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Program: Electrical and Information Engineering
Area: Information Engineering
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Professional Expertise

My research interests include bioinformatics, comparative genomics, metagenomics, biological database.

Research Fields of Interest

It is one of the most important tasks of life science to unveil unknown basic knowledge from a large amount of accumulated information of genomic sequences. Self-Organizing Map (SOM) is an effective tool for clustering and visualizing high-dimensional complex data on a two-dimensional map. We developed a modified SOM (Batch Learning SOM; BLSOM) for comprehensive analyses of species-specific genomic sequence characteristics.

1. Comparative genome analyses for unveiling genome signature

We found that BLSOM could classify genomic sequence fragments according to species without any information other than oligonucleotide frequencies in a wide range of genomes. The BLSOM, which can systematically characterize species-specific genome signature of all prokaryotes and eukaryotes analyzable, proves a new powerful bioinformatics strategy to study biodiversity and molecular evolution.

2. A novel bioinformatics strategy for unveiling microbial diversity and protein functions of metagenome sequences

Metagenomic approach, which is the genome analysis on a mixture of uncultured microorganisms, has been recently developed to search for novel and industrially useful genes and to study microbial diversity in a wide variety of environments. Using a BLSOM, most of the sequences obtained by metagenomic studies were classified (self-organized) according to phylotypes without any phylogenetic information. Because the BLSOM is a powerful tool for phylogenetic classification of genomic fragments, BLSOM could provide a new systematic strategy for revealing basic knowledge obtained from uncultured microorganisms including viruses in a wide variety of environmental samples.

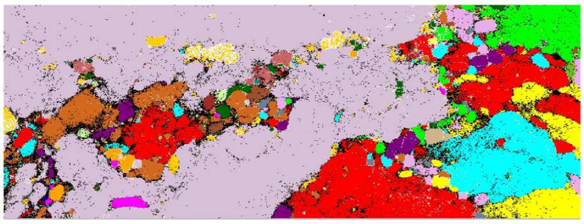

Figure. DegeTetra-BLSOM of 5-kb sequences derived from species-known 2,813 prokaryotes, 111 eukaryotes, 1,728 mitochondria, 110 chloroplasts, and 31,486 viruses.

Education

2004: Ph.D. in Genetics, Graduate School of Life Science, The Graduate University for Advanced Studies, Japan
2001: M.S. in Engineering, Graduate School of Science and Engineering, Yamagata University, Japan
1999: B.S. in Engineering, Faculty of Engineering, Yamagata University, Japan

Awards

Society of Genome Microbiology, Japan, Award for Young Scientists, 2011

Major Publications

Papers

[1] "A novel bioinformatics strategy for searching industrially useful genome resources from metagenomic sequence libraries.", Hiroshi Uehara, Yuki Iwasaki, Chieko Wada, Kennosuke Wada, Toshimichi Ikemura and Takashi Abe., Genes & Genetic Systems, Vol.86, pp.53 - 66(2011)

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[6] "The genome of Pelotomaculum thermopropionicum reveals niche-associated evolution in anaerobic microbiota.", Tomoyuki Kosaka, Souichiro Kato, Takefumi Shimoyama, Shunichi Ishii, Takashi Abe and Kazuya Watanabe., Genome Research, Vol.18, pp.442 - 448(2008)

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[10] "Novel Phylogenetic Studies of Genomic Sequence Fragments Derived from Uncultured Microbe Mixtures in Environmental and Clinical Samples.", Takashi Abe, Hideaki Sugawara, Makoto Kinouchi, Shigehiko Kanaya and Toshimichi Ikemura., DNA Research, Vol.12, pp.281 - 290(2005)

[11] "Direct cloning of genes encoding novel xylanases from the human gut.", Hidenori Hayashi, Takashi Abe, Mitsuo Sakamoto, Hiroki Ohara, Toshimichi Ikemura, Kazuo Sakka and Yoshimi Benno., Canadian Journal of Microbiology, Vol.51, pp.251 - 259(2005)

[12] "Substrate-induced gene-expression screening of environmental metagenome libraries for isolation of catabolic genes.", Taku Uchiyama, Takashi Abe, Toshimichi Ikemura and Kazuya Watanabe., Nature Biotechnology, Vol.23, pp.88 - 93(2005)

[13] "Informatics for unveiling hidden genome signatures.", Takashi Abe, Shigehiko Kanaya, Makoto Kinouchi, Yuta Ichiba, Tokio Kozuki and Toshimichi Ikemura., Genome Research, Vol.13, pp.693 - 702(2003)

[14] "Analysis of codon usage diversity of bacterial genes with a self-organizing map (SOM) : characterization of horizontally transferred genes with emphasis on the E. coli O157 genome.", Shigehiko Kanaya, Makato Kinouchi, Takashi Abe, Yoshihiro Kudo, Yuko Yamada, Tatsuya Nishi, Hirotada Mori and Toshimichi Ikemura., Gene, Vol.276, pp.88 - 99(2001)

Book Chapters

[1] Takashi Abe, Shigehiko Kanaya and Toshimichi Ikemura. 2010. "Sequences from prokaryotic, eukaryotic and viral genomes currently available clustered according to phylotype on a large-scale Self-Organizing Map.", Knowledge-Based Bioinformatics; Gil Alterovitz and Marco Ramoni (Eds.) Wiley & Sons, Ltd. pp.233-249