

## CURRICULUM VITAE SATORU MIYANO

### CURRENT POSITION

**Director, Human Genome Center**, The Institute of Medical Science,  
The University of Tokyo

Date of Birth : December 5, 1954

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### ACADEMIC QUALIFICATION

- 1984 Doctor of Science, Kyushu University
- 1977 –1979 Master of Science, Department of Mathematics, Kyushu University
- 1973–1977 Bachelor of Science, Department of Mathematics, Kyushu University

### CAREER HISTORY

- April, 1996 – Professor, Human Genome Center, Institute of Medical Science, The University of Tokyo
- March, 1993 – March, 1996 Professor, Research Institute of Fundamental Information Science, Kyushu University
- 1994 Guest Professor, University of Paris VII, France
- December, 1987 – February, 1993: Associate Professor, Research Institute of Fundamental Information Science, Kyushu University
- 1985 - 1987 Alexander von Humboldt Research Fellow, University of Paderborn, Germany
- July, 1981 – March, 1984 Assistant Professor, Department of Mathematics, Kyushu University
- September 1981 – July 1982 Visiting Researcher, Department of Electrical Engineering and Computer Science, Northwestern University, USA
- June, 1979 – June, 1981 Assistant Professor, Research Institute of Fundamental Information Science, Kyushu University

### INSTITUTIONAL APPOINTMENTS

- April 1, 2014 - Director, Human Genome Center, The Institute of Medical Science, The University of Tokyo
- April 1, 2004 - March 31, 2005, Deputy Director, The Institute of Medical Science, The University of Tokyo
- April 1, 2000 - March 31, 2003, Deputy Director, The Institute of Medical Science, The University of Tokyo
- April 1, 1994 - March 31, 1996, Director, Research Institute of Information Science, Kyushu University

### AWARDS

- 2013: Fellow of the International Society for Computational Biology  
<http://www.iscb.org/iscb-fellows>
- 1994: IBM Science Award

- 1994: Sakai Special Award

## ACADEMIC SOCIETIES

- President, Japanese Society for Bioinformatics (April 2002 – March 2004)
- Board of Directors, International Society for Computational Biology (2004 -2006)
- President, Association of Asian Societies for Bioinformatics (2003-2004, 2009)

## RESEARCH AREAS

Bioinformatics, Systems Biology, Computational Biology

1. **Gene network analysis:** His group has developed a series of computational methods for mining gene networks from DNA microarray gene expression data and various genome-wide data such as protein-protein interactions, etc. Bayesian networks, state space model, and Boolean networks are investigated for modeling, estimating and analyzing gene networks consisting of several thousands genes. This gene network technology has been applied for searching drug-response pathways.
2. **Modeling and simulation of biological systems:** His group has been developing a software tool Cell Illustrator (CI) (<http://ciconline.hgc.jp/>) with which we can model and simulate various biological mechanisms and pathways in cells by organizing and compiling biological data and knowledge, and an XML format Cell System Markup Language (CSML) (<http://www.csml.org/>) for describing biological systems with dynamics and Cell System Ontology (CSO). Since CI employs CSML/CSO and equips biology-oriented sophisticated GUIs, we can model very complex biological processes like with a drawing tool.
3. **Peta flops computing for biomedical applications:** Since 2006, his group has been involved with the RIKEN's grand challenge project for life sciences called "[Next-Generation Integrated Simulation of Living Matter](#)". We are developing (i) peta-scale computational methods for inferring molecular networks of tens of thousands nodes, and (ii) a new statistical and computational method called "data assimilation" that "blends" simulation models and observational data rationally.
4. **International leadership in bioinformatics and computational biology:** He organized the International Conference on Genome Informatics for 11 years since 1996. He served as program committee chair and member for the most important international conferences on bioinformatics and computational biology such as RECOMB, ISMB, ECCB, APBC, CSB, etc. He also has been serving on editorial boards of PLoS Computational Biology, Bioinformatics, J. Computational Biology and Bioinformatics, IEEE/ACM Transactions on Bioinformatics and Computational Biology, etc.