

# Dizzy: a stochastic simulator



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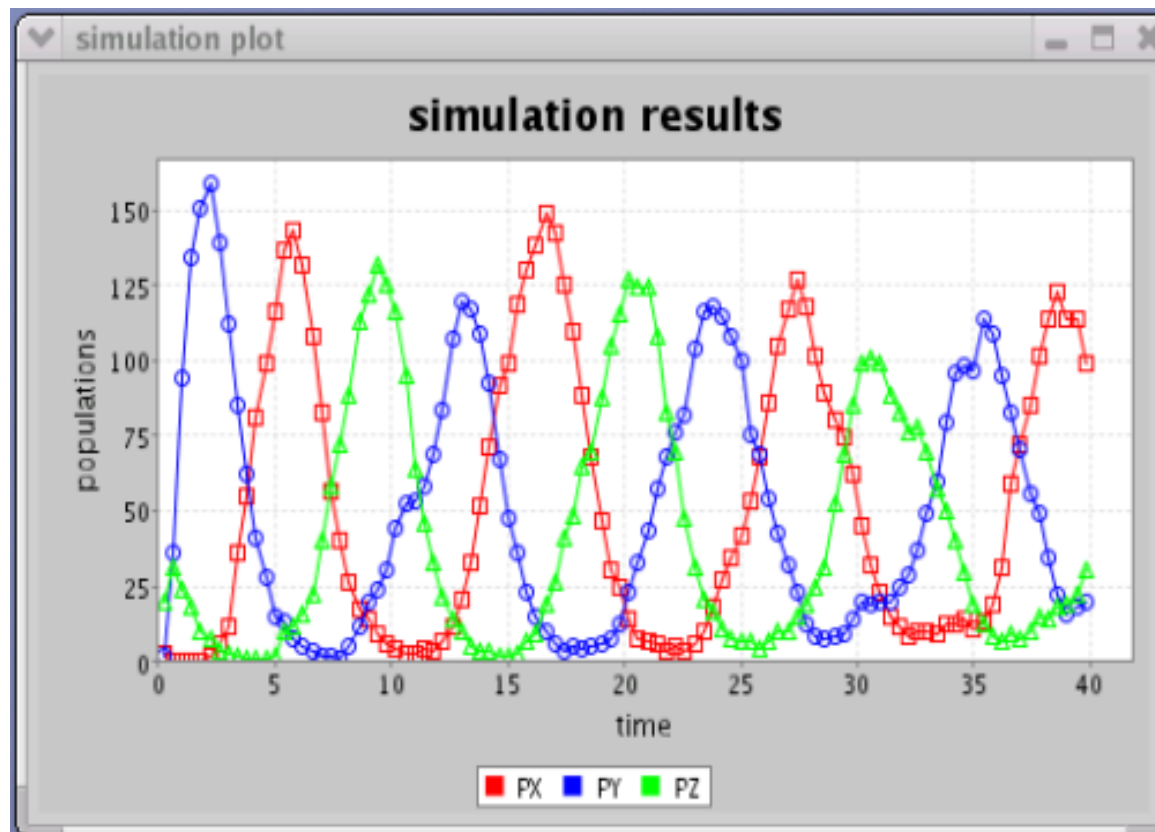
# Dizzy Overview

- SBML import/export
- Java with Swing GUI
- Stochastic simulators
- ODE simulators
- “Dizzy” language
- SBW integration
- Cytoscape integration

The screenshot displays the Dizzy software interface, which is divided into several windows:

- Dizzy (Code Editor):** Shows the model definition in the "Dizzy" language. The code includes parameters for initiation rate, activation strength, translocation rate, and inter-PCOM distance, along with model definitions for species and reactions.
- simulation plot:** A line graph showing the population of nRNA over time. The y-axis is labeled "populations" and ranges from 0.0 to 1.0. The x-axis is labeled "time" and ranges from 0 to 40. The plot shows a sharp initial rise in nRNA population, reaching a steady state around 0.9 after approximately 5 time units.
- Dizzy: simulator:** A control panel for running simulations. It includes a "simulation:" section with "start", "cancel", "stop", and "resume" buttons. A "simulators:" list shows options like "ODE-RK5-adaptive", "ODE-RK5-fixed", "gibson-bruck", and "gillespie-direct". The "gillespie-direct" simulator is currently selected. Other settings include "start time: 0.0", "stop time: 40", "num samples: 100", and "number of ensembles / number of timesteps: 1000". A "view species:" list shows "PCOM\_at\_base\_1", "PCOM\_at\_base\_100", "PCOM\_at\_base\_1000", "PCOM\_at\_base\_101", "PollI", and "nRNA". The "Output Type" section has radio buttons for "print" (selected) and "plot", and a "save results as a text (CSV) file:" option.

# SBML Import: Repressilator



Stochastic simulation of “Repressilator” model of Elowitz et al. (2000)

Dizzy can import SBML Level 1, versions 1 and 2 (exports L1,V1)

# Dizzy Language

- Symbolic mathematical expressions:  $R = [A * B * (1.0 - \text{time}) * k]$   
 $R1, A + B \rightarrow C + D, [R]$
- Define simple chemical reactions:

```
loop (i, 1, 10)
{
    "r[i]", "A[i]" + "B[i]" -> "C[i]", k;
}
```
- Loop constructs:
- File inclusion:

```
include "foo.dizzy";
```
- Compartments:

```
A @ myCompartment;
```
- Multi-step reactions:

```
transcribe, pcomplex -> pcomplex + rna, rate, 1000;
```
- Comments:

```
// this is a comment
```
- Comments:

# Future Work

- Template feature for reusable model elements
- Support for SBML Level 2 import (export?)
- Improve performance of ODE simulators
- Model diffusion and transport
- Interoperate with BioTapestry
- Automatically obtain steady-state

# Software Used

- ISBJava: ISB ([labs.systemsbiology.net/bolouri](http://labs.systemsbiology.net/bolouri))
- Graphing: Jfreechart ([www.jfree.org](http://www.jfree.org))
- JNLP: NetX ([jnlp.sourceforge.net/netx](http://jnlp.sourceforge.net/netx))
- JavaHelp: Sun ([java.sun.com/products/javahelp](http://java.sun.com/products/javahelp))
- SBW: SBW Dev Grp ([www.sbw-sbml.org](http://www.sbw-sbml.org))
- SBML lib: SBML Dev Grp ([www.sbw-sbml.org](http://www.sbw-sbml.org))
- Ant: Apache Project ([ant.apache.org](http://ant.apache.org))
- InstallAnywhere: Zero-G ([www.zerog.com](http://www.zerog.com))

# Dizzy on the Web

<http://labs.systemsbiology.net/bolouri/software/Dizzy>