The AB05 NIAB Tools Workbench for Building Automatic Biopathway Maps for Agricultural Organisms

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Summary

For the past several years, we have built various tools for automatic construction of biopathways to help biological experts, especially in the field of agriculture. We integrated several systems for constructing web applications for analyzing biological pathway information for agricultural species, constructing optimized pathway maps. In addition to building web applications for agricultural pathway information, we developed several stand-alone software tools, which are publicly downloadable under proper license agreements.

Availability: The website for the system is http://biopath. niab.go.kr/index.jsp. Technical manuals for the project are available.

Keywords: visualization, pathway map, interaction, bioinformatics

The AB05 Modules

We have been building a software system-the NIAB AB05 Tools Workbench-for analyzing and visualizing biological pathways and networks for efficient exploitation. It is based on a comprehensive, extensible data model that can be used to model biological pathways and networks. The system aims to be a portal site for agricultural genome and pathway information sites, combining genome and pathway informatics modules on the web. The system has been uniformly written in Java for portability, composed of several web application modules and stand-alone modules, including ABIS, MPV, PathFinder, BioPathCAD, BioNetView, Biopathway XML Conversion Parser, PDB3D, BioTextMiner, WeSAT, Interfacer, and WASPIV. These modules can be further divided into web-based tools and stand-alone modules.

The ABIS, MPV, BioNetView, and BioTextMiner modules are web-based service modules. To explain some of the features of these modules, the ABIS (Fig. 1(a)) and MPV (Fig. 1(c)) modules are designed as three-tier applications: a tier for providing interfaces to existing databases, a tier for analyzing biopathway data, and a tier for visualizing the result of the analysis. They are based on an SVG[1])-based tool for visualizing metabolic pathways and regulatory pathways. The goal of BioNetView (Fig. 1(b)) is to create a clear and useful protein-interaction visualization model that is fully automated to handle large datasets. The browser is a tool that hierarchically lists the pathways, processes, and molecular entities in the database. BioTextMiner in Fig. 1(d) is also a web-based application tool designed to handle textual information related to biological pathways through the internet. Because important background knowledge in bioinformatics is often buried in textual documents, the role of BioTextMiner is to search the literature and automatically extract information from online abstracts and papers.

Other tools are stand-alone modules at this time, although converting stand-alone applications into web-based services is not difficult. To explain several modules among them, PDB3D in Fig. 1(e) is a simple PDB (Protein Data Bank) visualization tool for biomolecular structures, sequences, and sequence alignments. The view of the structure can be changed in several ways. Residues selected through the sequence view will be highlighted by a brighter-than-usual color. The BioCAD module in Fig. 1(f) is also a stand-alone pathway editor for drawing and annotating biological pathways. It integrates the different possibilities of charting elements with different attributes, drawing connections between elements with distinct characteristics. The result of the editing process is an XML (eXtended Markup Language) file for the appropriate links.

Due to limited space, we have briefly introduced only several exemplary modules of the NIAB AB05 Workbench. We expect that by combining these modules in the future, we will create a software environment that enables users to conduct a large number of bioinformatics analyses, combined with smooth data management and excellent

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1) **Scalable Vector Graphic (SVG)** is an XML specification and file format for describing two-dimensional vector graphic, both static and animated.

graphical viewing and output options.

Software Release Stage

Implementation of each module has progressed far beyond what was initially planned and now incorporates concepts required for representing many other biological pathways. However, some AB05 NIAB Tools still await full testing of all their functionalities and is not feature complete. The current release is the first version released outside the organization that developed the software, for the purpose of evaluation or real-world testing. Our software generally includes all features but may also include known issues and bugs of a less serious variety. For example, BioCAD in Fig. 1(f) is only an alpha release. Identification of appropriate knowledge discovery problems, integration design of each module, and development of evaluation methods are also ongoing. We expect to have a bioinformatics solution that continuously evolves through frequent program updates with the latest scientific developments.
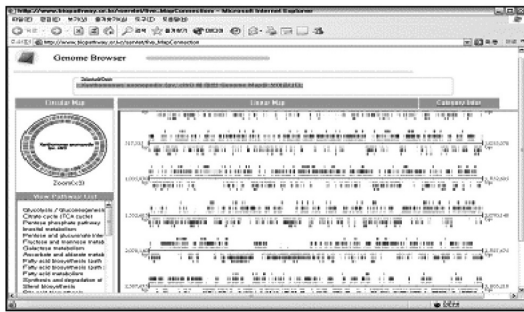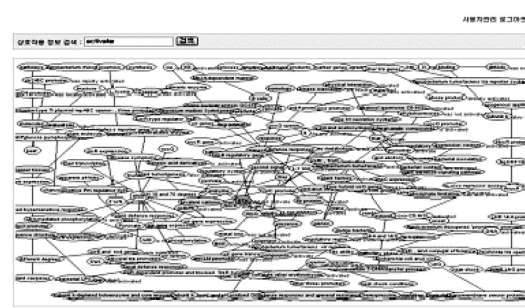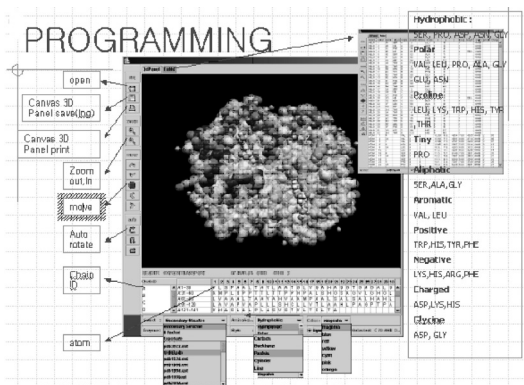

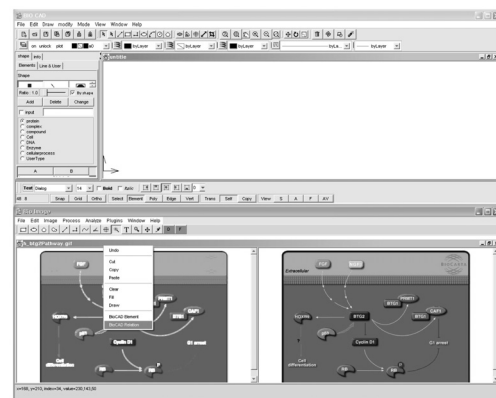(a) The ABIS System
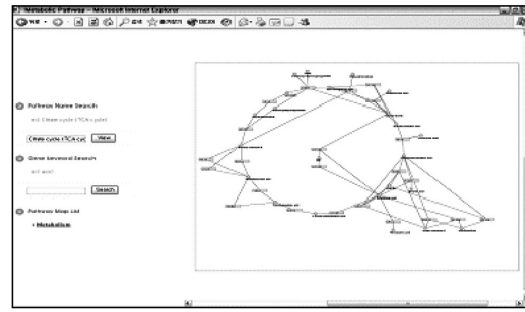
(b) Multi Pathway Viewer
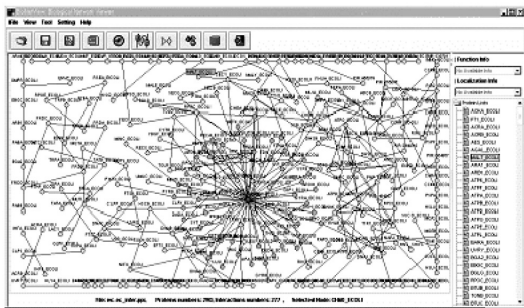
(c) BioNetView

(d) BioTextMiner

(e) PDB3D

(f) BioCAD

Fig. 1. AB05 Tools

Acknowledgments

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