What do biological and production networks have in common?

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We will discuss the differences and communalities of biological and production networks. Two case studies will be presented: i) Self-organizing Kanban production analogous to the synchronization of enzyme molecules leads to smoother production cycles, ii) discrete event simulations allow to extend traditional methods for modeling stochastic biochemistry to study the dynamics of single molecule enzyme reactions. Steps towards the goal of developing tools to understand functional networks in biology, production systems and logistics and to determine their common structures are outlined.

Modelling of experience dependent behavior - Fighting among male crickets

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Animals have evolved nervous systems to adapt changing environment. Insects have rather simple and identical nervous systems than mammalian brain. Thus insects must be good model animals to reveal neuronal mechanisms underlying adaptive behavior. They perceive signals as stimulation from environment and they adjust their behavior. They do not always respond the same way to the same external stimuli. The state of central nervous system must be dependent on their experiences as well as internal and/or external conditions. These factors would mediate threshold of introducing a behavior or behavioral pattern. Insect neuroethology has already provided valuable insight into how nervous systems organize and generate sophisticated behavior. It has made important contributions to brain science researches, expanding our overall understanding of sensory and motor systems. However, numbers of mechanisms to understand how adaptive behavior emerges have been still remained unclear.

One of the common goals of biologists and robotics researchers must be to understand how nervous systems adapt animal behaviors to the changing environments. For further elucidation, we combine neuronethological approaches and engineering approaches by constructing dynamic model to understand neuronal mechanisms of socially adaptive behavior.

It is important topic to investigate social adaptation in animal behavior. Previous social experience such as mating behavior and agonistic behavior must drastically mediate following behavior. We have focused on insect agonistic behavior using male crickets to understand how animals establish social organization and how they emerge adaptive behavior in the society.

Fig. 1. Fighting between male crickets.

Cricket aggressive behavior is one of the pheromone behaviors released by cuticular pheromone on the surface of cricket body. The main components of the cuticular substances are hydrocarbons. The male and female cuticular pheromones introduce different behaviors in male crickets. When male crickets encounter a female to perceive female pheromone, they start courtship behavior. When they, on the other hand, encounter conspecific male, they introduce agonistic behavior (Fig. 1). The interaction usually escalated to hard fighting. After the fighting, the dominant (winner) starts aggressive song with chasing after the loser (subordinate). The subordinate crickets wouldn't fight again against other male crickets more than 1 hr. This indicates that cricket behavior can be modified by the

previous experiences. How do subordinate animals retain the previous experiences and change their behaviors after they lose the fighting? We have investigated neuronal mechanism of the cricket agonistic behavior. Behavioral and pharmacological experiments suggest that NO generation in the brain could play important role on the formation of dominant hierarchy. We also hypothesize that NO-cGMP system could regulate biogenic amines in the brain to meditate aggressive behavior of the crickets. In order to understand dynamic activities of the cricket's brain, we are trying to construct a neuronal circuit model based on biological experiments. We consider neuromodulators in the neuronal model that consists of a diffusion equation for NO level, differential equations for biogenic amine levels and a threshold model for behavior selection.

We have also constructed a cricket behavior model based on behavior experiments. First of all, observation ability and motion ability of artificial cricket are assumed based on animal behavior. The behavior of the artificial crickets was described by using a probability that is defined by the parameter α. A personal field of an artificial cricket was defined and the behavior was simplified to three major primitive patterns that were wandering, avoiding and fighting. Artificial cricket fight each other when they encounter other agents. After fighting, subordinate turns and escapes from dominant opponent and avoid them for a while. On the other hand, dominant retreat others from its personal field. Animals change their behavior based on their experiences. Hence, we need at least one internal state variable for the cricket model. The probability (P) of losing at cricket fighting depends on a parameter α that runs from 0 through 1. The parameter α describes an internal state of the cricket. We determined this parameter from the behavior experiments of crickets. The value of α gradually decrease depending on time. Losing at fight increases the value of α, but winning at the fight decreases the value of α.

$$P = \alpha (0 \le \alpha \le 1) \tag{1}$$

The value of α is revised with the following equation.

$$\alpha_{n+1} = (1-\omega)\alpha_n + \varepsilon_{lose}\eta_{lose} - \varepsilon_{win}\eta_{win} \tag{2}$$

Here,

$$\eta_{lose} = \begin{cases} 1 & \text{if lose} \\ 0 & \text{else} \end{cases}, \eta_{win} = \begin{cases} 1 & \text{if win} \\ 0 & \text{else} \end{cases}$$

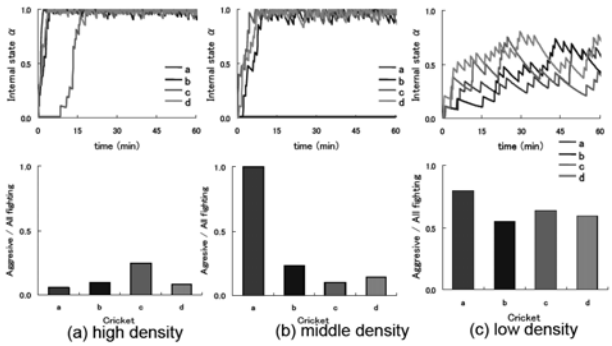

Fig. 2. Simulation results of the artificial cricket behavior. Three kinds of fields (128×128(pix), 256×256(pix) and 512×512(pix)) are utilized for simulations. The number of crickets was fixed to four. In case of higher density, the value of α converged to rather high and most of all avoided from others. In case of the middle density, one of the crickets increased the α value to become the dominant. In case of the low density, α did not converge. The aggressiveness of each cricket becomes similar and α value is not so low.

We simulated how crickets change their behavior depending on the density of animal population (Fig. 2). The simulation results are similar to that of behavior observation results of crickets, suggesting that the parameter α would contain internal model that must be neuronal modulation system in the animals. Adequate parameter tuning in the simulation model also suggests that cricket behaviors among males were mainly influenced by the previous fighting experience, in particular previous losses.

A Mathematical Model of Amoeboid Locomotion

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Amoeboid locomotion is widely observed in the single cell movement. In this paper, we concentrate on the locomotion of the naked amoebae which are crawling around on the substrate. An amoeba extends the part of its body to the direction of movement, which is called pseudopod. Cytoplasm of the amoeba is composed of the gel layer under the cell membrane and the cytosol exhibiting a strong flow. During the locomotion, contraction of the actomyosin fibers produce a power, a part of the cell is extended, and also sol-gel transformation is taking place. To guarantee the normal amoeboid locomotion, lots of processes are going simultaneously in the coordinated manner. A mathematical model is presented, in which we adopt the combination of the two models of different type, the one is a phase field model and the other is a smoothed particle hydro-dynamics (SPH). Phase field is used as an expression of cell membrane since the phase filed model is quite tough to the large deformation of interfaces. Also, SPH particles are used for the expression of gel phase and sol phase, which are considered to be two type of fluids with different mobility. We will demonstrate simulations of our model which reproduce realistic amoeboid locomotions.

Large scale movement on spatial networks: from the global cargo shipping network to bird migration

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Bioinvason, either as the spatial spread of infectious diseases or as the invasion of exotic species into new habitats, constitutes one the major aspects and challenges of a globalized world. The dynamics of bioinvasion ultimately is related to the spatial movement of individual organisms, which are frequently able to bridge large distances, either on their own or mediated by human transportation (e.g. ships or airplanes).

The presentation emphasises the role of complex spatial networks for understanding the movement of biological organisms on a global scale. This is illustrated with two case-studies. First, we investigate the global network of cargo ship movements. We use information about the itineraries of 16,363 cargo ships in 2007 to construct a network of links between ports and show that the network has several features which set it apart from other transportation networks. The second example studies a network model for bird migration, i.e. the seasonally driven movement of birds between wintering and breeding areas. The analysis is based on ring recovery and satellite telemetry data of the white stork (Ciconia ciconia). We propose a stepping stone model for global avian migration which describes a number of discrete breeding, resting and wintering sites which are linked by a network of fast, directed migratory flight routes. The stochastic transitions of individual birds between different habitat patches are described as seasonal functions of time. The model can be generalized to the problem of transport on a complex network where each directed link is associated with a complex number describing the strength and seasonal phase of transportation along this link.

Generalized models: Analyzing the dynamics of diagramatic representations of complex heterogeneous networks.

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To investigate the dynamics of large heterogeneous networks is an important challenge in many areas of science and technology. In many cases the structure of the system, i.e., the topology of the network, is well known, while only limited information on the precise nature of interactions is available. An example of such a system is for instance an ecological food web, in which we know who-eats-who, while the amount of prey that is consumed is very difficult to describe by a specific mathematical function. In generalized models we therefore avoid to restrict processes to specific functions, Instead, a given generalized model describes the class of all dynamical systems that are consistent with a given diagramatic representation of the network. A normalization procedure is used to capture all information that is necessary to determine the local dynamics around all steady states of the system in a number of meaningful parameters.

Local bifurcation theory is then used to identify important parameters, compute the thresholds at which local stability is lost, and extract certain insights on global dynamics. In this talk I will illustrate generalized modelling with examples from different disciplines, including an ecological model with several hundred unknown parameters.

A step toward understanding the principle of biological networks

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The world is composed of unavoidable and specific interactions. A network in the world is a shadow of such interactions (*idea*) and it opens a window on how it has been composed.

We have been investigated protein-protein interaction network (PPI) of the yeast based on the yeast two hybrid assay (Y2H). It is well known that Y2H may include many false-positives, however Y2H becomes de-facto standard for investigating the PPI.

It has been considered that topological structure of the PPI is different from other networks such as social networks, World Wide Web and so on. However, we confirmed that topological structure of the PPI is no different from other networks. In order to investigate the topological structure of networks, we developed a method, which stratifies the network according to the degree of each node (the network stratification method). By using this method, we confirmed that topological structure of the PPI does not have unique topological structure.

As we mentioned, since Y2H is not appropriate for a shadow of *idea*, we investigate protein-glycan interactions. Around fifty percent of proteins are modified by glycans that mediate protein-protein interactions *in vivo* and protein-glycan interactions have been precisely examined in Biochemistry. We regenerate PPI from the experimental data of protein-glycan interactions. We speculate the principal of these interactions.

Mathematical Model for the Foraging Tactics of Ants Colony under Unsteady Food Supply

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A mathematical model for the foraging behavior of ants colony is considered which gives two kinds of characteristic features: i) Shape of foraging trail is varied depending on the feeding schedule to realize optimal foraging under each schedule. ii)The heterogeneity of a colony provides more efficient foraging than the homogeneous case, here the heterogeneity means the inclusion of proper number of pheromone-insensitive ants within the colony. In the present lecture we show some details of numerical results and simple mathematical analysis for the above model, and the rest of time is devoted to discuss on the more general relation between heterogeneity of a group and its efficiency.

Towards Synthesis of Mammalian Circadian Clocks

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The logic of complex and dynamic biological networks is difficult to elucidate without comprehensive identification of network structure[1-3], prediction and validation based on quantitative measurement and perturbation of network behavior[4] and, ultimately, design and implementation of biological networks driven by the same logic as the original network. Mammalian circadian clock is such a system consisting of complexly integrated regulatory loops composed of 20 transcription factors, and three type of DNA elements[1,2] including "morning" element (E-box), "day-time" element (D-box) and "night-time" element (RevErbA/ROR binding element, RRE), and displaying the intriguing dynamical properties such as temperature independence of oscillatory period over the wide range of temperature.

In this symposium, I present current progresses in the design and implementation of the three type of DNA elements, and transcriptional networks governing the day-time and night-time transcriptional programs[5,6]. I will also present our on-going research activities on the design/implementation of evening and morning transcriptional programs, as well as the reconstruction of temperature-compensation.

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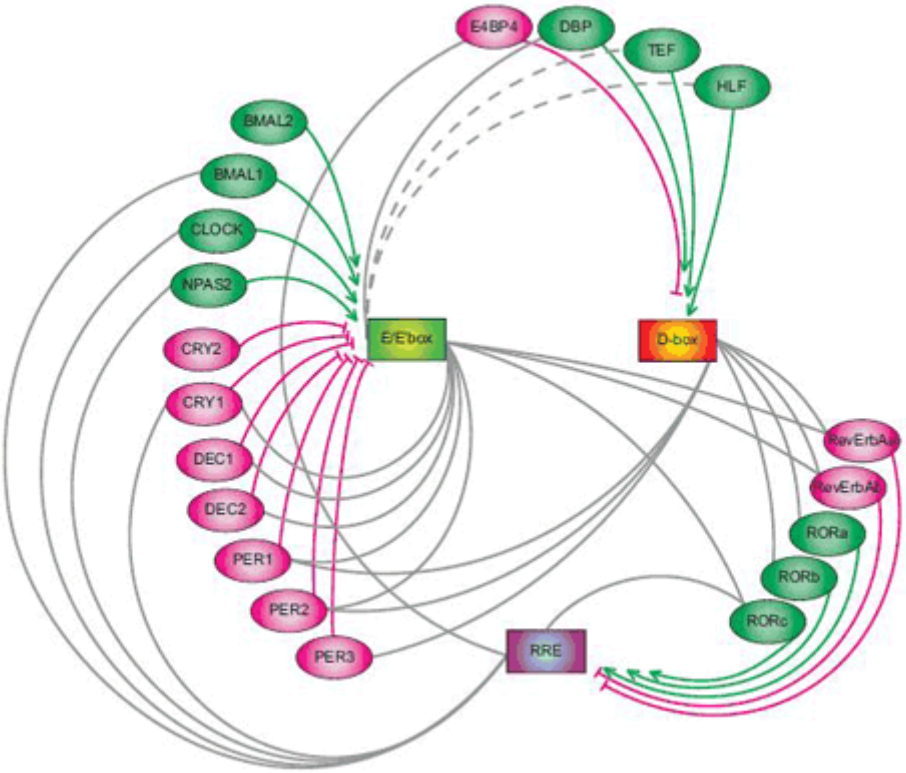

Figure1. Scheme of identified transcriptional network for mammalian circadian clocks (Reference 1,2,3, 6)

Oblique collisions in dissipative systems

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Spatially localized patterns are ubiquitous such as chemical blobs, discharge patterns, morphological spot, and binary convection cells. When they are moving in space, it is unavoidable that they collide each other, and the generic manner of collision becomes oblique.

Unlike the solitons of conservative systems, there are much more variety of outputs after collisions in dissipative systems, in fact, repulsion, annihilation, coalescence, and splitting are observed depending on the parameters. Moreover, for oblique case, it also depends on the incident angle. In order to understand the complicated transient collisional process of traveling spots, it is imperative that we have to overcome the difficulty of large deformation at collision.

A new approach is presented to clarify a backbone structure behind those dynamics. A key ingredient lies in a hidden network of unstable solutions called scattors, which plays a crucial role to understand the input-output relation for collisional process. A remarkable thing is that there appears a time-periodic rotational motion as a scattor for oblique collision. This approach is also useful to understand the dynamics of traveling spots in heterogeneous media. This is a joint work with T. Teramoto, K.-I. Ueda, Yuan Xiaohui, and K. Suzuki.

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Evolutionary engineering of complex functional networks

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From a single cell to the brain and the human society, functional dynamical networks play a fundamental role. The networks which are a product of natural evolution have properties far exceeding those of rationally designed networks, currently used in industrial manufacturing, transportation logistics or information processing systems. In this talk, I show how evolutionary optimization methods can be used for engineering of efficient artificial functional networks. As examples, design of flow distribution networks which are robust against local damage, construction of networks with prescribed dynamics, and design of easily controllable oscillator networks are considered.

Network evolution of body plans: a modeling approach for evolutionary developmental biology.

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One of the major goals in evolutionary developmental biology is to understand the relationship between gene regulatory networks and the diverse morphologies and their functionalities. Are the diversities solely triggered by random events, or are they inevitable outcomes of an interplay between evolving gene networks and natural selection? Segmentation in arthropod embryogenesis represents a well-known example of body plan diversity. Striped patterns of gene expression that lead to the future body segments appear simultaneously or sequentially in long and short germ-band development, respectively. Moreover, a combination of both is found in intermediate germ-band development. Regulatory genes relevant for stripe formation are evolutionarily conserved among arthropods, therefore the differences in the observed traits are thought to have originated from how the genes are wired. To reveal the basic differences in the network structure, we have numerically evolved hundreds of gene regulatory networks that produce striped patterns of gene expression. By analyzing the topologies of the generated networks, we show that the characteristics of stripe formation in long and short germ-band development are determined by Feed-Forward Loops (FFLs) and negative Feed-Back Loops (FBLs) respectively, and those of intermediate germ-band development are determined by the interconnections between FFL and negative FBL. Network architectures, gene expression patterns and knockout responses exhibited by the artificially evolved networks agree with those reported in the fly *Drosophila melanogaster* and the beetle *Tribolium castaneum*. For other arthropod species, principal network architectures that remain largely unknown are predicted. Our results suggest that the emergence of the three modes of body segmentation in arthropods is an inherent property of the evolving networks.

Synchronization effects in transportation networks with biologically inspired self-organized control

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The efficient and reliable operation of material flows in transportation networks is a subject of broad economic interest. Traditional approaches to controlling such networks are however known to have severe disadvantages: centralized controllers suffer from their high computational demands that make an on-line control hardly possible in larger networks, while a decentralized control using clearing policies leads under rather general conditions to instabilities. As an alternative approach that may help overcoming these problems, a self-organization mechanism of conflicting flows is proposed which is inspired by oscillatory phenomena of pedestrian and animal flows at intersections or bottlenecks. The proposed method allows sequentially serving the different flows at an intersection in a fully demand-dependent way.

The presented approach yields a self-organization of alternating traffic flows at the different intersections of a transportation network using only "local" information about the status of neighboring intersections. The resulting oscillatory service dynamics is further characterized in terms of synchronization. For simple grid topologies, different synchronization regimes are found depending on the inertia of the switching from one service state to the next one. This multiplicity of synchronization windows may be understood as the result of two concurring time scales (free-flow traffic time and intrinsic cycle time of the controller) in the system. Although the basic approach considered here does not necessarily yield an optimum solution to the problem of network flow control, it is demonstrated that it can be modified in a way that allows reducing queue lengths, delay times, and their variations in terms of a flexible coordination principle.

Jamology – Research on jams of self-driven particles

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Jamming phenomena are seen in various kinds of flow, such as vehicles on highway, pedestrians in a corridor, data packets in internet and productions in a supply chain network. Jamology is an interdisciplinary research of analyzing and solving these jams. In this study, vehicles and pedestrians, etc., are all regarded as self-driven particles, which are active particles and do not satisfy the Newton's laws in general. The dynamics of these particles are studied by using rule-based models such as cellular automata.

In the talk, starting from the background of this research, a simple mathematical model, called the asymmetric simple exclusion process, is introduced as basis of all kinds of traffic flow. Then it is extended in order to account real traffic phenomena, and the comparison between theory and experiment is shown. It turns out that models are able to capture fundamental features of observations. Some solutions of traffic jams are also shown and investigated in detail by numerical simulations and experiments.

Consistency Principe for Robust Biological Systems

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ERATO Complex Systems Biology, JST

Biological system generally consists of a hierarchy of different levels, each of which is under stochastic dynamics. We propose consistency between different levels, as a guiding principle to understand such system, and apply it to unveil general relationship between genotype and phenotype that allows for evolution of robustness in developmental process.

First, proportionality among evolution speed, phenotypic plasticity, and isogenic phenotypic fluctuation is derived as an extension of fluctuation-response relationship in physics. Following an evolutionary stability hypothesis we then derive a general relationship between phenotypic fluctuation and genetic variance. As these variances work as indices for developmental and mutational robustness, the relationship suggests a link between robustness to mutation and to noise, and sets a general condition for the evolution of robustness. The obtained relationship is confirmed in models of gene expression dynamics, as well as in laboratory experiments in bacterial evolution. Relevance of the relationship to design of robust dynamical systems is briefly discussed.

If I have time, I hope to discuss a novel, general adaptation mechanism in a cell that does not rely on specific signal transduction network but takes advantage of the stochasticity in gene expression, and also robustness in developmental process in relationship with interaction mediated control of chaotic gene expression dynamics.

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The logistics of metabolism

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The network of metabolic reactions in a cell is responsible for providing a wide range of substances at the right time in the right proportions. The logistic challenges are quite remarkable: How does the system ensure robustness with respect to perturbations? How can the system react rapidly to important changes in its environment? Here I explore metabolism from a logistics perspective. In particular I discuss relations between topology and dynamics in metabolic networks and describe heuristics to predict the system's reactions to perturbations and changes in the environment. These heuristics are compared with simulations based on flux-balance analysis.

Control of hybrid systems: a new framework for control of complex systems

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A hybrid system is defined as a dynamical system composed of discrete dynamics and continuous dynamics, where the discrete dynamics are usually expressed by finite automata and the continuous dynamics are by ordinary differential equations. The class of this system includes a lot of kinds of dynamical systems such as power-train systems, car engines, electric power systems, chemical plants, robots, biological networks, and communication networks, and so on. Since 1990's various approaches to modeling, analysis, and control synthesis of such hybrid systems have been extensively developed within the computer science community and the systems and control community from the different points of view, and currently this field is considered as one of the most significant and prospective research topics in the systems and control community.

This talk provides an introduction to control theory of hybrid systems. After the overview of this research field is given, several research topics on well-posedness (uniqueness of solution), controllability, and optimal control synthesis are explained together with examples of iron reheating process, gene regulatory network, and robot walking, etc.

Collective molecular motor using chiral liquid crystalline thin films

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Chirality often plays a decisive role in determining structures and properties of liquid crystalline phases. In certain circumstances, the chirality, macroscopic and molecular, can also manifest itself in dynamical behaviors. 100 years ago, Lehmann was the first to observe an unusual nonequilibrium dynamics of a chiral nematic liquid crystal subjected to a temperature gradient, now referred to as the Lehmann effect, in which the liquid crystal director makes a continuous precession at an angular velocity proportional to the magnitude and sign of the temperature gradient. In recent years, there is a resurgence of interest in the Lehmann effect, partly inspired by the authors' discovery of mass flow-induced continuous precession of molecules in monomolecular thick film (Langmuir monolayer) of chiral liquid crystals [1], which may serve as a collective molecular motor. Given the absence of macroscopic twist in Langmuir monolayers, a naive interpretation of this phenomenon is that the chiral molecule behaves like a propeller placed in mass flow (typically water molecules), and the angular momentum at the molecular level is transferred to the macroscopic director rotation by a mechanism which we do not understand yet. I shall review the present state of our understanding of this phenomenon drawing on our recent experimental and simulation studies.

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Self-propelled particles with nematic interactions: From simple agent-based models to experiments with rod-shaped bacteria

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Co-workers: F. Peruani, F. Ginelli, H. Chate (ICS Paris), A. Deutsch, J. Starruss (TU Dresden), V. Jakovljevic, L. Sogaard-Andersen (MPI Marburg)

Self-propelled, polar particles with polar, “ferromagnetic” interactions as well as apolar particles with apolar, “nematic” interactions have been studied extensively within recent years. Here, we address a third case that mixes properties of these systems: self-propelled, polar particles with apolar, nematic interactions. First, we study collective phenomena in a simple two-dimensional stochastic system of self-propelled particles (SPP) interacting locally through an apolar, nematic alignment mechanism [1]. Extensive simulations show that there are four qualitatively different regions of spatial organisation. At high noise intensity, disordered spatially homogeneous distributions are found, while at low noise intensity long-range nematic order is found. For intermediate noises and large enough system size, the system segregates into macroscopic areas of high and low density. The high density areas take the form of bands that can take on stable straight shapes or can be dynamically changing depending on the size of the system, band width and noise intensity. A second more detailed model consist of self-propelled rods interacting through volume-exclusions in two dimensions. Herein, nonequilibrium clustering is observed in simulations and rationalized with a mean-field theory [2].

A suitable experimental realization of self-propelled particles with nematic interactions are gliding rod-shaped bacteria on a substrate. Such bacteria – as other microorganisms - exhibit a transition to multicellularity which starts with the onset of clustering and aggregation. We have studied the combined effects of active, adventurous motion and anisotropic cell shape in assemblies of a mutant strain of myxobacteria that exhibit neither social motility nor so-called C-signalling. We observe a transition to clustering and collective motion, that is presumably caused by simple physical volume-exclusion interactions only. Our results show that in gliding bacteria, the combination of anisotropic cell shape and active motion, leads to an primitive effective alignment mechanism. The transition to clustering is correctly predicted by the hard-rod model in [2] and verified by comparison of cluster-size statistics predicted by the model with corresponding statistics taken from experimental data.

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Splashes by a frog diving into water

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Types of splash generated by a frog diving into water were investigated experimentally by using a high speed CCD camera. The type of splash depends on diving speed, characteristics of surface material of a body and body shape. To categorize types of splash, I also observed splashes by impinging bodies with different shapes. Fluid dynamics related to formation of splash is discussed in the presentation.

Integrated study of insect flight: from aerodynamics, maneuverability to optimization

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How can insects fly freely as they do? A simulation-based study may answer this simple but complicated question. We have developed an integrated and rigorous simulator for modeling flapping-wing bio-flights. This simulator is very versatile, easily integrating the modeling of realistic wing-body morphology, realistic flapping-wing and body kinematics, and unsteady aerodynamics in insect flight; and of evaluation of flapping energetics on inertial and aerodynamic forces, torques and powers. The simulator is further coupled with a multi-body dynamics solver and a complex method-based optimization algorithm. Application to the integrative evaluation of the aerodynamics with/without fluid-structure interaction (FSI), the maneuverability and the optimization in hovering and/or forward flights of insects demonstrates its feasibility in modeling realistic bio-flights of insects and birds and also points to its importance in the design of micro air vehicles.

Fluid dynamics of a suspension of micro-organisms

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Micro-organisms play a vital role in many biological and medical phenomena; such as plankton blooms in the oceans that affect the oceanic ecosystem, bioreactors for medicine or food, human digestion assisted by enterobacteria. It is known that systems of swimming micro-organisms exhibit an interesting variety of collective behaviour such as clustering and migration; examples include coherent structures of swimming bacteria. The mechanism of these collective behaviours is still not well understood, and currently one of the most active research areas in biophysics. In this lecture, I will explain how swimming micro-organisms, such as Paramecia, Volvox and bacteria, interact in a suspension, and how the interaction can be modelled computationally. I also will explain how the suspension properties, such as the rheology and the diffusion, are affected by the interaction of micro-organisms. Interestingly, the simulation results illustrate that various coherent structures, such as aggregation, meso-scale spatiotemporal motion and band formation, can be generated by purely hydrodynamic interactions between micro-organisms.

Theory of flapping flight using vortices

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I will show recent results of the theoretical study on 2D flapping-flight problem [1]. First I will introduce a generalized Blasius formula, an exact formula for a force that acts on a moving body, based on the incompressible Navier-Stokes equations. Then, using this formula, I will show that the time-averaged force can be calculated solely in terms of the time-averaged far-field flow if the flow is temporally periodic. Applying this result, a paradox concerning the flight of insects is identified, that is, insects maintaining their bodies in a particular position (hovering) cannot, on average, generate hydrodynamic force if the induced flow is temporally periodic and converges to rest at infinity. On the basis of these assumptions, the relationship between this paradox, numerical results, and real insects that actually achieve hovering will be discussed.

Reference:

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Single molecule nanoscience: Fluctuation and function of life

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The aim of our research is to reveal the engineering principles inherent in adaptive biological systems by uncovering the unique functions of biological molecular motors. My specific interest is the molecular motors in muscle, which are considered to be standard molecular motors, having used single molecule nano-detection to study their dynamics. Here, I will explain how molecular motors do not overcome Brownian motion (thermal noise) but rather exploit it to economize their use of energy. Furthermore, our computer simulations show that a system based on stochastically fluctuating molecular motors can modulate its motion with a high degree of flexibility and adaptability, all in response to its environment. We are currently applying these results to develop artificial muscle.

Coordination of Cell Shape and Motility in Spontaneous Cell Migration

Masaki Sano
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There is growing interests in self-propelling systems ranging from artificial self-driving particles to migrating biological cells. Understanding dynamics and mechanism of cell motility is an important issue in cell biology. Yet only little is known about how cells change their own shape and how cells coordinate shape dynamics and movement. I will present our recent study on cell shape dynamics and motility during spontaneous cell migration. We found ordered pattern dynamics; elongation, oscillation, and rotation in seemingly random shape dynamics of Dictyostelium cells. These ordered patterns appear in the absence of external stimuli. We found that the emergence of these ordered patterns are related to spontaneous localization of molecules, PTEN, Pi3K and F-actin. The polarization due to spontaneous localization of molecules breaks symmetry in cell adhesion strength on the substrate. We compare these results with the stress distribution exerted by cells to the elastic substrate measured by traction force microscopy. I will also discuss how cell uses the switching among different ordered patterns to ensure overall exploration.

Dissipative patterns in heterogeneous BZ systems.

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It is well known that a homogeneous BZ system usually exhibits trigger waves that form target or spiral waves. Nano-heterogeneous BZ-AOT system, which is a BZ system dispersed in water nano-droplets of aerosol OT reversed microemulsion, demonstrates a zoo of dissipative patterns like Turing structures, standing waves, localized patterns, and different types of propagating waves (dash-waves, jumping waves, accelerating waves, anti-waves, and chaotic waves). If we significantly increase the radius of water droplets swimming in the continuous oil phase up to tens of micrometers, then the direct communication between droplets due to fusion-fission process is no longer possible and BZ droplets can communicate only through oil-soluble molecules like Br_2 and BrO_2 radical. This is similar to synaptic communication through special signaling molecules (neurotransmitters) or similar to chemoattractants and chemorepellants in chemotaxis. An ensemble of coupled BZ microdroplets is able to demonstrate complex synchronous behavior. We have found Turing-like patterns and anti-phase oscillations in 1D (D = dimension) configuration, as well as several oscillatory patterns in 1.5D and 2D geometry. We compare patterns found in different heterogeneous BZ systems and analyze a possibility to use coupled BZ droplets for a chemical computer.

Deformable self-propelled particles

Takao Ohta
Department of Physics, Kyoto University

A theory of self-propelled particles is developed in two dimensions assuming that the particles can be deformed from a circular shape when the propagating velocity is increased. A coupled set of equations in terms of the velocity and a tensor variable to represent the deformation is introduced to show that there is a bifurcation from a straight motion to a circular motion of a single particle. Dynamics of assembly of the particles is studied numerically where there is a global interaction such that the particles tend to cause an orientational order. A transition from a localized state to a delocalized state of the particles and a crossover from diffusion to ballistic motion are discussed.

Reference:

[1] T. Ohta and T. Ohkuma, arXic:0811.3281v1 [cond-mat.soft] 20 Nov. 2008

Hypotheses on the functional roles of chaotic transitory dynamics

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In contrast to the conventional static view of the brain, recent experimental data show that an alternative view is necessary for an appropriate interpretation of its function. Some selected problems concerning the cortical transitory dynamics are discussed. First, we propose five scenarios for the appearance of chaotic itinerancy, which provides typical transitory dynamics. Second, based on the concepts of chaotic itinerancy, Milnor attractors, and Cantor coding, we present nine hypotheses on the formation of dynamic memory and perception, focusing on the dynamics embedded in data and the dynamical interpretation of brain activity within the framework of cerebral hermeneutics. These hypotheses may account for dynamic functional processes such as episodic memory and the itinerant process of cognition. These hypotheses also clarify the biological significance of the chaotic activity observed in the brain.

Synchronization of a circadian clock in vitro.

Hiroshi Ito
Ochanomizu University, Academic Production

Circadian rhythms are the physiological oscillations with about 24 h periods that show the period stability under various circumstances. While the transcription/translation feedback loop system has been proposed for the model of the origin of the circadian oscillation, my colleagues and I had proposed an alternative model. The cyanobacterial circadian clock can be reconstituted *in vitro* only by mixing the three clock proteins, KaiA, KaiB, and KaiC, with ATP. Namely, the ratio of phosphorylated KaiC oscillates every 24hr in the mixture. This simple biochemical reaction shows self-sustained oscillation as the Belosov-Zhabotinsky reaction. In this presentation, I will discuss synchronization of this “in vitro clock” between KaiC molecules and entrainment by temperature cycles.

I examined the robustness of the KaiC phosphorylation rhythm by mixing together samples with six different oscillation phases and then monitored rhythm of the mixture. I found that immediately after mixing the samples, the overall KaiC phosphorylation of the mixture showed a rhythmic pattern with an amplitude comparable to those observed for the original, individual samples.

I also examined the entrainment of in vitro clock by temperature cycle. This oscillatory system has a prominent property, period of temperature compensation. Though that property is thought to imply insensibility to temperature, I observed the temperature cycle of 30 ºC and 45 ºC can entrain the in vitro clock. In my talk, we will discuss the issue how the in vitro clock acquires the both property, temperature compensation and entrainment.

Nonequilibrium Phase Transition to Synchronization in Small World Networks of Phase Oscillators

Ralf Tönjes[1)] ,
Hiroshi Kori[1),3)] and Naoki Masuda[2),3)]
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We have studied directed networks of identical phase oscillators with and without driving by a pacemaker. Depending on the link density of the network we have found that the driving can excite a nonequilibrium state of complete desynchronization or partial synchronization which persists independently of the periodic forcing. It coexists with the state of complete synchronization of the identical oscillators which is always stable. Upon variation of the link density or another system parameter (nonisochronicity) we observe transitions between complete desynchronization, partial synchrony and complete synchronization. We present the results of extensive numerical simulations to characterize these transitions.

Individual vs. Collective Descriptions of Coupled Oscillators

Yoshiki Kuramoto
Research Institute for Mathematical Science, Kyoto University

Statistical mechanics of matter interrelates between the descriptions at the two levels with vastly different space-time scales. If we go one step out of the physics of matter, however, there is virtually no established theoretical framework to deal with similar problems. This is unfortunate because hierarchical structures of nature calling for our scientific understanding seem to exist everywhere in the world.

To approach the latter class of problems, I will focus on large assemblies of rhythmic elements, and argue how it is possible to find their collective description from the knowledge of the individual oscillatory units and their interaction. Making full use of the so-called phase description will turn out crucial there. Although such theories still stays at their infancy, their potential relevance to a broad area of science, particularly to life science, should be great.

Linking cell-level and system-level responses in oscillator networks with any network structure

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JST PRSTO researcher

We report on a new reduction theory that describes the response of an oscillator network as a whole to external forcing applied nonuniformly to its constituent oscillators. Our theory is applicable to a wide variety of oscillator networks undergoing frequency synchronization. Any network structure can systematically be treated. In addition, the algebraic expression of the left zero-eigenvector of the Jacobian matrix, which is relevant to collective dynamics, is found. For networks composed of identical oscillators, the Jacobian matrix is identical to the Laplacian matrix defined for directed, weighted networks. Thus, our study would also be of interest to those working on complex networks as well as those working on nonlinear dynamics. A few examples are given to illustrate our theory.