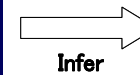
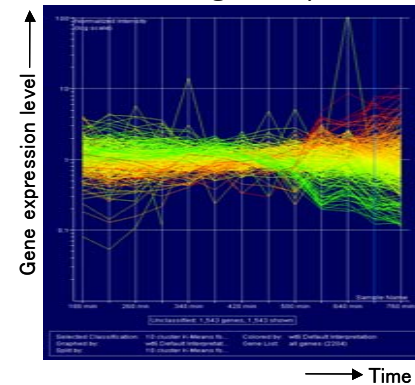


R&D field: Life science

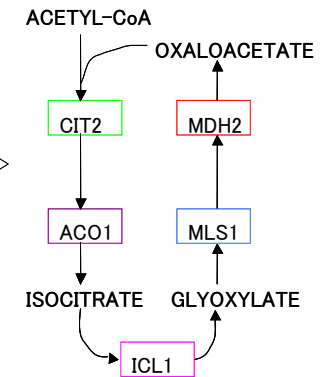
Inference of Genetic Networks from Experimental Data of Gene Expression

- Program name: GNISC
- Developer
 - Shuhei Kimura, Associate Prof. of Tottori Univ.
- Abstract
 - Inference of gene regulations in actual cells from gene expression levels measured with DNA microarrays.
 - Reduction of genetic network inference to parameter estimation of simultaneous differential equation models.
- Algorithm
 - Decomposition of genetic network inference into several sub-problems.
 - C++ and MPI.
- Current computation size
 - Inference of genetic network of 30 genes.
 - Sustained performance 12 GFlops (PC Cluster : PentiumIII × 32 CPUs).
 - Memory 100 MB and disk 10 MB.
- Future computation in 2010
 - Inference of genetic network of 1000 genes.
 - About 33 times of the number of sub-problems and about 33 times of the search dimension in each problem, totally 33,000 times of the current computation amount.
 - Memory 3 TB and disk 300 GB.

Time-series data of gene expression levels



A genetic network model



- Expected results
 - GNISC is an essential method to understand life phenomena that can infer genetic networks of about $10^3 - 10^4$ genes interacting with each other in live cells.
 - GNISC can determine target genes for drug discovery and understand gene functions through numerical simulations based on the inferred genetic network models.
- Reference
 - S.Kimura, K.Ide, A.Kashihara, M.Kano, M.Hatakeyama, R.Masui, N.Nakagawa, S.Yokoyama, S.Kuramitsu and A.Konagaya: Inference of S-system models of genetic networks using a cooperative coevolutionary algorithm, Bioinformatics, Vol. 21, No. 7, pp. 1154-1163, 2005.