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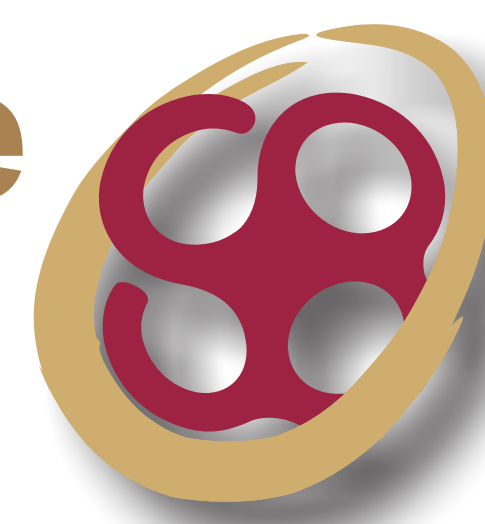COGNITIVE SYSTEMS · PROF. DR. A. ZELL

KEGGtranslator: visualizing and converting the KEGG PATHWAY database to various formats

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The KEGG PATHWAY database provides a widely used service for metabolic and nonmetabolic pathways. It contains manually drawn pathway maps with information about the genes, reactions and relations contained therein. To store these pathways, KEGG uses KGML, a proprietary XML-format. Parsers and translators are needed to process the pathway maps for usage in other applications and algorithms.
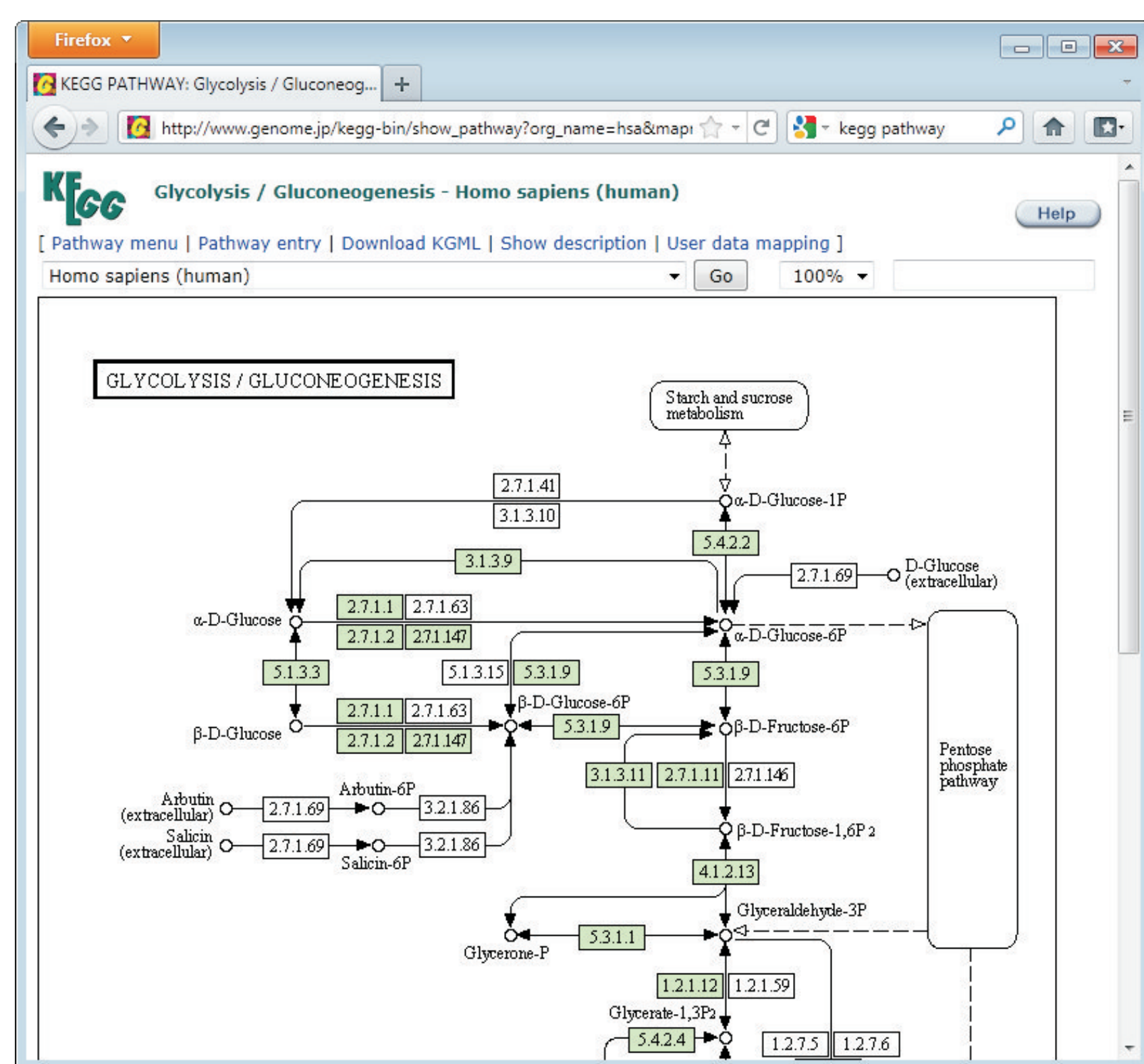

Fig. 1: The KEGG database contains information about a large collection of compounds and pathways that qualitatively describe the interplay between these compounds. In order to make use of this rich source of information it is often required to manually extract and convert the given pathway diagrams into data formats that can be imported to other applications for further processing.

KEGGtranslator

We have developed KEGGtranslator, an easy-to-use stand-alone application that can visualize and convert KGML formatted XML-files into multiple output formats. Unlike other translators, KEGGtranslator supports a plethora of output formats, is able to augment the information in translated documents (e.g., MIRIAM annotations) beyond the scope of the KGML document, and amends missing components to fragmentary reactions within the pathway to allow simulations on those.

Availability

KEGGtranslator is freely available as a Java™ Web Start application and for download at http://www.cogsys.cs.uni-tuebingen.de/software/KEGGtranslator. KGML files can be downloaded from within the application.
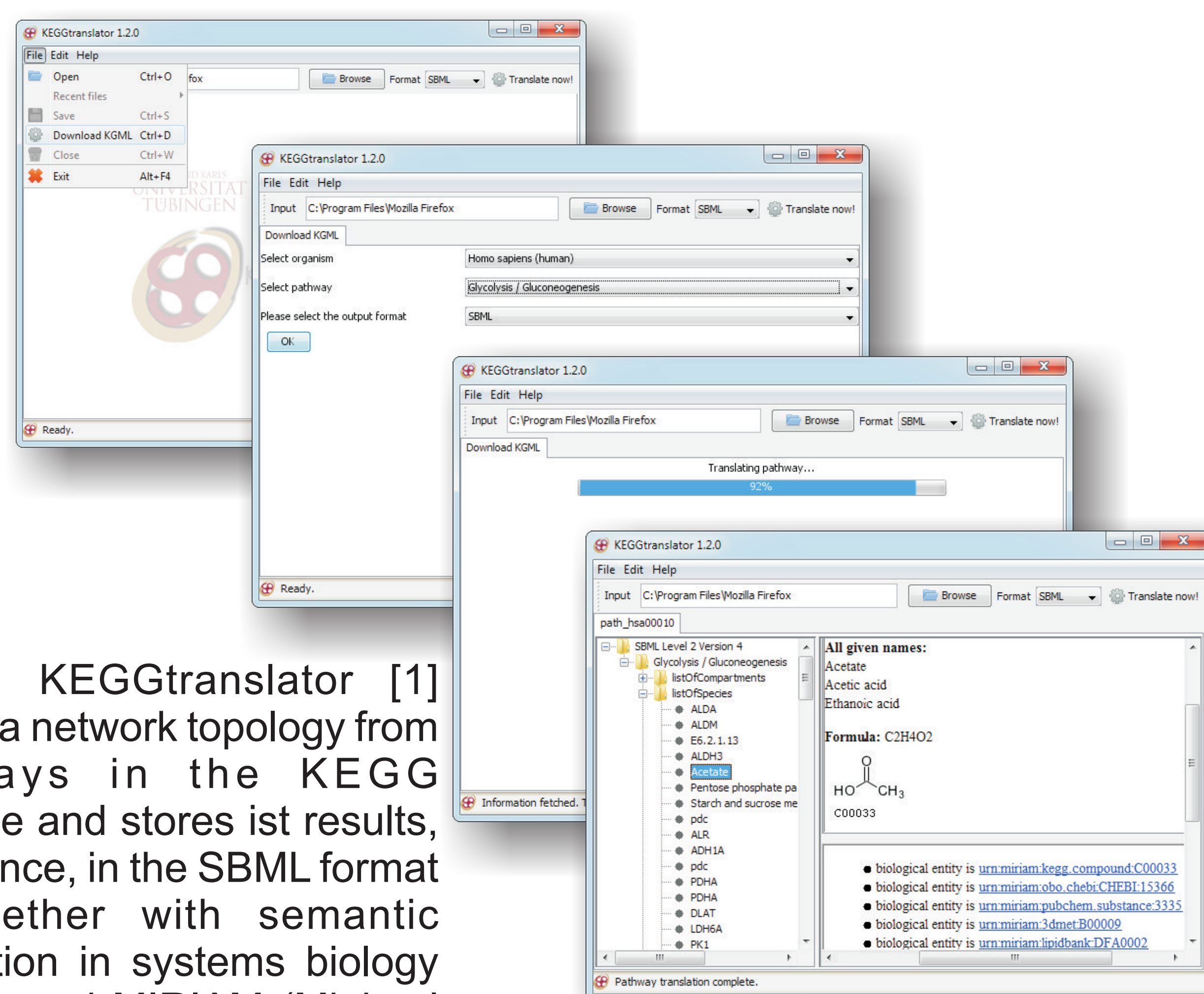

Fig. 2: KEGGtranslator [1] creates a network topology from pathways in the KEGG database and stores ist results, for instance, in the SBML format [2] together with semantic information in systems biology ontology and MIRIAM (Minimal Information Required in the Annotation of Models). It also includes all graphical annotations in form of CellDesigner tags. KEGGtranslator guides the user through the conversion, allows command-line batch processing, automatic download of KEGG pathways, and conversion to various graphical formats.
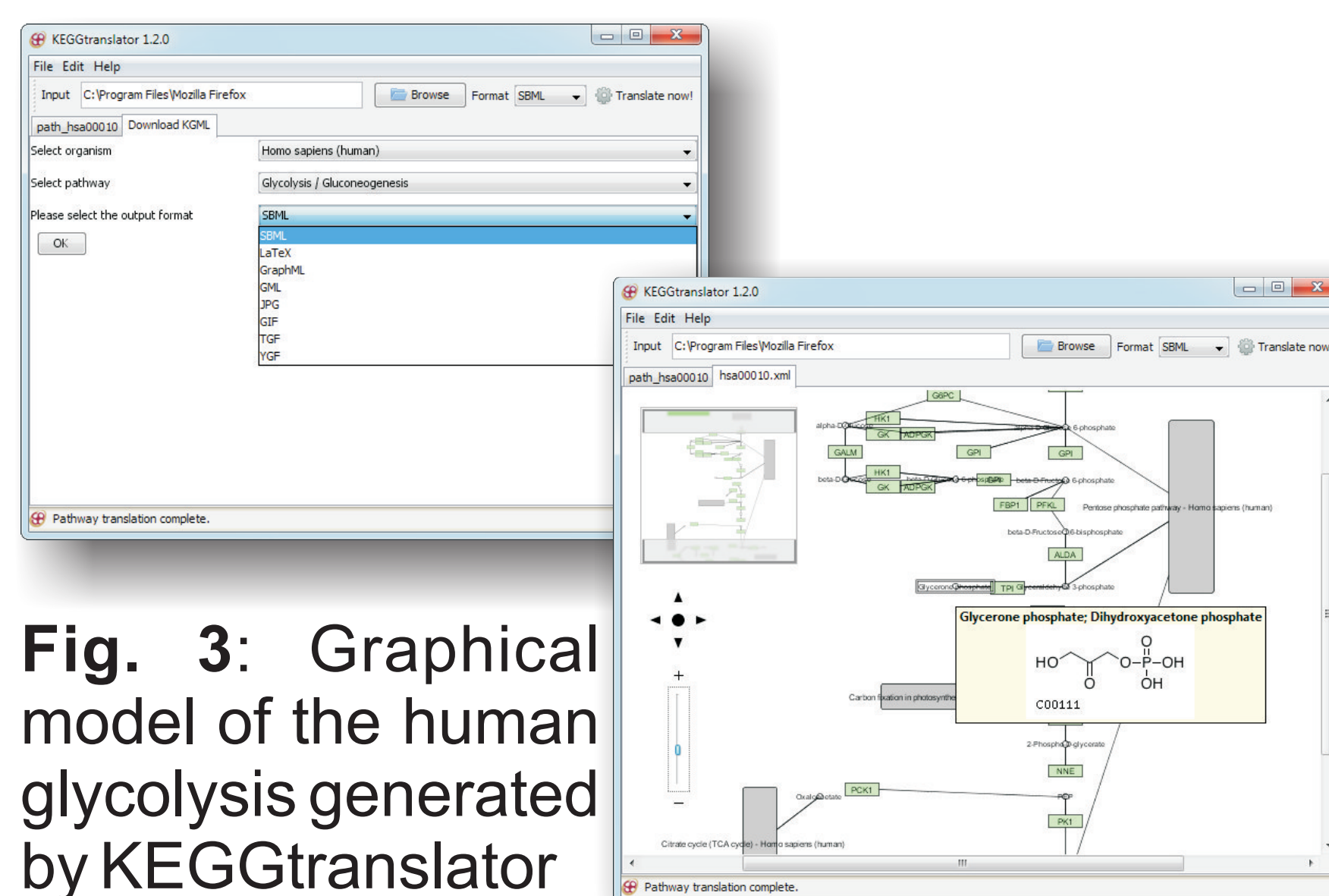

Fig. 3: Graphical model of the human glycolysis generated by KEGGtranslator

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[2] Hucka M, Finney A, Sauro HM et al. The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. Bioinformatics 19 (4): 524–31, 2003.

[3] Dräger A, Rodriguez N, Dumousseau M, Dörr A, Wrzodek C, Le Novère N, Zell A, Hucka M. JSBML: a flexible Java library for working with SBML. Bioinformatics, 27(15):2167-2168, June 2011.

[4] Dräger A, Planatscher H, Wouamba DM et al. SBML2LaTeX: Conversion of SBML files into human-readable reports. Bioinformatics, 25(11):1455-1456, April 2009.

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