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Establishment of statistical computing and mathematical modeling for understanding of biological functions with 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. To discover the new knowledge from genomic big data, I will introduce the novel statistical computing and mathematical modeling method for understanding of biological functions with genomic big data named PMC machine learning which is based on Monte-Carlo Methods and parallel computing. Monte-Carlo Methods is random sampling methods such as bootstrap, jackknife and Markov-chain Monte-Carlo methods. Parallel computing was implemented by (1) High Performance Computing (HPC) with many core CPUs, (2) Cloud computing based on a computer cluster, (3) GPGPU (General-purpose computing on graphics processing units) and (4) A parallel FPGA cluster. In this presentation, I will show some clinical, agricultural or ecological applications of PMC machine learning.

Biography

Kazuo Ishii is the Professor of Genomic Science of the Graduate School of Agriculture, Tokyo University of Agriculture and Technology in Japan. In 2011, he got the job and he has dedicated to the Human Resource Development Program in Agricultural Genomic Sciences in Tokyo University of Agriculture and Technology, funding supported from the Ministry of Education, Culture, Sports, Science and Technology of Japan (MEXT). His main interest is statistical computing and mathematical modeling for understanding of biological functions with big data.

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