RMT2015 (Program)

Talkers:
Andersen (Aarhus), Fuji(Kagawa),Hatano(Tokyo), Ihara(Tokyo), Katori(Chuo), Kikkawa(OIST), Nagao(Nagoya), Nelson(Harvard), Sakasai(Tokyo), Sasamoto(Tokyo Tech), Takeuchi(Tokyo Tech), Zinn-Justin(Paris)

Schedule:
11-2, 10:00-12:00 Sasamoto
12:00-14:00 Lunch
14:00-15:00 Takeuchi
15:00-16:00 Coffee
16:00-17:00 Nagao
17:20-18:30 Short talks (posters)
18:30-20:30 Banquet
11-3, 10:00-12:00 Katori
12:00-14:00 Lunch
14:00-16:00 Zinn-Justin
17:00-18:00 Sakasai
18:30-20:30 Dinner
11-4, 10:00-12:00 Andersen
12:00-13:00 Lunch
13:00-18:00 Excursion
18:30-20:30 Dinner
11-5, 10:00-12:00 Nelson
12:00-14:00 Lunch
14:00-15:00 Hatano
15:30-16:30 Kikkawa
17:00-18:30 free
18:30-20:30 Dinner
11-6, 10:00-12:00 Ihara
12:00-14:00 Lunch
14:00-15:00 Fuji

A determinantal structure for a finite temperature polymer model

Tomohiro Sasamoto (Tokyo Institute of Technology)

abstract:
For the Gaussian unitary ensemble (GUE), it is well known that the eigenvalues are determinantal because the probability density of the eigenvalues is written in the form of a product of two determinants. For the O'Connell-Yor(OY) model, which is a finite temperature directed polymer model, a generating function of the partition function can be written as a Fredholm determinant but the underlying determinant structure is not well understood.
We show that there is a product of determinant structure associated with the OY polymer model, which is related to the above-mentioned Fredholm determinant. This can be regarded as a generalization of Warren's Brownian motion in the Gelfand-Tsetlin cone for zero temperature case.
This is based on a collaboration with T. Imamura. [Ref] arXiv:1506.05548

Bessel Process, Schramm-Loewner Evolution, and Dyson Model

Makoto Katori (Chuo University)

The purpose of my lecture is to introduce recent topics in mathematical physics and probability theory, especially the topics on the Schramm-Loewner evolution (SLE) and in- teracting particle systems related with random matrix theory. A typical example of the latter systems is Dyson's Brownian motion model. For this purpose I have considered one story to tell the SLE and the Dyson model as 'children' of the Bessel processes [1]. The Bessel processes make a one-parameter family of one-dimensional diffusion processes with parameter D, in which the D-dimensional Bessel process, $\mathrm{BES}^{(D)}$, is defined as the radial part of the D-dimensional Brownian motion, if D is an integer. This definition implies that Bessel processes are 'children' of the Brownian motion, and hence, the SLE and the Dyson model are 'grandchildren' of the Brownian motion.

First the parenthood of Brownian motion in diffusion processes is clarified and $\mathrm{BES}^{(D)}$ is defined for any $D \geq 1$. There, the importance of two aspects of $\mathrm{BES}^{(3)}$ is explained. SLE is then introduced as a complexification of $\mathrm{BES}^{(D)}$. I show that rich mathematics related with the conformal field theory and the fractal physics involved in SLE are due to the nontrivial dependence of the Bessel flow on D. Finally Dyson's Brownian motion model with parameter β is introduced as a multivariate extension of $BES^{(D)}$ with the relation $D = \beta + 1$. I will concentrate on the case where $\beta = 2$. In this case the Dyson model inherits the two aspects of $BES^{(3)}$ and has very strong solvability. That is, the process is proved to be determinantal in the sense that all spatio-temporal correlation functions are given by determinants, and all of them are controlled by a single function called the correlation kernel.

[1] Katori, M.: *Bessel Process, Schramm-Loewner Evolution, and Dyson Model*, to be pub- lished in the series *SpringerBriefs in Mathematical Physics*, Springer (2015+).

Random-matrix distributions under microscope: evidence for universal interfacial fluctuations

Kazumasa A. Takeuchi (Tokyo Institute of Technology)

I will present recent developments on universal fluctuation properties of growing interfaces, known by the name of the Kardar-Parisi-Zhang (KPZ) universality class. While KPZ scaling exponents have been known for 30 years, recent studies on the one-dimensional KPZ class provided exact solutions to finer properties such as the distribution and correlation, unveiling a non-trivial link to random matrix theory and many other fields in physics and mathematics [1]. The purpose of the talk is to illustrate such developments, along an experimental realization that I and a coworker found in turbulent convection of liquid crystal [2].

Measuring interface fluctuations of growing domains of turbulence (photos below), we found not only the KPZ scaling exponents, but also the particular distribution functions derived for solvable models (figure): namely, the Tracy-Widom distributions, known as the largest-eigenvalue distributions for Gaussian random matrices. Interestingly, circular and flat interfaces show the Tracy-Widom distribution for different matrix ensembles as shown in the figure. This implies that the KPZ class splits into a few universality subclasses, determined by the global geometry of interfaces, or equivalently by their initial condition.

I will also briefly present our latest attempt to characterize KPZ time correlation properties [2,3], which remain analytically intractable in large part. Our analysis showed that time correlation is also different between circular and flat interfaces, even qualitatively [2]. Moreover, we found an interesting connection to the renewal theory, studied in the context of aging and ergodicity breaking [3].

[1] For a review, see I. Corwin, Random Matrices Theory Appl. 1, 1130001 (2012).
[2] K. A. Takeuchi and M. Sano, Phys. Rev. Lett. 104, 230601 (2010); Sci. Rep. 1, 34 (2011); J. Stat. Phys. 147, 853 (2012).
[3] K. A. Takeuchi and T. Akimoto, arXiv:1509.03082 (2015).

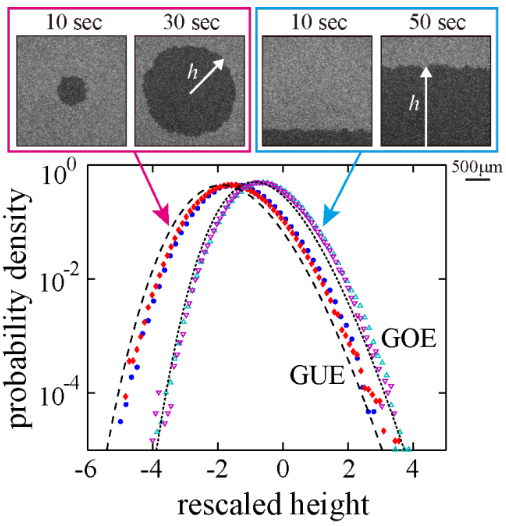

Figure: Growing domains of liquid-crystal turbulence. Fluctuations of the height h (as defined in the top images) for the circular and flat interfaces show the Tracy-Widom distribution for the Gaussian unitary and orthogonal ensembles, respectively. [2]

Two methods of computing the inverse localization length in one dimension

Naomichi Hatano
Institute of Industrial Science, University of Tokyo
hatano@iis.u-tokyo.ac.jp

I will present two independent methods that I have found to compute numerically the inverse localization length (the Lyapunov exponent) of the one-dimensional random Anderson model. They indeed give consistent results for the random-potential model.

I proposed the first method as a by-product of studying the spectrum of the non-Hermitian random Anderson model [1]. We obtain the inverse localization length of the Hermitian model as the edges of the bubble of the complex spectrum of the non-Hermitian model.

The second method is the kernel-polynomial expansion [2] of the inverse localization length. I transform the Chebyshev-polynomial expansion of the den- sity of states [3] to that of the localization length, using the Thouless formula [4]. The expansion produces a smoother dataset than the expansion of the den- sity of states because the expansion coefficients become smaller in high orders. I noticed this method during the collaboration with A. Amir and D.R. Nelson [5].

References

[1] N. Hatano and D.R. Nelson, Phys. Rev. Lett. 77, 570 (1996); Phys. Rev. B 56, 8651 (1997).

[2] A. Weiße, G. Wellein, A. Alvermann and H. Fehske, Rev. Mod. Phys. 78, 275 (2006).

[3] R.N. Silver and H. Röder, Int. J. Mod. Phys. C 5, 735 (1994); R.N. Silver, H. Roeder, A.F. Voter and J.D. Kress, J. Comp. Phys. 124, 115 (1996); R.N. Silver and H. Röder, Phys. Rev. E 56, 4822 (1997).

[4] D.J. Thouless, J. Phys. C 5, 77 (1972); B. Derrida, J.L. Jacobsen and R. Zeitak, J. Stat. Phys. 98, 31 (2000)

[5] A. Amir, N. Hatano and D.R. Nelson, in preparation.

Correlation functions for products of truncated unitary matrices

Taro Nagao (Nagoya Univ.)

Abstract:

We study the products of M complex random matrices obtained by removing L rows and L columns of unitary random matrices uniformly distributed on the group U(N+L). The correlation functions for the complex eigenvalues of the products are investigated and various large N limits at fixed M are evaluated.

Title: H-bond rotations in proteins and H-bond networks.

Jørgen Ellegaard Andersen

Abstract: First we will review our joint work with Bob Penner, Ebbe Andersen, Jens Ledet Jensen, Jakob Nielsen and the rest of the Aarhus team concerning rotations for H-bonds in proteins. We will then discuss our latest results joint with Jens Ledet Jensen, Rasmus Villemoes and Jakob Nielsen, regarding relations between H-bond rotations and the local networks the H-bonds form.

Non-Hermitian Localization in Ecological and Neural Networks

David R. Nelson
Lyman Laboratory of Physics Harvard University

In the 70 years since Phillip Anderson proposed his ideas about localized states in disordered systems, it has become clear that virtually all electronic states are localized in one-dimension. We show that the situation is quite different when the hopping matrix becomes non-Hermitian. Non-Hermitian matrices, with complex eigenvalue spectra, arise naturally in simple models of complex ecosystems, with many interacting predator and prey species. Recent work has revealed particularly striking departure from the conventional wisdom in the one-dimensional non-Hermitian random matrices that describe sparse neural networks.[1] Approximately equal numbers of random excitatory and inhibitory connections lead to an intricate fractal eigenvalue spectrum that controls the spontaneous activity and induced response. When rings of neurons become directed, with a systematic bias for the transfer of excitations in the clockwise direction, an hole centered on the origin opens up in the density of states in the complex plane. All states are extended on the rim of this hole, while the states outside the hole are localized. Time permitting, we will review a simpler application of non-Hermitian localization to biology, relevant to Fisher-Kolmogorov-Petrovsky-Piscounov population waves and growth in disordered media.[2]

[1] A. Amir, N. Hatano and D. R. Nelson, to be published.
[2] D. R. Nelson, Biophysical dynamics in disorderly environments, Ann. Rev. of Biophysics, 41, 371 (2012).

Annulus Diagram of Modules in Biological Molecules

Sigeo Ihara*
Institute for Biology and Mathematics of Dynamic Cellular Processes (iBMath), Research Center for Advanced Science and Technology & Graduate School of Mathematical Sciences, The University of Tokyo
Mail: ihara@genome.rcast.u-tokyo.ac.jp

A major challenge in working with structural biology is to elucidate the implications hidden in the three-dimensional atomic configurations of a given structure. The easier-to-use representation of biological molecules other than 3D computer graphics is important. We introduce the annulus diagram for proteins, where the peptide units in protein backbone structure are mapped onto the annulus. Using this annulus diagram for the data in Protein Data Bank (PDB), the *SO(3)* rotation of the peptide units and the interactions between them are studied with the distribution of water molecules and compounds. We show that our representation is useful in characterizing the protein structure and the role of water molecule, and thereby able to detect the change due to the mutation or the time evolution. Applying our approach to a specific protein complex, we found that a previously unrecognized role of the water molecules. We also discuss the extensions of our method to the wider range of biological molecules.

* Collaboration with Y. Ohta, H. Kodama, A. Sugiyama, M. Matsuoka, H. Doi, T. Tsuboi, J.E. Andersen, and R.C. Penner

Matrix models for the topological enumeration of RNA molecules

Hiroyuki Fuji (Kagawa Univ.)

Abstract:
In this talk, the construction of matrix models to enumerate the topological configuration of RNA molecules will be discussed. Among

various secondary structures, the pseudo-knot structures cause interesting topological structure of the RNA folding. To study such structure of RNA molecules, we will consider the enumerative problem of topological configurations on basis of the chord diagram. Such problem is efficiently studied by applying matrix model techniques, and some new matrix models can be proposed recently. I discuss about the construction of RNA matrix models that enumerate the number of chord diagrams. This talk is based on the work in progress with Joergen Andersen et.al.

Symmetric functions and solvable lattice models

Paul Zinn-Justin (Universite Pierre et Marie Curie)

Abstract:

This is joint work with I. Ikhlef, R. Weston and M. Wheeler. I will discuss the interplay between two properties of two-dimensional statistical models, namely integrability (or exact solvability) and discrete holomorphicity. After introducing these concepts, I will explain how the Bernard-Felder construction of nonlocal currents out of quantized affine algebras provides a link between them, relating the discrete holomorphicity equation with conservation of these nonlocal currents. I will discuss as an example the case of the Temperley--Lieb (dense) loop model.

Random matrix analysis for molecular networks in biological systems

A. Kikkawa (OIST)

Abstract:

The proteins interact with each other inside/outside cells and their interacting networks regulate the biological responses to the ever-changing environments. For example, the study of protein – protein interaction (PPI) network is very important in order to understand the functions and the dynamics of the biological systems. The application of the random matrix theory (RMT) is one of the methods for the investigation of the topology of

the PPI networks. We study the behavior of eigenvalues of interaction matrices where the elements are generated by the pair of the interacting proteins or transcripts. We compare several networks such as PPI in cancer cells and micro RNA – target genes (transcripts) interactions.