

Tools for Molecular Interaction Maps and a Graphical Notation Validation Framework for PathVisio

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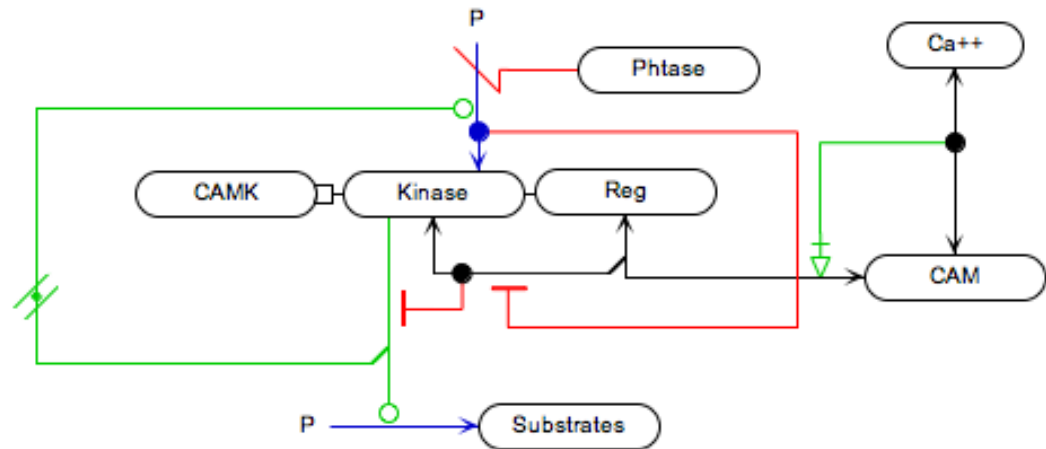


Overview

- Overview of Molecular Interaction Map (MIM) software
 - Update specification, format, API, and diagram editor
 - Network analysis
- Validation framework (Kumar Chandan/GSOC)
 - Validator plugin
 - Features
 - Groovy and Schematron ruleset support
- Issues in validator development
- Extending Schematron
- Future work

Molecular Interaction Maps (MIMs)

- A graphical notation for bioregulatory networks created by Kurt Kohn in 1999
- Creation of large diagrams that remain intuitive for use by biologists by minimizing redundant elements
- Precursor to SBGN-ER
- Tools for biologists and programmers



Luna A. et al., 2011

Current MIM Tools

```
23 <mimVis:EntityGlyph visId="f1327" pos
24 <mimVis:EntityGlyph visId="e1fe7" pos
25 <mimVis:EntityGlyph visId="d73bd" cer
  ="20.000000000000018" color="000000" type
26 <mimVis:GenericProperty key="Numk
27 <mimVis:GenericProperty key="Shay
28 </mimVis:EntityGlyph>
29 <mimVis:EntityGlyph visId="e4900" cer
  ="20.0" color="000000" type="SimplePhysic
30 <mimVis:GenericProperty key="Numk
31 <mimVis:GenericProperty key="Shay
32 </mimVis:EntityGlyph>
33 <mimVis:EntityGlyph visId="c0757" cer
  "20.0" color="000000" type="SimplePhysic
34 <mimVis:GenericProperty key="Numk
35 <mimVis:GenericProperty key="Shay
36 </mimVis:EntityGlyph>
37 <mimVis:EntityGlyph visId="a482c" cer
  type="SimplePhysicalEntity" displayName="
38 <mimVis:GenericProperty key="Numk
39 <mimVis:GenericProperty key="Shay
40 </mimVis:EntityGlyph>
41 <mimVis:EntityGlyph visId="d8200" cer
```

Machine-Readable
Format

```
1 package gov.nih.nci.lmp.mim.mimExample;
2
3 import java.io.File;
4 import java.io.FileOutputStream;
5 import java.io.OutputStream;
6 import java.util.HashMap;
7
8 import org.apache.xmlbeans.XmlOptions;
9
10 import gov.nih.nci.lmp.mim.mimVisLevel1.*
11
12 /**
13  * An class that shows an toy example for
14  */
15 public class CaCamExample {
16
17     /** The MIM-Vis doc. */
18     public DiagramDocument visDoc;
19
20     /**
21      * Create a DiagramDocument from scra
22      * physical entity (SPE), Ca++, bindi
23      */
24     public void createCaCam() {
25         visDoc = DiagramDocument.Factory.
26
27         // Create a new diagram to go wit
28         DiagramType dia = visDoc.addNewDi
29         dia.setWidth(84.7);
30         dia.setHeight(146.3);
31
32         // Create a new entity and add it
33         EntityGlyphType ca = dia.addNewEn
34         ca.setVisId("b4357");
35         ca.setCenterX(47.0);
36         ca.setCenterY(38.0);
37         ca.setWidth(60.0);
38         ca.setHeight(20.0);
39         ca.setColor("000000");
40         // This shows the way to access e
41         ca.setType(EntityGlyphType.Type.S
```

Programming
Interface

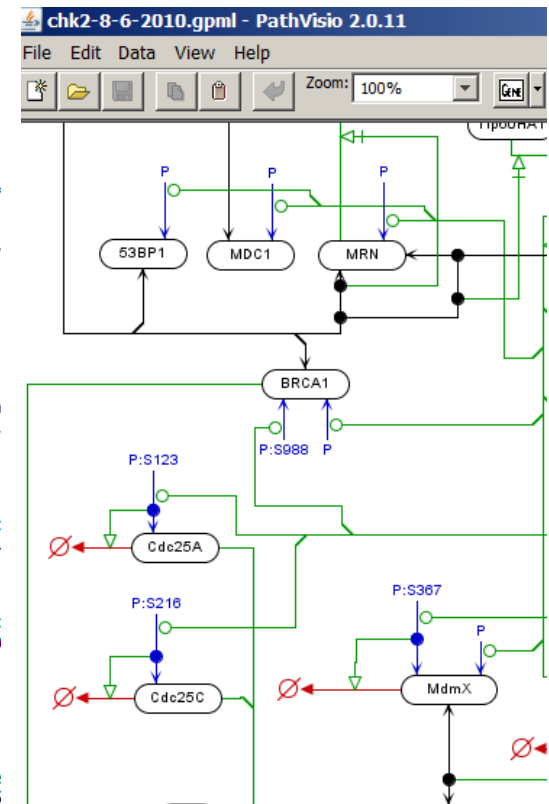


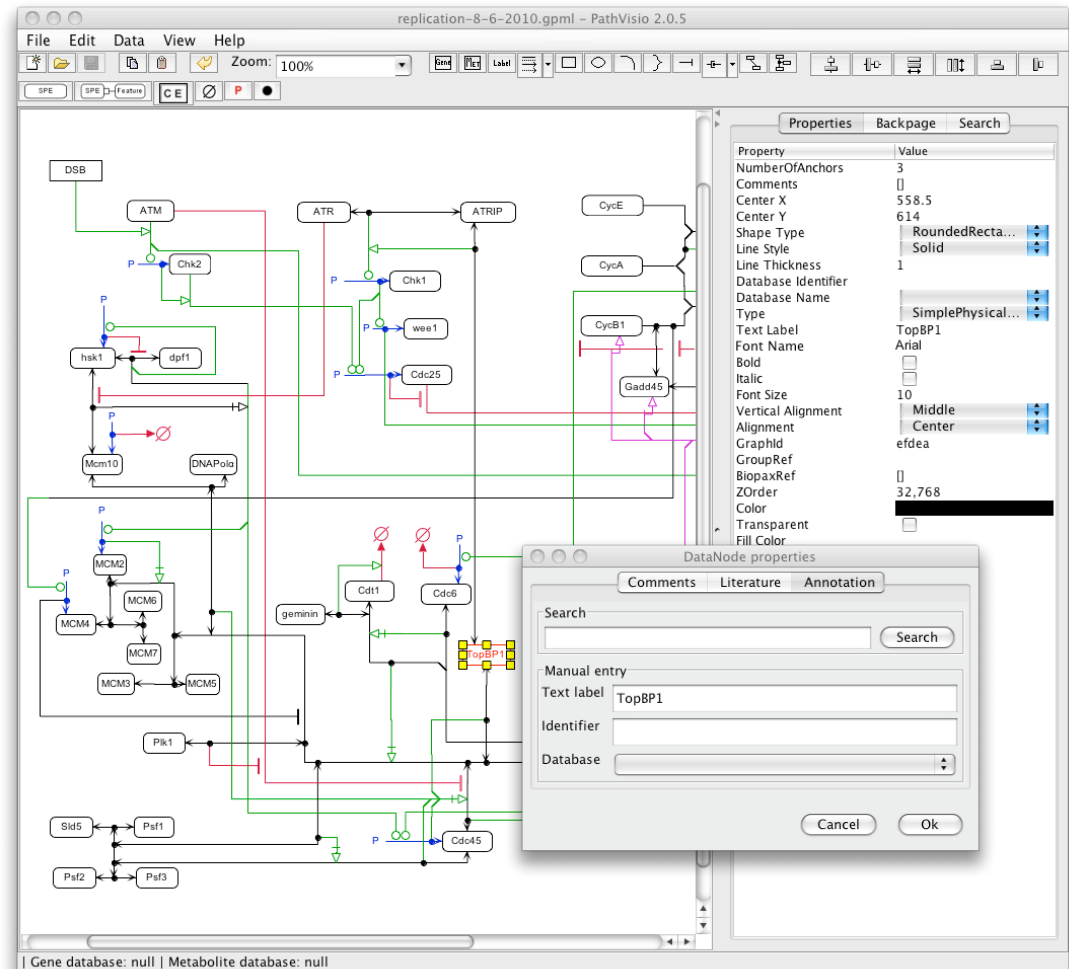
Diagram Editor

Current MIM Tools

- Updated MIM specification to make MIM “machine-friendly”
- MIM format similar on GPML
- API being generated with XMLBeans for Java
- Syntactic validation using Schematron
 - Makes assertions about the presence or absence of patterns in XML documents using XPath
 - Processed into XSLT

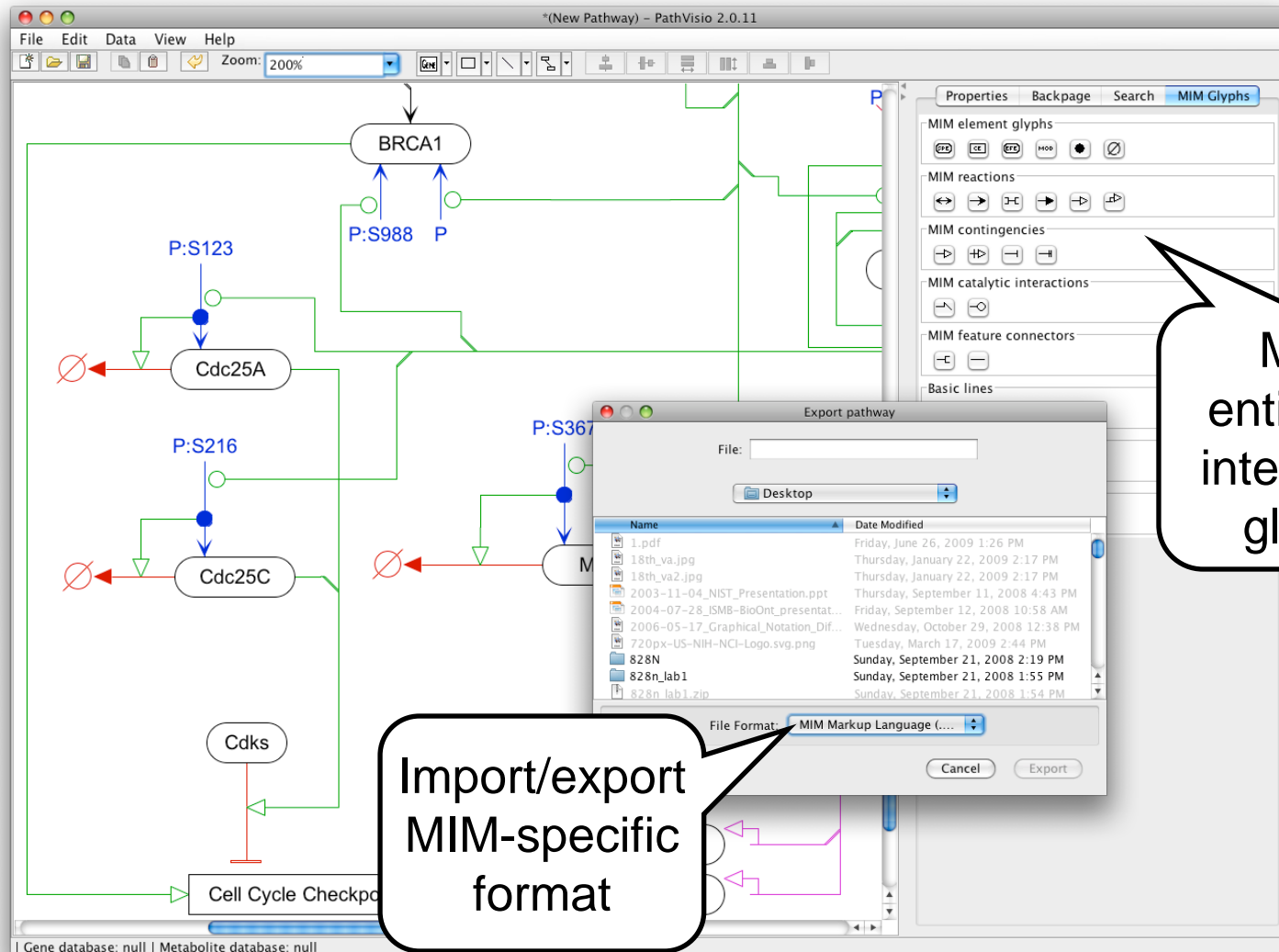
Choosing PathVisio for MIM Diagrams

- Open-source
- Java
- Plugins
 - Cytoscape
 - BioPAX
 - SBGNML
- WikiPathways

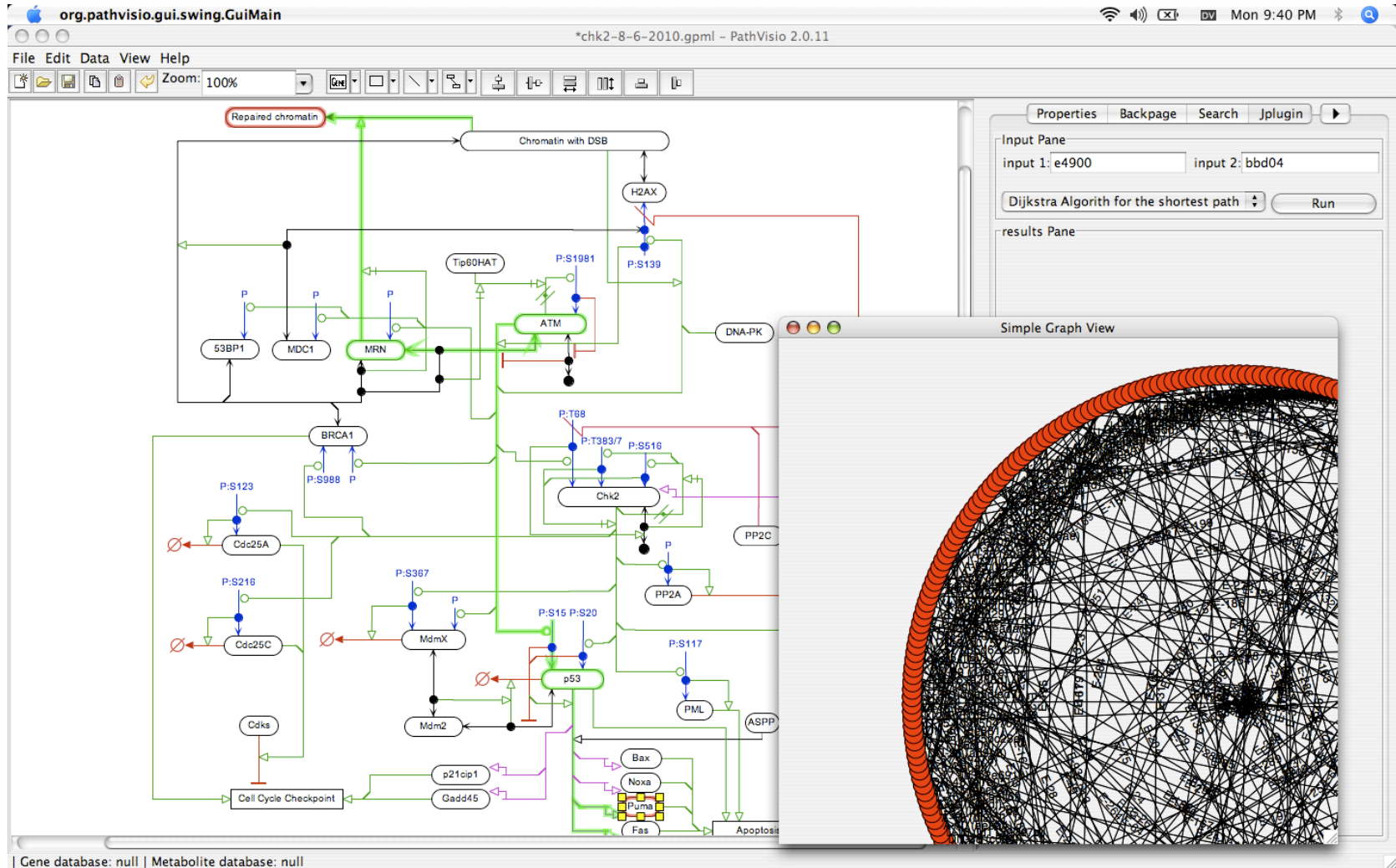


van Iersel, M. et al. 2008

PathVisio-MIM Plugin



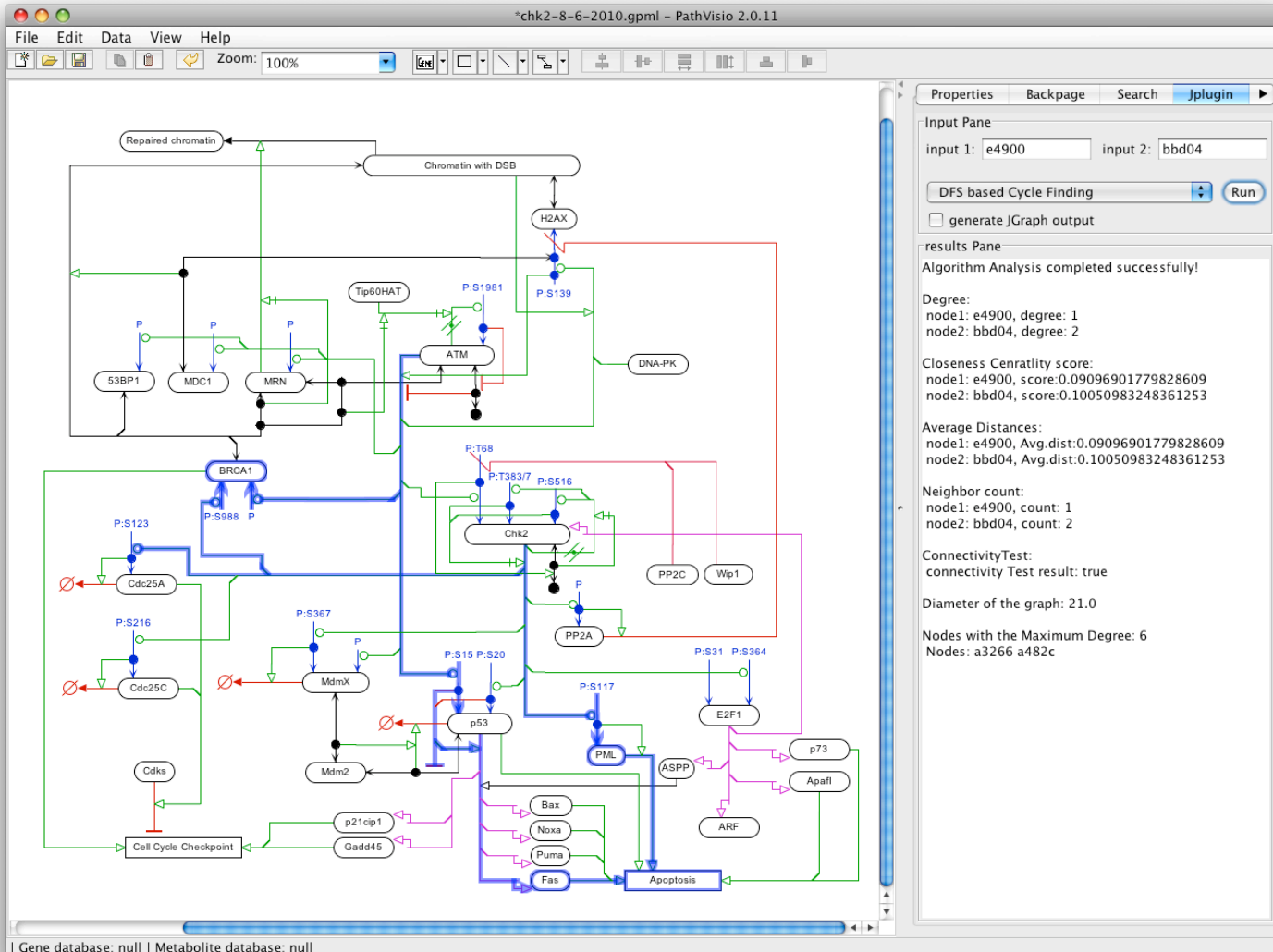
Network Analysis: Shortest Path



Chandan, K. and Luna, A. (unpublished)

9/6/2011

Feedback Cycle Finding



Chandan, K. and Luna, A. (unpublished)

9/6/2011

PathVisio Validator Plugin

The screenshot displays the PathVisio Validator Plugin interface. The main window shows a metabolic pathway diagram with various entities (A, B, C, D, E, F, G, H, I, J, K, M) and interactions. A callout labeled "Error: Unattached Line" points to a blue line segment that is not connected to any entity. Another callout labeled "Highlighted Errors" points to a specific error in the diagram. The right-hand panel displays validation results for the "mimmi_validation" ruleset. It shows 3 errors and 0 warnings. The errors are listed as follows:

- 1.) Error - The end of an interaction should possess a visRef attribute.
- 2.) Error - Non-branched interactions possessing a 'CovalentBondCleavage' arrowhead should be terminated with a 'Line' arrowhead.
- 3.) Error - A covalent bond cleavage interaction should be connected to one of the following entity types: entity feature, simple physical entity, implicit complex, conceptual entity, or explicit complex.

The interface also includes a "Rule Groups" dropdown menu, a "Ruleset Selection" dropdown menu, and a "Filter Message Type" dropdown menu. At the bottom, there are buttons for "Highlight All", "Validate", "Errors & Warnings", and "Choose Ruleset". The status bar at the bottom indicates "Gene database: null | Metabolite database: null".

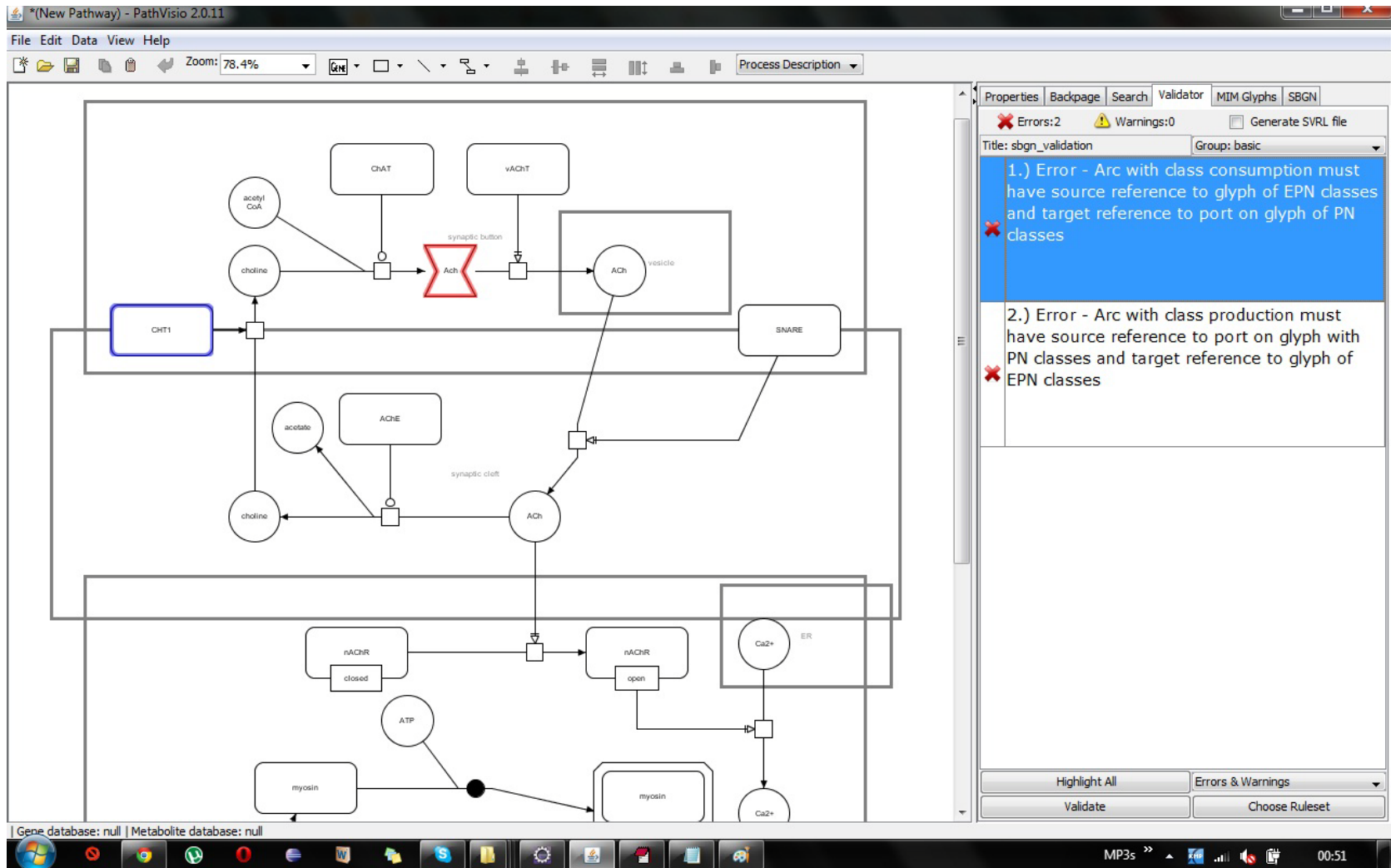
Chandan K. et al. (submitted)

9/6/2011

PathVisio Validator Plugin Features

- Current Rulesets: MIM, WikiPathways, SBGN expected
- Selective rules
 - Validation on rule subsets
 - Users can filter out errors or warnings
 - Ignore diagram element or message instance
 - Ignore in session or permanently
- Groovy and Schematron support
 - Groovy:
 - Easier to write for Java developers
 - Tied to internal workings of PathVisio
 - Schematron:
 - Reusable in software with access to an XSLT processor
 - Standardized validation report language

SBGN Validation Support in PathVisio



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Comparison Schematron and Groovy: Unattached Line Check

Groovy

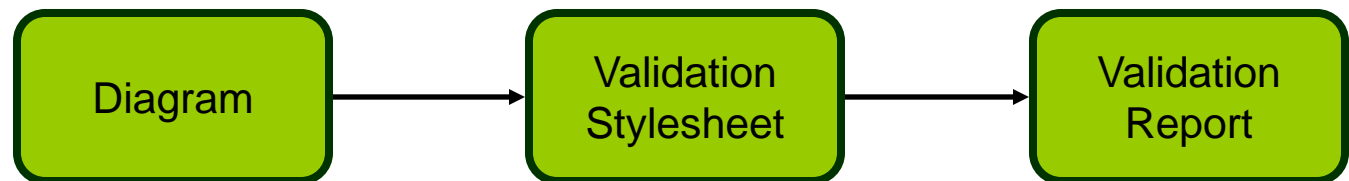
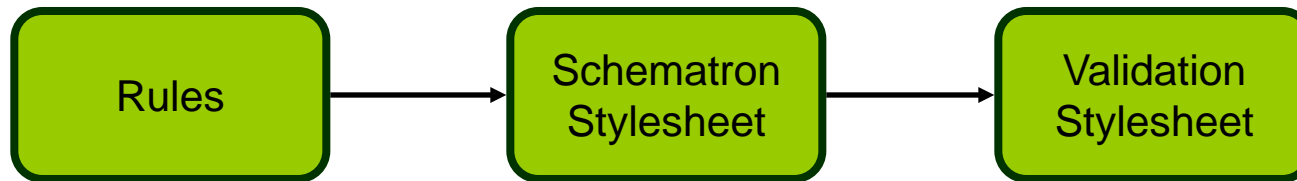
```
4 //The rule below checks for unattached lines by checking each of the "Line" element's first and last "GraphRef" attributes.
5 ArrayList<String>[] ruleUnattachedLines(Pathway pw) {
6     String[] result = null; // the intermediate result to be added to the final result
7     ArrayList<String>[] totalResultForThisRule = null; // the final result which is sent to the Validator
8     for(PathwayElement pwe: pw.getDataObjects()){
9         if(pwe.getObjectType()==ObjectType.LINE && // check if the Pathway element is of the type : "Line"
10            ( pwe.getStartGraphRef()==null | pwe.getEndGraphRef()==null // check its "GraphRef" values
11              | pwe.getEndGraphRef().equals("") | pwe.getStartGraphRef().equals("") ) ){
12             if(totalResultForThisRule==null){
13                 totalResultForThisRule=new ArrayList<String>[]>();
14             }
15             //result[0]: "error" / "warning"; result[1]: diagnostic message; result[2]: element's Graph-Id
16             result = ["error", "Lines should be attached at both ends.", pwe.getGraphId()];
17             totalResultForThisRule.add(result);
18         }
19     }
20     if(totalResultForThisRule==null) System.out.println("All the lines are attached");
21     return totalResultForThisRule; // this final result is passed to the Validator
22 }
```

Schematron

```
5 <!-- Check that all lines are attached at both ends -->
6 <iso:pattern name="check-unattached-lines" id="check-unattached-lines">
7     <!-- Check "Line" elements -->
8     <iso:rule context="gpml:Line" role="error">
9         <!-- Get the unique identifier for the line -->
10         <iso:let name="graph-id" value="@GraphId"/>
11
12         <!-- Get the GraphRefs (these indicate the GraphIds of the objects the line is connected to) of the first and last points for a line -->
13         <iso:let name="start-graph-ref" value="gpml:Graphics/gpml:Point[position()=1]/@GraphRef"/>
14         <iso:let name="end-graph-ref" value="gpml:Graphics/gpml:Point[last()]/@GraphRef"/>
15
16         <!-- Assert that the GraphRef attributes on the first and last points are present and not empty, otherwise output error message and identifier -->
17         <iso:assert test="$start-graph-ref and $end-graph-ref and not($start-graph-ref='') and not($end-graph-ref='')"
18             diagnostics="graph-id">Lines should not be unattached.</iso:assert>
19     </iso:rule>
20 </iso:pattern>
```

Validation Mechanism Using Schematron

Step 1: Generating Validation Stylesheet



Step 2: Validation of Diagram

Validation Process

- Groovy
 1. Validate diagram
 2. Display messages
- Schematron
 1. Generate validation stylesheet
 2. Export diagram
 3. Transform diagram to validate
 4. Parse validation report
 5. Display messages

Schematron Rule and Validation Report

```
<iso:pattern name="check-int-visref" id="check-  
int-visref">  
<iso:rule context="mimVis:InteractionGlyph">  
<iso:let name="vis-id" value="@visId"/>  
<iso:assert test="mimVis:Point[1]/@visRef"  
diagnostics="vis-id">The start of an  
interaction should possess a visRef  
attribute.</iso:assert>  
<iso:assert test="mimVis:Point[last()]/@visRef"  
diagnostics="vis-id">The end of an  
interaction should be possess a visRef  
attribute.</iso:assert>  
</iso:rule>  
</iso:pattern>
```

Validation Schematron File

```
<svrl:active-pattern id="check-int-visref" />  
<svrl:failed-assert  
test="mimVis:Point[1]/@visRef"  
location="...">  
<svrl:text>The start of an interaction should  
possess a visRef attribute.</svrl:text>  
<svrl:diagnostic-reference diagnostic="vis-  
id">idcd72516b</svrl:diagnostic-reference>  
</svrl:failed-assert>  
</svrl:active-pattern>
```

SVRL Validation Output

Issues Encountered

- Validating files with non-MIM glyphs
 - Exporter could not function because of enumerated types in XML schema
 - Resolution: Moved enumeration validation to Schematron
- Issues incorporating Saxon XSLT processor
 - As of Saxon 9.2, some useful features (e.g. extensions) were removed from the free version
 - Resolution: Used Saxon-B (Saxon 9.1)

Schematron Extensions with Saxon XSLT Processor

Schematron File

```
<iso:schema
  xmlns:iso="http://purl.oclc.org/dsdl/schematron"
  xmlns:xsl="http://www.w3.org/1999/XSL/Transform">
  <iso:ns prefix="sbgn" uri="http://sbgn.org/libsbgn/0.2"/>
  <iso:ns prefix="sbgn-ext" uri="java:org.sbgn.SaxonTools.Extensions"/>
  <iso:pattern name="saxon-test" id="00001"><iso:rule context="sbgn:arc">
    <iso:assert
      test="not (sbgn-ext:return-true()) ">Saxon extension worked.</iso:assert>
    </iso:rule></iso:pattern>
</iso:schema>
```

Java Extension

```
package org.sbgn.SaxonTools;
public class Extensions {
    public static Boolean returnTrue() {
        Boolean b = new Boolean("true");
        return b;
    }
}
```

Next Steps

- Molecular Interaction Maps (MIMs)
 - Continued work network analysis components for MIMs
- Validation
 - Extend to other notations:
 - SBGN ruleset
 - KEGG ruleset?
 - Incorporate validator into WikiPathways (<http://wikipathways.org/>)
 - Continuous background validation
 - COMBINE validation report language ([combinevrl](http://combinevrl.org/))
- Software Links
 - MIM software: <http://discover.nci.nih.gov/mim>
 - Validator plugin: <http://pathvisio.org/wiki/PathwayValidatorHelp>

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 - Mine Edes
 - Ruth Nussinov
 - Can Ozturan
- BioPAX Community
- SBGN Community