



**Journal of Pesticide Science**  
Pesticide Science Society of Japan

[Available Issues](#) | [Japanese](#) >> [Publisher Site](#)

Author:  Keyword:   **ADVANCED**



[TOP](#) > [Available Issues](#) > [Table of Contents](#) > [Abstract](#)

ONLINE ISSN : 1349-0923

PRINT ISSN : 1348-589X

**Journal of Pesticide Science**

Vol. 31 (2006) , No. 3 pp.282-288



[\[PDF \(384K\)\]](#) [\[References\]](#)

## **G-language System as a platform for large-scale analysis of high-throughput omics data**

**Kazuharu Arakawa<sup>2)</sup> and Masaru Tomita<sup>1)</sup>**

1) Institute for Advanced Biosciences, Keio University

2) Japan Society for the Promotion of Science

(Received: June 13, 2006)

### **Abstract:**

The advent of high-throughput measurement technologies has resulted in the rapid accumulation of “omics” information including genome, transcriptome, proteome, and metabolome data. This increase in data acquisition has led to a demand for an efficient computational platform for *in silico* analysis. The G-language software suite provides a comprehensive workbench for large-scale omics research and systems biology. The suite includes a bioinformatics research framework G-language Genome Analysis Environment, which contains a Gene Prediction Accuracy Classification benchmarking tool for the quantification of the sensitivity of genome informatics analysis methods to genome annotation completeness. Omics data processed in this environment can be visualized with KEGG-based pathway mapping web service, and Genome-based Modeling System enables automatic prototyping of metabolic pathway models from the genome. The software suite covers various domains of omics, with the goal of integrating all of these data for research into systems biology.

### **Keywords:**

bioinformatics, omics, G-language System, software tools, analysis pipelines, systems biology, post-genome



[\[PDF \(384K\)\]](#) [\[References\]](#)

To cite this article:

Kazuharu Arakawa and Masaru Tomita, "G-language System as a platform for large-scale analysis of high-throughput omics data". *J. Pestic. Sci.* Vol. **31**, pp.282-288 (2006) .

---

doi:10.1584/jpestics.31.282

JOI JST.JSTAGE/jpestics/31.282

*Copyright (c) 2006 Pesticide Science Society of Japan*

---



---

[Japan Science and Technology Information Aggregator, Electronic](#)

