Bioinformatics Center
– Mathematical Bioinformatics –

https://www.bic.kyoto-u.ac.jp/takutsu/index.html

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Scope of Research

Due to the rapid progress of genome sequencing technology, whole genome sequences of organisms ranging from bacteria to human have become available. In order to understand the meaning behind the genetic code, we have been developing algorithms and software tools for analyzing biological data based on advanced information technologies such as theory of algorithms, artificial intelligence, and machine learning. We are currently studying the following topics: systems biology, scale-free networks, metabolic networks, phylogenetic trees, neural networks, chemo-informatics, and discrete and stochastic methods for bioinformatics.

KEYWORDS

Complex Networks
Boolean Networks
Neural Networks
Metabolic Networks
Phylogenetic Trees
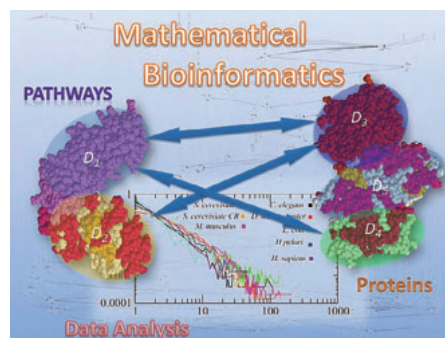
Recent Selected Publications

Ghafoor, M.; Akutsu, T., On the Generative Power of ReLU Network for Generating Similar Strings, *IEEE Access*, **12,** 52603-52622 (2024).

Pan, Q.; Zhong, J.; Akutsu, T.; Liu, Y.; Liu, R., Distributed Pinning Control: Stabilizing Large Boolean Networks Subjected to Perturbations, *IEEE Trans. Cybern*., **54,** 7094-7102 (2024).

Tokuhara, Y.; Akutsu, T.; Schwartz, J-M.; Nacher, J. C., A Practically Efficient Algorithm for Identifying Critical Control Proteins in Directed Probabilistic Biological Networks, *npj Syst. Biol. Appl*., **10,** 87 (2024).

Tamura, T., Trimming Gene Deletion Strategies for Growth-Coupled Production in Constraint-Based Metabolic Networks: TrimGdel, *IEEE ACM Trans. Comput. Biol. Bioinform*., **20,** 1540-1549 (2023).

Tamura, T., MetNetComp: Database for Minimal and Maximal Gene-Deletion Strategies for Growth-Coupled Production of Genome-Scale Metabolic Networks, *IEEE ACM Trans. Comput. Biol. Bioinform*., **20,** 3748-3758 (2023).