

Next-Generation Integrated Simulation of Living Matter



Project Outline

The "Next-Generation Supercomputer" project, began in 2006 by MEXT, is a close collaboration between government, industry, and academia centered on RIKEN under a MEXT initiative, and carried out in a unified way in order to maintain Japan's lead in a wide range of fields including science and technology, academic research, industry, medicine, and pharmacy. It has the following objectives:

- 1.Develop a world-leading and maximum performance "Next-Generation Supercomputer";
- 2.Develop and distribute software to make maximum use of the Next-Generation Supercomputer (the "Grand Challenge Applications");
- 3. Construct a world-class supercomputing research and education base centered on the Next-Generation Supercomputer.

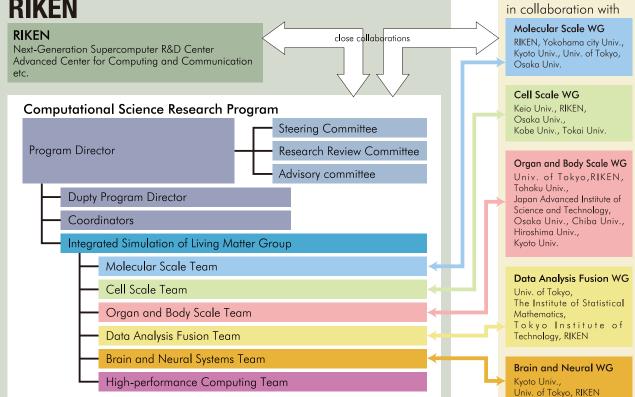
The RIKEN Wako Institute has been selected as the research and development base for "Grand Challenge Applications" in the life sciences, and is carrying out research and development for the "Next-Generation Integrated Simulation of Living Matter".

This promotes the research and development of simulation software which helps understand phenomena from molecules to entire organisms. We are trying to develop simulation software both from an analytic approach, where we will study phenomena through basic principles, and a data-analysis approach, where we will attempt to discover new processes and laws by analyzing large quantities of experimental data.

Core viewpoints set in order that this project contributes to life science are:

- 1. Development of application software aimed at use in the completed supercomputer.
- 2.Long-term "grand challenges" aimed at the construction of a basis for future life science unifying experiments and computer simulations to gain new knowledge for the first time.





From the director

The twenty-first century has been called the "era of prediction", and the need for the computational science to make this a reality is acknowledged worldwide. Computational science is based on theory, but underlined by experimental data, and this link between theory and experiment is vital for the future of science and technology.

In particular, a lead in the development and use of supercomputers is vital for Japan's international competitiveness. It has been given the status of a National Critical Technology in the third Basic Program for Science and Technology, and MEXT is promoting it under the title of "Next-Generation Supercomputer Project". RIKEN has been entrusted with the construction of the project, and has responsibility not only for its research and development, but for promoting its basis, computational science.



This project requires not only world-class hardware, but also research and development of leading-edge software. We aim to make possible simulations which use the next-generation supercomputer to its fullest potential by developing application software to synthetically understand natural phenomena, the "grand challenge applications".

From October 2006, in close collaboration with other institutions, we at RIKEN started the "Research and Development of Next-Generation Integrated Life-Science Simulation Software", a "grand challenge application" for the life sciences, to make full use of the power of the Next-Generation Supercomputer and enable ground-breaking new simulations.

This will establish computational science as a new methodology for the life sciences, and we are determined to bring about breakthroughs. At the same time as its development, we also plan to distribute the software to industry in order that these results may be used in real-world applications, and contribute to the success of the next-generation supercomputer.

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Data Analysis Fusion Team Team Leader





Brain and Neural System Team Team Leader

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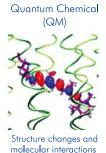
High-Performance Computing Team Team Leader

Makoto TAIJI

Molecular Scale Team

Molecular simulations try to elucidate the molecular basis of biological functions brought about by proteins and other biomolecules at the atomic level. Hierarchical nature of biological functions can be modeled by the multi-scale simulation combining quantum chemical (QM), molecular dynamics (MM), and coarse-grained model (CG) simulations, i.e., QM/MM and MM/CG. Developing these methods, we try to simulate large-scale systems containing long-time dynamics with high-precision. Our scope covers a wide-range of biological problems, from enzymatic reaction to molecular events in the cellular environment. These techniques should form a fundamental basis for rational drug design.

Three-Layers of Biomolecular Simulation

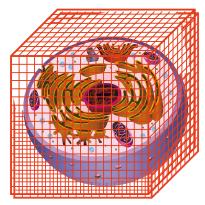






events in cellular context

Cell Scale Team



Simulation of metabolism in various organelles and subcellular localization of material and enzyme

We are developing the integrated cell simulation platform which is important system of cell scale research. This platform is a common base system which takes into consideration of an intracellular place and the coupled simulation. In the space of a fixed lattice, the model parameter obtained from experiment data can simulate various cell reactions on our platform. We section a cell in 1,000,000 voxels and take the

to various cell reactions. Our first target is hepatocyte. We reproduce the energy metabolism or

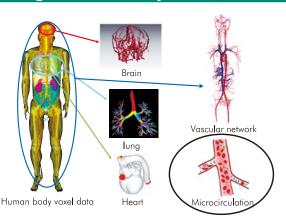
information such as the quantity or

movement of material. Then we

simulate a phenomenon in the cell

the drug metabolism based on the experimental data. We hope for the achievement of biology and the medical significant simulation. It is thought that it becomes a useful tool to understand the disease and the clinical condition.

Organ and Body Scale Team



We are developing a living human body model which has the circulation system, the musculoskeletal system, all sorts of organs and the nervous system. Using this model, we are trying to develop the simulation-based supporting system for the next-generation medical treatment.

For example, as one of the blood flow simulators, thrombosis simulator is developed through the introduction of the coupling method between continuum scale simulation for blood flow and cell level simulation for the aggregation of platelets. This simulator will be used for the prediction and treatment of the thrombotic disease.

gene



Molecule



Cell



tissue





Body

Data Analysis Fusion Team

We are facing with the explosion of measurement data related to genes and genomes. This team is developing algorithms and their applications for data analysis which cannot be realized without peta-scale computing. In parallel with this data analysis challenge, we are creating a peta-scale modeling technology

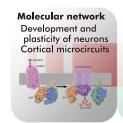
based on data assimilation that fuses observational data and simulation models

nductive Detective Data Can run, but requires a steering for direction Modeling Engine for Science

In the future, these developments will form the fundamental information technology that will contribute to drug target discovery and medicine with the full scope of all human genes and their variations. Currently, by sharing "lung cancer and drugs" as a common theme in the team, the members are making a strong synergy to establish the technology that can predict large biological network structures and their dynamic models from data and will produce personalized models from "general models" with "personal data" with the innovation of data assimilation.

Brain and Neural Systems Team

The brain is a profound biological system where information emerges on the basis of physical molecules. We perform simulation studies of development and plasticity of single neurons, dynamics of cortical neuron ensembles, and processing of invertebrate's olfactory system and vertebrate's visual system; they will lead not only to elucidation of information processing functions of brain and neural systems but also to understanding how development/learning disorders arise in the brain.



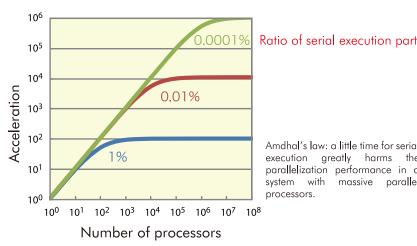
Software Model and database Real-time simulation

Information processing in the brain Olfactory system of insects Visual system of mammals

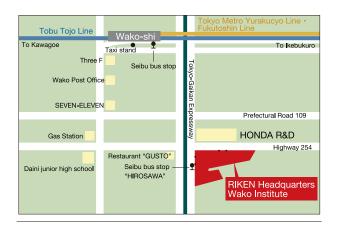
In order to reveal the functions of processing units in the brain, we develop models and software to simulate molecular networks related to development and plasticity of single neurons, and highly-complicated cortical neural microcircuits. Moreover, we develop models, databases and software about insects' processing from odor stimuli to odor-source exploration and animals' processing from visual stimuli to eye movements, so as to simulate the real-time information processing by the brain

High Performance Computing Team

The developments of highly-parallel software is essential to enhance the potential of the next-generation supercomputer system. We contend with the difficult problems in massive parallelization with the other research teams. Also, we develop the parallelized libraries for the basic simulation software such as molecular dynamics, molecular orbital methods and fluid/elastic mechanics, as well as visualization and work-flow tools.

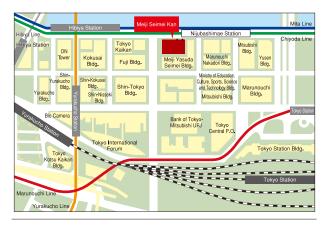


Amdhal's law: a little time for serial execution greatly harms the parallelization performance in a system with massive parallel processors.



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