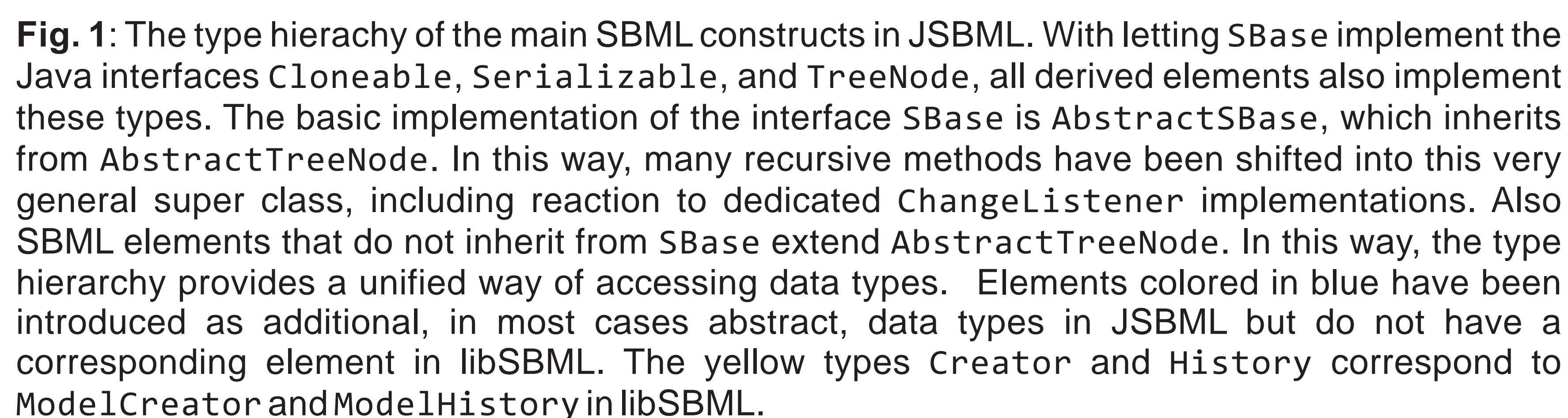


Source code, binaries and documentation for JSBML can be freely obtained under the terms of the LGPL2.1 from the website <http://sbml.org/Software/JSBML>.

JSBML provides an SBML parser and programming library that maps all SBML elements to a flexible and extended type hierarchy (Fig. 1). JSBML strives to attain compatibility with libSBML's Java API, to ease a switch from one library to the other. JSBML supports all constructs for SBML up to the latest Level 3 Version 1, including an API to add SBML extensions. More complex functions of libSBML, e.g., model consistency checking, SBML validation, and the conversion between different SBML Levels and Versions are expected to be included as separate community efforts via web services.



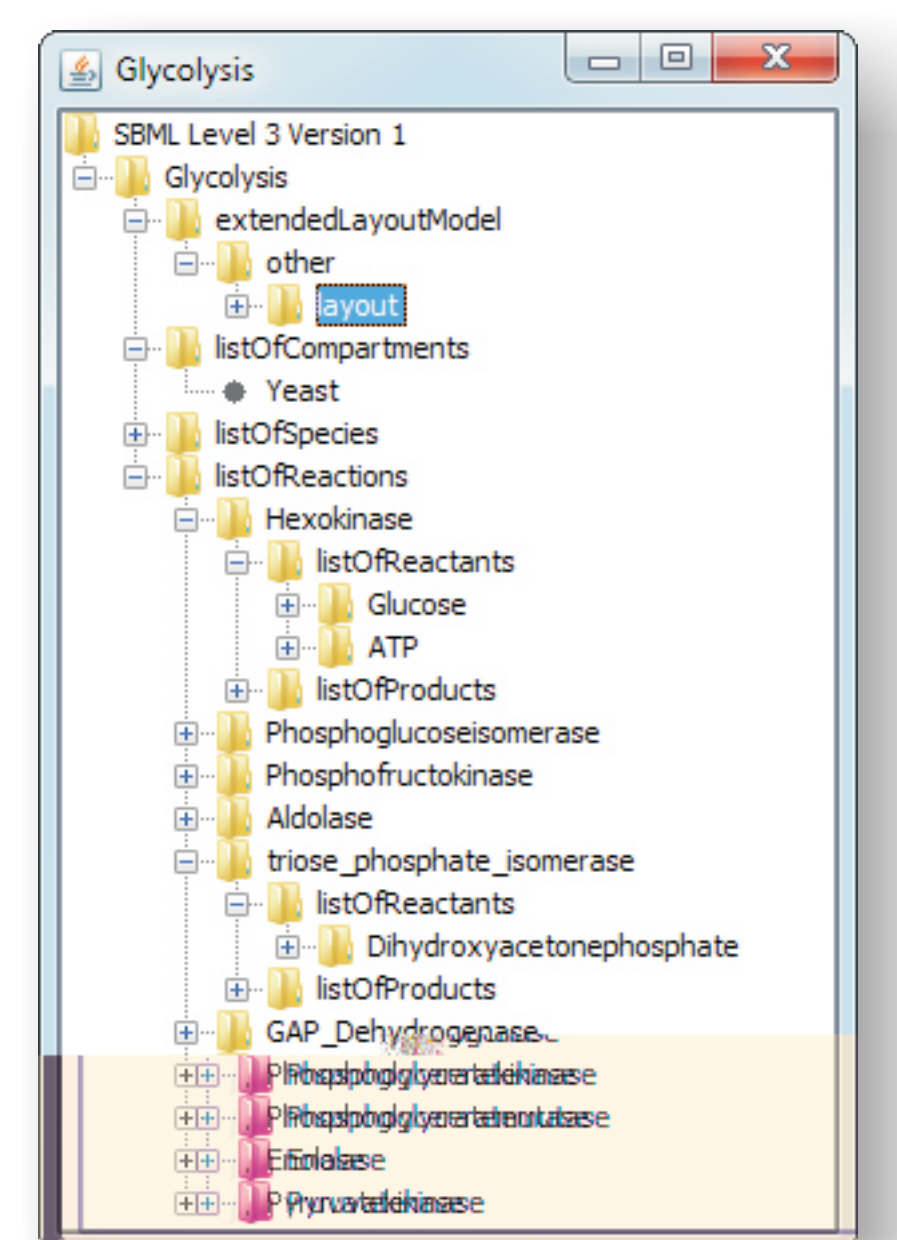
A minimal example for a visual representation of the content of an SBML file using JSBML with source code and output for an SBML test model of the glycolysis that includes a layout extension:

```
import javax.swing.*;
import org.sbml.jsbml.SBMLDocument;
import org.sbml.jsbml.xml.stax.SBMLReader;

public class JSBMLvisualizer extends JFrame {

    public JSBMLvisualizer(SBMLDocument document)
    {
        super(document.getModel().getId());
        getContentPane().add(new JFree(document));
        pack();
        setVisible(true);
    }

    // Expects file name as command line argument
    public static void main(String args[])
        throws Exception
    {
        new JSBMLvisualizer(
            SBMLReader.readSBML(args[0]));
    }
}
```



JSBML is written entirely in Java version 1.5 and does not require additional non-Java software. It is distributed in source-code form as well as pre-compiled JAR files in different versions (including/excluding third-party libraries). JSBML is a young, ongoing software project that provides comprehensive and entirely Java-based data structures to read, write, and manipulate SBML files. Its layered architecture allows for the creation of Java web start applications and CellDesigner plug-ins based on stand-alone programs with very little effort. One program, SBMLsqueezer [4] 1.3, has already been re-implemented and released using JSBML, a simulator that is benchmarked on the SBML test suit will be available soon, and many other projects are planned.

- [1] 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.
- [2] Bornstein BJ, Keating SM, Jouraku A, Hucka M. LibSBML: An API Library for SBML. *Bioinformatics*, 24(6):880–881, 2008.
- [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, 2011.
- [4] Dräger A, Hassis N, Supper J, Schröder A, Zell A. SBMLsqueezer: a CellDesigner plug-in to generate kinetic rate equations for biochemical networks. *BMC Systems Biology* 2008. 2:39. 2008.