

5th World Congress on **Cell & Stem Cell Research**

March 23-25, 2015 DoubleTree by Hilton Chicago - North Shore, USA

Statistical computing and mathematical modeling for understanding of biological functions using big data

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Emergence of the next generation sequencing technologies and its application to clinical and biological research opened the door of the era of genomic big data. Today, realizing the personal medicine with big data is fascinating topic in the current clinical research. For manipulation and processing of genomic big data, we are utilizing four strategies of information technology: (1) Monte-Carlo Simulation, random sampling from the genomic big data. (2) HPC (high performance computing), possessing Many Core CPU and Large Memory. (3) Cloud-based Hadoop technology containing distributed file systems (HDFS) and distributed processing systems (MapReduce) on the Amazon Web Services (AWS). (4) non-Hadoop Shell scripting technology including distributed file systems and distributed processing system without hadoop. Monte-Carlo Simulation is a powerful method for optimization and elucidation of the biological functions using genomic big data. Here we will focus on the powerful and novel application of Monte-Carlo Simulation for genomic big data.

Biography

Kazuo Ishii, Ph.D. is the Professor of Genomic Sciences, the Graduate School of Agriculture, Tokyo University of Agriculture and Technology. After receiving the Ph.D. degree from the University of Tokushima Graduate School of Medicine in 1995, he began the professional career in genomic sciences. He has studied data analysis and data mining for microarray and next generation sequencing since 2003. His present interest is statistical computing and mathematical modeling for biology.

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