International Active Matter Workshop 2025

VENUE:
Meiji University (Nakano Campus)

DATE:
24 - 25 January, 2025

Organiser

MEXT Joint Usage/Research Center Meiji University
"Center for Mathematical Modeling and Applications" (CMMA)

Co-organiser

JSPS Core-to-Core Program
"Advanced core-to-core network for the physics of self-organizing active matter"

Organising committee

Hiroyuki Ebata (Kyushu Univ.)
Hiroyuki Kitahata (Chiba Univ.)
John Molina (Kyoto Univ.)
Nobuhiko J. Suematsu (Meiji Univ.)
Mitsusuke Tarama (Kyushu Univ.)
Ryoichi Yamamoto (Kyoto Univ.)

Web page

https://sites.google.com/view/activematter2025

Contact

email: active2025@googlegroups.com

Program

2025/1/24 Fri.

09:20 - 09:45	Registration
09:45 - 09:50	Opening remark
09:50 - 10:50	[IL] **Toshiyuki Nakagaki** (Hokkaido University) "Remodeling of biological form driven by load-induced local modulation of growth rate: vessel, bone and tree"
10:50 - 11:00	Break
11:00 - 11:20	**Hongmei Xu** (Nanyang Technological University) "Practical guidelines for using spatial correlation functions to understand the collective motion of living matter"
11:20 - 11:40	**Isabelle Shiiba** (Kyoto University) "The Role of DNA Hybridization as a Control for Self-Assembling Active Cytoskeleton Proteins"
11:40 - 12:40	Lunch
12:40 - 13:00	**Susumu Ito** (Tohoku University) "Selective decision making and collective motion of fish by visual attention"
13:00 - 13:20	**Takahiro Kanazawa** (The University of Tokyo) "Locomotion on a lubricating fluid with spatial viscosity variations"
13:20 - 13:40	**Simon Schnyder** (The University of Tokyo) "Nash Epidemics"
13:40 - 13:50	Break
13:50 - 14:10	**Mitsusuke Tarama** (Kyushu University) "Interaction between synchronizing elevators"
14:10 - 14:30	**Riccardo Muolo** (Institute of Science Tokyo) "Higher-order interactions hamper synchronization: a data-driven analysis on the 3-body Kuramoto model"
14:30 - 14:50	**John Molina** (Kyoto University) "Differentiable Physics for Inverse Problems"
14:50 - 15:10	Group photo / Coffee break
15:10 - 16:50	**Poster presentations**
16:50 - 17:00	Break
17:00 - 18:00	[IL] **Yasumasa Nishiura** (Hokkaido University) "High-index saddles and hidden singularities"
18:20 - 20:30	Social meeting

2025/1/25 Sat.

09:10 - 09:30 Registration

09:30 - 09:50 **Bappaditya Roy** (Tohoku University)
"Estimation of spatial and time scales of collective behaviors of active matters through learning hydrodynamic equations from particle dynamics"

9:50 - 10:10 **Hideyuki Miyahara** (Hokkaido University)
"Vicsek Model Meets DBSCAN: Cluster Phases in the Vicsek Model"

10:10 - 10:30 **Hiroyuki Kitahata** (Chiba University)
"Collective behavior of dimer-shaped active Brownian particles moving in their minor-axis direction"

10:30 - 10:50 Coffee break

10:50 - 11:50 [IL] **Masaki Sano** (Shanghai Jiao Tong University)
"Active matter: a methodology to decipher biological tissue"

11:50 - 12:50 Lunch

12:50 - 13:10 **Jun Li** (Wenzhou University)
"Time-correlation functions of stochastic three-sphere micromachines"

13:10 - 13:30 **Shigeyuki Komura** (Wenzhou Institute, University of Chinese Academy of Sciences)
"Ornstein-Uhlenbeck information swimmers with external and internal feedback controls"

13:30 - 13:50 **Kento Yasuda** (Kyoto University)
"Statistical formulation of the Onsager-Machlup variational principle"

13:50 - 14:10 Coffee break

14:10 - 14:30 **Takuya Kobayashi** (Kyoto University)
"Single Spherical Microswimmers in Non-Newtonian Fluids"

14:30 - 14:50 **Haruki Hayano** (The University of Tokyo)
"Revealing the Mechanism of Anomalous Rheology in Microswimmer Suspensions"

14:50 - 15:10 **Kangeun Jeong** (Nagoya University)
"Crystallization of Chiral Active Brownian Particles at Low-Densities"

15:10 - 15:20 Break

15:20 - 16:20 [IL] **Kaoru Sugimura** (The University of Tokyo)
"Mechanical control of epithelial morphogenesis"

16:20 - 16:30 Closing remark

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Presentation time

Invited lectures [IL] [60 min each, including discussions]
Contributed talks [20 min presentation, including discussions]

Poster list

1. Nakamura, Sohei (Kyushu university)
   “Optimal substrate stiffness for cell migration”
2. Zhao, Luekai (Department of Physics, Tohoku University)
   “Emergence of attractors with nonreciprocal skin effect from dissipative coupled Duffing oscillators”
3. Katayama, Daisuke (Department of Physics, Kyushu university)
   “Torque-free rotation of cells crawling on a substrate”
4. Zhang, Jiawei (The University of Tokyo)
   “Active Matter in Human Crowds: A Framework for Analyzing Congestion Dynamics”
5. Qin, Zichen (Department of Physics, Tohoku University)
   “Collective Behaviors of Aligning Self-Propelled Particles with Frustration”
6. Watanabe, Takeshi (Nagano University)
   “Global bifurcation structure of steady solutions characterizing free energy landscape of coupled Cahn-Hilliard equations”
7. Nakayama, Bokusui (Kyoto University)
   “Active Mean Filter”
8. Chan, Chung Wing (Graduate School of Science, Kyoto University)
   “Anisotropic Swarming of Photoresponsive Microtubules in Opical Landscript”
9. Shimokawa, Michiko (Nara women's University)
   “Bifurcation phenomena of a rotating camphor boat”
10. Negi, Archit (Kyushu University, Kyoto University)
    “Confining geometry determines the contracted shape of active cytoskeleton”
11. Kershner, Liliana (University of Tokyo Department of Physics)
    “Geometry-dependent motion of L-shaped microswimmers near a planar wall”
12. Sakurai, Shun (Department of Physics, Tohoku University)
    “Boltzmann-Ginzburg-Landau theory for autochemotaxis of self-propelled rods”
13. Goto, Takashi (Department of Physics, The University of Tokyo)
    “Response of collective orientation of magnetotactic bacteria to a stationary magnetic field ”
14. Sato, Ryoga (Grad. Sch. of Sci. and Eng., Chiba Univ.)
    “Transition processes of a camphor particle in a three-state chamber”
15. Tateyama, Yuta (Chiba University)
    “Bifurcation structure in the one-dimensional non-reciprocal Swift-Hohenberg model”
16. Ohshima, Suguru (Tokyo Metropolitan College of Industrial Technology (TMCIT))
    “Chemotaxis based on rotational fluctuation of bubble-propelled spherical Janus particle”
17. Dam, Duc (Nagoya University)
    “Melting of Two-Dimensional Disordered Persistent Active Particles”
18. Tani, Marie (Kyoto University)
    “Deformation of Microtubule Bundles by External Mechanical Stress”

19. Ebata, Hiroyuki (Kyushu University)
    "Mobility of an active particle in dense passive colloids"
20. Shiina, Jintaro (Keio university)
    "Photo- excited micro-droplet robotics"
21. Koyano, Yuki (Kobe University)
    "Activity-induced diffusion recovery in crowded colloidal suspensions"

Core poster presentation time:

Odd numbers → 15:10 - 16:00
Even numbers → 16:00 - 16:50

Abstracts

Day 1
24 Jan., 2025 (Fri.)

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17:00 - 18:00	[IL] **Yasumasa Nishiura** (Hokkaido University)
18:20 - 20:30	Social meeting

Remodeling of biological form driven by the load-induced local modulation of growth rate: vessel, bone, and tree.

NAKAGAKI Toshiyuki[1]

[1]Research Institute for Electronic Science, Hokkaido University

The form of organisms is often functional in some sense. For example, C.D. Murray showed that the flow rate of blood vessel is proportional to the cube of the tube diameter, minimizing the sum of the energy dissipation associated with blood flow and the volume cost of blood. This is known as the Murray rule, which was recently found to hold in protozoan slime mold. However, the mechanism by which this tube-network is formed to satisfy the Murray rule is still under study. In plasmodial slime mold, a local rule of current-reinforcement (a rule in which the tube diameter varies depending on the flow rate) was discovered and a simplified mathematical model was proposed to reproduce the formation of tube-network under various environmental conditions. Similar current-reinforcement rules have been found in vascular systems in animals, leaf-veins in plants, and mycelial network in fungi, and are widespread in biological transport systems.

C.D. Murray also showed that when defining a single starting point and multiple arrival points for mass transport, the network of branching tubes connecting them minimized the energy function of Murray law. He considered that the similar idea was applied to the branching structure of tree branches, and indicated that the maximum bending stress at the branch base was constant regardless of the size of the branch. The relative growth rate of tree depends on the local stress applied there. Areas subjected to higher stress due to their own weight will develop more and lower the applied stress. This growth law was formulated similarly to the current-reinforcement model of transport systems. Specifically, a model similar to the current-reinforcement model in plasmodial slime mold has been proposed and applied to the remodeling of animal bones (trabecular bone of the femoral head), but its application to trees remains a future challenge.

Growth control laws for localized loading are widely found not only in flow systems but also in structural systems, and are interesting as a general mechanism that leads to distinctive structure-function correlations in biological systems. I would like to discuss the possibilities that expand from this perspective, focusing on a study of plasmodial slime mold.

References:

1. D'Arcy W. Thompson (1917) On Growth and Form, The Cambridge University Press.
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4. Katherine A. McCulloh, John S. Sperry, Frederick R. Adler (2003) Water transport in plants obeys Murray's law, Nature. 421 (6926): 939–942.
5. Dai Akita, Itsuki Kunita, Mark D. Fricker, Shigeru Kuroda, Katsuhiko Sato and Toshiyuki Nakagaki (2017) Experimental models for Murray's law, J. Phys. D: Appl. Phys., Vol. 50, 024001(11pp).
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7. C. D. Murray (1927) A relationship between circumference and weight in trees and its branching angles."J. Gen. Physiol., 10, 725–729.
8. Ken-ichi Yamakoshi, Tatsuo Togawa, Akira Kamiya, Teizo Fujii, Kiichi Tsuchiya (1976) IYODENSHI TO SEITAIKOGAKU Vol. 14, 296-302.

Practical guidelines for using spatial correlation functions to understand the collective motion of living matter

Xu Hongmei[1], **Huo Yucheng**[1], **K. Jimmy Hsia**[1,2], **Endao Han**[3]

[1]School of Mechanical and Aerospace Engineering, Nanyang Technological University, 50 Nanyang Avenue 639798, Singapore
[2]School of Chemical and Biomedical Engineering, Nanyang Technological University, 50 Nanyang Avenue 639798, Singapore
[3]School of Physical and Mathematical Sciences, Nanyang Technological University, 50 Nanyang Avenue 639798, Singapore

Active matter systems exhibit a wide range of motion patterns and complex phenomena, contributing to the formation of hierarchical structures within these systems. Quantitative descriptions of active matter rely heavily on correlation functions, which measure the degree of collectivity within the system. However, the definitions and mathematical formulations of these functions have been divergent and controversial, leading to inconsistent calculations and incommensurable results within the active matter community, thereby hindering the advancement of a unified theoretical framework.

We will address the ambiguities in the definitions of the correlation function by reviewing the existing ones in the literature, highlighting the inconsistencies that may confound result interpretation, and proposing our suggestions. Through comprehensive calculations and meticulous analysis of both artificial fields and various experimental active systems, we have identified robust frameworks for calculating correlation functions and correlation lengths and provide a practical approach to understanding collective cell motion with the help of spatial correlations, especially velocity correlations.

Overall, our goal is to improve the clarity in interpreting spatial correlation measurements, propose a standardized definition to address existing inconsistencies, offer a valuable data analysis tool for the broader biological and bioengineering communities and aim to enhance our comprehension of collective motion in biological systems.

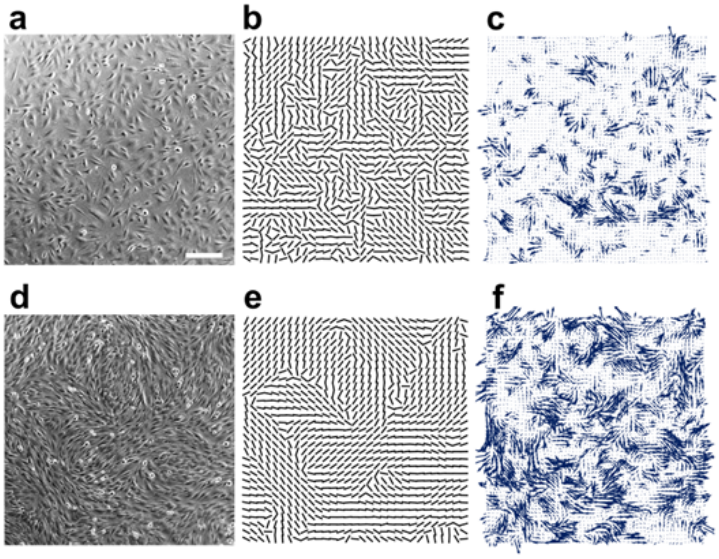

Fig. 1: C2C12 cell monolayers with lower (top row) or higher (bottom row) nematic order.
(a) Bright field image of a C2C12 cell monolayer with lower cell concentration. Scale bar: 200 μm.
(b-c) Orientation (director) field and velocity field of (a).
(d) Bright field image of a C2C12 cell monolayer with higher cell concentration.
(e) Orientation (director) field of (d), which shows stronger nematic order compared to (b).
(f) Velocity field of (d). Larger groups of cells move collectively in (f) compared to (c).

The Role of DNA Hybridization as a Control for Self-Assembling Active Cytoskeleton Proteins

Isabelle Shiiba[1], Rubaya Rashid[1,2], Ibuki Kawamata[1], Marie Tani[1], Masatoshi Ichikawa[1], Akira Kakugo[1]

[1]Graduate School of Science, Kyoto University, Kyoto, Japan
[2]Department of Physics, Texas Southern University, Houston, USA

The collective behavior of swarming is a natural inspiration for molecular robotics that can harness active matter to reproduce biological organization and motility. We use a reconstituted system by leveraging microtubules (polar cytoskeletal filaments essential for cellular organization, migration, and mitosis) capable of active movement due to chemically driven molecular motors[1]. DNA hybridization is a strong method to bind microtubules (MTs) to each other to build functional and controllable molecular robots[2]. So far we have established controlling DNA hybridized swarms to transfer and deliver cargo[3], and associate and dissociate due to photoresponse[4] or DNA linkers[5]. However, the bounds of effective DNA crosslinking sequence, length, and concentration are still unknown. Using a bottom-up approach of DNA modified MTs gliding on a kinesin-coated surface, we show how changing DNA sequence length and concentration affect energetic descriptions, association rates, and interaction mechanisms (Fig 1). We found an effective region of DNA lengths that induce alignment at greater collision angles than steric-induced MT alignment, and found that the crticial angle of swarm formation increase with increasing DNA length and concentration. We continue to explore the phase space of nematic polar alignment of microtubules in order to predict and reproduce swarm dynamics for optimal applications.

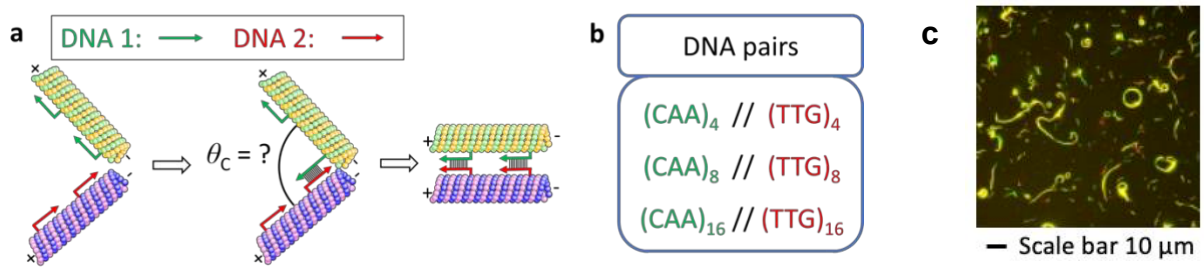

Fig. 1: a) DNA interactions aid swarm formation of MTs based on the critical angle, θ_C (angle of collision). b) Complementary DNAs that have different θ_C with varying repeating base pairs. c) Snapshot of MT swarm, crosslinked with 90 µM of CAA_8//TTG_8 DNA.

Thank you to Fulbright Japan, Japan-U.S. Educational Commission and the Active Matter Lab for supporting this research.

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4. Keya, J.J. *et al.* Control of swarming of molecular robots. *Sci Rep* **8**, 11756 (2018).
5. Ibuki Kawamata *et al.*Autonomous assembly and disassembly of gliding molecular robots regulated by a DNA-based molecular controller.*Sci. Adv.***10**,eadn4490 (2024).

Selective decision making and collective motion of fish by visual attention

Dept. of Phys., Tohoku Univ. **S. Ito and N. Uchida**

Various approaches have been taken to model the fish school [1], but the fundamental question (i.e. how to read the positional and the temporal information of a neighbor and reflect it in own movement) is not yet fully answered. In this study, we focus on visual interaction.

Previous models using visual interaction [2] implicitly assume that an agent interacts with all visible neighbors, but this method of the interaction is too heavy load for fish with small brains. A recent experiment [3] shows that fish selects and approaches one neighbor even if there are multiple neighbors within the visible range.

In this study [4], we construct the equations of motion that takes into account the motion of visual attention induced by the visual stimulus from the images on the retina. A signal whose magnitude depends on the vertical angular diameter of the image is generated in each bin of the visual field, and they are superimposed to a synthesized signal. Next, the agent reads the position and velocity of the neighbor on the line of sight and reflects it in own movement.

In this model, the vortex pattern and polarized school are spontaneously emerge (Fig. 1(d)-(e)). Even when multiple neighbors are visible at the same time, an agent tends to track one of the neighbors rather than the average position of all particles, and this result reproduces the selective decision making in the experiment (Fig. 1(f)-(g)). Thus, for the first time, we have constructed a visual model that can simultaneously show the spontaneous appearance of various collective patterns and the experimental coincidence of selective decision making.

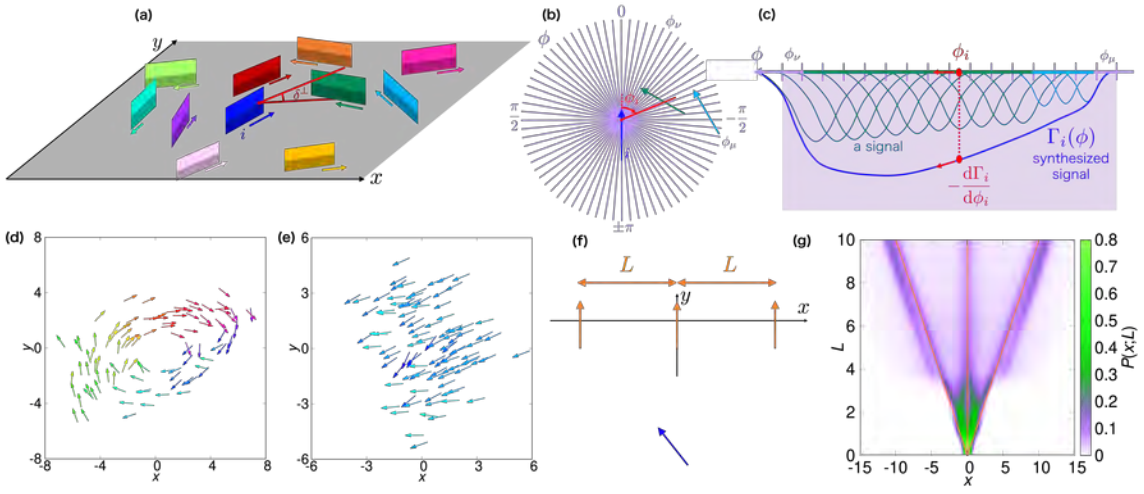

Fig1: (a) A flat plate agent moves on a two-dimensional plane. The blue agent i measures the vertical angular diameter $\delta^{\perp}$ of the green agent. (b) The blue, green, and cyan agents in (a), viewed from above. ϕ_i is the angle of the line of sight. (c) The generation of a single signal at $\phi \in [\phi_\mu, \phi_\nu]$ in (b) and the synthesized signal $\Gamma_i(\phi)$. (d) The vortex pattern (e) the polarized at 100 agents. (f) A blue agent chases orange agents moving along the y-axis with a distance of L. (g) The probability distribution $P(x;L)$ of the position x of the blue agent with respect to L in the situation in (f). The solid line corresponds to the position x of the orange agents at each L.

[1] 伊藤将，内田就也, 日本物理学会誌 **78**, 198 (2023).
[2] R. Bastien and P. A. Romanczuk, Sci. Adv. **6**, eaay0792 (2020).
[3] V. H. Sridhar *et al.*, Proc. Natl. Acad. Sci. U.S.A. **118**, e2102157118 (2021).
[4] S. Ito and N. Uchida, PNAS Nexus **3**, pgae264 (2024).

Locomotion on a lubricating fluid with spatial viscosity variations

Takahiro Kanazawa[1,2], **Kenta Ishimoto**[3]

[1]Department of Physics, The University of Tokyo
[2]RIKEN Center for Biosystems Dynamics Research
[3]Research Institute for Mathematical Sciences, Kyoto University

Viscosity plays an important role in locomotion, e.g., in the navigation of active particles through torques resulting from spatial inhomogeneities, known as viscotaxis [1]. Since locomotion usually involves repeated cycles of gates, two characteristic timescales naturally arise: a fast timescale for a single cycle of gates and a slow timescale for the entire locomotion. In inefficient locomotion such as crawling, these two timescales are sufficiently separated. This leads us to study the long-time behavior of the cumulative effects of a viscosity inhomogeneity through leveraging multiple time-scale analysis.

In this study, we theoretically investigate locomotion on a thin Newtonian fluid film whose viscosity depends on position, via the lubrication approximation [2]. In crawling locomotion with a peristaltic wave, two modes are known: a retrograde (direct) wave whose traveling direction is opposite to (the same as) that of the locomotion. To examine these two types of modes, we consider a crawler whose surface deformation is given as a combination of traveling waves with longitudinal and transverse oscillations. By asymptotic expansions with small surface deformation, we obtain asymptotic locomotion velocities and find that under uniform viscosity, a transverse wave leads to a retrograde crawler, whereas a longitudinal wave leads to a direct crawler. We then analyze locomotion with (i) a sharp viscosity interface and (ii) a linear viscosity gradient, as two illustrative examples of spatial inhomogeneity. To properly account for the nonlinear effects, we employ multiple scale analysis. (i) For a viscosity interface, the time-averaged locomotion speed is lower than that in locomotion under uniform viscosity, regardless of the wave type. The speed reduction is significant when the crawler's front enters the more viscous layer and the crawler's rear exits from the same layer. (ii) For a linear viscosity gradient environment, the locomotion speed becomes slower for a transverse wave, while it remains almost the same for a longitudinal wave, compared to a homogeneous viscosity environment.

Our analysis can be applied to locomotion on a fluid film, such as crawling snails with secreted mucus, and locomotion in a fluid near a wall such as slithering sperms and gliding bacteria. Our study offers a methodological basis for understanding the complex interactions between locomotor and its environment.

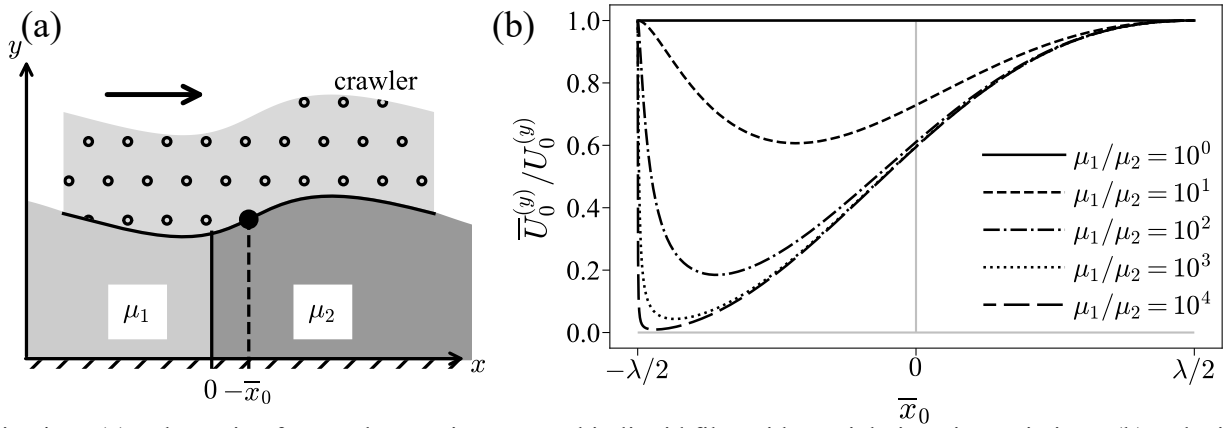

Fig. 1 : (a) Schematic of a crawler moving over a thin liquid film with spatial viscosity variations. (b) Velocity reduction while the crawler crossing over a viscosity jump. μ_1, μ_2 is a viscosity of each fluid layer and $-\overline{x}_0$ is a position of the crawler's midpoint in the laboratory frame, where the viscosity interface is located at $x = 0$.

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Nash Epidemics

S. K. Schnyder[1], **J. J. Molina**[2] , **R. Yamamoto**[2], **Matthew S. Turner**[3, 4]

[1] Institute of Industrial Science, The University of Tokyo, Tokyo 153-8505, Japan
[2] Department of Chemical Engineering, Kyoto University, Kyoto 615-8510, Japan
[3] Department of Physics, University of Warwick, Coventry CV4 7AL, UK
[4] Institute for Global Pandemic Planning, University of Warwick, Coventry CV4 7AL, UK

The collective behavior of social agents is a classic example of active matter. Social distancing behavior during epidemics is a self-organized and collective phenomenon: Faced with a dangerous epidemic, humans spontaneously social distance to reduce their risk of infection at a socio-economic cost. In this way, they exhibit a behavior in reaction to disease dynamics which is itself generated by the behavior of the population. Game theoretic analysis shows that such dynamics can give rise to a Nash equilibrium, in which no individual can deviate from their own behavior without reducing their utility. Previously, our analytic understanding of Nash equilibria in epidemics had been extremely limited, leaving us reliant on numerical solutions. Here, we combine a SIR compartmental disease model with an individual utility for self-organized decision-making. We identify an exact analytic expression for fully time-varying Nash equilibrium behavior and resultant disease dynamics, Fig. 1 [1]. In particular, the strength of social distancing is proven to be proportional to both the perceived infection cost and prevalence, see Fig. 1c. Remarkably, this gives a posteriori justification for the sort of simple heuristics developed to understand diseases like HIV.

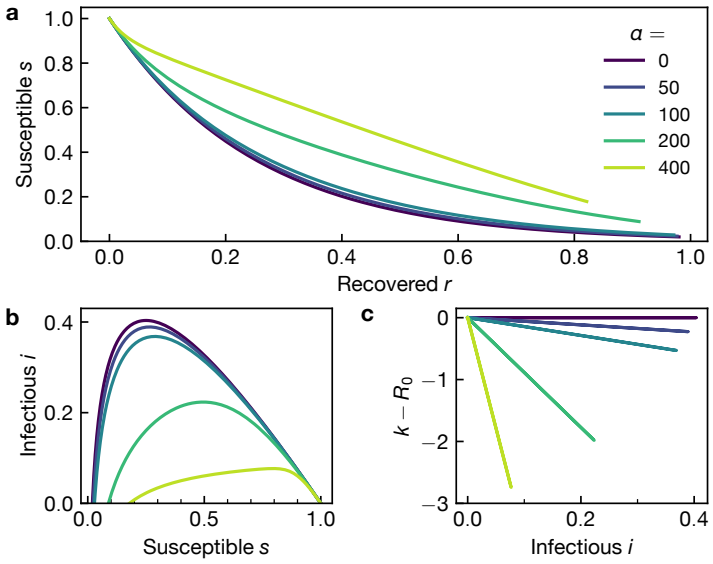

Fig. 1 : **Analytic Nash equilibrium solution.** a) Susceptible fraction vs. recovered. b) Infectious fraction vs. susceptibles. c) Deviation of social distancing behaviour k from the pre-epidemic default R0 vs. infectious.

Acknowledgements
We fondly acknowledge the generous wisdom of Prof. George Rowlands, who was involved in the early discussions leading to this work and who has since sadly passed away. We thank Paul François, Shuhei Horiguchi, Tetsuya J. Kobayashi, and Takehiro Tottori for helpful discussions. This work was supported by JSPS KAKENHI Grants No. 20H00129 (RY), 20H05619 (RY), 22H04841 (SKS), 22K14012 (SKS), 23H04508 (JJM), and the JSPS Core-to-Core Program "Advanced core-to-core network for the physics of self-organizing active matter" JPJSCCA20230002 (all of us). MST acknowledges JSPS Fellowship, ID L19547, the Leverhulme Trust, Ref. IAF-2019-019, and the kind hospitality of the Yamamoto group.

References
1. S. K. Schnyder, et al: "Nash Epidemics", *https://arxiv.org/abs/2407.04366* (under review).

Interaction between synchronizing elevators

Mitsusuke Tarama[1], and **Sakurako Tanida**[2]

[1]Department of Physics, Kyushu University
[2]Department of Astrophysics, The University of Tokyo

Synchronization is a ubiquitous phenomenon in nonequilibrium oscillations. A unique example is elevators, which are driven by the flow of passengers. It is known that two elevators synchronize their motion while delivering the passengers to the ground floor [1]. To understand this mechanism, we investigate the interaction acting between two elevators by measuring phase susceptibility [2]. Astonishingly, we found the existence of both attractive and repulsive interactions. By tuning the parameters of the microscopic model relevant to changing the impact of these conflicting interactions, we are successful to show that the dynamical behaviour transitions from in-phase to anti-phase synchronizations. Our results can readily be tested with real elevators by applying the same method once we obtain observation data. We believe that this study provides a novel approach to design optimal transportation, which is of great importance in improving sustainable social systems.

[1] S. Tanida, PRE 2021.
[2] M. Tarama and S. Tanida, in preparation.

Higher-order interactions hamper synchronization: a data-driven analysis on the 3-body Kuramoto model

Riccardo Muolo[1], **Hiroya Nakao**[1], **Marco Coraggio**[2]

[1]Department of Systems and Control Engineering, Institute of Science Tokyo, Tokyo, Japan
[2]School for Advanced Studies, Naples, Italy

Networks are powerful tools in the modeling of complex systems, but they may not capture the right interactions when multiple units are involved simultaneously. Such many-body interactions are encoded by higher-order structures which can be thought as extensions of networks [1]. The most general form is a hypergraph, in which interactions of any order can coexist without any constraint [2]. Over the last years, higher-order structures have been the focus of great excitement, since this novel framework has enormous potential for applications [3]. Particular interest has been devoted in the effects of higher-order interactions on the dynamics, including but not limited to synchronization [4], pattern formation [5], and also applications in the framework of active matter, e.g., the swarmalator [6].

In this talk, I will focus on the effects on synchronization and, in particular, on the higher-order Kuramoto model [4], by showing the results of a data-driven study [7] (paper currently in preparation). I will first briefly introduce the structure of higher-order interactions and their effects on the dynamics. Then, I will show the derivation of the higher-order Kuramoto model, which is the starting setting of our analysis. By performing the simulations in different settings, we show how the attraction basin of the synchronous solution shrinks when higher-order interactions are stronger. Stated differently, it is easier to obtain synchronization when the oscillators interact pairwise, while higher-order interactions enrich the dynamics, making synchronization more difficult. Our results are consistent with a recent work [8], which is complemented by our thorough analysis with different higher-order topologies.

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Differentiable Physics for Inverse Problems

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Differentiable Physics (DP) simulations, which refer to physical simulations that are end-to-end differentiable, have emerged at the intersection of Physics and Machine Learning, and have opened up a new avenue of research within the physical sciences [1,2]. The core-technology behind DP is the same one responsible for the enormous success of deep-learning, i.e., automatic-differentiation (AD). AD makes it possible to efficiently differentiate through simulations, allowing one to perform (nested) meta-optimizations. In particular, this can be used to solve inverse problems for material design, for example, to find the underlying model parameters Θ that result in a given target property A (see Fig.1). In this talk we will provide a brief overview of DP, discuss its benefits and limitations, and present select examples within the broad realm of Soft/Active Matter. Furthermore, we will show how DP can be combined with Machine Learning to construct physics-informed Neural Networks that encode the structure of the underlying Physics, and how this allows us to analyze/learn complex systems.

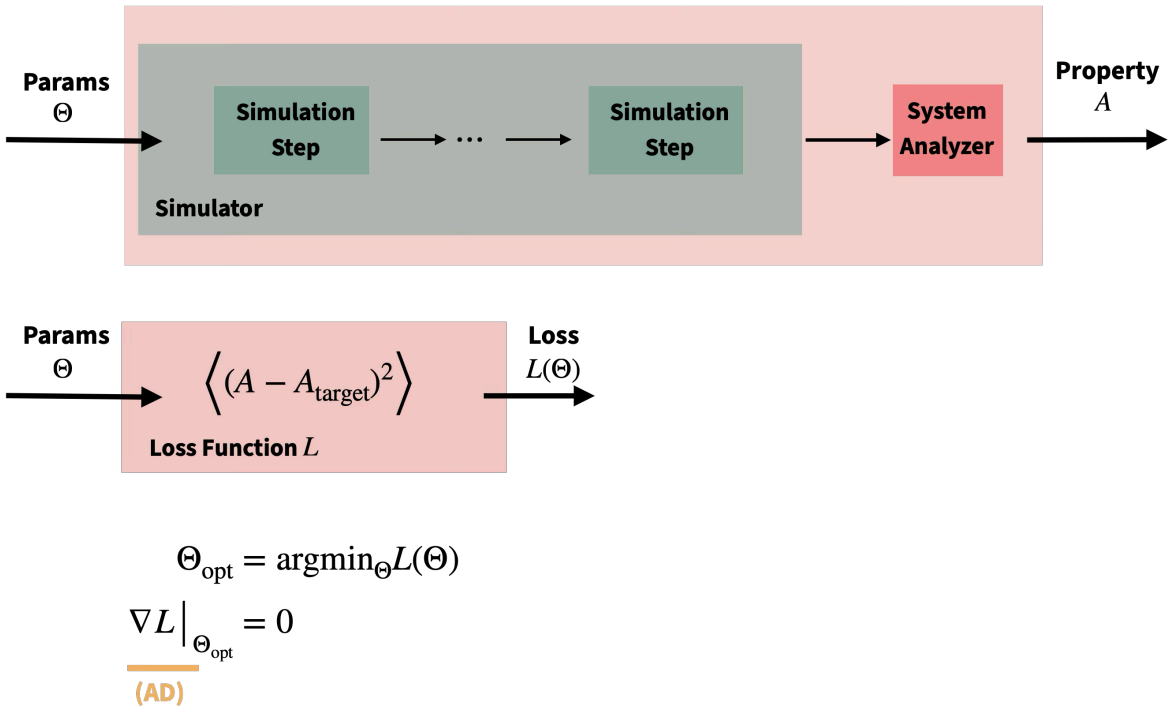

Fig. 1. Schematic representation of the DP framework. Being end-to-end differentiable allows us to optimize the loss through the simulator and system analyzer.

Acknowledgements
This work was supported by a Grant-in-Aid for Scientific Research (JSPS Kakenhi No. 23H04508) as well as the JSPS Core-to-Core Program "Advanced core-to-core network for the physics of self-organizing active matter (JPJSCCA20230002)"

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High-index saddles and hidden singularities

Yasumasa NISHIURA

Hokkaido University

This talk addresses two key challenges in nonlinear dynamics:

1. How can we understand the large deformations of localized patterns that arise during collisions, splitting, annihilation, and automatic pattern generation processes [1–3]?
2. Can we reconstruct the global landscape of free energy, capturing all minimizers, saddle points, and transitional pathways [4,5]? Moreover, how can we systematically guide the system to a desired minimizer from random initial conditions?

First, I will emphasize the role of high-index saddle points and hidden singularities in understanding large deformations of localized patterns. The collision dynamics are governed by a hierarchical network of saddle points, where the diversity of outputs originates from the variety of high-index saddles. Pattern splitting, annihilation, rotation, and generation emerge from codimension-2 singularities such as drift-saddle-node, drift-Hopf, drift-pitchfork, and double-homoclinic bifurcations embedded within the parameter space.

Second, reconstructing the global free energy landscape in infinite-dimensional systems remains a formidable challenge due to its rugged structure, which comprises a vast number of local minima and saddles. I will demonstrate how the hierarchical organization of high-index saddles forms the backbone of this landscape. As an illustrative example, I consider a simplified 1D coupled Cahn-Hilliard system and reconstruct its associated free energy, which serves as an "atlas" for systematically exploring the landscape.

Despite the vast number of minimizers, only a small subset can be detected theoretically or experimentally. A fundamental limitation arises because orbits near high-index saddles are constrained by the governing PDEs and the historical trajectory (itinerancy) of the system. To overcome this, I propose a novel approach using a *one-parameter family of PDEs*, parametrized by the ratio of relaxation parameters for systems with two variables. While steepest-descent dynamics are a common but suboptimal choice, this parameterization enables us to significantly broaden the accessible portion of the free energy landscape. I will present evidence of the efficiency of this method, demonstrating how orbits initialized from random data can systematically explore a wide range of the landscape.

Acknowledgements
We acknowledge the following people for the discussion and long-term collaboration: T. Watanabe (Nagano University), K. Ueda (Toyama University), T. Teramoto (Kyoto Woman's University), K. Kagawa (Hokkaido University), and E. Avalos (Tohoku University).

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Day 2
25 Jan., 2025 (Sat)

09:10 - 09:30 Registration

09:30 - 09:50 **Bappaditya Roy** (Tohoku University)
09:50 - 10:10 **Hideyuki Miyahara** (Hokkaido University)
10:10 - 10:30 **Hiroyuki Kitahata** (Chiba University)

10:30 - 10:50 Coffee break

10:50 - 11:50 [IL] **Masaki Sano** (Shanghai Jiao Tong University)

11:50 - 12:50 Lunch

12:50 - 13:10 **Jun Li** (Wenzhou University)
13:10 - 13:30 **Shigeyuki Komura** (Wenzhou Institute, University of Chinese Academy of Sciences)
13:30 - 13:50 **Kento Yasuda** (Kyoto University)

13:50 - 14:10 Coffee break

14:10 - 14:30 **Takuya Kobayashi** (Kyoto University)
14:30 - 14:50 **Haruki Hayano** (The University of Tokyo)
14:50 - 15:10 **Kangeun Jeong** (Nagoya University)

15:10 - 15:20 Break

15:20 - 16:20 [IL] **Kaoru Sugimura** (The University of Tokyo)
16:20 - 16:30 Closing remark

Estimation of spatial and time scales of collective behaviors of active matters through learning hydrodynamic equations from particle dynamics

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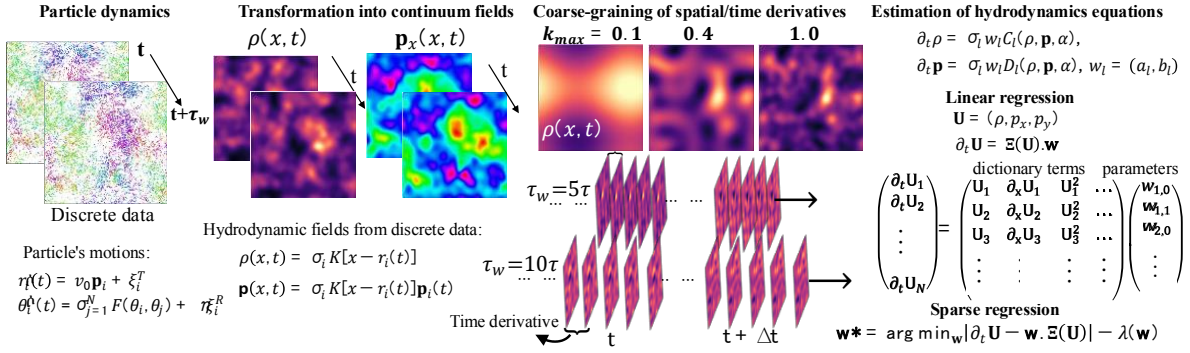
In nonequilibrium systems, a collective movement of microscopic active particles often displays several common emerging properties, such as swarming, motility-induced phase separation, nonequilibrium disorder-order transitions, anomalous density fluctuation, spatiotemporal patterning, and unusual rheological properties. However, those universal aspects of collective behaviours are hardly captured from microscopic particle-based simulation methods. The macroscopic properties obtained from nonlinear hydrodynamic equations help us understand those aspects. Therefore, we start from the numerical Langevin simulations of the microscopic particle dynamics and present a data-driven strategy for the collection of self-propelled particles to develop the hydrodynamics equations [1]. In our method, microscopic particle data is our input. Hence, the hydrodynamics fields are obtained by coarse-graining from the discrete description of particle dynamics. For partial differential equation (PDE) learning[2], the spectral representation gives the efficient and accurate computation of spatial and temporal derivatives of density and polarization density fields. Using sparse regression on the fields, we generate hydrodynamic equations[3]. The estimated PDEs from microscopic models are beneficial to understanding the universal features of the system in comparison to standard supervised learning. Hence, the macroscopic features will be shared both by microscopic models and hydrodynamic equations.



Schematic illustration of estimation of hydrodynamic equations from particle dynamics

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Vicsek Model Meets DBSCAN: Cluster Phases in the Vicsek Model

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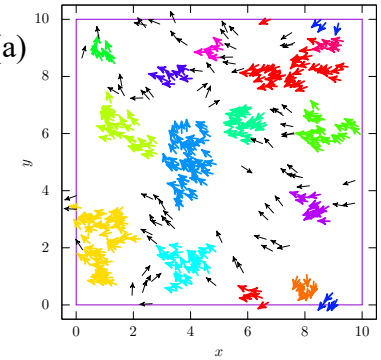
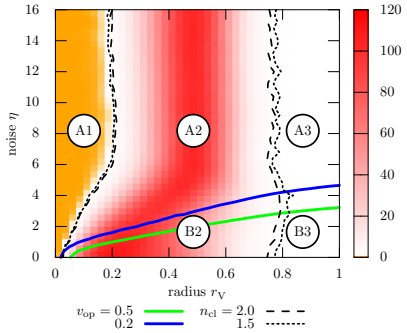
The Vicsek model, originally proposed to elucidate the dynamics of bird flocking, undergoes a phase transition concerning the absolute value of the mean velocity. While clusters of agents are readily observed through numerical simulations of the Vicsek model, there is a lack of qualitative studies. We examine the clustering structure of the Vicsek model by employing DBSCAN, a widely used density-based clustering algorithm in the machine learning field. We find that as the radius specifying the interaction of the Vicsek model increases for a fixed noise magnitude, the model undergoes a phase transition in the number of clusters from *O(N)* to *O(1)*, where *N* represents the number of agents. Additionally, we also propose a new order parameter to characterize flocking within clusters by utilizing the results of DBSCAN. Then, we identify at least four phases of the Vicsek model by combining the order parameter proposed by Vicsek et al. with the number of clusters. To underscore the novelty of DBSCAN, we conduct mean shift, which is an alternative density-based clustering algorithm, demonstrating its lack of a linear relationship between the num- bers of agents and clusters. This fact implies that we cannot define an order parameter in a naive manner using mean shift.

We here briefly demonstarte the resutls of this study by showing some figures while we will not get into the details. We depict a snapshot of the Vicsek model and the result of DBSCAN in Fig (a) and the phase diagram of the Vicsek model determined by DBSCAN in Fig (b). The meaning of labels are shown in Fig (c). See Ref. [1] for detailed analysis.

(a)



(b)



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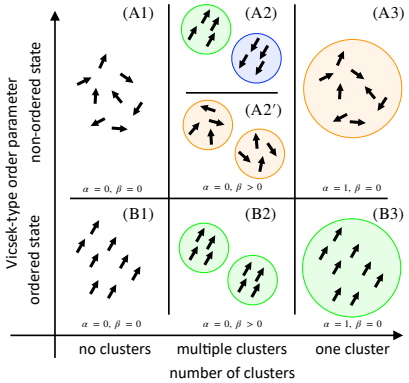

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Collective behavior of dimer-shaped active Brownian particles moving in their minor-axis direction

Hiroaki Ishikawa, Hiroaki Ito, Hiroyuki Kitahata

Department of Physics, Chiba University

Self-propelled particles in nonequilibrium systems have intensively attracted interest since they often exhibit spatio-temporal pattern formation originating from their collective behavior. Various kinds of mathematical models for the spatio-temporal pattern formation have been reported. These models can be classified into two, the so-called “wet” and “dry” ones. The momentum conservation among self-propelled particles and surrounding medium is considered in the wet models, while the momentum conservation is not included in the dry models. Viscek model and active Brownian particle model are the most famous dry models for collective motion. These models can reproduce collective motion and show interesting characteristic spatio-temporal pattern formation like traveling band formation and motility-induced phase separation (MIPS). However, these models do not include the effect of the particle shape, though the particle shape plays an important role in actual systems. In order to include the effect by the particle shape, the excluded volume effect is often included. Even if the shape effect is included in the model for self-propelled particles, the elongated particles that move their major-axis direction are often considered [1-3], but the ones that move in their minor-axis are rarely investigated. In actual systems, there are several examples in which the self-propelled particle moves in their minor-axis direction [4,5]. Therefore, we investigate the shape effect in both cases.

Therefore, we investigate the collective motion of dimer-shaped active Brownian particles with exclusive volume effect, in which the particles move either in the major-axis or minor-axis direction, by numerical simulations. By varying the dimer shape and the area fraction, several phases are observed such as disordered phase, uniform nematic phase, uniform polar phase, and MIPS phase. The uniform nematic phase is only observed in the system with the dimer-shaped particles moving in its minor-axis direction. We focus on the uniform nematic phase of the self-propelled particles that move in their minor-axis direction. We discussed the features of the transition between the disordered phase and the uniform nematic phase by evaluating the time evolution of the order parameter. We also discussed the mechanism of the appearance of the uniform nematic phase by focusing on the collision process of the two particles.

Acknowledgements
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Active matter: a methodology to decipher biological tissue

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Abstract
The concept of active matter has evolved since the particle (Vicsek) model was proposed. The continuum theories such as Toner-Tu model, active gel model, and active liquid crystal model have been applied for many experimental systems including bird flocks, bacterial suspension, reconstructed cytoskeleton systems, and active colloidal suspensions. In this talk, I would like to explain how these models can be applied more quantitatively to collective motions of eukaryotic cell layers (or biological tissue in other words). Collective motion frequently occurs in tissues composed of various types of cells. Depending on the type of cell, some cell tissues behave like active solids, while others behave like active liquids. Classifications of cell types or tissue properties often use extensile-contractile dichotomy based on the direction of the forces exerted by the cells to neighbors. Such a classification is thought to be possible by observing the behavior around topological defects. Recently, we observed accumulation/depletion behavior of cell monolayers around induced integer topological defects and have found that this extensile-contractile dichotomy is not sufficient to classify tissue properties. Near the topological defect, nonlinear active forces, which are usually ignored, play an important role. As a result, two new categories were identified in both experiments and theory. We proposed a new method for quantifying and classifying cell layers using this framework. We also discuss the effects of these forces from a broader perspective.

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Time-correlation functions of stochastic three-sphere micromachines

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We discuss and compare the statistical properties of two stochastic three-sphere micromachines, i.e., odd micromachine and thermal micromachine [1]. We calculate the steady state time-correlation functions for these micromachines and decompose them into symmetric and antisymmetric parts. In both models, the cross-correlation between the two spring extensions has an antisymmetric part, which is a direct consequence of the broken time-reversal symmetry. For the odd micromachine [2], the antisymmetric part of the correlation function is proportional to the odd elasticity, whereas it is proportional to the temperature difference between the two edge spheres for the thermal micromachine [3]. The entropy production rate and the Green-Kubo relations for the two micromachines are also obtained. Comparing the results of the two models, we argue an effective odd elastic constant of the thermal micromachine. We find that it is proportional to the temperature difference among the spheres, which causes an internal heat flow and leads to directional locomotion in the presence of hydrodynamic interactions.

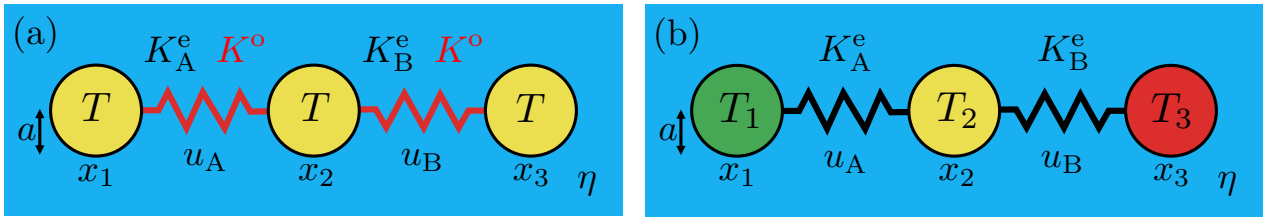

Fig.1 Two stochastic three-sphere micromachines consisting of three spheres with a radius a and two springs with a natural length ℓ. The positions of the spheres are denoted by x_i $(i = 1, 2, 3)$ in a one-dimensional coordinate, and the spring extensions with respect to ℓ are denoted by $u_\alpha(\alpha = \mathrm{A}, \mathrm{B})$. (a) Odd three-sphere micromachine in which the two springs have the odd elastic constant K^{o} in addition to the even elastic constants $K^{\mathrm{e}}_{\mathrm{A}}$ and $K^{\mathrm{e}}_{\mathrm{B}}$ [2]. The temperature of all the spheres is T. (b) Thermal three-sphere micromachine in which the two springs have only the two elastic constants $K^{\mathrm{e}}_{\mathrm{A}}$ and $K^{\mathrm{e}}_{\mathrm{B}}$ [3]. The three spheres are in equilibrium with independent heat baths at different temperatures T_i.

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Ornstein-Uhlenbeck information swimmers with external and internal feedback controls

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Recently, much attention has been paid to active systems that utilize information instead of energy, i.e., informational active matter [1]. During the last decade, there have been many studies on "information engines" that use information to extract mechanical work. One example of such an engine proposed by Huang *et al*. is the model of "information swimmer" in which the swimmer periodically measures its velocity and adjusts its friction coefficient [2]. They showed that the information swimmer can achieve a steady-state velocity without external energy input although it does not violate the extended second law of thermodynamics with information. In the absence of measurement and feedback, the information swimmer proposed by Huang *et al*. is passive and purely governed by thermal fluctuations.

Using an underdamped active Ornstein-Uhlenbeck particle, we propose two information swimmer models having either external or internal feedback control and perform their numerical simulations [3]. Depending on the velocity that is measured after every fixed time interval (measurement time), the friction coefficient is modified in the externally controlled model, whereas the persistence time for the activity is changed in the internally controlled one. In the steady state, both of these information swimmers acquire finite average velocities in the noisy environment, and the efficiency can be maximized by tuning the measurement time. The internally controlled swimmer is more relevant to biological systems and can generally achieve larger average velocity and efficiency than the externally controlled model.

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Statistical formulation of the Onsager-Machlup variational principle

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[2]Wenzhou Institute, University of Chinese Academy of Sciences,

Onsager's variational principle provides us with a systematic way to derive dynamical equations for various soft matter and active matter. In this principle, we construct a functional quantity called Rayleighian by summing up the dissipation function and the change rate of free energy. Minimization of the Rayleighian under appropriate constraints provides us with overdamped deterministic equations that describe the change rate of the state variables.

Doi et al. proposed the OnsagerMachlup variational principle (OMVP) using a quantity called the Onsager-Machlup integral, which is the time integral of the Rayleighian. In contrast to OVP, which is a time-local principle, OMVP is a time-global variational principle, and it allows us to obtain the most probable trajectory over a long time. However, statistical properties of stochastic trajectories and effects of thermal fluctuations, such as the mean square displacement of a Brownian particle, cannot be directly obtained within OVP or OMVP, which remains an important issue especially for active systems.

By reformulating OMVP, we propose a new method to incorporate thermal fluctuations [1] and call it the statistical formulation of OMVP (SOMVP). In SOMVP, we introduce an observable that is determined by the system variables and it allows the OM integral to explore trajectories deviating far from the most probable path. We propose a modified OM integral that should be maximized to obtain the cumulant-generating function (CGF) of the observable.

To demonstrate the utility of SOMVP, we obtain the diffusion constant of a Brownian particle embedded in a viscous fluid (Fig.1) by maximizing the modified Onsager-Machlup integral for the surrounding fluid. Notably, the obtained diffusion constant recovers the Stokes-Einstein relation or the fluctuation-dissipation relation without any additional requirements. We also apply our formulation to a Brownian particle in a steady shear flow, which is a typical nonequilibrium system.

We further show the application of SOMVP to the active particle model called information swimmers [2], which can rectify its random motion by using measurement and feedback loops. We obtain the analytical expression of swimming velocity, which has not been reported, and confirm good agreement with numerical simulations. We will discuss other possible extensions of our formulation to internally driven active systems.

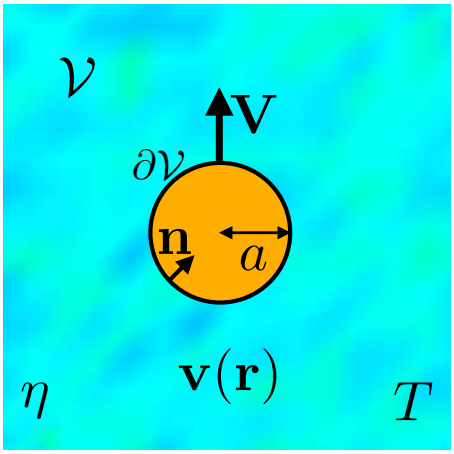

Fig. 1 ： A spherical particle is embedded in a fluctuating viscous fluid.

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Single Spherical Microswimmers in Non-Newtonian Fluids

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In biological systems, microswimmers often propel themselves through complex media. However, many aspects of swimming mechanisms in non-Newtonian fluids remain unclear. This study considers the propulsion of two types of single spherical microswimmers (squirmers) in shear-thickening and shear-thinning fluids. The slip-driven squirmer propels faster/slower in shear-thickening/thinning fluids than in Newtonian fluids [1]. In contrast, we discovered that a traction-driven squirmer exhibits the opposite trend, moving slower/faster in shear-thickening/thinning fluids than in Newtonian fluids (Fig.1) [2]. In addition, we have shown theoretically that Purcell's scallop theorem does not hold in non-Newtonian fluids when a squirmer with reciprocal surface motions is used. The present findings open up possibilities for the design of new types of microswimmers that can achieve translational motion from a single reciprocal motion in non-Newtonian fluids. Furthermore, we demonstrated that traction-driven squirmers swim faster and more efficiently in shear-thinning fluids than in Newtonian fluids. These findings highlight how the non-Newtonian rheology enhances both swimming speed and efficiency, suggesting further potential for optimizing locomotion performance otherwise impossible in Newtonian fluids.

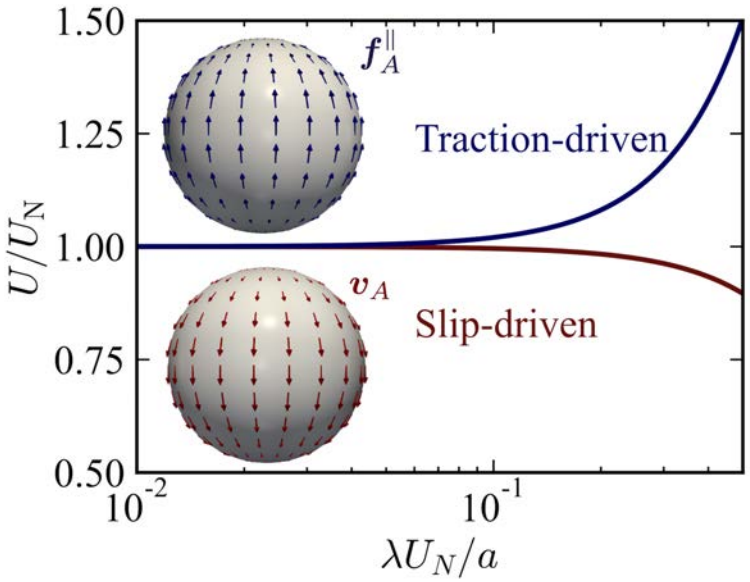

Fig. 1 ：Swimming speed of two types of microswimmers: a slip-driven squirmer and traction-driven squirmers.

Acknowledgements
We acknowledge Raymond E. Goldstein and Ronojoy Adhikari for the discussion.

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Revealing the Mechanism of Anomalous Rheology in Microswimmer Suspensions

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Active suspensions containing microswimmers, such as swimming bacteria dispersed in solvent fluids, demonstrate anomalously distinctive properties not observed in passive suspensions. For example, *E. coli* suspensions, categorized into pusher-type microswimmers, exhibit a notable decrease in viscosity, even dropping to zero under certain conditions [1]. On the contrary, *Chlamydomonas* suspensions, classified into puller-type microswimmers, show a steeper increase in viscosity compared to non-motile cell suspensions [2].

In a seminal study by Hatwalne *et al*., it was predicted that when orientational order is achieved under shear flow, additional stress arising from the active forces of microswimmers could emerge, potentially leading to negative stress [3]. In dilute and semi-dilute microswimmer suspensions, hydrodynamic interactions (HIs) are expected to play a crucial role in determining the orientational distribution of swimmers and their resultant rheological properties. However, the highly nonlinear and nonequilibrium nature of HIs has still prevented a comprehensive understanding of their substantial effects in active suspensions.

In this study, we investigate the mechanisms underlying the anomalous rheology of model active suspensions using direct hydrodynamic simulations (Fig. 1) [4,5]. Our simulations qualitatively reproduce the anomalous rheology observed in experiments. Furthermore, for pusher-type swimmers, HIs under shear flow systematically promote the alignment of swimmers along the extension direction, leading to a significant reduction in viscosity. In contrast, for puller-type swimmers, those near the boundary walls exhibit a strong polar order. Notably, the direction of this polar order for puller swimmers is highly dependent on the aspect ratio of their bodies, which determines whether the viscosity is enhanced or reduced. Our findings indicate that the rheological properties of active suspensions vary widely depending on the swimmer's properties, such as their shapes and swimming mechanisms.

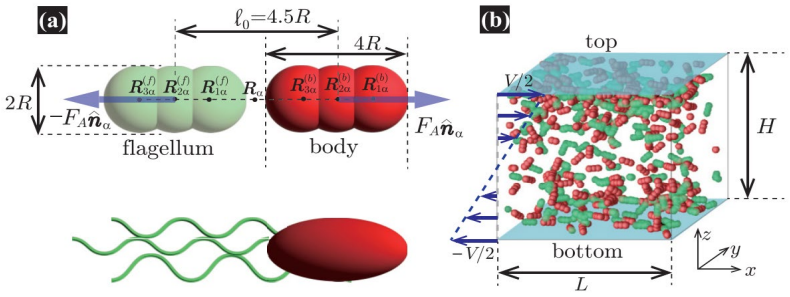

FIG. 1: (a) Our pusher-type model swimmer
(b) Simulation system (cited from [4])

Acknowledgements

This work was supported by JSPS KAKENHI (Grants No. 20H05619) and JSPS Core-to-Core Program "Advanced core-to-core network for the physics of self-organizing active matter" (Grants No. JPJSCCA20230002) and JST SPRING (Grants No. JPMJSP2108).

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Crystallization of Chiral Active Brownian Particles at Low-Densities

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Chiral active matter is defined as a collection of active objects whose motion breaks the left-right symmetry, such as circular motion in two dimensions, and has attracted much interest [1]. Among many theoretical models of chiral active matter, chiral active Brownian particles (cABP) is a simple model that is often used. In the model, the behavior is characterized by three parameters: the persistence time τ_p, the radius of a circular trajectory R, and the packing fraction φ. So far, several studies have revealed phenomena that are absent in non-chiral counterparts. For example, in the limit $\tau_p \to \infty$, the system undergoes an absorbing phase transition at low densities [2] and two-dimensional crystallization with long-range translational order at high densities [3]. However, the phase behavior of the model has not yet been fully understood.

Here, we study cABP for a broad range of parameters, τ_p, R, and φ, and show that crystallization takes place even at low densities. We observe that as R decreases for a fixed τ_p, the first peak of the structural factor sharpens, indicating a crystalline structure. To quantify this, we measure the hexatic order parameter and construct a liquid-solid phase diagram on the plane $(1/\tau_P,\ R)$ for different φ (see figure 1). We also compute the spatial correlation functions of the hexatic and translational order parameters and find power-law behaviors like those observed in two-dimensional melting in equilibrium [4] (see figure 2). In the spatial correlation function of the hexatic order parameter near the transition point, it exhibits power-law decay behavior with an exponent of $\eta_6 = 1/4$, consistent with equilibrium melting theory [4]. For the spatial correlation function of the translational order parameter, the power-law decay behavior observed near the solid state shows an exponent of $\eta_G \approx 0.8$ or even closer to 1, which disagrees with the melting theory ($\eta_G = 1/3$) and appears too large [4].

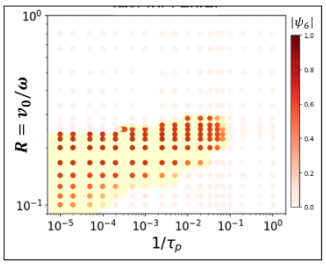

Figure 1. a liquid-solid phase diagram of cABPs on the plane $(\boldsymbol{1/\tau_P},\ \boldsymbol{R})$ at $\boldsymbol{\varphi = 0.4}$. red dots are a solid phase and the rest of it is a fluid phase

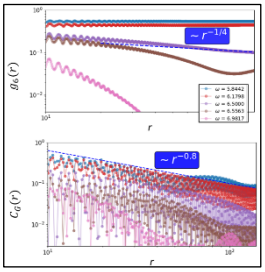

Figure 2. the two spatial correlation function of the hexatic order parameter (top) and the translational order parameter (bottom) for $\boldsymbol{\tau_p = 100, \varphi = 0.4}$ and different $\boldsymbol{\omega}$.

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Mechanical control of epithelial morphogenesis

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How do cells push and pull each other to trigger precise deformations of a tissue when shaping the body? Answering this central question is essential for understanding the development of animal forms, including our body. To address this, we have formulated Bayesian force inference and mechanical parameter inference, both of which utilize image data of epithelial cells to derive physical quantities. In this symposium, I will discuss how these approaches have helped uncover the mechanisms underlying cell rearrangement, cell packing, and cell division during epithelial morphogenesis. If time permits, I will also present our ongoing research on the dynamics of soft, deforming cell populations.

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Abstracts
for Poster presentations

Optimal substrate stiffness for cell migration

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Durotaxis is a phenomenon where cells change their migration behavior depending on substrate stiffness [1]. This phenomenon has been observed in many experiments including those using epithelial and cancer cells and is important for cancer metastasis and wound healing. In this presentation, we address how cells crawling on a substrate respond to the stiffness of the substrate underneath by using a mechanochemical model that combines intracellular biochemical reactions and cell mechanics [2]. We found that cell migration behavior changes nonmonotonically depending on the substrate stiffness (Fig.1), which is compared with experimental observation.

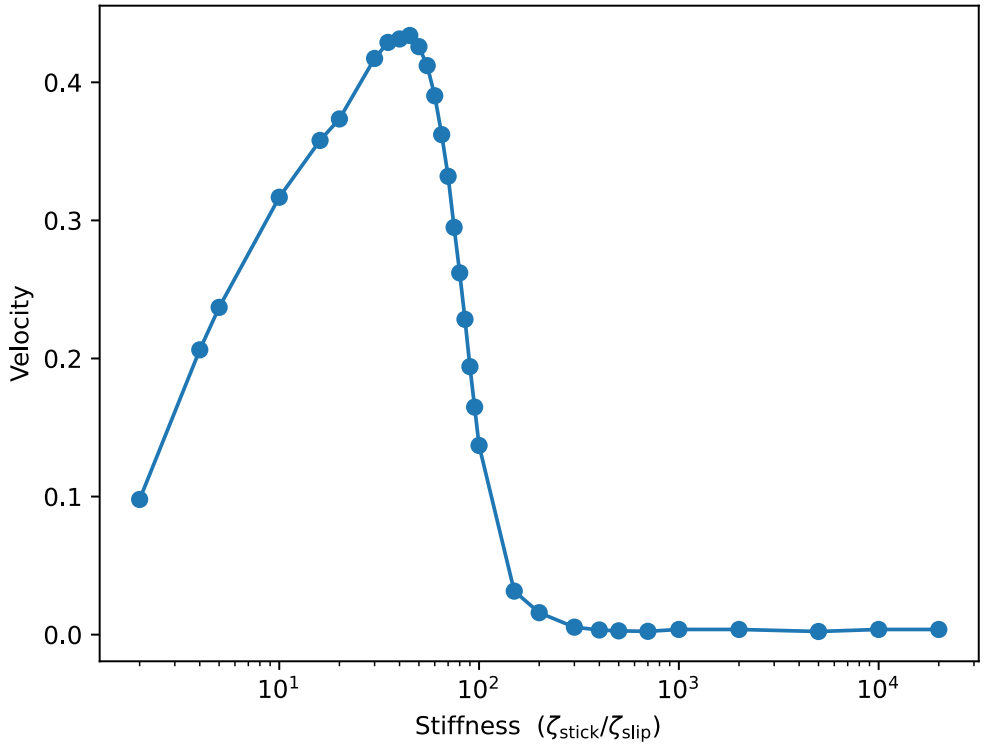

Fig.1 Cell speed at different substrate stiffness.

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Emergence of attractors with nonreciprocal skin effect from dissipative coupled Duffing oscillators

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In linear quantum systems, the Non-Hermitian Skin Effect (NHSE) [1] has drawn much attention these years. Local perturbation of boundary conditions gives rise to non-local shift of eigenstates. The localization of eigenstates toward the ends of the system is the NHSE. However, few works delve into the nonlinear systems to reproduce the NHSE [2].

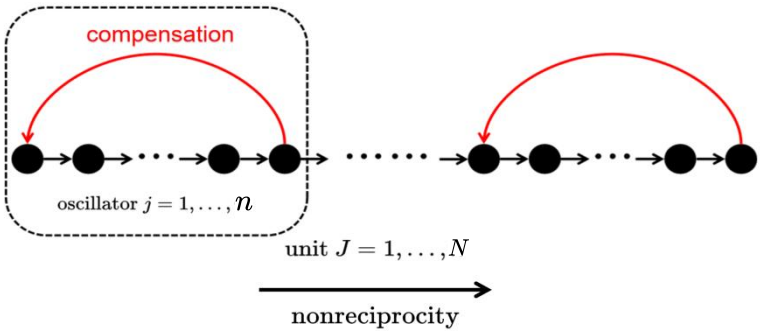

Fig.1： The 1D chain model of Duffing oscillators

Here, we investigate the emergence of attractors with nonreciprocal skin effects (NRSE) in dissipatively coupled Duffing oscillators and uncover a novel route to chaos in high-dimensional systems. The model we used is composed of *N* units, each formed by *n* oscillators; see Fig.1. The arrows are unidirectional couplings with the black ones generating nonreciprocity and red ones compensating for the energy loss caused by the damping term. Throughout this work, numerical analyses are applied in order to determine the Lyapunov spectrum [3] and phase portraits.

Based on the previous researches [4] on the unit of a ring of non-reciprocally coupled Duffing oscillators, we first illuminate the mechanism of bifurcations in view of concerted effects of both the nonreciprocity and compensation couplings. Then, the observation of localized modes resembling the NRSE and an unconventional way to chaos in higher dimensional phase space of the 1D chain system are systematically discussed. To be specific, a novel synthesis of attractors from different subspaces is presented, where the unidirectional couplings play an important role. Besides, Duffing nonlinearity imposes saturation on the NRSE, establishing a boundary for attractor growth. With the length of the system increasing, the NRSE is ceased at a certain length and the amplitude maintains the saturation value, which is quite distinct from the linear case.

To summarize, this work bridges the gap between non-Hermitian physics and nonlinear dynamical systems, offering insights into the interplay of nonlinearity, nonreciprocity, and dimensionality in emergent chaotic phenomena.

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Torque-free rotation of cells crawling on a substrate

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Dynamics of cells crawling on a substrate has been studied from a various viewpoint. Among them, recent studies shed light on its chirality. That is, some cell types tend to draw trajectories that curve leftwards or rightwards on average. Although many theoretical studies have been conducted to understand cell migration, such rotational motion is not well understood yet.

To investigate the active rotation of cells, we construct a model in which a cell is represented by two particles connected by a viscoelastic spring. We introduce a torque dipole to this model cell, which tend to rotate the two particles in the opposite directions. Although the net torque acting on this model cell vanishes, the cell exhibits spatial migration if the substrate adhesion characteristics change in time. To characterize its dynamics, we measure three quantities: the average rotation angle around the center of mass, the displacement of the center of mass and its squared value. In particular, we analyze in detail the condition where the cell fails to achieve migration or rotation. By combining our results with the translational motion induced by active force dipole, we expect that we can understand more complex dynamics of real cells.

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Active Matter in Human Crowds: A Framework for Analyzing Congestion Dynamics

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1 Introduction

Crowd dynamics research has introduced various metrics to evaluate congestion, such as Congestion Level and Congestion Number, which are derived from velocity rotation calculations of vector fields [1]. While effective, these metrics rely heavily on vector analysis and require extensive trajectory data over significant time intervals, making real-time calculations challenging. Other approaches, including acceleration percentiles based on shock wave propagation relative to crowd movement [2] and crowd entropy derived from area and population [3], offer insights into density but remain situation specific. These methods often fail to capture the nuanced influence of pedestrian micro dynamics, particularly in densely packed scenarios where movement persists even under high congestion. This gap highlights the need for metrics that better connect individual behavior with collective crowd dynamics to address challenges in understanding and managing highly dense crowds.

2 Concept

To evaluate crowd congestion, individuals in a crowd are modeled similarly to particles in active matter systems, where collective behavior arises from local interactions. Congestion levels are quantified by analyzing the variance in individual speeds within a defined area, calculated as $Vov \propto \frac{1}{N}\sum_i^N (v_i - \bar{v}_i)^2$,where v_i is the speed of each individual, $\bar{v}_i$ is the average speed, and N is the total number of individuals. The area for this calculation is determined using Voronoi diagrams [4] are employed to define the calculation area, capturing local interactions and reflecting how individuals' movements are influenced by their neighbors. This approach aligns with active matter theories by treating the crowd as a non-equilibrium system, emphasizing local interactions and collective dynamics. Similar to active matter, the variance metric highlights the system's disorder, with greater speed variance indicating more chaotic and uncoordinated movement, often associated with higher congestion levels. The analysis not only draws inspiration from thermodynamic analogies but also reflects principles of active matter by linking individual dynamics to macroscopic crowd behavior.

3 Method & Result

This study analyzed the relationship between turning angles and movement smoothness. Specifically, an experiment was conducted where pedestrians going straight merged with those turning at five different angles. This experiment examined the correlation between velocity variance and smoothness with respect to angle dependency and crowd size. In conclusion, this study compared three key congestion indicators, each offering unique insights into crowd dynamics. **Density** reflects the spatial distribution of the crowd, highlighting areas of high occupancy. ***CN*** identifies localized high-density zones that may pose safety risks, emphasizing critical areas for intervention. $\boldsymbol{Vov}$, on the other hand, captures the smoothness of movement and the overall distribution of congestion, providing a dynamic perspective.

Acknowledgements
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Collective Behaviors of Aligning Self-Propelled Particles with Frustration

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Many active matter systems found in nature and studied in experiments, including bacteria, actin filaments or microtubules driven by molecular motors, and Janus particles, can be understood as collections of self-propelled particles. Previous studies on self-propelled particles with nematic interactions have primarily focused on rod-like particles. In such systems, particles align their velocities when the incoming angle is small, whereas they anti-align when the incoming angle is large. In this study, we consider cone-shaped particles with an extended nematic alignment rule, as described in Fig. 1. When particles collide at a small angle, they separate by a certain angle α. Consequently, the angular differences between neighboring particle pairs cannot be satisfied simultaneously, thereby introducing frustration into the system.

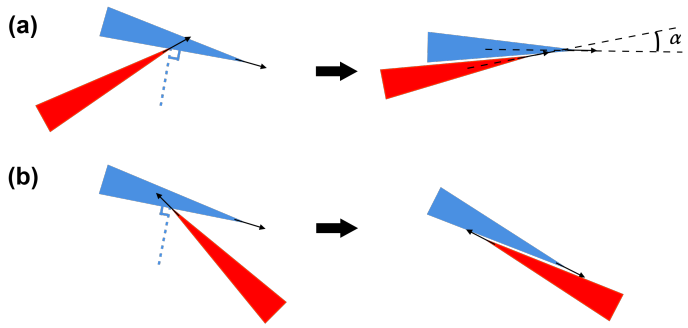

Figure 1: Illustration of the alignment interaction between cone-shaped particles. (a) A collision at a small angle causes the angle difference α. (b) A collision at a large angle results in the anti-parallel alignment.

We performed numerical simulations based on a Vicsek-type description and observed distinct phenomenology in the new model compared to the original one [1]. Between the homogeneous ordered phase and the homogeneous disordered phase, we observed anti-parallel polar bands instead of nematic bands. These anti-parallel bands resemble recent observations in studies of the two-species Vicsek model [2].

We also studied the continuous description based on the Boltzmann approach. Following Ref. [3], we conducted a linear stability analysis of the homogeneous states and found that, in the intermediate parameter range, the most unstable wavevector is parallel to the nematic order, which is consistent with observations from the microscopic model.

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Global bifurcation structure of steady solutions characterizing free energy landscape of coupled Cahn–Hilliard equations

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Block copolymers can form nanoscale particles exhibiting diverse three-dimensional morphologies, driven by particle shape and internal microphase separation. A suitable free energy F (given in Eq. (1)) allows a coupled system of the Cahn-Hilliard model to emerge as a gradient system[1]. However, it remains unclear where specific target morphologies, like Platonic solids[2], lie within the free energy landscape.

Here, we present an approach that shows global atlas of all relevant saddles and minimizers shaping the landscape of free energy, which guides us toward these exotic shapes. Here we employ a simplified one-dimensional Cahn-Hilliard equations:

$$\begin{aligned} \tau_u \frac{\partial u}{\partial t} &= \nabla^2 \frac{\delta G}{\delta u} = \frac{\partial^2}{\partial x^2}\left(-\varepsilon_u^2 \frac{\partial^2 u}{\partial x^2} - u + u^3 + \alpha v + \beta v^2\right), \\ \tau_v \frac{\partial v}{\partial t} &= \nabla^2 \frac{\delta G}{\delta v} = \frac{\partial^2}{\partial x^2}\left(-\varepsilon_v^2 \frac{\partial^2 v}{\partial x^2} - v + v^3 + \alpha u + 2\beta uv\right), \end{aligned}$$

where

$$G = \frac{\varepsilon_u^2}{2}|\nabla u|^2 + \frac{\varepsilon_v^2}{2}|\nabla v|^2 + \frac{(1-u^2)^2}{4} + \frac{(1-v^2)^2}{4} + \alpha uv + \beta uv^2, \quad F = \int_\Omega G \mathrm{d}x, \tag{1}$$

and u is phase field of block copolymer and solvent, v is phase field of two polymers B and A, ε_u and ε_v are gradient energy coefficient of u and v, respectively. α is an indicator of the relative hydrophilicity or hydrophobicity of each polymer, and β is a coupling parameter. Note that $u \approx 1$ is regarded as polymer rich whereas -1 solvent rich, and $v \approx 1$ is regarded as polymer B is rich whereas -1 A is rich. In the present investigation, periodic boundary condition is imposed as $x \in \Omega = [0, 2.56)$. Parameters are fixed as $\bar{u} = \int_\Omega u \mathrm{d}x / \left(\int_\Omega \mathrm{d}x\right) = 0.0005$, $\bar{v} = \int_\Omega v \mathrm{d}x / \left(\int_\Omega \mathrm{d}x\right) = 0.0055$, and $\beta = -0.3$, whereas α varies.

In the present study bifurcation analysis is introduced to provides global atlas of the free energy (1). Using the global atlas, it becomes possible to predict the itinerancy of the orbit and asymptotic state without calculating time evolution for each case[3]. Therefore it is expected to identify the set of initial conditions that approach a specific target morphologies in the landscape.

α is chosen as bifurcation parameter. The larger $|\alpha|$ becomes, the stronger polymer A and B repel each other and thus a variety of patterns appear around $|\alpha| = 0$ whereas only a small number of patterns exist for larger $|\alpha|$. Although the present model is simplified one-dimensional model, it provides very rich energy landscape, transition processes, and asymptotic states. It gives an abundant clues for original three-dimensional system.

This work was supported by JSPS KAKENHI Grant Number 23K19003 and 23K17653.

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Active Mean Filter

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Active matter systems, characterized by collectively self-propelled particles, have been widely studied due to their ability to exhibit self-organized patterns and long-range order. A prominent example is the Viscek model, which demonstrates critical phase transitions in collective polar order depending on interparticle interactions and noise amplitude [1]. While this model focuses on mobile agents directly interacting with each other in free space, in our system, fixed agents interact via shared cargo transport.

Fig. 1 shows a schematic image of our model. In this model, unit agents (termed "veyors") are arranged on a two-dimensional grid with random initial orientation. These veyors are fixed on the platform and themselves do not move around, that is akin to a classical XY model [2]. Instead, they can potentially push a contacting object to their orientations, and their orientations can be aligned to the mean direction of neighboring veyors when in contact with a finite-sized cargo. This operation is like a mean-filtering function that is usually used as image image-processing technique. Once the collective veyors sharing a single cargo are aligned with each other, the cargo starts to move in the direction, changing its contacting combination of veyors. This dynamic interplay not only induces alignment among directly interacting neighborhoods but also propagates alignment across distant regions indirectly through cargo transport. Here, in our system, while agents are immobile, instead the interacting window moves, therefore we call this an "active mean filter". To investigate the emergent behaviors in this system, we performed simulations exploring how the density of cargo affects the global alignment of veyors. Our results are compared to existing active matter models, emphasizing the unique role of indirect interactions mediated by cargo.

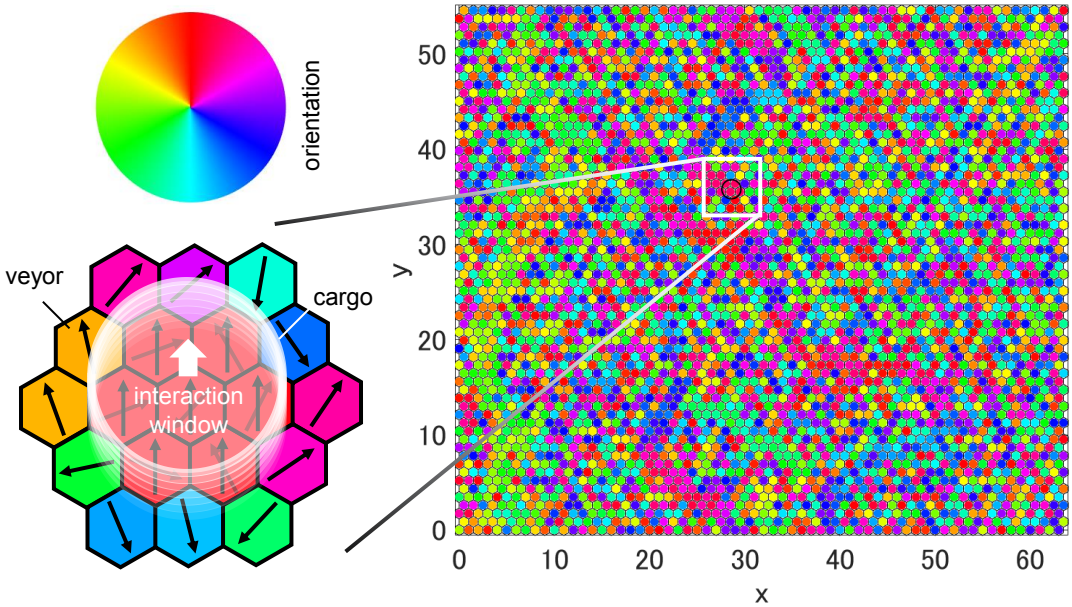

Fig.1: A schematic image of active mean filter system.

Acknowledgments
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Poster 8

Anisotropic Swarming of Photoresponsive Microtubules in Optical Landscape

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Introduction

Active matter systems, a diverse range of non-equilibrium system that each agent can convert environmental energy into self-propelled motion. Such systems often display different emergent collective behaviors, for instance, swarming and phase separation, offering advantages like robustness and flexibility to complete tasks like cargo and sensing. However, achieving programmable self-assembly on micro-scale remains challenging. Microtubules (MTs)-kinesin systems show potential in overcoming this challenge as molecular robot.

Results

In our study, we show the swarm of MTs modified with photo-responsive DNA(p-DNA) can be controlled by UV and visible light, presenting new opportunities for optical control of swarming behavior. To gain more physical insights from the experimental system, we also combine numerical simulation with Vicsek type model and effective hydrodynamic theory to investigate the swarming dynamics of p-DNA-conjugated MTs in optical patterns. Our preliminary result suggests that swarming direction of MT swarm can be oriented by the optical pattern. The critical noise for order-disorder phase transition and the mechanism of oriented swarm direction are also well explained by the effective hydrodynamic theory. Based on it, by manipulating optical patterns, our research can facilitate the controlling MTs swarm, advancing the understanding of collective dynamics in optical landscape.

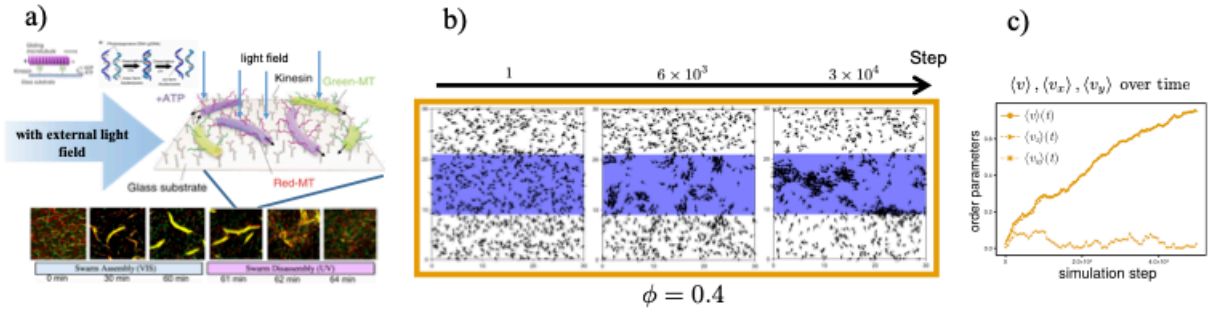

Fig. 1 (a) Schematic of the experimental setup. The bottom figures illustrate the swarm assembly and disassembly under homogeneous UV illumination [1]. (b) Snapshots from simulations at three distinct time steps. (c) Measured order parameter reveals a bias in the swarm direction.

Acknowledgement

This work was supported by JST SPRING, Grant Number JPMJSP2110.

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Bifurcation phenomena of a rotating camphor boat

Michiko Shimokawa[1], **Hiroyuki Kitahata**[2]

[1]Nara Women's University, [2]Chiba University

A Camphor boat is one of the self-propelled particles. When a camphor particle is placed on the surface of water, the camphor molecules diffuse to the water surface. The camphor molecules decrease its surface tension, and then, a camphor boat moves toward the low surface tension region around the boat.

We can control the movement of a boat by controlling the camphor concentration around the boat. We proposed a new camphor boat as shown in Fig. 1(a). The rotational axis, which is an acrylic rod with 3.0 mm diameter, is penetrated the pore of the camphor boat. It forbids the translational movement of the camphor boat. The camphor boat is placed on the water surface as shown in Fig. 1(b). The rotational motion is dominant in this system.

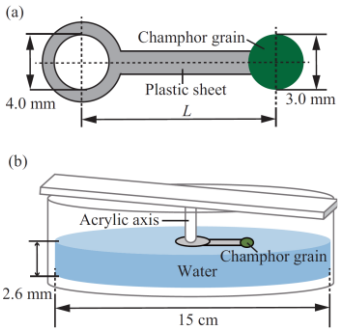

Fig.1：(a)Camphor boat, (b) Experimental setup.

We found the bifurcation phenomenon of the camphor boat's movement in an increasing arm length L of the boat in our experiments. Figure 2 shows the time series of the velocity v of the camphor boat obtained from experiments with several L. The boat shows the stational state (Fig. 2(a)), the intermittent motion (Fig. 2(b)), the rotational motion with an oscillating velocity (Fig. 2(c)), and that with a constant velocity (Fig.2(d)) in an increase of L. In order to evaluate this bifurcation, we investigated T/T_0 against L, where T_0 and T mean a measurement time in our experiments and total time when $v > 30$ mm/s in T_0, respectively. Figure 3 supports the appearance of the bifurcation phenomena in our experiments.

We confirm that the contact condition between the edge of the pore and the rotational axis changes in a change of L. As shown in the previous paper [1], the contact condition is important to determine the rotational phenomena. We considered that the contact condition would be determined by the balance between the centrifugal force to work on the boat and the force towards the radial direction due to the difference of the surface tension, because the bifurcation depends on v. We will show detailed experimental results and discuss the mechanism of the bifurcation in this presentation.

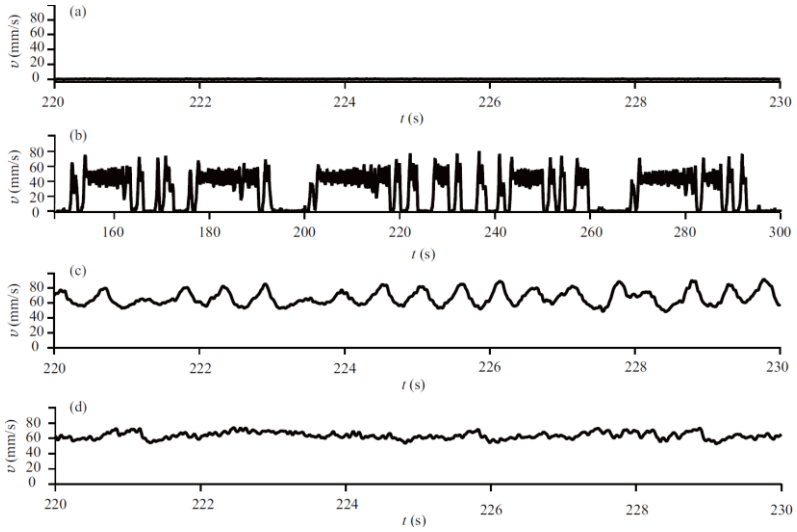

Fig.2：Time series of velocity v obtained from the arm length of the camphor boat L = (a)4.5 mm, (b)5.0 mm, (c) 6.0 mm, and (d) 25 mm.

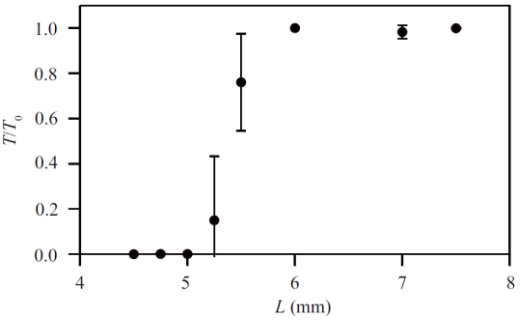

Fig.3：Relationship between L and T/T_0, where T_0 and T are a measurement time in our experiments and an time where $v > 30$ mm/s in T_0, respectively.

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Confining geometry determines the contracted shape of active cytoskeleton

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Living cells are dynamic systems that can spontaneously self-organize ordered structures from constituent molecules. In this process, an important role is played by molecular motor proteins, which can convert chemical energy into mechanical work and are responsible for controlling cell-specific structures and functions. This is particularly true in the cytoskeleton of a cell, where actin filaments and myosin molecular motors together form the actomyosin complex and regulate the cell shape, cell motility as well as cell division. We are interested in uncovering the underlying physical principles that govern such varied orderings of the actomyosin complex.

While there have been numerous studies on how actomyosin self-organizes inside cell-sized confinements [1,2], the effect that the cell geometry itself has on self-organization is relatively less explored, and addressing this point is the aim of this work. We confine cytoplasmic extracts containing the actomyosin complex inside microwells in the shape of circular segments (Fig. 1, a, b). We find that in these microwells, the actomyosin network contracts to form a nucleus-like cluster, and that the cluster shape changes with the microwell shape (Fig. 1, c). Thus, the clusters play a role akin to transcribing artificial cell shape into an intracellular body.

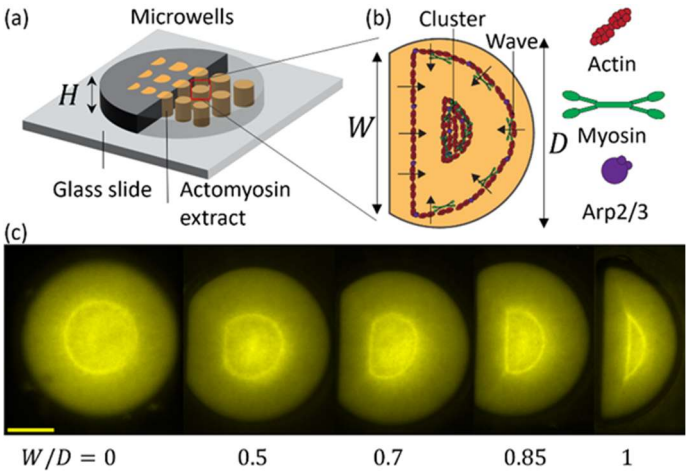

Fig. 1: (a) Schematic of the experimental setup (b) microwell and actomyosin dynamics schematic, major components of the cytoplasmic extract (c) cluster shape changes as microwell shape changes and W/D goes from 0 to 1 (scale bar, 100 μm)

To clarify the mechanism by which cell boundary shapes are transferred to internal clusters, we utilize an active gel theory of actomyosin [3] and find that the numerical simulation agrees with the experiments, meaning our active gel model is sufficient to explain the geometric effect in cluster formation. Hence, this work reveals how the feedback due to the interplay between the asymmetric confinement and the actomyosin network leads to self-organization previously unseen in circular confinements.

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Kershner, Liliana

Boltzmann-Ginzburg-Landau theory for autochemotaxis of self-propelled rods

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Department of Physics, Tohoku University

We address the interplay between chemotaxis and orientational interactions in active rod-like particles, such as *E. coli* and Janus rods. Starting from a discrete model of self-propelled rods with chemotactic responses, we employ a Boltzmann-Ginzburg-Landau (BGL) approach[1] to derive a coarse-grained dynamical equations for the density, polar and nematic orientational order parameters of the particles and concentration field of the chemoattractant.

We set up a two-dimensional model of self-propelled rods with chemotactic interactions mediated by the concentration field $c(\mathbf{r},t)$ of the chemoattractant. We start from the discrete time-evolution equations

$$\mathbf{r}_j^{t+\Delta t} = \mathbf{r}_j^t + v_0 \Delta t\, \mathbf{e}\left(\theta_j^t\right) + \zeta_{tr} \nabla c(\mathbf{r}_j^t)\Delta t,$$

$$\theta_j^{t+\Delta t} = \arg\left[\sum_{|r_j - r_k|<d_0} \mathrm{sign}[\cos\left(\theta_k^t - \theta_j^t\right)]\exp\left(i\theta_k^t\right)\right] + \zeta_{rot}\partial_\theta \mathbf{e}(\theta_j^t)\cdot\nabla c(\mathbf{r}_j^t)\Delta t + \eta_j^t.$$

$$\frac{\partial c}{\partial t} = D_c \nabla^2 c + a_1 \sum_j \delta(\mathbf{r} - \mathbf{r}_j^t) - a_2 c$$

where $\mathbf{r}_j^t$ and θ_j^t are the position and angle of the j-th particle at time t, respectively, Δt is the time increment, $\mathbf{e}(\theta) = (\cos\theta, \sin\theta)$, v_0 is the speed of self-propulsion, d_0 is the radius of orientational interaction, ζ_{tr} and ζ_{rot} are the translational and rotational chemotactic susceptibilities[2], and η_j^t 's are white noises that share the Gaussian distribution $P(\eta)$ with zero mean and standard deviation σ. The chemoattractant is produced by each particle with the rate a_1, spreads with the diffusion constant D_c, and dissociates with the rate a_2.

Linear stability analysis is performed for fluctuations around the uniform steady solutions that correspond to the disordered and ordered phases; see Fig.1. For both phases, we find that the translational chemotactic response enhances instability, while the rotational one suppresses it. We further examined which elements contribute to instability by analyzing the mode structure.

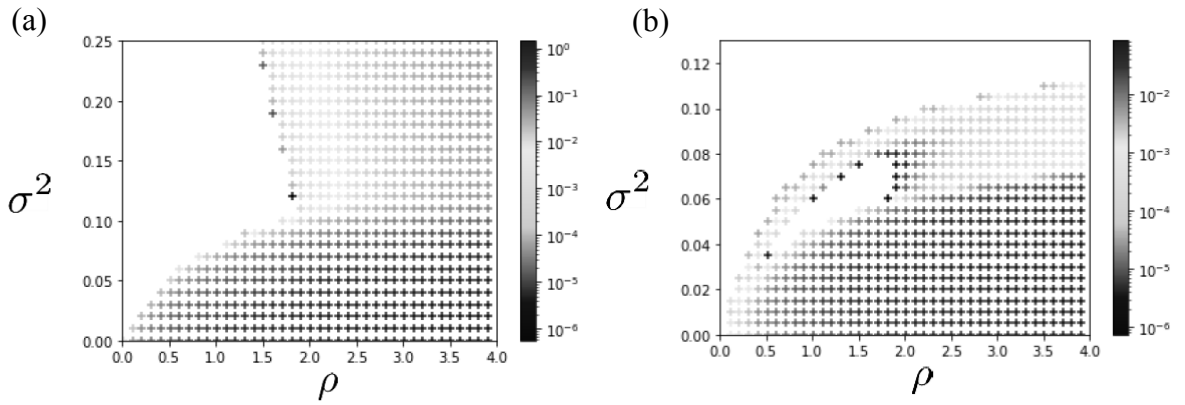

Fig. 1 : Stability diagrams for (a) the disordered phase and (b) the ordered phase in terms of the particle density ρ and noise strength σ. The unstable regions are shown in gray with the grayscale showing the linear growth rate of the most unstable mode.

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Response of collective orientation of magnetotactic bacteria to a stationary magnetic field

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The emergence of order is one of the popular research themes in active matter. The application of external fields is a means of approaching order formation by manually breaking the system's symmetry. In active matter, attempts to understand order formation from the response to external fields have been well-developed in theory [1, 2]. If experimental understanding is provided by measuring the external field response, the theory designed so far can be brought closer to real systems. In this study, by using the magnetic field response of magnetic bacteria, which is considered to have a simple mechanism [3], we constructed an experimental system to measure the magnetic field response of the collective motion of active matter.

In our experiment, the orientation of cells of magnetic bacteria confined in a quasi-two-dimensional well was observed. Without a magnetic field, the cell population is not globally oriented. Next, the response of collective motion to a steady magnetic field was examined. Applying a magnetic field resulted in global order in the nematic orientational field (Figure 1). As a future perspective, we will apply a magnetic field with time development to measure the emergence and collapse of order.

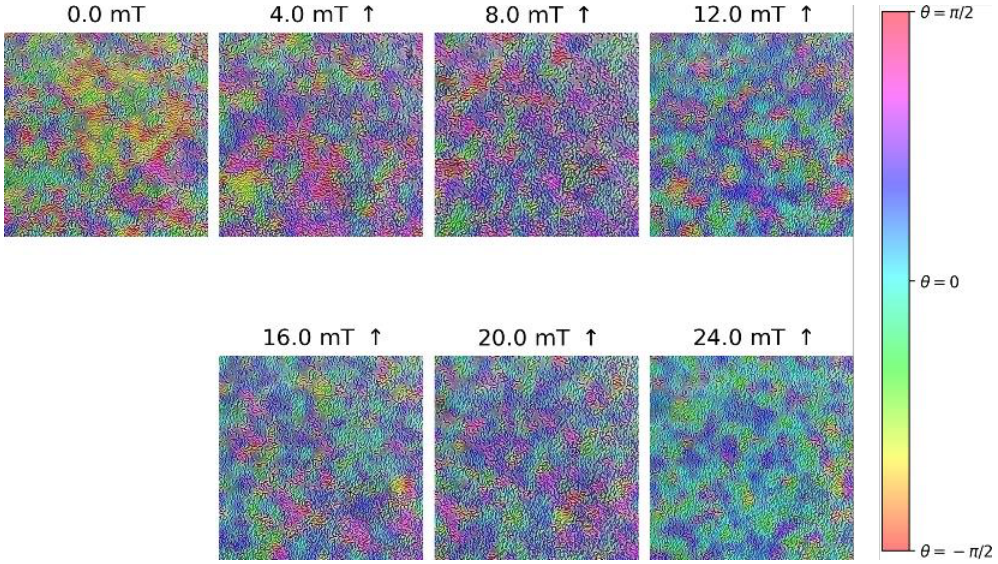

Fig. 1 ： Figure 1: Response of the orientation to the magnetic field. The color indicates the orientation of cells.

Acknowledgments

We acknowledge A. Taoka (Kanazawa Univ.) for offering the AMB-1 strain of magnetotactic bacteria and providing me with basic knowledge, techniques, and discussions about magnetotactic bacteria. Without his support, I could not have incubated magnetotactic bacteria. T. Goto is supported by the University of Tokyo's World-leading Innovative Graduate Study Program for Materials Research, Information, and Technology (MERIT-WINGS).

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Transition processes of a camphor particle in a three-state chamber

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Self-propelled motion has been studied in the field of non-equilibrium physics. A single self-propelled particle confined in a finite region exhibits various behaviors depending on the boundary shape [1, 2]. Investigating the relationship between boundary geometry and self-propelled motion is important for controlling such motion.

A camphor tablet floating on water is a simple and easily prepared non-living self-propelled particle. It exhibits self-propelled motion driven by surface tension gradient caused by inhomogeneous spatial distribution of camphor molecules. Many studies have examined the influence of the water chamber shape on the motion of a camphor particle. Notably, a spontaneously rotating camphor scraping moves between interconnected two circular regions [3].

In this study, we utilized a camphor particle floating on water and adopted a chamber with interconnected three circular regions (Fig. 1). Using this chamber, the particle should select its direction of the transition between the circular regions. This setup allows for several possible transition modes: transition to the other two regions with an equal probability, transition with a biased probability, or oscillation between two regions. We investigated the particle motion in both experiment and simulation, and analyzed transitions as discrete stochastic processes.

In our experiments, we observed probabilistic transitions, with a tendency to transit in the same direction in the case of short time interval between the sequential two transitions.

In our simulation, we utilized a mathematical model comprising the equation of motion for the camphor particle position and the reaction-diffusion equation for the camphor concentration field [4] with the boundary condition corresponding to the experimental setup. We reproduced the motion and transitions between the regions and compared with the experimental results.

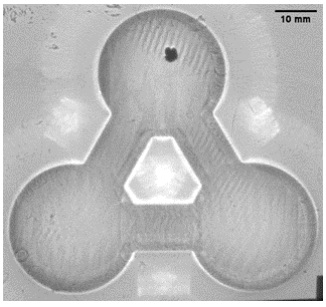

Fig. 1: A chamber with interconnected three circular regions.

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Bifurcation structure in the one-dimensional non-reciprocal Swift-Hohenberg model

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The concept of non-reciprocity has recently attracted attention in non-equilibrium physics, including pattern formation and active matter physics, since non-reciprocity leads to novel non-equilibrium phenomena [1]. Non-reciprocity is characterized by asymmetric interactions that do not satisfy the law of action and reaction. It also induces non-reciprocal phase transitions to time-dependent phases that break time and space inversion symmetries. In recent years, the concept of non-reciprocity has been extended to gradient systems [2], which are described by a free energy functional, and the bifurcation structure of non-reciprocal phase transitions has been studied [3]. The introduction of non-reciprocity into gradient systems leads to the emergence of spatiotemporal oscillatory patterns that do not appear in the reciprocal case. Several characteristic spatiotemporal patterns have been reported in the one-dimensional coupled Swift-Hohenberg equations with both reciprocal and non-reciprocal linear interactions [1, 4].

This study elucidated the bifurcation structure of characteristic spatiotemporal patterns in the one-dimensional non-reciprocal Swift-Hohenberg (NRSH) model using numerical calculations and theoretical analyses based on amplitude equations [5]. The one-dimensional NRSH model is given by

$$\partial_t \phi = \left[\varepsilon - (1+\partial_x^2)^2\right]\phi - \phi^3 - (\chi+\alpha)\psi,$$
$$\partial_t \psi = \left[\varepsilon - (1+\partial_x^2)^2\right]\psi - \psi^3 - (\chi-\alpha)\phi,$$

where ε is the destabilization parameter, and χ and α are the reciprocity and non-reciprocity, respectively. Since the Swift-Hohenberg equation has a characteristic wave number of destabilization, this model's spatial Fourier modes contributing to the spatiotemporal dynamics are minimal. We derived amplitude equations for the characteristic wave number modes. We showed that the bifurcation analysis of the reduced dynamical system can understand the bifurcation structure of the characteristic spatiotemporal patterns in the NRSH model. The presentation will explain the detailed bifurcation structure, including global bifurcations, of the amplitude equation system derived from the one-dimensional non-reciprocal Swift-Hohenberg model.

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Chemotaxis based on rotational fluctuation of bubble-propelled spherical Janus particle

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1 Tokyo Metropolitan College of Industrial Technology (TMCIT)

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We have investigated a chemotaxis principle of bubble-propelled spherical Janus particles (BPSJP), focusing on the concentration dependence of rotational fluctuations. BPSJP, which contain platinum catalysts, are propelled by bubble generation resulting from catalytic reactions with hydrogen peroxide. Numerical simulations of the mathematical model show that BPSJP move toward lower concentrations under concentration gradient conditions (negative chemotaxis) and that the chemotactic velocity increases with BPSJP radius. Studies by Jeffrey et al. show that Pt/Au self-propelled rods accumulate in areas of low motility. And there was good agreement between the experiment and the Brownian dynamics simulation. [1]. However, we observed non-Gaussian diffusion, differing from Brownian motion, at low concentrations for BPSJP with sizes of several tens of micrometers. We hypothesized that this difference in diffusion due to concentration might be caused by rotational fluctuations of BPSJP. We investigated diffusion and chemotaxis behaviors based on this hypothesis.

First, we analytically derived the probability density function for rotational angles in cases where the bubble generation angle changes randomly. Based on the probability density function, we calculated the transition probabilities for moving forward, P_F, and backward, P_B, at each concentration (Fig. 1). The results show that P_F and P_B have equal probabilities at high concentrations, whereas they exhibit unequal probabilities at low concentrations. Additionally, the concentration C_{ip} at which P_F=75% increases with increasing radius of BPSJP.

Next, we examined numerical simulations of the lattice model based on the computed transition probabilities. Under homogeneous concentration conditions, the time evolution of the position distribution showed Gaussian diffusion and non-Gaussian diffusion are high concentrations and low concentrations reapectively. These results are consistent with those of the mathematical model. Furthermore, under concentration gradient conditions, they show negative chemotaxis (Fig.2). In contrast, negative chemotaxis were not seen when the transition probabilities were set constant at every position. Therefore, these results suggest that the transition probability due to rotational fluctuations causes negative chemotaxis. Finally, we examined the transition probabilities obtained at each radius to investigate chemotaxis in the lattice model. (Fig. 2). The result shows that the slope of the gravity center of position (GCP), which representing the chemotactic velocity, increased with BPSJP radius. These results suggest that the increase in chemotactic velcity with increasing radius is caused by a shift of C_{ip} to higher concentrations as the radius increases.

These results suggest that negative chemotaxis and radius-dependent chemotactic velocity under concentration gradient are caused by difference in diffusion due to rotational fluctuations.

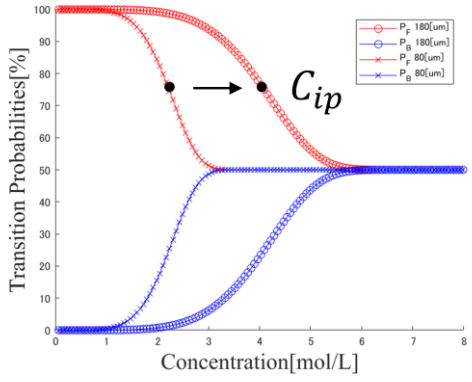

Fig. 1：transition probabilities at each concentration.

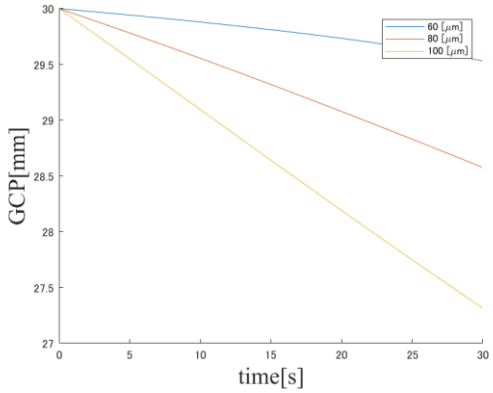

Fig. 2：Time variation of the gravity center of position

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Melting of Two-Dimensional Disordered Persistent Active Particles

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Active matter is any system composed of self-propelled particles. The constant input of energy drives active matter systems out of equilibrium. This gives rise to a wide range of collective behaviors, including bacterial swarms and bird flocks, which are absent in typical equilibrium systems. Remarkably, these behaviors can be explained by minimal models which demonstrate their universal nature. A key example is that of Active Brownian particles (ABPs). The translational motion of ABPs is governed by interparticle interactions, Brownian motion, and an active self-propelling velocity. The direction of the self-propelling velocity diffuses over a persistence time τ_r. Previous research on ABPs has focused on the intermediate density range where self-propulsion triggers a motility-induced phase separation (MIPS) when the active forces are sufficiently strong. Conversely, much less is known about the melting of such a system at high density. The majority of existing studies show that for small persistence time τ_r, dense active particles behave similarly to passive thermal systems. In contrast, persistent ABPs ($\tau_r \to \infty$) exhibit significant deviations from thermal systems [1]. This indicates that persistent active forces strongly influence the phase behavior of dense systems. Moreover, a recent study has demonstrated that active particles never crystallize when the persistent time diverges [2]. However, the melting scenario in disordered solids due to persistent active force remains unclear. In this work, we investigate whether disordered solid states are stable against a persistent active force.

We employ numerical simulations to study the melting of a minimal model of dense disordered persistent active particles. A persistent active force is introduced into a high-density, two-dimensional disordered solid system. Each particle is propelled by a constant force pointing in a randomly assigned, fixed direction. By analyzing dynamical quantities, we measure the critical active force at which the system melts and verify whether the disordered solid state is stable against a persistent active force as the system size increases. We extend our study to investigate the melting of disordered chiral persistent active particles and compare our results to the crystalline counterpart [2].

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Deformation of Microtubule Bundles by External Mechanical Stress

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Microtubules (MTs) are essential cytoskeletal filaments that provide structural support and serve as tracks for intracellular transport. In cells, especially in axons of neurons, MTs are flexibly crosslinked by MT associated proteins to form continuous bundles. While the behavior of single MT under mechanical stress has been extensively studied, the dynamics and functional implications of MT bundles to understand their roles in maintaining cellular architecture and to adapt to mechanical stresses remain less understood.

Here, we investigate the effect of mechanical deformation on MT bundles, focusing on how tensile and compressive forces influence their structural integrity in comparison with single MT. Using in vitro reconstitution assays on micro-stretcher combined with fluorescence microscopy, we demonstrate that MT bundles exhibit distinct mechanical properties compared to individual filaments, including enhanced resistance to buckling under compressive forces and fragmentation under tensile stress. We reveal that the MT bundles exhibit strain rate-dependent mechanical behavior indicating their viscoelastic nature which was not observed in the case of single MT. We explain these findings by a viscoelastic model. These results provide new insights into the mechanobiology of MT bundles and their role in cytoskeletal mechanics, potentially enabling cellular adaptation to mechanical stresses.

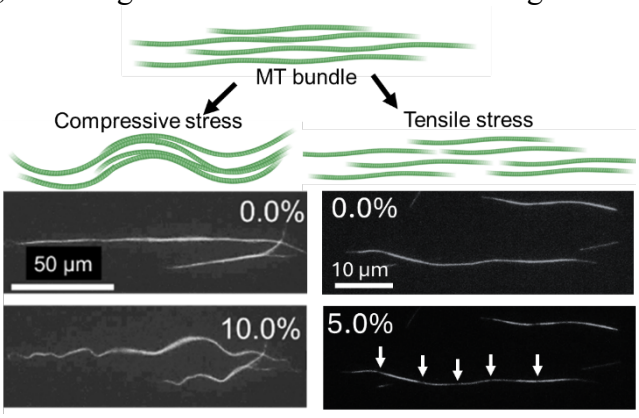

Figure: Microtubule bundles subjected to compressive stress (Left) and tensile stress (Right). White vertical arrows indicate the breakage in the bundles.

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Mobility of an active particle in dense passive colloids

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The cell cytoplasm harbors a dense population of macromolecules, constituting 20 – 40 % of the total volume of the cell [1]. Additionally, it suspends mesoscopic colloidal components, including organelles and condensates formed via phase separation [2]. Thus, active agents such as motor proteins should migrate in the environment crowded with nano-particles to maintain cell functions.

Recent studies have focused on the dynamics and mechanical properties of densely packed active matter, often referred to as active glass [3]. A key characteristic of active matter is that each component generates active forces, leading to non-thermal fluctuations that can surpass the thermal fluctuations of the system. These non-thermal fluctuations could induce fluidization of active colloids. However, it is still unclear how an active agent efficiently moves in passive dense colloids using self-generated non-thermal fluctuations.

To address this, we conducted 2D Brownian dynamics simulations to investigate the mobility of a particle exhibiting non-thermal fluctuations within passive colloids near the glass transition point (Fig. 1 (a)). Mobility $M = \langle v \rangle_t / F$ was calculated by applying a constant force F to the particle, where $\langle v \rangle_t$ represents the time-averaged velocity of the particle. Figure 1 (b) illustrates the trajectories of 20 passive particles (without non-thermal fluctuations) under a steady pulling force. The particles exhibit intermittent, step-like motions due to the applied force. In contrast, Fig. 1 (c) demonstrates that when the particle is active (experiencing non-thermal fluctuations), the frequency of step-like motions increases significantly, resulting in faster movement. This suggests that the non-thermal fluctuation of a particle enhances the rearrangement of surrounding particles. Figure 1 (d) compares the mobility of particles with different types of non-thermal fluctuations, where ABP, Vib, and Vibn represent active Brownian particles and particles with sinusoidal vibration parallel and perpendicular to the pulling force, respectively. The labels "1s" and "33s" indicate the persistence time or oscillation period of the non-thermal fluctuations. The data reveal that high-frequency fluctuations and those perpendicular to the pulling force are less effective in enhancing particle mobility in dense colloids. This suggests that specific types of locally generated non-thermal fluctuations are particularly effective at facilitating particle transport in crowded environments.

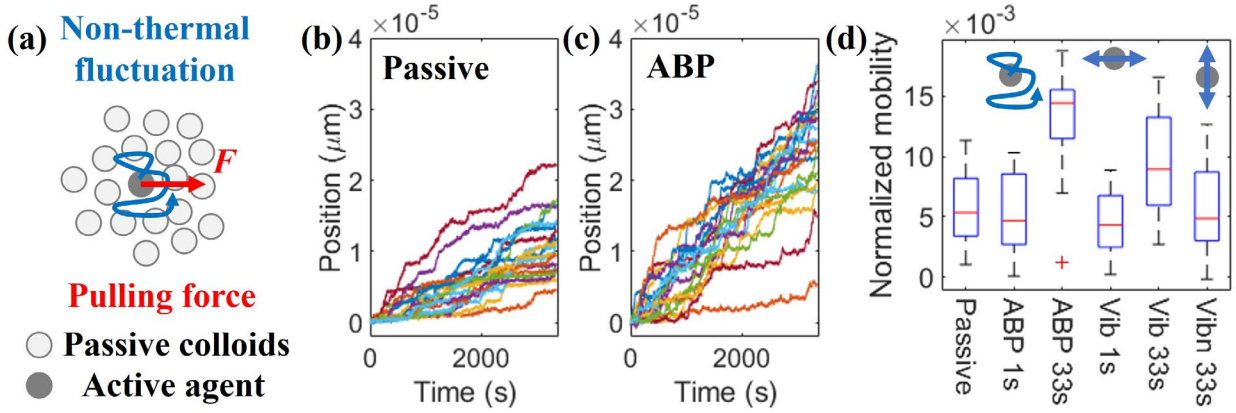

Figure 1. (a) Schematic illustration of the numerical simulation. (b, c) Trajectories of passive and active Brownian particle (persistent time 33 s) under pulling force. (d) Mobility of the particle with/without non-thermal fluctuations. Mean square of active force $\langle f_a^2 \rangle_t$ is identical among ABP, Vib, and Vibn.

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Photo-excited micro-droplet robotics

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Experimental results are presented on the behavior of micro-droplet robots by laser light irradiation. The laser-driven droplets interact with each other and show something that seems to be like collective behavior. We aim to observe various behavior of the droplets by changing parameters. We discuss how this behavior is caused and suggest the very new agent of collective behavior.

A mixture of a volatile, low surface tension liquid (ethanol) and a nonvolatile, high surface tension liquid(PEG200) is sandwiched between a glass substrate and a substrate with gold thin layer (25nm). When the laser beam is focused and irradiated to the bubbles in the mixture sandwiched by substrates, single droplet is formed on the laser spot. This is because the ethanol evaporates preferentially due to the heat by laser and the concentration of PEG comes to be higher locally around the laser spot. PEG has so high surface tension that it gathers the liquid from surroundings and form a droplet(Marangoni convection). The droplet rotates and vibrates around the laser spot. This phenomenon is thought to result from the saturation of ethanol gas. The gas evaporates intensely on the laser spot and saturates. Thus the droplet move and change the shape to avoid saturation. So far we use 2 laser spot, but this time we make multiple laser spot and observe the complex interaction of several droplets. If the vibrating droplets get close each other, they have the same vibration frequency. We think this is because the droplets exchange their body and they have the same volume. Such behavior is a crucial factor when considering flock of nature and biological system. In this report we discuss the physical principles of synchronization phenomenon and suggest the very new liquid robots.

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Activity-induced diffusion recovery in crowded colloidal suspensions

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In crowded colloidal systems, the normal diffusion of colloids is observed for shorter time scale than the mean free time of collisions. The diffusion becomes sub-diffusive for longer time scale due to the cage effect, i.e., the mean square displacement (MSD) is not proportional to time duration t but t^{α} where the index α satisfies $0 < \alpha < 1$. Further longer time scale, the diffusion becomes normal again since the colloids can escape from the cages. In cells, the diffusion is an important substance transport process, where the crowdedness cannot be ignored. The biochemical reaction also can affect the diffusion but its effect is nontrivial.

To clarify the effect of crowdedness and chemical reaction, we have studied the diffusion of Brownian particles in the enzyme catalysis of urease and urea [1]. The enzyme was introduced in the aqueous phase or on the surface of the particles. As the experimental results, it has revealed that the diffusion is enhanced by the enzyme catalysis; Both of the MSD and the index α becomes greater. To discuss the detailed mechanism, we have modeled the system by the two-dimensional Langevin dynamics. The enzyme was modeled as the dimer, and we supposed that its conformational change during the enzyme catalysis can be approximately reproduced by the dimers' length oscillation. We also assumed that the Brownian particles interact mechanically with the enzymes. We simulated the multibody system of the Brownian particles and enzymes, and compared with the experimental results.

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