

Keynote Speech

Hiroaki Kitano

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Sony CSL, Inc./ ERATO Kitano Symbiotic Systems Project



Hiroaki Kitano is a senior researcher at Sony Computer Science Laboratories, Inc. and a Project Director of Kitano Symbiotic Systems Project, Japan Science and Technology Corporation. He received a B.A. in physics from the International Christian University, Tokyo, and a Ph.D. in computer science from Kyoto University. Since 1988, he has been a visiting researcher at the Center for Machine Translation at Carnegie Mellon University. Kitano received Computers and Thought Award from the International Joint Conferences on Artificial Intelligence in 1993, and received Prix Ars Electronica 2000. His research interests include AI, Robotics, and Systems Biology.

Plenary Invited Talk

Yusuke Nakamura

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Institute of Medical Science, The University of Tokyo



Dr. Yusuke Nakamura is the Director of Human Genome Center and Professor of Laboratory of Molecular Medicine in Institute of Medical Science, The University of Tokyo. He graduated from Osaka University Medical School and was Research Assistant Professor, Department of Human Genetics, University of Utah during 1987-1989. He serves as a member in the Editorial Board for Annals of Human Genetics, Cancer Research, Clinical Genetics, Genes Chromosomes & Cancer and also the Editor-in-Chief for Journal of Human Genetics.

Software Platform and Data Resources

Hamid Bolouri

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Caltech and University of Hertfordshire /
ERATO Kitano Symbiotic Systems Project



Hamid Bolouri is Professor of Neural Systems at the Science & Technology Research Centre, University of Hertfordshire and has been a Visiting Associate in the Division of Biology at the California Institute of Technology since 1996. He received the BS, Ms and PhD degrees in Electronic Engineering from the Universities of Sussex, Southampton and Brunel in the UK in 1984, 1985, and 1990 respectively. He joined the ERATO Kitano Project in 1999.

Masaru Tomita

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Laboratory for Bioinformatics, Keio University



Masaru Tomita is a professor and the Director of Laboratory for Bioinformatics, Keio University. He received B.S (1981) in Mathematics from Keio University, M.S (1983) and Ph.D (1985) in Computer Science from Carnegie Mellon University, and another Ph.D (1994) in Molecular Biology from Keio University. Dr. Tomita is a recipient of Presidential Young Investigators Award from National Science Foundation of USA (1988). Research fields are Bioinformatics, Genome Informatics, Theoretical Molecular Biology, Natural Language Processing, and Artificial Intelligence.

Pedro Mendes

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Virginia Bioinformatics Institute



Dr. Pedro Mendes is a Biochemistry graduate (University of Lisbon, Portugal, 1988) and has a PhD in "Computer Simulation of Biochemical Pathways" (University of Wales Aberystwyth, UK, 1994) supervised by Prof. Douglas B.Kell. After a position as Program Leader at the National Center for Genome Resources (Santa Fe), he is now a Faculty member of the new Virginia Bioinformatics Institute, at Virginia Tech. Pedro is best know for being the author of biochemical simulation software Gepasi.

Thomas Simon Shimizu

University of Cambridge

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Thomas Simon Shimizu began his research in computational biology during his undergraduate (1992-1996) and masters (1996-1998) degrees at Keio University, where he was involved in launching and developing the E-CELL project with Masaru Tomita. He now works as a PhD student with Dennis Bray at the Department of Zoology, University of Cambridge, where in 1998 he took over the development of StochSim, a stochastic simulator for biochemical reactions. His current research utilises StochSim and other computational tools to study the intracellular signalling pathway controlling bacterial chemotaxis.

Key Publications:

Shimizu, T.S., Le Novère, N., Levin, M.D., Bevil, A.J., Sutton, B.J. & Bray, D. Molecular model of a lattice of signalling proteins involved in bacterial chemotaxis. *Nature Cell Biology* 2, 792-796(2000) Morton-Firth, C.J., Shimizu, T.S. & Bray, D. A free-energy-based stochastic simulation of the Tar receptor complex. *Journal of Molecular Biology* 286, 1059-1074 (1999) Tomita, M., Hashimoto, K., Takahashi, K., Shimizu, T.S., Matsuzaki, Y., Miyoshi, F., Saito, K., Tanida, S., Yugi, K., Venter, J.C. & Hutchison, C.A. E-CELL: software environment for whole-cell simulation. *Bioinformatics* 15, 72-84 (1999) Shimizu, T.S., Takahashi, K. & Tomita, M. CpG distribution patterns in methylated and non-methylated species. *Gene* 205, 103-107 (1997)

Jörg Stelling

P 29

Max-Planck-Institute for Dynamics of Complex Technical Systems



Born 1969. Studies in Biotechnology at the Technical University Braunschweig (until 1996). Scientific assistant at the Institute for system dynamics and control, Stuttgart University (until 1998). Currently assistant researcher at the Max-Planck-Institute for dynamics of complex technical systems / Bioprocess engineering group and Peter-und-Traudl-Engelhorn foundation fellow. Research interests focus on mathematical modelling of cellular regulatory networks especially in eukaryotes. Author of 5 papers.

Reconstruction & Reverse Engineering of Genetic Network

Zoltan Szallasi

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Uniformed Services University of the Health Science



Zoltan Szallasi, M.D. is an assistant professor at the Department of Pharmacology, Uniformed Services University. He has been active in both the theoretical and experimental aspects of genetic network analysis of cancer. His lab is conducting cDNA microarray based large-scale gene expression measurements in breast cancer and developing experimental and computational analytical tools in order to achieve a more complex understanding of this disease. His other main interest is to determine the theoretical limitations of predictive power in molecular biology.

Mattias Wahde

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Chalmers University of Technology



I received my Ph.D. from Chalmers University of Technology in Goteborg, Sweden in 1997, and thereafter held a postdoc position at Nordita in Copenhagen between 1997 and 1999. In 1999, I returned to Chalmers University of Technology, where I presently hold a position as assistant professor. My research interests include bioinformatics as well as adaptive algorithms and their applications in the field of autonomous intelligent robots. One of my recent papers on bioinformatics can be found in Biosystems, vol 55, pp.129-136, 2000.

Minoru Kanehisa

Kyoto University

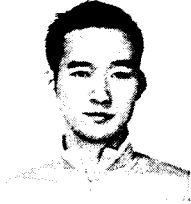


After receiving D.Sc. in physics from the University of Tokyo in 1976, Minoru Kanehisa worked in the Johns Hopkins University School of Medicine, in the Los Alamos National Laboratory where he was one of the cofounders of GenBank, and in the National Institutes of Health. Since 1987 he has been Professor in the Institute for Chemical Research, Kyoto University. He has been Principal Investigator of the Japanese Genome Informatics Project for a decade and has just become President of the newly established Japanese Society for Bioinformatics.

Koji Kyoda

ERATO Kitano Symbiotic Systems Project

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Koji Kyoda is a research assistant at the Kitano Symbiotic Systems Project, ERATO, JST and a Ph.D. candidate in Keio University. His research interests include inference of a gene regulatory network from gene expression data. He received a MS in computer science from Keio University.

System –Level Analysys

Adam P. Arkin

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Lawrence Berkeley National Laboratory



EDUCATION AND RESEARCH INTERESTS

Ph.D., Massachusetts Institute of Technology, Physical Chemistry, 1992

Major awards: Technology Review Top 100 Innovative Young Scientist Award, (1999)

Research interests: genetic and biochemical reaction network analysis and simulation, computational biology and genomics, control theory and biology, multichannel and cell-based biosensors

PROFESSIONAL EXPERIENCE

2000-present Assistant Investigator, Howard Hughes Medical Institute
1999-present Assistant Professor, Departments of Bioengineering and Chemistry University of California, Berkeley

1999-present Faculty Scientist, Computational and Theoretical Biology Department
Physical Biosciences Division, Lawrence Berkeley National Laboratory
1998-1999 Staff Scientist, Physical Biosciences Division Lawrence Berkeley Laboratory

SELECTED PUBLICATIONS

McAdams, H.H., Arkin, A.P., "Genetic Regulation at the Nanomolar Scale: It's a Noisy Business!", *TIGS*, 15(2): 65-69, 1999.

Arkin, A.P., "Signal Processing by Biochemical Reaction Networks", In: *Biodynamics*, J. Walleczek, ed., Cambridge University Press, 1999.

Dennis Bray

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University of Cambridge



Received his Ph.D. from M.I.T. and postdoctoral training at Harvard Medical School. Since then he has been employed as a research scientist by the Medical Research Council, UK, at laboratories in London and in Cambridge. At various times he has served as visiting professor at the University of Otago, at Washington University, and at California Institute of Technology. He is the author of over a hundred research papers in neurobiology, cell biology, and computational biology and an author of text books, including "The Molecular Biology of the Cell," "Essential Cell Biology" and "Cell Movements."

John Doyle

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California Institute of Technology



John Doyle works on the mathematics of complex systems, emphasizing robustness and methods for uncertainty management, with recent application interests in engineering and biological networks and theoretical physics. His research career started as a consultant with Honeywell in 1976, and he is currently a Professor in Control and Dynamical Systems at Caltech. He received his BS and MS in EE from MIT in 1977, and PhD in Math from Berkeley in 1984.

Tau-Mu Yi

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Caltech / ERATO Kitano Symbiotic Systems Project



Dr. Yi is currently a post-doctoral research fellow in the Division of Biology at Caltech and a member of the ERATO-Kitano Symbiotic Systems Biology Project. He received his B.S. degree from Harvard University, and his Ph.D. degree from Dr. Eric Lander's laboratory at M.I.T. The focus of his research is modeling biochemical networks, especially signal transduction pathways. His most recent paper (Yi et al., 2000) investigated the relationship between robustness and feedback control in bacterial chemotaxis signaling.

Yi, T. -M., Huang, Y., Simon, M. I., and Doyle, J. (2000). Proc. Natl. Acad. Sci. USA, 97: 4649-4653.

Andre Levchenko

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California Institute of Technology



Andre Levchenko is an awardee of a Borroughs-Wellcome fellowship in computational molecular biology, doing his post-doctoral studies at Biology and Electrical Engineering divisions Caltech. He obtained his Ph.D. in 1999 at Columbia University. In 2001 he will join Johns Hopkins University as Assistant Professor. His interests lie in theoretical and experimental studies of signal transduction. Currently, his work is focused on mechanisms of eukaryotic gradient sensing, stress response cells and myogenesis. His prior experience included theoretical and experimental analysis of drug resistance in cancer.

Eric Mjolsness

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California Institute of Technology



Eric Mjolsness is a principal computer scientist at the Jet Propulsion Laboratory of the California Institute of Technology, and a Faculty Associate in Biology at the California Institute of Technology. His research interests include gene regulation networks, cell simulation, statistical pattern recognition, neural networks, computer vision, and large-scale optimization methods. He earned his AB in Physics and Mathematics from Washington University and his PhD in physics and computer science from the California Institute of Technology. He is a member of the IEEE and the ACM. Contact him at the Jet Propulsion Laboratory, MS 126-346, 4800 Oak Grove Drive, Pasadena CA 91109-8099, mjolsness@jpl.nasa.gov; www-aig.jpl.nasa.gov/mls

Comprehensive Measurement

Shinya Kuroda

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Columbia University/Kawato Dynamic Brain Project, ERATO



Current affiliation

Postdoctoral fellow (JPSP Postdoctoral Fellowships for Research Abroad)
Center for Neurobiology and Behavior, Columbia University, c/o Eric R Kandel

Education

- (1) M.D: Kobe University School of Medicine (1991)
- (2) PhD: Department of Molecular Biology and Biochemistry, Osaka University Medical School (1995)

Career

- (3) Post doctoral fellowship of Cancer Research, JSPS (1995)
- (4) Research Assistant: Division of Signal Transduction, Nara Institute of Science and Technology
- (5) Committee member of Kawato Dynamic Brain Project, ERATO, JST (1999)
- (6) Inheritance and Variation Group, PRESTO, JST (1999)

Specialty

Biochemistry, Molecular Biology, Neurobiology

David Polidori

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Entelos, Inc.



David Polidori is the technical leader for metabolism modeling at Entelos, Inc. Dave leads a group of 11 engineers and scientists working on computer-based models of obesity, diabetes, and adipocytes for pharmaceutical research. His group collaborates with many leading academic researchers. Before joining Entelos, Dave received a Ph.D. in applied mechanics from Caltech and a B.S. in engineering mechanics from the University of Wisconsin.

Satoru Kuhara

P 95

Graduate School of Genetic Resources Technology, Kyushu University



I received the B.S and M.S. degree in Faculty of Agriculture from Kyushu University and received Doctor of Agriculture from Kyushu University. In 1995 he joined as a professor in the Faculty of Agriculture in Kyushu University. I have been engaged in Bioinformatics research.

Yuji Kohara

National Institute of Genetics

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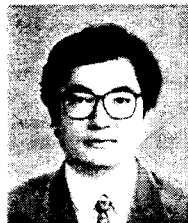


Yuji Kohara is Professor and Head of the Center for Genetic Resource Information, National Institute of Genetics, Mishima, Japan. His first work in genome research is the physical mapping of the *E.coli* genome in 1987, and then he joined the *C.elegans* genome project at MRC-LMB, Cambridge, UK. After returning to Mishima, Japan, he has conducted a gene expression/function project of the *C. elegans* genome. His ultimate interest is to reconstruct the developmental process of the worm in the computer.

Shohei Mitani

Tokyo Women's Medical University School of Medicine

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Shohei Mitani is an associate Professor at the Department of Physiology, Tokyo Women's Medical University School of Medicine. He graduated Medical School at the University of Tokyo in 1984. He is major on the molecular genetics using the nematode *Caenorhabditis elegans*. His special interest is in the developmental mechanisms of the nervous system. To address this issue, he and his colleagues have developed an efficient method to isolate deletion mutants (Gengyo-Ando and Mitani, 2000) and are now on the way to isolate many mutants.

Shuichi Onami

ERATO Kitano Symbiotic Systems Project

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Shuichi Onami, Ph.D. is the group leader of System Biology Group, Kitano Symbiotic Systems Project, Japan Science and Technology Corporation and a visiting associate at Department of Control and Dynamical Systems, California Institute of Technology. His main interest is computer simulation of life. His group is studying early *C. elegans* embryogenesis, and developing software for automatic cell lineage acquisition and computer simulation. He is also conducting a study for gene regulatory network inference from large-scale experimental data.