engraulis japonicus) 자원에 대한 자원평가 방법 개발 (정동원)

② Prey-Induced Dispersal in Predator-Prey Model (Youngseok Chang)

③ The population dynamics of red eared slider in Korea (Yunju Wi)

④ Analysis of the invasive species spread using cellular automata classification and machine learning (Gyujin Oh)

11:40- **Closing**

Plenary Lectures

Plenary Lecture I

Application of Artificial Intelligence in Medical Field

Do-Young Kang

Institute of Convergence Bio-Health, Department of Nuclear Medicine
College of Medicine, Dong-A University
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The format of medical data is largely divided into text, image, and waveform. Among them, since the image data was built as big data by PACS in the hospital, artificial intelligence-based analysis of image data was most actively carried out. Various types of medical data are publicly available and can be used for research.

There are various fields of application of AI technology in medicine, such as diagnostic imaging, genetic diagnosis, electrodiagnosis, clinical laboratory, and mass screening. The leading 10 disease types considered in the artificial intelligence, such as neoplasms, nervous, cardiovascular, urogenital, pregnancy, digestive, respiratory, skin, endocrine, and nutritional systems.

The main types of machine learning and deep learning algorithms used in medicine are support vector machine, neural network (deep, convolutional, recurrent), logistic regression, Random Forest, linear regression, Naïve Bayes, nearest neighbor, decision tree, hidden Markov etc.

Dozens of medical AI algorithms have been approved by the FDA and the KFDA, and they are being clinically applied to patients. However, to apply the real data to medical treatment in hospitals, it is not enough to simply evaluate the accuracy of the algorithm, and it is necessary to verify it with internal and external data. Technical performance, clinical performance, and clinical utility are all indicators of efficacy of different levels and characters.

Plenary Lecture II

Mathematical AI and COVID-19

Hyung Ju Hwang

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Mathematics is closely related to the theory and algorithms of AI and machine learning. In this talk, we investigate how Mathematical AI can help us understand the biomedical and epidemic mechanisms of COVID-19 by three recent studies. First, we look into real-world implications of a rapidly-responsive COVID-19 spread model via deep learning and mathematical modeling. The methodology could also be employed for short-term prediction of COVID-19, which could help the government prepare for a new outbreak. Second, we developed a machine learning model that predicts the mortality of infected patients by using basic patients' information such as age, residence, comorbidity, and past medical history, which can lead to a medical system that allows patients to check their own severity. Third, we analyzed the difference in the immune response of T cells between COVID-19 patients and non-patients using artificial intelligence. This method was superior to the existing statistical methods in classifying COVID-19 patients and was also effective in predicting the severity of the disease.

References

[1] S.Y. Jung, H. Jo, H. Son, H.J. Hwang, Real-World Implications of Rapidly Responsive COVID-19 Spread Model with Time Dependent Parameters Via Deep Learning: Algorithm Development and Validation, Vol 22, No 9 (2020): September, Journal of Medical Internet Research

[2] S.Y. Jung, H. Jo, M. Park, H.J. Hwang, COVID-19 patients severity prediction using machine-learning model on the past medical history data, preprint

[3] E. Lee, S. Park, S. Lee, J. Jang, J. Park, H.J. Hwang, Leveraging artificial intelligence to elucidate T cell immune response of COVID-19 patients, preprint

Sessions

General Session A1

Infectious Disease Modeling I

Date/Time: 8월 26일(목) 16:00

Speakers:

1. Youngsuk Ko	**(Konkuk University)**
2. Jiyeon Suh	**(Yonsei University)**
3. Jongmin Lee	**(Konkuk University)**
4. Boyeon Kim	**(Yonsei University)**

Mathematical modeling of COIVD-19 epidemic in the Republic of Korea considering heterogeneous transmission

Youngsuk Ko[1], Jacob Lee[2], Yubin Seo[2], Yeonju Kim[3], Donghyok Kwon[3], and Eunok Jung[1]

1) Department of Mathematics, Konkuk University, KOREA
2) Division of Infectious Disease, Department of Internal Medicine, Hallym University College of Medicine, KOREA
3) Division of Public Health Emergency Response Research, Korea Disease Control and Prevention Agency, KOREA
**Corresponding Author: Eunok Jung, junge@konkuk.ac.kr*

Since the end of 2019, COVID-19 has caused a serious burden on the healthcare system and economical-and-social losses worldwide. Governments around the world have implemented non-pharmacological interventions such as lockdown and social distancing campaign. The first vaccination (AZD1222, known as AstraZeneca) initiated in England after acquiring emergency-use authorization. In the Republic of Korea, along with non-pharmacological interventions that have already been implemented, the vaccination began on February 26th.

In this research, we developed mathematical model of COVID-19 epidemic in the republic of Korea considering heterogeneous transmission (age or epidemic-related group). By using maximum likelihood estimation method, we estimated transmission rates between different groups. Using estimated transmission rates and phase-dependently estimated reproductive number, we discuss about best vaccine allocation strategy and risk structure of COVID-19 transmission. Our research depicts the importance of adequately implemented non-pharmacological interventions, not only the vaccination.

References

[1] Johns Hopkins University; COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE),

[2] Myung IJ; Tutorial on maximum likelihood estimation. Journal of mathematical Psychology. 2003 Feb 1;47(1):90-100,

[3] Kim S, Kim YJ, Peck KR, Ko Y, Lee J, Jung E. Keeping Low Reproductive Number Despite the Rebound Population Mobility in Korea, a Country Never under Lockdown during the COVID-19 Pandemic. International journal of environmental research and public health. 2020 Jan;17(24):9551.,

Modeling the Impact of Rapid Diagnostic Tests and Tafenoquine on the *Plasmodium Vivax* Malaria Burden in North Korea

Jiyeon Suh, Hye Seong, Joon-Sup Yeom, and Jeehyun Lee

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In North Korea, *Plasmodium vivax* malaria has been prevalent since its reemergence in 1997 [1]. The number of malaria cases peaked at over 110,000 in 2000 and has declined steadily with fluctuations, reporting 1,869 cases in 2019 [2]. In addition, the malaria risk area in North Korea is more extensive than in South Korea [2,3]. Therefore, a lot of resources and efforts are needed to eliminate malaria in North Korea. In this study, we developed a dynamic compartmental model for *P. vivax* malaria transmission in North Korea and estimated the impact of introducing rapid diagnostic tests (RDTs) and tafenoquine (TQ). The model was calibrated to fit annual malaria incidence data between 2014-2018 using maximum likelihood estimation and then predicted incidences over the next ten years. The model simulations demonstrated that introducing RDT alone averted total cases by 65.3%, TQ alone prevented relapse cases by 91%, and both RDT and TQ reduced total and relapse cases by 96.4% and 68.7%, respectively. Moreover, probabilistic sensitivity analysis was performed to evaluate the influences of uncertainties in the model parameters on the results. In conclusion, the RDT and TQ introduction could significantly reduce total and relapse malaria cases, respectively. Furthermore, the simultaneous and continuous implementation of RDT and TQ would be an effective way to reduce the malaria burden in North Korea.

References

[1] PT. Chol, N. Suwannapong, and N. Howteerakul, Evaluation of a Malaria Control Project in DPR Korea, 2001-2003, Southeast Asian Journal of Tropical Medicine and Public Health, **36,** 565-571 (2005)

[2] World Health Organization and others, World Malaria Report 2020: 20 Years of Global Progress and Challenges, World Health Organization, (2020)

[3] J.-H. Kim, A.-Y. Lim, and H.-K Cheong, Malaria Incidence of the Regions Adjacent to the Demilitarized Zone in the Democratic People's Republic of Korea, 2004-2016, Journal of Korean Medical Science, **34,** e227 (2019)

Mathematical modeling of COVID-19 in the Republic of Korea and scenario-based-study for the estimation of herd immunity achievement

Jongmin Lee, Youngsuk Ko, and Eunok Jung

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After the emergency-use authorization, COVID-19 vaccines have been continuously implemented since the end of 2020. In many countries, including Korea, uncertainties about the supply of vaccines are raised as the production is below in its demand. In this study, we developed the mathematical model of COVID-19 epidemic in Korea considering 2-shots of vaccination. By setting that herd immunity is achieved when the reproductive number is below 1, we estimated the herd immunity timing under various scenarios which consider different vaccine effectiveness, vaccine supply, and intervention policies. As a result, in the scenario with the same amount of vaccine as Korean government planed, herd immunity can be achieved between August and September. We found that to achieve herd immunity (or reduce the daily confirmed cases to 100 or less), more than 50 (75) million of vaccine doses are necessary. Our study emphasizes the importance of maintain social distancing in stable level and vaccine supply, simultaneously.

References

[1] ANDERSON, Roy M., et al. Challenges in creating herd immunity to SARS-CoV-2 infection by mass vaccination. The Lancet, 2020, 396.10263: 1614-1616.

[2] MACINTYRE, C. Raina; COSTANTINO, Valentina; TRENT, Mallory. Modelling of COVID-19 vaccination strategies and herd immunity, in scenarios of limited and full vaccine supply in NSW, Australia. Vaccine, 2021.

[3] WEITZ, Joshua S., et al. Modeling shield immunity to reduce COVID-19 epidemic spread. Nature medicine, 2020, 26.6: 849-854.

The impact of the Covid-19 on Tuberculosis in South Korea

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Vigorous government efforts have decreased the incidence of Tuberculosis (TB) in South Korea, but it still has a considerable TB burden. Since the first outbreak of Covid-19 in January 2020, the ongoing pandemic has led to various control measures. Policies adopted in response to the pandemic cause unintended consequences on other infectious diseases [1]. Health system overload due to Covid-19 may limit the service availability and result in delayed diagnosis and treatment of TB cases. On the other hand, interventions such as social distancing have the potential to decrease the transmission of tuberculosis by reducing contacts. This study is to evaluate the overall impact of Covid-19 on Tuberculosis incidence and deaths in Korea by 2025 through mathematical modeling. The results depend on the balance between negative effect by health service disruption and positive one by reduced contacts.

References

[1] Pai , M. COVID-19 coronavirus and tuberculosis: we need a damage control plan. Forbes. (2020) https://www.forbes.com/sites/madhukarpai/2020/03/17/covid-19-and-tuberculosis-we-need-a-damage-control-plan/#f72dd45295caExternal Link

General Session A2

Mathematical Modeling of Biological Systems

Date/Time: 8월 26일(목) 16:00

Speakers:

1. Kwangjoong Kim	**(Kookmin University)**
2. Seokjoo Chae	**(KAIST)**
3. Taeyong Lee	**(Yonsei University)**

Reaction-advection-diffusion competition models under lethal boundary conditions

Kwangjoong Kim[1], Wonhyung Choi[2] and Inkyung Ahn

1) College of General Education, Kookmin University
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2) Department of Mathematic, Korea University
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In this talk, we present a Lotka-Volterra reaction-advection-diffusion model for two competing species under homogeneous Dirichlet boundary conditions, which describe a hostile environment at the boundary. In particular, we deal with the case wherein one species diffuses at a constant rate, whereas the other species has a constant rate diffusion with a directed movement toward a better habitat in a heterogeneous environment under a lethal boundary. We show that stability of semi-trivial solution and the convexity of the environment is important for coexistence. The mathematical results will be expressed through numerical simulation.

First passage time approach reveals sources of noise in the timing of intracellular events

Seokjoo Chae[1,2], Dae Wook Kim[1,2] , Seunggyu Lee[3] and Jae Kyoung Kim[1,2]

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2) Biomedical Mathematical Group, Institute for Basic Science
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Intracellular events are required to occur on time for proper functioning of cells. How cells retain the temporal precision in the timing of intracellular events against a heterogeneous environment is poorly understood. Here, we investigate timings of various intracellular events by using a first-passage time framework. To be specific, we derive some formulae which quantify the randomness in the timing of events and use the formulae to understand the timing of complex intracellular events. Our result sheds light on biological conditions to reduce the fluctuation of the timing of cellular processes.

Optimal Control for Oncolytic Virus Treatment

Taeyong Lee, Hee-Dae Kwon and Jeehyun Lee

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Oncolytic viral therapy is one of the promising treatment in order to get rid of tumor cells. With virus infecting cancer cells and inducing cell death, this protocol treats cancer. Moreover, the treatments are duplicated by themselves in the host, which helps to maintain the amount to suppress cancer growth. However, when cancer grows faster than the replication, treatment is ineffective to prevent the growth of cancer at desired level. On the other hand, an excessive dose of virus may be toxic in spite of attenuation or cause unexpected side-effects.

Therefore, it is important to derive the optimal strategy of treatment protocol to get the best results with a set amount. We formulate the optimal control problem to minimize the amount of susceptible cancer cells at the end of the terminal time and during the whole time with the fixed amount of viruses. Numerical results and other findings are illustrated for the optimal strategies with various terminal time.

References

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General Session A3

Modeling and Data analysis in Medical Science

Date/Time: 8월 26일(목) 16:00

Speakers:

1. Junho Lee	**(Konkuk University)**
2. Donggu Lee	**(Konkuk University)**
3. Tae-Rin Lee	**(Seoul National University)**
4. Hyeryoung Cho	**(Seoul National University)**

Atorvastatin-mediated rescue of cancer-related cognitive changes in combined anticancer therapies

Junho Lee, Jin Su Kim and Yangjin Kim

Department of Mathematics, Konkuk University
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Acute administration of trastuzumab (TZB) may induce cognitive impairment. These cancer-related cognitive changes (CRCC) is an adverse biological process involving cancer stem cells (CSCs) and IL-6. Recent study has reported that atorvastatin (ATV) may change the dynamic of cognitive impairment in a combination (TZB+ATV) therapy. In this study, we investigate the mutual interactions between cancer stem cells and the tumor cells that facilitate cognitive impairment during long term TZB therapy by developing a mathematical model that involves IL-6 and the key apoptotic regulation. These include the densities of tumor cells and CSCs, and the concentrations of intracellular signaling molecules (NF_B, Bcl-2, BAX). We apply the mathematical model to a single or combination (ATV+TZB) therapy used in the experiments to demonstrate that the CSCs can enhance CRCC by secreting IL-6 and ATV may interfere the whole regulation. We show that the model can both reproduce the major experimental observation on onset and prevention of CRCC, and suggest several important predictions to guide future experiments with the goal of the development of new anti-tumor and anti-CRCC strategies. Moreover, using this model, we investigate the fundamental mechanism of onset of cognitive impairment in TZB-treated patients and the impact of alternating therapies on the anti-tumor efficacy and intracellular response to different treatment schedules.

References

[1] Lee S, Lee HJ, Kang H, Kim EH, Lim YC, Park H, et al. Trastuzumab Induced Chemobrain, Atorvastatin Rescued Chemobrain with Enhanced Anticancer Effect and without Hair Loss-Side Effect. J Clin Med. 2019;8(2):E234.

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Mathematical model of STAT signaling pathway in cancer development and optimal control approaches

Donggu Lee[1], **Jonggul Lee**[2], **and Yangjin Kim**[1,3,4]

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2) Korea Disease and Prevention Agency
3) Mathematical Biosciences Institute, Columbus, USA
4) Department of Neurosurgery, Harvard Medical School & Brigham and Woman's Hospital
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In many diseases, STAT family displays various responses, such as cellular immunity, apoptosis, proliferation, and differentiation. In this study, we investigate how an intracellular signaling network (STAT1, STAT3, Bcl-2, and BAX) regulates an important cellular fate, either anti-apoptosis or apoptosis. We developed a mathematical model of a signaling network using a set of ordinary differential equations. We show that network can generate a bi-stability condition so that it will induce either apoptosis or anti-apoptosis status of tumor cells. Then, we use this model to develop several anti-tumor strategies including injection of IFN-beta and DDP. The model provides a visual display of the complex behavior of a population of STAT and tumor in response to various IFN-beta and JAK2 stimuli. The simulation results from the mathematical model were show agreement with experimental data. In addition, the effect of anti-tumor drug administration is incorporated in the model in an effort to achieve optimal anti-tumor efficacy by optimal control theroty.

References

[1] Y. Kim, D. Lee, J. Lee, S. Lee, and S. Lawler, Role of tumor-associated neutrophils in regulation of tumor growth in lung cancer development: A mathematical model, PLoS One, **14,** e0211041 (2019)

[2] Y. Kim and A. Friedman, Interaction of tumor with its microenvironment: A mathematical model, Bull. Mth. Biol, **72,** 1029-1068 (2010)

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Data analysis of patient-specific lifelogging obtained from wearable devices

Tae-Rin Lee, Hee-jeong Park, Seeun Kim and Hyeryoung Cho

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Recently, various wearable devices have been utilized to monitor personal healthcare data or lifelogging data, e.g. heart rate, steps, calories, sleep status, etc. These data may be useful for understanding personal lifestyle. However, due to complex and high fluctuating data signals, it is difficult to precisely quantify personal lifestyle form the lifelogging data. In this talk, we present a sample set of lifelogging data obtained from patients. The lifelogging data acquisition was performed by commercial wearable devices for a year. Three different groups of patients were selected for this study. As a result, the lifelogging data from patients were compared with their blood test results. In addition, a data analysis method was suggested for quantifying their daily life.

Computer simulation of blood flow in the cerebrovascular structure of brain

Hyeryoung Cho and Tae-Rin Lee*

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As the scanning techniques advance, it promotes fast and detailed visualization of three-dimensional of the brain. However, due to a paucity of information of microvasculature, it is difficult to figure out mass transport from the vasculature to the brain tissue at the clinical level. In this talk, we suggest a computational model to predict quantify cerebral blood flow in the whole brain[1]. The patterns of blood pressure, flow velocity, and direction were numerically estimated by integrating the cerebrovascular geometry and the brain tissue. To represent the mass transport from the vasculature to the tissue, we use a diffusion model with multiple sources. Additionally, we discuss the changes of hemodynamic properties in case that the vascular network was partially blocked at specific areas in the brain.

References

[1] T.-R. Lee, J.-A. Hong, S. S. Yoo, and D. W. Kim, “A computational modeling of blood flow in asymmetrically bifurcating microvessels and its experimental validation,” International journal for numerical methods in biomedical engineering, vol. 34, no. 6, p. e2981, 2018.

Special Session B1

Medical Mathematics in Data Science and Applications

Organizer: Hyojung Lee (National Institute for Mathematical Sciences, NIMS)

Date/Time: 8월 27일(금) 09:00

Speakers:

1.	**Changhoon Kim**	**(Pusan National University)**
2.	**Hyoung Suk Park**	**(NIMS)**
3.	**Hyojung Lee**	**(NIMS)**
4.	**Kyungtaek Jun**	**(NIMS)**

Modeling for Mathematical Biology Potential epidemiologic indicators in the infectious disease control and their future use

Changhoon Kim

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There is a growing interest in research on probabilistic or mechanistic methodologies for epidemic infectious diseases. In particular, the monitoring of infection control measures using Rt and the evaluation of the impact of social distancing are typical examples. It is expected that promising research achievements will be possible and be utilized soon. However, many potential indicators necessary for field epidemiologic activities are not being utilized in the current response to Covid-19 as a limitation of appropriate data sources and methodologies.

In this talk, we will introduce indicators necessary for the implementation and evaluation of infection control measures, and introduce examples of data collection, analysis, and utilization in Busan metropolitan city. It is intended to provide opportunities for the development of various indicators necessary for future infection control measures and methodologies that can effectively estimate them.

References

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Recent works in Division of Medical Mathematics at NIMS

Hyoung Suk Park

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The Division of Medical Mathematics in National Institute for Mathematical Sciences (NIMS) conducts research for the development and application of medical diagnosis and disease prediction solutions using integrated mathematical theory. In this presentation, we introduce our recent works: (1) low-dose CT image reconstruction [1] (2) 3D cephalometric landmark identification [2] (3) developmental dysplasia of the hip (DDH) disease detection in X-ray [3]. The presented works were carried out in collaboration with Chungnam National University, Severance Hospital, and, Seoul National University Hospital, respectively.

References

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Approach to solve the mathematical problems using medical data

Hyojung Lee

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The Busan Center for Medical Mathematics (BCMM) of National Institute for Mathematical Sciences (NIMS) has been actively working with hospitals and medical companies in Busan since April 2020. In this talk, first, I would like to describe how to define the mathematical problems from real-world medical problems suggested by medical doctors and how to solve those problems. Second, I'd like to present several research topics of mathematical modeling of COVID-19 transmission dynamics. COVID-19 infection has continued to spread worldwide since December 2020. We constructed a mathematical model to assess the control interventions including the social distancing implemented in Korea. Finally, we assessed the effect of the control strategies as time-dependent interventions using mathematical model approach on the COVID-19 spread to suggest the most effective intervention.

References

[1] Hyojung Lee, Yeahwon Kim, Eunsu Kim, and Sunmi Lee, Risk Assessment of Importation and Local Transmission of COVID-19 in South Korea: Statistical Modeling Approach, JMIR Public Health & Surveillance, 7(6), 2021.

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Application of a Virtual Alignment Method to the dental prostheses and diagnosis

Kyungtaek Jun

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In this talk, we present some topics in mathematical biology. In cone-beam computed tomography (CBCT), it is difficult to obtain clean CT images when patient movement occurs during scanning. Due to the geometrical difficulties of CBCT, researchers have yet to find a solution to the alignment problems. To improve the geometric difficulties with CBCT, there has been ongoing researches on using Göbel mirror or X-ray compound lenses to alter the type of x-ray beams. This study deals with the reconstructed CT images when the X-ray shape is converted from a cone-shaped geometry to a parallel-shaped geometry. Here, to obtain clean CT images, we suggest utilizing cone-beam computed tomography system that can transform divergent beam of x-ray into parallel beam. In this study, the new alignment method, the virtual alignment method[1,2], shows promising results by reducing the error range down to several μm, offering the possibility to produce high-quality dental prostheses with accuracy and precision. In addition, the CT image used shows the internal detailed structure that has not been seen through the CBCT system so far. Therefore, we would like to show the benefits of using an X-ray mirror in a CBCT system. We expect that the newly suggested CT system along with the alignment method can be further investigated to be applied more readily in the field of dentistry to provide better quality images of patients to make a more accurate diagnosis and prostheses.

References

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Special Session B2

Mathematical Modeling in Medicine

Organizer: Wanho Lee (National Institute for Mathematical Sciences, NIMS)

Date/Time: 8월 27일(금) 09:00

Speakers:

1. **Wanho Lee**	**(NIMS)**
2. **Junhong Jo**	**(NIMS)**
3. **Minha Yoo**	**(NIMS)**
4. **Seunggyu Lee**	**(Korea University)**

Computational simulation of guidewire motion in a blood vessel

Wanho Lee

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The guidewire is made of a thin stainless-steel wire, inserted into the human body and moved through the blood vessel, and is an essential tool for the treatment and diagnosis of vascular diseases. In this study, Kirchhoff rod theory is applied to develop a guidewire model as an elastic rod, and to simulate moving within a given blood vessel. Particularly, the inherent characteristics (shape, strength, torque, and elasticity) of the guidewire are applied to the model, and the reaction of the guidewire to the axial movement and rotation of the operation portion is simulated. The blood vessel is presented with single branch, and the movement of guidewire along the shape of the vessel is examined. It will be also discussed the tip shape of the guidewire that must be selected to navigate to the desired path. The development of guidewire simulations can provide a safe environment for practitioners to practice as often as necessary while avoiding bioethics issues. In addition, it is possible to find an optimal pathways and controls for moving the guidewire to the clinical target with minimal stress on the environments within the vessel.

Axial Green function Method for viscous fluids and its applications

Junhong Jo[1], Wanho Lee[1] and Do Wan Kim[2]

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Axial Green function Method (AGM) is a technique for numerically solving multi-dimensional partial differential equations using only one-dimensional Green function [1-3]. In this talk, we introduce a method of solving Navier-Stokes equation which describe the motion of viscous fluid by applying AGM to the projection method [4]. Numerical results demonstrate the performance of our method. The application deals with two-dimensional coronary artery with stenosis.

References

[1] D. W. Kim, S.-K. Park, and S. Jun, "Axial Green's function method for multi-dimensional elliptic boundary value problems," *Int. J. Numer. Methods Eng.*, vol. 76, no. 5, pp. 697-726, Oct. 2008.

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Global Well-Posedness of Nutrient-Taxis Systems Derived by a Food Metric

Jaewook Ahn[1], **Sun-Ho Choi**[2] **and Minha Yoo**[3]

1) Department of Mathematics, Dongguk University
2) Department of Applied Mathematics and the Institute of Natural Sciences, Kyung Hee University
3) Division of Medical Mathematics, National Institute for Mathematical Sciences
mhyoo@nims.re.kr

In this talk, we deal with a nutrient-taxis system derived by a food metric, a metric defined by the density of nutrients, proposed by Choi and Kim, [1]. We show the existence and uniqueness of the model with assumptions that the initial nutrient density has uniform lower bounds. We also show the limit behavior when the diffusions of nutrient converges to zero. Finally, we discuss the existence of solutions when the initial of nutrients do not have any positive lower bounds.

References

[1] Sun-Ho Choi, Yong Jung Kim, *Chemotactic traveling waves by metric of food*, SIAM J. Appl. Math., **75,** (2015), 2268-2289.

Modelling for Functions of Anatomical Structures

Seunggyu Lee[1], Mi-Sun Hur[2] and Chang-Seok Oh[3]

1) Division of Applied Mathematical Sciences, Korea University
2) Department of Anatomy, Catholic Kwandong University College of Medicine
3) Department of Anatomy and Cell Biology, Sungkyunkwan University School of Medicine
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In this talk, we discuss some mathematical models used in recent studies of anatomical structures and their corresponding numerical simulation results. It is presented how mathematics and 21st century anatomy meet to investigate the function of human organs including prostatic urethral wall, facial muscles, channels in the interatrial septum of the heart, and pyloric sphincter.

References

[1] M. Hur, H. Lee, H. Yang, H. Kwon, J. O, S. Lee and C. Oh, Longitudinal muscular column in the prostatic urethral wall: its form, shape, and possible function based on mathematical simulation in ejaculation, Prostate, **80**(6), 471-480 (2020)

[2] M. Hur, J. O, H. Yang, H. Kwon, S. Lee, H. Lim, S. Lim and C. Oh, Heights and spatial relationships of the facial muscles acting on the nasolabial fold by dissection and three-dimensional microcomputed tomography, PLoS One, **15**(8), e0237043 (2020)

[3] M. Hur, S. Lee, C. Oh and Y. Choe, Newly-found channels in the interatrial septum of the heart by dissection, histologic evaluation, and three-dimensional microcomputed tomography, PLoS One, **16**(2), e0246585 (2021)

[4] M. Hur, S. Lee, T. Kang and C. Oh, The three muscle layers in the pyloric sphincter and their possible function during antropyloroduodenal motility, under review

Special Session B3

Analysis and Modeling of PDEs in Biological Systems

Organizer: Hantaek Bae, Kyudong Choi (UNIST)

Date/Time: 8월 27일(금) 09:00

Speakers:

1.	**Sun-Ho Choi**	**(Kyung Hee University)**
2.	**Min-Gi Lee**	**(Kyungpook National University)**
3.	**Ohsang Kwon**	**(Chungbuk National University)**
4.	**Myeongju Chae**	**(Hankyong National University)**

Chemotaxis system derived by food metric

Sun-Ho Choi, Jaewook Ahn, and Minha Yoo

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In this talk, we consider the global well-posedness of the nutrient-chemotaxis model derived from the food metric [2]. This model has a diffusion coefficient depending on nutrient density with singularity when nutrient density is zero. Here, we consider an energy estimate method [1] and a new transformation to obtain the global existence when the initial nutrient density has zero boundary condition at infinity.

References

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[2] Choi, S.-H. and Kim, Y.-J.: Chemotactic traveling waves by metric of food. SIAM Journal on Applied Mathematics 75 (2015), 2268–2289.

A system arises from plasticity and chemotaxis: result in stable regime

Min-Gi Lee

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We consider a system of equations

$$u_t = \Delta\left(\frac{u^n}{\gamma}\right),$$

$$\gamma_t = u^m - \gamma, \quad n, m > 0$$

in a smooth bounded domain with zero flux boundary condition. This system in one space dimension has an interpretation of a plasticity system of solid, and in general of a chemotactic system of micro-organisms. Dependency on γ in the first equation shows the control of diffusive nature by γ, while γ solves the second equation of relaxation type. This effects in the opposite ways depending on the parameters n and m. Linearized analysis shows the bifurcation by the sign of $n-m$. We expect the appearance of the aggregation phenomena, the blow-up, in the unstable regime while we expect the stabilization to a constant state in the stable regime. In this talk, the stable regime is considered first, where we show the global existence of a classical solution.

References

[1] L. Desvillettes, Y.-J. Kim, A. Trescasesc, and C. Yoon, A logarithmic chemotaxis model featuring global existence and aggregation, Nonlinear Analysis: Real World Applications, **50,** 562-582 (2019)

Spatial Segregation in Homogeneous Environment

Ohsang Kwon, Min-gi Lee and Youngae Lee

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Mutually attractive and repulsive interaction of species derives various pattern formations. For example, S-K-T model shows segregation phenomenon even in homogenous environment. In this talk, we prove the existence of non-symmetric positive solutions of homogeneous elliptic system which implies other type of spatial segregation phenomenon.

Modeling for Mathematical Biology

Jaewook Ahn, Myeongju Chae, and Jihoon Lee

School of applied mathematics and computer engineering, Hankyong National University
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Cell-cell adhesion is an inherently nonlocal phenomenon. Numerous partial differential equation models with nonlocal term have been recently presented to describe this phenomenon, yet the mathematical properties of nonlocal adhesion model are not thoroughly understood. We consider a model with two kinds of nonlocal cell-cell adhesion, satisfying no-flux conditions in a multidimensional bounded domain. In this talk we present the result on the global-in-time well-posedness of the solution to the model and discuss corresponding stochastic particle models.

References

[1] H. Amann, Semigroups and nonlinear evolution equations, Linear algebra and its applications, **84,** 3-32 (1986)

[2] N. J. Armstrong, K. J. Painter and J. A. Sherratt, A continuum approach to modelling cell-cell adhesion, Journal of Theoretical Biology, **243,** 98-113 (2006)

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Special Session C1

Mathematical Analysis and Methods in the Dynamics of Biological System: Cancers and Circadian Clock I

Organizer: Yangjin Kim (Konkuk University)

Date/Time: 8월 27일(금) 13:30

Speakers:

1. **Eunjung Kim**	**(Korea Institute of Science and Technology)**
2. **JaeKyoung Kim**	**(KAIST)**
3. **Chaeyoung Lee**	**(Korea University)**
4. **Hyejin Park**	**(Asia Pacific Center for Theoretical Physics)**

Mathematical and computational modeling for cancer treatment

Eunjung Kim

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In this talk, we will discuss the integrated approach of mathematical/computational modeling, biological experimental, and the clinics to better understand and treat cancer. First, I will introduce model-driven adaptive therapy strategies. Here, we developed two models that explain two modes of interaction between drug-sensitive and -resistant cell populations in a tumor. The models were parameterized using serological biomarker data from patients with advanced melanoma. The trained models were used to determine patient-specific adaptive therapy on and off schedule, resulting in improved progression-free survival compared to a one-size-fits-all therapy strategy. Next, we will discuss a mathematical model of cell signaling pathways to predict targeted therapy outcomes. The model was trained by minimizing the difference between model-predicted protein expression and experimentally measured protein phosphorylation under different microenvironmental conditions. The calibrated model predicts distributional responses to kinase inhibitors and suggests drug resistance mechanisms that can be exploited in drug combination strategies. The suggested combination strategies are validated using in vitro experimental data. The validated in silico cells are further interrogated through an unsupervised clustering analysis and then integrated into a hybrid cellular automata model of tumor growth in a spatially heterogeneous microenvironment. As a proof of concept, we simulate tumor responses to targeted therapies in a spatially segregated tissue structure containing tumor and stroma and predict complex cell signaling responses that suggest a novel combination treatment strategy.

REFERENCES

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Oscillatory timeseries data sheds light on molecular mechanisms

Jae Kyoung Kim

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I will talk about a fundamental question underlying the model-based time-series analysis: “Can we always fit a model to given oscillatory timeseries data as long as the number of parameters is large?”. That is, is Von Neumann's quote “With four parameters I can fit an elephant, and with five I can make him wiggle his trunk” true? From this, I will describe an inference algorithm for biochemical reaction network.

Mathematical modeling and computational simulation of a cytokine shield formation of senescent tumor cells

Chaeyoung Lee[1], Jun Ho Lee[2], and Yangjin Kim[2]*

1) Department of Mathematics, Korea University
2) Department of Mathematics, Konkuk University
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Treatment of cancer development are still a big challenge in the field of medical science because of physical barriers that prevent immune cells from penetrating into the tumor. However, the onset of a chemical barrier, called Cytokine Shield, that protects cancer cells from immune attack has recently been identified [1]. It has been found that two substances secreted by senescent tumor cells in colorectal cancer impede the infiltration of immune cells (called CD8+ T cells) into the tumor and weaken the activity of immune cells, thereby exacerbating the progression of colorectal cancer: C-X-C motif chemokine ligand 12 (CXCL12) and colony stimulating factor 1 (CSF1). A high concentration of CXCL12 from senescent tumor cells prevents infiltration of CD8+ T cells, and CSF1 change monocyte differentiation into M2 macrophages, which prevent CD8+ T cell activation. In this talk, we introduce a mathematical model, based on hybrid approaches involving nonlinear PDEs and intracellular signaling network, and computational simulation of a cytokine shield formation of senescent cells. Our proposed model can be potentially used for developments of antitumor immune mechanism.

References

[1] Y. W. Choi, Y. H. Kim, S. Y. Oh, K. W. Suh, Y. S. Kim, G. Y. Lee, et al. Senescent tumor cells build a cytokine shield in colorectal cancer. Advanced Science, **8**(4), 2002497 (2021).

Reducing the risk of accumulating mutations via cell competitions in a hierarchical tissue

Hye Jin Park[1], ArneTraulsen[2], and Da Zhou[3]

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A hierarchical structure of cells in tissue has been recognized for a long time; the stem cells become mature cells through several differentiation steps. Previous studies have shown that such structures could reduce cancer risk by suppressing the accumulation of mutations, suggesting the hierarchical structure could be an evolutionary outcome. However a huge volume of model studies has ignored the interaction between cells that is an essential ingredient of the frequency-dependent evolution. Here we introduce competition between cells and develop a minimal model to study the role of interaction. The results show that competition can enhance wildtype cells even without no competition advantage for wildtype cells. The key underlying mechanism is that the benefit of wildtype cells can be effectively larger for smaller population size.

Special Session C2

Population Model

Organizer: Tae-Soo Chon (Enfra), Young-Seuk Park (Kyung Hee University)

Date/Time: 8월 27일(금) 13:30

Speakers:

1. **Young-Seuk Park**	**(Kyung Hee University)**
2. **Nam Jung**	**(Inha University)**
3. **KyoungEun Lee**	**(National Institute of Ecology)**
4. **Thakur Dhakal**	**(Kangwon National University)**
5. **Tae-Soo Chon**	**(Ecology and Future Research Institute)**

Recent Trends of Data-Driven Models in Ecology

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Various types of ecological models have been developed depending on the objectives of the studies including development of strategies to conserve or restore concerning ecosystems and test of ecological hypothesis. Modeling techniques can be classified to various types based on interests of researches. Among them, two different types such as a process model and a data-driven model. A process model is based on the description of the system behavior by hypothesizing relationship between the variables in the data set where the nature of the relationship is specified in terms of the physical, chemical or biological processes. Therefore, the process models need several parameters to characterize these processes in the concerning system, and they can be obtained by experiments. The process models are useful to predict novel dataset and evaluate the causality between variables. However, it is hard to obtain accurate and general range of parameters, and takes much of effort and time to develop the models. Meanwhile, data-driven models are based on the analysis of the data by aiming to find relationships between variables without explicit knowledge of the concerning system behavior. They assume the information is imbedded in the data. Therefore, the relationship between variables seeks to describe the data, and in turn sufficient observed data are required to address the condition of the system. Statistical models such as liner regression and machine learning methods are included in this category. This study present recent trends of data-driven models in ecology and environmental science.

A spatially explicit model applied to nutria (*Myocastor coypus*) population dispersal in field conditions in Korea

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Nutria (*Myocastor coypus*) is the species for a well-known example of population invasion in Korea: the population was introduced to Republic of Korea in 1985 for fur farming but released to the wild due to failure of nutria farm, inhabiting over the area of 23,384 km^2 along the Nakdong River resultantly. A spatially explicit model (SEM) was developed to present essential life events of nutria, including growth and movement rates, effects of carrying capacity and Allee effects, and human capture concurrently. The model outputs were compared with the field data from late 1990s to late 2010s in the Nakdong River watershed area. Overall, simulated results reflected the area of population invasion observed in field conditions. The movement rate appeared to be a main cause of spatial dispersal under the fixed condition of human capture while the other parameters related to carrying capacity and Allee effect contributed to diffusion in association with local environmental and biological conditions during the course of population advancement. The model was able to find the cause of delayed advancement locally due to low values of habitat preferences. The simulation model based on SEM was efficient to address causality of spatio-temporal dispersal and to monitor and manage invasive populations under various environmental conditions.

Predicting dispersal of invasive sika deer (*Cervus nippon*) in a novel group-based model

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Incidents such as an outbreak of invasive alien species give rise to ecological instability and disturbance including dramatic biodiversity loss. Causality of sika deer (*Cervus nippon*) invasion is currently a subject for scrutiny due to the rapid increase of its population in Korea, leaving numerous accounts. It has been reported many traces of sika deers in the invaded area, Songnisan National Park. We introduce a group-based model for sika deer dispersal dynamics in the Songnisan National Park area, specifically linking with group behavior, which is one of distinct characteristics of deers. The group dynamics of sika deer is addressed by group size change and biased levy walk across different life stages (normal, birth, and mating), concurrently considering the habitat preference and carrying capacity in each cell. Simulation was conducted in the invaded area around the Songni mountain for 20 years (from January 2008 to December 2027). Numerical database based on the model results presented the direction and area of population dispersal in spatio-temporal domain effectively. Specifically, populations were mostly spreading along the mountain ranges from the released point, Beopjusa, within the Songni mountain. However, some are spreading out of bounds of the mountain, even across the road. The model results were efficient in revealing both global dispersal patterns in one hand and local incidences of group advancement in the other hand. The model could be further incorporated to practical problems related to sika deer dispersal, for example, roadkill, crop damage and so on, in the future. This simulation-based, predictive framework will enable us to identify the ecological as well as environmental consequences in revealing invasion causality of species spreading in the target area under various biological and environmental conditions.

Individual-based simulation for wild boar (*Sus scrofa*) dispersal and disease transmission in linking with behaviour states defined by hidden Markov model

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Wild boar (*Sus scrofa*) has expanded rapidly in Korea, critically linked with spread of African swine fever (ASF). An individual based model (IBM) was developed to present life events of wild boars, including movement, growth rate, carrying capacity and Allee effects. Specifically, movements of individuals were simulated according to hidden Markov model (HMM). Based on telemetry data obtained in field conditions, the parameters, transition probability matrices (TPMs) and emission probability matrices (EPMs) were estimated through the HMM training. According to TPMs and EPMs movements of individuals were generated in IBM in selecting habitats with different resources such as shelter, food and water. The model results were effective in revealing both population dispersal and disease transmission globally and individual visits to habitats locally. Based on the life events of healthy individuals, transmission of ASF was further incorporated to the model when susceptible individuals encountered infected individuals; prognosis was possible in presenting spatio-temporal transmission of disease under different simulation conditions. Effectivity of IBMs with an emphasis on individual behaviour states is further discussed in monitoring and management of both the host population and disease transmission.

Hidden Markov model applied to behavioural states in wild boar (*Sus scrofa*) movements in linking with self-organizing map

Tae-Soo Chon[1,2], Thakur Dhakal[2], Sang Jin Lim[2],
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Wild boar (*Sus scrofa*) has been recently a critical issue in Korea regarding rapid population expansion in one hand and transmitting African swine fever in the other hand. Understanding movement behaviour of wild boar individuals is critical in predicting spatial advancement patterns of host population and disease transmission. Movements of animals, however, are complex and difficult to analyse. The hidden Markov model (HMM) was utilized to objectively define behaviour states of wild boars in choosing habitats in each time unit. Movement data for wild boar individuals continuously tracked in field conditions (Bukhan Mountain, Seoul, Korea, from June, 2018 to May, 2019) were used for HMM training. The time-series observable events were expressed as the habitats with different resources (forest, leaf types and water) as input. Transition probability matrices (TPMs) and emission probability matrices (EPMs) were estimated according to combinations of initial conditions through HMM training. Subsequently self-organizing map (SOM) was used to identify all output results as clusters on the component map to reveal local/global maxima of the calculated parameters. The obtained states were identifiable including probabilistic preference of the most suitable habitat (broad-leaf with water) followed by either needle-leaf with water or broad-leaf without water according to the individuals. The effectivity of utilizing HMM in linking with SOM is further discussed in extracting ecologically useful information from complex field data.

Special Session C3

Pharmacokinetic and Pharmacodynamic Model (PKPD)

Organizer: Il Hyo Jung (Pusan National University)

Date/Time: 8월 27일(금) 13:30

Speakers:

1. **In-Soo Yoon**	**(Pusan National University)**
2. **Jong Hyuk Byun**	**(Pusan National University)**
3. **Yong-Jung Kim**	**(KAIST)**
4. **Yun Min Song**	**(KAIST)**

Development of physiologically based pharmacokinetic model of entrectinib in rats and humans

Seong-Wook Seo[1], Dong-Gyun Han[1], Eugene Choi[1], Taeuk Park[2], Jong Hyuk Byun[3], Hyun-Jong Cho[4], Il Hyo Jung[3], and In-Soo Yoon[1]

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A physiologically based pharmacokinetic (PBPK) model is recognized as a powerful tool for the quantitative analysis of kinetic behavior of a compound in the body after administration. The use of real anatomical structure and physiological parameters enables a PBPK model to quantitatively predict the drug exposure levels in various tissues of animals and humans through in vitro-in vivo extrapolation and/or interspecies scaling. In the present study, we developed a PBPK model for entrectinib, an oral antineoplastic agent that was approved by the US Food and Drug Administration in 2019 for the treatment of c-ros oncogene 1 (ROS1) fusion-positive non-small cell lung cancer and neurotrophic tyrosine receptor kinase (NTRK) fusion-positive solid tumor. Using the model, the contributory roles of gut and hepatic metabolism on the oral bioavailability of entrectinib in rats and humans were investigated.

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A transit and fractional order derivative model of lapatinib

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Lapatinib is an orally active drug for breast cancer and other solid tumors. It is a dual tyrosine kinase inhibitor that interrupts the HER2/neu and epidermal growth factor receptor (EGFR) pathways. In this study, we consider how to apply the model considered *in vitro* 2D to 3D cell lines. The morphology of the 2D cell line is altered due to disturbances in interactions with the external environment, in which cells lose their polarity. This discrepancy between them leads to difficulty to model. To address this, a new model is developed to describe cell dynamics in 2D. The growth rate from 2D to 3D is considered time-dependent. The process of cell damage by the drug effect is considered age-structured. If the drug's cell growth inhibition occurs slowly, a fractional-order derivative equation (FDE) can be applied. The FDE model has the advantage of reducing the number of parameters and models. Based on data, various models are compared to validate the result.

References

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Can you tell how effective a COVID-19 prevention strategy is at elementary schools?

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Predicting the spread of epidemic using an epidemic model has never been successful. In this talk, we consider a new use of epidemic models, i.e., we use it to estimate the effect of epidemic spreading prevention strategies. The basic idea is to use epidemic models to compute the basic reproduction number R_0 under various strategies using epidemic models such as SIR, SIRS, etc.

Accurate Prediction of Drug Clearance in Liver

**Yun Min Song[1,2], Hyukpyo Hong[1,2], Eun Han Goo[1], Hyun-Moon Back[3],
Hwi-Yeal Yun[4], Sang Kyum Kim[4], Jung-Woo Chae[4], and Jae Kyoung Kim[1,2]**

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Clearance (CL), the amounts of a drug metabolized by enzymes per unit time, is the major pharmacokinetic parameter for developing medications. *In vivo* hepatic CL for a drug has usually been predicted by extrapolating measured in vitro intrinsic CL, the ratio between the maximal rate of metabolism and Michaelis-Menten constant ($\frac{V_{max}}{K_M}$). This prediction is based on the Michaelis-Menten equation which is valid only when the K_M value of a drug is much higher than the hepatic concentration of the enzymes. However, this condition does not hold for many drugs, and thus the prediction of hepatic CL for such drugs can be inaccurate. In this presentation, we introduce an alternative approach which accurately predicts *in vivo* CL for drugs regardless of their K_M.

References

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Special Session D1

Mathematical Analysis and Methods in the Dynamics of Biological System: Cancers and Circadian Clock II

Organizer: Jae Kyoung Kim (KAIST)

Date/Time: 8월 27일(금) 15:20

Speakers:

1. **Jinsu Kim**	**(Korea Institute Radiological and Medical Sciences)**
2. **Euimin Jeong**	**(KAIST)**
3. **Masud M A**	**(Korea Institute of Science and Technology)**
4. **Hyukpyo Hong**	**(KAIST)**

PET tracing of biodistribution for orally administered ^{64}Cu-labeled polystyrene in mice

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Plastics are used commonly in the world because of its convenience and cost-effectiveness. Microplastics, an environmental threat and human health risk, are widely detected in food, and consequently ingested. However degraded plastics are found everywhere, which cause environmental threat and human health risk. Therefore, real-time monitoring of orally administered microplastics is tremendously important to trace them in the body. In this study, to visualize their absorption path, we labeled polystyrene with [^{64}Cu]Cu-DOTA. We prepared radiolabeled polystyrene with ^{64}Cu after, [^{64}Cu]Cu-DOTA-polystyrene was then orally administered to mice and evaluate its transit and absorption in mice using PET imaging. The absorption path and distribution of [^{64}Cu]Cu-DOTA-polystyrene were determined using positron emission tomography (PET) over 48 h. *Ex vivo* tissue-radio thin-layer chromatography (*Ex vivo*-radioTLC) was used to demonstrate the existence of [^{64}Cu]Cu-DOTA-polystyrene in tissue. PET images demonstrated that [^{64}Cu]Cu-DOTA-polystyrene began to transit to the intestine within 1 h. [^{64}Cu]Cu-DOTA-polystyrene accumulation in the liver was also observed. Biodistribution of [^{64}Cu]Cu-DOTA-polystyrene confirmed the observed distribution of [^{64}Cu]Cu-DOTA-polystyrene from PET images. *Ex vivo*-radioTLC was used to demonstrate that the detected gamma rays originated from [^{64}Cu]Cu-DOTA-polystyrene. This study provided evidence of microplastic accumulation and existence in tissue by using PET imaging, and cross confirmed by *ex vivo*-radioTLC. The information provided may be used as the basis for future studies on the toxicity of microplastics.

Mathematical Modeling for Pacemaker-neuron-dependent Molecular Rhythm Alteration by *Drosophila* Clock Mutant

**Eui Min Jeong[1,2], Miri Kwon[3], Eunjoo Cho[3],
Sang Hyuk Lee[3], Eun Young Kim[3], and Jae Kyoung Kim[1,2]**

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In Drosophila, circadian (~24h) rhythms are regulated by about 150 pacemaker neurons. In each pacemaker neuron, circadian gene expression is driven by a transcriptional-translational feedback loop (TTFL). Interestingly, with dCLK-Δ mutation, which has impaired binding with PER, the amplitude of PER rhythms is greatly reduced in small ventral lateral neurons (sLNvs), but not in posterior dorsal neuron 1s (DN1_ps). We investigated this unexpected difference between sLN$_v$s and DN1_ps by developing a mathematical model describing the TTFL. Our model predicted the differences in the molecular stoichiometry and regulatory mechanism of clock proteins between sLN$_v$s and DN1_ps, which were validated by the experiments. We will discuss the biological significance of those differences between LNvs and DN1s for circadian clock system to work.

Spatial Heterogeneity Mediated Treatment Response

Masud M A and Eunjung Kim

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A long-standing practice in cancer treatment is hit hard with maximum tolerated dose to eradicate the tumor. Such continuous therapy, however, selects for resistance cells leading to treatment failure. A different type of treatment strategy, adaptive therapy, has recently shown a degree of success in both preclinical xenograft experiments and clinical trials. Adaptive therapy aims to maintain tumor volume by exploiting the competition between drug-sensitive and resistant cells with minimum effective drug doses or timed drug holidays. To further understand the role of competition on adaptive therapy outcomes, we develop a 2D on-lattice agent-based model. Our simulations show that the superiority of adaptive strategy over continuous therapy depends on the local competition shaped by the spatial distribution of resistant cells. Cancer cell migration and increased carrying capacity drive a faster tumor progression time under both types of treatment by reducing spatial competition. The intratumor competition can also be affected by fibroblasts, which produce microenvironmental factors that promote cancer cell growth. Our simulations show that the spatial architecture of fibroblasts modulates benefit of adaptive therapy. Finally, as proof of concept, we simulate adaptive therapy outcomes on multiple metastatic sites composed of different spatial distributions of fibroblasts and drug resistance cell populations. Among the multiple metastatic sites, one is considered invisible in the sense that it has very few cancer cells at the beginning. Our simulations show that the cell configuration of the invisible metastasis critically determines the treatment response.

Inference of stochastic dynamics in biochemical reaction networks by exploiting deterministic dynamics

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M Ali Al-Radhawi[4], Eduardo Sontag[4], and Jae Kyoung Kim[1, 2]

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Biochemical reaction networks (BRNs) have a stochastic nature, so every reaction in BRNs display randomness. Inherent stochasticity can be captured only by stochastic models, but it is more challenging to analyze their dynamics while their deterministic counterparts are easier to be analyzed, in general. Thus, various methods exploiting deterministic dynamics to infer the stochastic one have been proposed. In particular, stochastic model reduction using deterministic quasi-steady-state approximations (QSSAs) of fast variables is widely used to efficiently simulate a stochastic model. For instance, Michaelis-Menten or Hill-type functions have been used for Gillespie stochastic simulation. In this talk, we provide a complete validity condition for stochastic model reduction using the deterministic QSSA to eliminate stochastic reversible binding, which is fundamental and ubiquitous in BRNs. Furthermore, we present a framework to analytically derive stationary distribution for a large class of BRNs using their deterministic steady states based on chemical reaction network theory.

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Special Session D2

정수생태계 변화 예측모델

Organizer: Young-Seuk Park (Kyung Hee University)

Date/Time: 8월 27일(금) 15:20

Speakers:

1. 이다영	(경희대학교)
2. 지창우	(전남대학교)
3. 이대성	(경희대학교)
4. 신지훈	(서울시립대학교)
5. 이정현	(㈜지오시스템리서치)

생물 모니터링 자료를 이용한 담수생태계의 먹이망 구축

이다영, 박영석

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생물 모니터링 자료는 환경 조건의 변화에 따른 생물 구성의 변화를 추적하는데 유용하다. 생물 군집 내에서는 구성원간에 다양한 상호작용이 일어나고 있으나 종 구성을 모니터링하는 자료만으로는 상호작용을 설명해줄 수 없다. 한편, 먹이망은 생태계 내 구성원들의 상호작용을 반영해줄 수 있다. 생물 모니터링 자료와 먹이망을 연결시킬 수 있다면 군집 구성뿐만 아니라 해당 생태계 내의 상호작용까지 반영해줄 수 있어 다양한 측면에서 생태계를 이해할 수 있다. 이 연구는 생물모니터링 자료과 먹이망 내 상호작용 관련 문헌을 바탕으로 통합 먹이망(metaweb)을 구축하고자 하였다. 이 연구에서는 담수생태계 내의 피식-포식 관계만을 고려하였다. 문헌 조사를 유기물, 식물플랑크톤, 동물플랑크톤, 저서성대형무척추동물, 어류의 먹이망에서의 관계를 조사하였다. 자료는 대부분 속 수준에서 구축되었다. 이 자료를 바탕으로 모든 가능한 피식-포식 관계를 포함하는 통합 먹이망을 구축한다. 통합 먹이망은 피식-포식 비율을 고려하지 않고 종의 출현 유무에 따라서만 구성하였다. 연구 대상지역의 모니터링 자료를 바탕으로 통합 먹이망에서 상호관계를 추출하여 각 지역의 먹이망을 구축하였다. 먹이망은 R 프로그램의 igraph 패키지를 이용하여 만들었다. 이 연구는 장기적으로 모니터링된 다양한 자료를 먹이망 연구와 연결시켜 군집 구성의 다양한 측면을 연구할 수 있도록 하는 디딤돌의 역할을 할 것이다.

국내 담수 어류의 45종과 멸종위기 어류 20종의 먹이원 분석

지창우 [1], 이대성 [2], 이다영 [2], 곽인실 [3], 박영석 [2]

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국내 담수 생태계 군집의 먹이망 자료 수집 및 분석을 위해 1차 담수 어류 12과, 28속, 45종 어류의 먹이원 문헌을 수집하고 수집하고 분석하였다. 먹이원이 보고된 45종의 어류 중 20종은 멸종위기 어류로 본 연구에서는 멸종위기 어류의 먹이원 자료를 추가적으로 분석하였다. 수집한 45종의 먹이원은 총 26목, 42강, 94목, 189과, 294속으로 조사되었으며 멸종위기 어류 20종의 먹이원은 20문, 31강, 58목, 116과, 154속으로 조사되었다. 동물류 먹이원 중 가장 많은 어류가 섭식한 먹이원은 분류군에 따라 절지동물문, 곤충강, 파리목, 깔따구과로 조사되었으며 식물류 먹이원은 규조류, 윷돌말강, 반달돌말목, 반달돌말과로 조사되었다. 먹이원 유형에 따라 어류의 섭식 형태를 분석하기 위해 SOM (Self-organizing map)과 NMDS (Non-metric multidimensional scaling), 계층적 군집분석(Hierarchical clustering) 분석을 하였고 추가적으로 어류와 먹이원과의 네트워크 분석을 시도하였다. 45종 어류의 먹이원에 따른 유형은 어류를 포식하는 어류군과 저서성무척추동물을 주로 섭식하는 어류군, 식물플랑크톤을 주로 섭식하는 어류군, 동물플랑크톤을 주로 섭식하는 어류군, 끝으로 잡식하는 어류군 5 가지로 구분되었다. 먹이원에 따른 멸종위기 어류 20종의 유형화는 파리목을 먹는 어류와 먹지 않는 어류로 2개의 그룹으로 나뉘었다. 45종의 어류와 먹이원의 네트워크 분석 후 조사된 허브 점수에서, 상위 5 종류의 먹이원은 파리목, 하루살이목, 이지목, 김발돌말목, 쪽배돌말목 순으로 조사되었다. 멸종위기 어류의 먹이원 중, 허브 점수가 높은 먹이원은 파리목, 하루살이목, 날도래목, 강도래목, 딱정벌래목으로 나타났으며 식물류 먹이원 중 허브 점수가 높은 쪽배돌말목과 반달돌말목, 김발돌말목으로 조사되었다.

한강 수계 내 호소에서 저서성 대형무척추동물 및 수질에 대한 어류 군집 구성 변화 예측

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어류는 담수생태계 내 최상위 소비자로서, 생태적, 사회적, 경제적으로 중요한 의미를 가진다. 그리고 생태계 내 어류 군집에 대한 생태학적 이해와 자원적 관리 및 활용을 위해서는, 생물 및 수질 요인과 어류 군집 간 관계를 이해하는 것이 선행되어야 한다. 본 연구에서는 한강 수계 내 어류 및 저서성 대형무척추동물 자료와 호소별 수질 자료를 바탕으로, 저서성 대형무척추동물 및 수질에 따른 어류 군집의 구성 변화를 모의하였다. 어류 군집의 구성 종은 분류학적 과(Family) 수준 및 섭식 특성에 따라 구분하였다. 연구 결과, 뱀장어과(Anguillidae)와 잉어과(Cyprinidae), 동자개과(Bagridae), 동사리과(Odontobutidae), 검정우럭과(Centrarchidae) 및 잡식종과 충식종에 대해, 해당 분류군의 구성 변화와 관련된 중요 생물 및 환경 변수를 확인하고, Random forest 모형을 이용하여 실제 채집 결과와 유의한 추세를 가지는 예측 모형을 제작하였다.

해석가능한 기계학습 기법을 활용한 녹조현상의 예측

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녹조현상에 대한 정확한 예측은 전세계적으로 수자원 관리에 있어 주요 관심사이다. 기계학습을 활용한 녹조발생 예측은 뛰어난 예측 성능을 보였으나, 예측 결과에 대한 해석력의 부재는 모델의 활용성 극대화에 있어 걸림돌이 되고 있다. 이에 따라 최근 해석력 증대를 위한 다양한 방법론들이 등장하고 있으며, 그 중 SHAP (SHapley Additive explanation)은 견고한 이론적 기반과 분석 상의 이점을 바탕으로 주목받고 있다. 본 연구에서는 SHAP을 활용하여 녹조현상에 대한 환경변수의 영향을 분석하였다. 다양한 기계학습 알고리즘을 활용해 녹조발생을 예측했으며, 예측변수로 다양한 수리수문, 기상, 수질 변수를 활용하였다. 기계학습 알고리즘은 모든 성능지표에 대해 양호한 예측성능을 나타냈다. SHAP의 적용을 통해 수온, 체류시간, 총 질소 등이 녹조발생에 대한 주요 환경변수임을 확인할 수 있었으며, 영향의 방향에 더해 변수 간 상호작용 또한 확인할 수 있었다. 게다가, 모든 상호작용의 영향을 제외한 단일 환경변수의 영향 또한 확인할 수 있었다.

Delf3D 모델을 활용한 주암호 물순환 및 수질변동 특성 분석

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최근 국내뿐만 아니라 국제적으로 환경보전과 지속적인 생태계 관리의 중요성이 부각되고 있다. 호소에서 발생하는 복잡한 동수역학적 운동(hydro-dynamics)과 생지화학적(biogeochemical) 반응특성, 그리고 이로 인한 생태계 상호작용을 이해하고, 선제적 수질·생태계 관리를 위해서는 수환경 모델(수리, 수질)과 수생태계 모델 연계를 통한 종합적인 분석과 예측이 필요하다[1]. 본 연구에서는 주암호 내에서 물순환 및 수질변동 특성을 보다 면밀히 분석하기 위하여 주암호를 대상으로 Delft3D 모델을 구축하였다. Delft3D 내 수질모듈인 DELWAQ를 적용하였으며, 조류의 적응과 경쟁 기작을 고려하기 위하여 BLOOM 모듈을 사용하였다. 모의에 사용된 수평격자 크기는 100 m, 연직격자는 주암호 내 수온성층 구조를 고려하여 1~3 m로 총 35개 층으로 구성하였다. 모델은 수위, 수온, 수질항목(DO, T-N, T-P, TOC, 클로로필-*a*)들의 연변동 특성을 잘 재현하였다. 보정된 모델을 활용하여 주암호 내에서의 물순환 특성과 수질변동 특성을 분석하였다.

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Special Session D3

의생명에 활용되는 데이터분석

Organizer: Gangjoon Yoon (NIMS)

Date/Time: 8월 27일(금) 15:20

Speakers:

1. **Wanho Lee**	**(NIMS)**
2. **Yongkeun Park**	**(Catholic Kwandong University)**
3. **Sangjeong Ahn**	**(Catholic Kwandong University)**
4. **YongKuk Kim**	**(Kyungpook National University)**

Computational approach to simulate microswimmers propelled by bacterial flagella

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Peritrichously flagellated bacteria swim in a fluid environment by rotating motors embedded in the cell membrane and consequently rotating multiple helical flagella. We present a novel mathematical model of a microswimmer that can freely run propelled by a flagellar bundle and tumble upon motor reversals. Our cell model is composed of a rod-shaped rigid cell body and multiple flagella randomly distributed over the cell body. These flagella can go through polymorphic transformations. We demonstrate that flagellar bundling is influenced by flagellar distribution and hence the number of flagella. Moreover, reorientation of cells are affected by the number of flagella, how many flagella change their polymorphisms within a cell, the tumble timing, different combinations of polymorphic sequences, and random motor reversals. Our mathematical method can be applied to numerous types of microorganisms and may help to understand their characteristic swimming mechanisms.

Machine learning approach using routine immediate postoperative laboratory values for predicting postoperative mortality

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Background: Several prediction models have been recommended for preoperative risk stratification. The patient's condition can significantly change after compared with before surgery. Hence, the status and prognosis of newly identified high-risk patients must be re-evaluated immediately after surgery. This study aimed to develop machine learning models using routine immediate postoperative laboratory values for predicting postoperative mortality.

Methods: A tertiary hospital database with publicly available datasets from South Korea was used in this research. The following machine learning algorithms were utilised for developing the models: lasso logistic regression, random forest, deep neural network and XGBoost. To validate the efficacy of the developed models, their performance was compared with that of the previouosly introduced SASA score combined modelscoring system. Furthermore, the models using only immediate postoperative blood test values were validated using data obtained from another tertiary hospital database.

Results: There were 5,940 patients included in the database. The performance of all models was superior to that of the SASA score combined modelscoring system. Moreover, the deep neural network had the best area under receiver operating characteristic curve and area under the precision recall curve. Of 5,940 patients, 3,817 had immediate postoperative blood test values. The models using only laboratory values were developed, and their efficacy was validated using data obtained from 21,640 patients in another database. The random forest model had the best performance, and phosphorus level had the highest contribution to the model.

Conclusions: Machine learning models using routine immediate postoperative laboratory values can help identify patients at a higher risk for postoperative mortality.

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Deep learning model for the prediction of EBV status in gastric cancer

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Background: Detection of EBV status in gastric cancer is crucial for clinical decision making, as it identifies patient with different treatment response and prognosis. Despite its apparent importance, EBV status is not readily testable because of limited medical resources. There is an unmet need for widely accessible and cost-effective tools for the testing. Here, we investigate the potential of a deep learning-based system for automated EBV prediction directly from hematoxylin and eosin (H&E)-stained whole-slide images (WSIs).

Methods: Our deep learning model (EBVNet) consists of two sequential components: a tumor classifier and an EBV classifier. The EBVNet was developed using 319 H&E-stained WSIs (26 with EBV positive and 293 with EBV negative), from The Cancer Genome Atlas, containing WSIs scanned at 40x and 20x magnification. Performance was primary evaluated using the sensitivity, specificity, negative predictive value (NPV), and F1-score on the hold-out test dataset.

Results: The tumor classifier achieved a NPV of 97.8%, sensitivity of 99.0%, specificity of 97.3%, and F1-score of 98.9%. The EBV classifier achieved a NPV of 99.3%, sensitivity of 92.4%, specificity of 99.3%, and F1-score of 92.4%.

Conclusion: Within the current universal EBV testing paradigm, such a model might contribute value as an automated screening tool to triage patients for confirmatory testing, potentially reducing the number of tested patients, thereby resulting in substantial test-related labor and cost savings.

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False promise of ending COVID-19 by vaccination without treatment

YongKuk Kim[1], Hwa Kil Kim[2], Hyebin Kim[1], Sang Il Kim[3], and Gangjoon Yoon[4]

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The COVID-19 global pandemic has posed the biggest medical challenge of the past two years. Because handling the pandemic cannot be limited to any national scale, significant joint cross-border efforts have been made to eradicate this infectious disease.

Recent studies claim that the development and distribution of vaccines is an effective approach to end this infectious disease. However, this study demonstrates that a vaccine alone may not solve this problem completely, mainly due to differences in the rates of waning immunity induced by infection and vaccination.

We propose that both vaccination and treatment are required to halt COVID-19 disease transmission and end the pandemic. From an epidemiological perspective, we employ the SVEIRS model by introducing vaccination and treatment into the compartmental epidemic model SIR.

The experimental results obtained via the proposed SVEIRS model suggest that the pandemic can be ended by performing both vaccination and treatment. Experiments have shown that it takes time to develop and distribute vaccines, develop treatments, and eradicate infectious diseases using both. Hence, the development of vaccines or treatments does not mark the immediate end of the disease, and procedures to control the spread of the disease must continue until it is completely eradicated.

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Special Session E1

Mathematical Modeling of COVID-19 and Beyond

Organizer: Sunmi Lee (Kyung Hee University)

Date/Time: 8월 28일(토) 10:00

Speakers:

1. Hee-Sung Kim	**(Chungbuk National University)**
2. Jung Eun Kim	**(UNIST)**
3. Sungchan Kim	**(Kyung Hee University)**
4. Kyeongah Nah	**(NIMS)**

Collateral health effects of COVID-19

Hee-Sung Kim

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The COVID-19 pandemic has resulted in both direct and indirect collateral effects on health care. From acute illnesses to chronic diseases, COVID-19 has already had a profound impact on a variety of diseases. For instance, infectious diseases prevalent in underdeveloped countries have increased due to shortages in medicines and disruption of health care system. Developed countries are in a similar situation. In the United states, for example the number of cardiovascular disease being treated in hospitals dropped by nearly 40% and cancelation or delay in cancer treatment due to overburdened hospitals pose negative impact on cancer patient. In this speech, I will introduce outstanding research in this field and identify areas requiring further research.

The effects of vaccination and Non-Pharmaceutical Interventions I on COVID-19 transmission dynamics in Korea

Jung Eun Kim, Sunmi Lee and Hee-Sung Kim

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Korea has been applying non-pharmaceutical intervention (NPI), such as social distancing policices, and started to vaccinate in February 2021. Although primary vaccination rates exceed 25% of the population, the number of COVID-19 cases is still not decreasing. We constructed an age structured mathematical model to investigate the transmission dynamics of COVID-19 according to high, intermediate, and low NPI policies and age-specific vaccination policies. In addition, according to the results of the study that patients with underlying conditions had a high mortality rate, a mathematical model was constructed that considered patients with underlying diseases, and the effect of preferential vaccination for patients with underlying conditions was also compared. Therefore, it can be seen that the proportion of the vaccinated population is also important when determining the timing of NPI level remission, but it is important to remit after being vaccinated as evenly as possible at all ages.

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Estimating the Basic Reproduction Number of COVID-19 on heterogeneous network

Sungchan Kim, Arsen Abdulali and Sunmi Lee*

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The assessment of the transmission dynamics of emerging disease is utmost important at its initial stage, where the intervention policies are needed to be designed. At this phase, the basic reproduction number is widely used to quantify the outbreak by describing the expected number of secondary cases produced by an infectious individual in a completely susceptible population [1]. The classic way of computing the basic reproduction number assumes the homogenous social interaction network. The actual social interaction network, as it has been reported in literature [2], is neither homogeneous nor random and rather follows the power-law distribution. The power-law distribution, on the hand, implies a high variance by having a fat tail leading to highly varied transmission at individual-level [3]. This has been found to a key factor causing a large super-spreading events [3, 4]. One of the vivid examples showing this phenomenon is the initial phase of COVID-19 in South Korea, where the super-spreader, as known as “Patient 31”, caused the large outbreak in Daegu city. In this situation, it is natural to ask the following questions: *Is the basic reproduction number computed with the assumption of homogenous network explain the actual transmission dynamics of the disease?* In this research, we propose a now metric describing the transmission dynamics of the infectious disease at its initial phase. We show that our can serve as a lower bound of the basic reproduction that occur at the beginning when the contact network is highly heterogeneous.

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A Model-informed Reopening Strategy based on a Case Study of Ontario, Canada

Kyeongah Nah

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As part of the COVID-19 pandemic recovery process, reopening plans and strategies have been developed for many countries around the world. Using a transmission dynamics model, parameterized through model fitting to cumulative incidence data during different social distancing escalation phases, we identify the optimal timing of reopening based on social-distancing de-escalation in a population. We also introduce a novel approach to inform the re-opening plan followed by a post-pandemic lockdown by integrating a stochastic optimization technique with a disease transmission model. We assess Ontario's re-opening plans as a case-study. Taking into account the uncertainties in contact rates during different re-opening phases, we find the optimal timing for the upcoming re-opening phase that maximizes the relaxation of social contacts under uncertainties, while not overwhelming the health system capacity before the arrival of effective therapeutics or vaccines.

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General Session E2

Infectious Disease Modeling II

Date/Time: 8월 28일(토) 10:00

Speakers:

1.	**Eunha Shim**	**(Soongil University)**
2.	**Yongin Choi**	**(UNIST)**
3.	**Nugyeom Moon**	**(Animal and Plant Quarantine Agency)**
4.	**James Slghee Kim**	**(UNIST)**

Impact of COVID-19 variants on the vaccination program in South Korea

Eunha Shim

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Two doses of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) vaccines are currently administered in South Korea; however, vaccine supply is limited. We evaluated the impact of the coronavirus disease (COVID-19) vaccination campaign using single-dose and two-doses regimes on reducing incidence, ICU hospitalization, and deaths in South Korea, considering constraints in vaccine supply and the emergence of variant strains. We developed an age-structured model of SARS-CoV-2 transmission parameterized with Korean demographics and age-specific COVID-19 outcomes. Our model incorporates the course of asymptomatic and symptomatic COVID-19 infection, as well as timey-varying rate of vaccination. In addition, we considered a higher transmissibility of SARS-CoV-2 variant compared to the pre-existing strain and reduced vaccine efficacy against the variant. Our results indicate that single-dose and two-dose vaccination can have a substantial impact on mitigating the severity of COVID-19. However, herd immunity is unlikely to be achieved with the administration of a single dose of COVID-19 vaccine, especially with the potential emergence of SARS-CoV-2 variants.

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Effects of social distancing on COVID-19 control in Korea based on age-structured modeling

Yongin Choi[1], James Slghee Kim[1], Heejin Choi[1], Hyojung Lee[2], and Chang Hyeong Lee[1]

1) Department of Mathematical Sciences, Ulsan National Institute of Science and Technology (UNIST)
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Since the end of 2019, a novel coronavirus disease 2019 (COVID-19) has occurred around the world. Before vaccines were available, contact tracing was used in Korea and non-pharmaceutical interventions such as social distancing, wearing masks, and closing work/schools were implemented in accordance with government guidelines. We then divided the data into seven distinct periods depending on the intensity of social distancing.

One of the epidemiological characteristics of COVID-19 is the difference in symptoms and fatality according to the age of the infected. A contact matrix was used to explain contact patterns between age groups, and the potential effects of social distancing in various scenarios were checked.

In this study, the effect of social distancing on the reduction of COVID-19 infections was confirmed by establishing an age-specific model and using epidemiological data of the first half of 2020 in Korea.

Risk assessment of HPAI on poultry farms in relation to migratory birds using a Maxent model

Mugyeom Moon, Ilseob Lee, Hachung Yoon, Eunesub Lee

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‘03년 국내 최초 발생 이후 최근까지 8번의 고병원성조류인플루엔자(HPAI)가 발생하여 심각한 사회 경제적 피해가 야기되었다. 국내 HPAI 유입 원인으로는 철새의 이동이 주요한 역할을 하는 것으로 알려져 있다. 이에 가금농장 HPAI 발생 데이터와 철새 AI 상시예찰 데이터, 철새행동권 및 철새 관련 환경 변수를 이용하여 종분포모델 중 하나인 Maxent 분석방법으로 가금농장 HPAI 발생 위험도를 평가하였다. Maxent 분석은 10,000회 iteration을 5회 반복 교차검증기법으로 실시하였다. 모델에 중요한 영향을 미치는 변수를 확인하기 위하여, 모델 트레이닝 과정 및 최종 선정된 모델에서 변수의 기여도를 확인하였으며, Jackknife 방법으로도 변수의 기여도를 확인하였다. 가금농장 HPAI 발생 위험도와 관련된 환경 및 철새 관련 변수의 특성은 response curve를 통해 확인하였다. 분석결과 모델의 예측력을 나타내는 Area Under Curve(AUC)는 0.87 이상으로 나타났다. 모델 분석 결과를 활용하여 가금농장 및 행정구역 단위의 HPAI 위험도를 산출하였다.

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Exploring the roles of vehicle transmission in inter-farm modelling for Foot-and-Mouth Disease.

James Slghee Kim[1], and Chang Hyeong Lee[1]

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In this study, we investigate the importance of vehicle transmission in Foot-and-Mouth Disease (FMD). In 2010, FMD was a major disaster for the livestock industry, Like many infectious diseases, once the outbreak starts, FMD can spread rapidly across the whole nation leading into difficult situations. What makes FMD extraordinary is that the disease happens only to livestock such as cows and pigs that are grounded in farms. However, the transmissions between farms in 2010 FMD show that there can be very long-distance transmissions. In this study, we try to simulate and reproduce the 2010 FMD using generated data and assess effective methods of preventing the spread.

General Session E3

Modeling in Ecology and Fisheries

Date/Time: 8월 28일(토) 10:00

Speakers:

1. **정동원**	**(Pukyong National University)**
2. **Youngseok Chang**	**(Korea University)**
3. **Yunju Wi**	**(Chonnam National University)**
4. **Gyujin Oh**	**(Chonnam National University)**

자료가 제한된 상황에서 한국 남동해역 멸치(*Engraulis japonicus*) 자원에 대한 자원평가 방법 개발

정동원[1], 김진영[2], 현상윤[1]

[1]부경대학교 해양생물학과

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한국에서 멸치(*Engraulis japonicus*)는 상업적으로 중요한 어종으로 지속가능한 어획을 위해 멸치 자원을 관리할 필요가 있다. 수산자원관리의 기반이 되는 수산자원평가는 이용가능한 자료의 정도에 따라 평가방법이 결정되는데, 멸치는 연령조성 자료와 체장 자료가 부재하므로 연령구조모델 혹은 체장기반모델을 적용할 수 없다. 따라서 본 연구는 연령조성 자료와 체장 자료의 이용이 제한된 상황에서 주요한 멸치 어장인 한국 남동해역(경상남도, 부산광역시 및 울산광역시) 멸치 자원에 대한 자원평가 방법 개발을 목적으로 한다. 2009년부터 2018년까지 한국 남동해역에서 기록된 멸치 어획량 자료, 단위노력당 어획량(CPUE) 자료 및 주요 멸치 어업인 기선권현망 어업의 체장 크기별 어획물 조성 자료 각각에 대해 6개월 단위로 정리하여 베이지안 상태공간 잉여생산모델에 적용하였다. 기존의 베이지안 상태공간 잉여생산모델에서 사용하지 않는 체장 크기별 어획물 조성 자료를 추가적으로 이용하여 모수 추정을 위한 목적함수에 다항분포 우도함수를 추가함으로서 자원량의 체장 크기별 조성을 추정하는 것이 본 연구의 모델과 기존 모델과의 차이점이다. 모수 추정을 위한 수치최적화에는 R 소프트웨어의 TMB 패키지가 사용되며, 도출 중인 예비결과는 본 발표 때 발표하고자 한다. 본 연구의 모델이 기존 모델 보다 자세한 자원상태를 파악할 수 있으므로 본 연구는 한국 멸치 자원관리에 도움이 될 것으로 기대된다.

Prey-Induced Dispersal in Predator-Prey Model

Youngseok Chang, Wonhyung Choi, and Inkyung Ahn

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In this talk, we consider a predator-prey model with non-uniform predator dispersal, called a prey-induced dispersal (PYID), representing the predator motility depending on the size of prey's density in a spatially heterogeneous region. To understand how PYID affects the dynamics and coexistence of the system in a heterogeneous region, we examine the model with some functional responses under no-flux boundary conditions wherein the predators move according to the PYID. We study the local stability of the semi-trivial solution of models with PYID and linear dispersal where the predator is absent. Furthermore, we investigate the local/global bifurcation from the semi-trivial solution of models with two different dispersals. We conclude that the PYID of predators usually promotes the predator's fitness but does not always increase it in a certain case.

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The population dynamics of red eared slider in Korea

Yunju Wi[1], Gyujin Oh[1], Hong Sung Jin[1], Hee-Jin Kang[2], Seung-ju Cheon[2]

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붉은귀거북은 주로 애완용으로 1970년대부터 국내에 수입되었고 2001년 대한민국 환경부에서 생태계교란야생생물로 지정되어 수입이 금지될 때까지 다량의 붉은귀거북이 국내에 유입되었다. 붉은귀거북이 성장함에 따라 관리가 어려워져 인간의 접근성이 좋은 공간에 많은 양이 방사되었다또한 종교적인 방생으로 야생으로 대량 유입되는 일이 매년 일어났으며 주변 환경에 대한 적응력이 높은 것으로 알려져 다양한 생태계에 쉽게 적응하고 생태적 교란 및 피해를 야기하는 것으로 알려져 있다. 붉은귀거북은 자연적인 번식에 의한 개체들로 추정되는 유체 수준의 작은 개체들도 발견되어 번식에 의한 확산도 이루어지고 있는 것으로 판단된다 붉은귀거북은 발견된 지역 빈도와 범위가 넓었고, 분포하는 서식지의 유형이 다양하다. 본 연구에서는 붉은귀거북의 서식지 확산에 따른 개체수의 변화와 생존률에 따른 개체수의 변화를 연단위로 시뮬레이션 해보았다. 서식지 확산은 인위적인 확산과 자연적인 확산으로 나눌 수 있을 것이다. 인위적인 확산은 방사 등을 통해 새로운 서식지로 유입되고 정착하는 형태로 나타나며 서식지의 증가로 표현하였다. 인위적인 확산이 일어남과 동시에 환경에 적응하고 번식하게 되면 이동에 의한 자연적인 서식지의 확산 현상이 일어날 것으로 예측되었으며 붉은귀거북의 이동도 최근에 확인되었다. 인위적인 요인과, 자연적인 요인이 복합적으로 나타나 서식지가 증가하게 되면 붉은귀거북의 개체수도 변화하게 될 것이며 여러 시나리오를 가정하여 개체수의 변화를 시뮬레이션 해보았다.

This work was supported by Korea Environment Industry & Technology Institute(KEITI) through the Project for the Development of Biological Diversity Threats Outbreak Management Technology (2018002270004), funded by Korea Ministry of Environment(MOE).

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Analysis of the invasive species spread using cellular automata classification and machine learning

Gyujin Oh[1] and Yunju Wi[1], Hong Sung Jin[1], Hee-Jin Kang[2], Seung-ju Cheon[2]

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외래침입종이 한국에 들어와 정착후 확산하는 양상을 분석하였다. 분석 도구로는 1차원 셀룰라 오토마타의 규칙성을 활용하였다. 먼저 규칙을 일정세대가 지난 후 세대별로 같은 분포를 가지는 것끼리 분류하였다. 먼저 짝수 규칙에 대하여 짝수세대와 홀수세대별로 분류를 하였고, 또한 모든 세대에서 같은 결과를 가지는 37가지 그룹으로 분류하였다.

분류된 규칙을 두가지 방법으로 훈련 데이터를 만들어 기계학습을 시켰다. 첫 번째 방법으로는 분류된 37가지 규칙에 대하여 초깃값 100, 200, 300의 값을 가지는 20x20행렬을 만들고, 한 세대 후의 행렬을 만들어 규칙을 분류하는 머신러닝 모델(CNN)을 만들었다. 추가적으로 모든 규칙에 대하여 분류하는 모델과 3개의 스텝을 가지는 모델을 만들었다. 두 번째 방법으로는 5개의 초기값을 주고 200세대후의 분포를 20x20행렬로 만들어 37가지 규칙을 분류하는 모델을 만들었다. 그리고 외래 생물의 예시로 황소개구리 분포를 가지고 클러스터링하여 여러 클러스터링 방법을 이용하여 규칙을 예측하고 분석했다. 또한, Maxent 확률 분포를 가지고 각 방법에 대하여 규칙을 예측하고 분석했다.

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