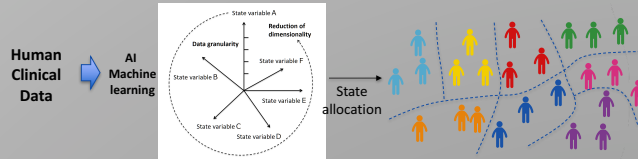
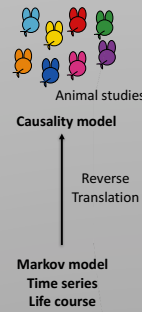
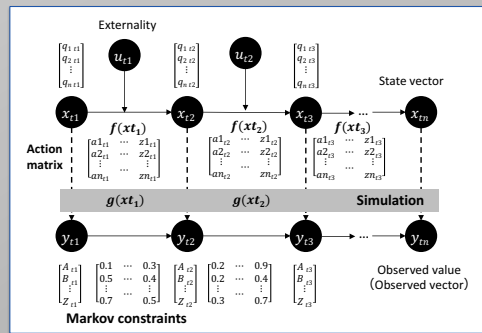


Although linear causations and correlations have been used in the explanation of biological phenomena, biological systems form complex network whose collective behavior cannot reduce to simple correlations. In addition, explanation usually eliminate information on differences between each individual people. To overcome these problems, I am developing a new bio-medical science based on pure description of the body condition by using multi-omics data.

To describe personal differences, it is necessary to consider the historic changes during life-course. I have applied the discretization model and Markov chain model to describe the life-course changes of individual people. Markov chain model is a well-known tool to model temporal properties of many phenomena.

The state allocation is done by the reduction of dimensionality and the granularity control using machine learning and energy landscape model. Relation between the present and future state is described by Markov constraints. The order observed in the sequence of symbols is defined which can overcome the concept of program in biology.

The data is gathering from patients of immune disorders, cancer and developmental disorders by collaborating with medical schools all over Japan. Knowledge obtained from human data is reversed translated in animal studies. The causality model is developed by animal studies.



The Description of biological phenomena as open system

Dr. Kazuhiro Sakurada

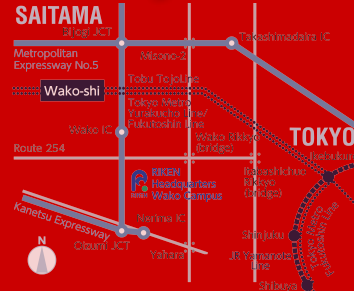
Deputy Program Director

RIKEN Medical Sciences Innovation Hub Program

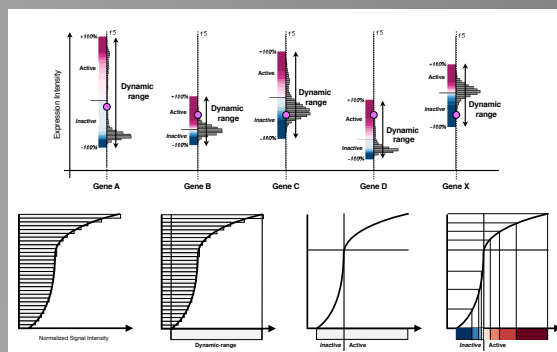


April 23rd (Mon.) 15:00~
Okochi Hall (Building C32)

RIKEN Wako campus AICS 6F auditorium Kobe



Now massive amount of bio-medical data are flowing into statistical analysis and machine learning. However, every biological variable has a different dynamic-range, thus prior data normalization is quite important. In this talk, I will introduce an open platform for objective gene expression profiling named Gene Expression Commons (<https://gexc.riken.jp>) in which expression dynamic-range of each gene is provided by global-scale meta-analysis has been to make use of supersymmetry. Recently, however, we have shown that higher-order derivative interactions typical in generalized G-inflation can also make the potential effectively flat even though they contain much larger values of parameters than usually assumed. This provides another arena for model building of realistic inflation. I will introduce these new trends in inflationary cosmology.



Every Biological Variable has a Different Dynamic-range

Dr. Jun Seita

Unit leader, AI based Healthcare and Medical Data Analysis Standardization Unit

RIKEN Medical Sciences Innovation Hub Program

