



#### AMEBA Interactive visualization of metabolic networks

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## Include even more information: reaction fluxes







### Visualization of metabolic networks







## Visualization of metabolic networks





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### Metabolic context





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#### **NetworkX**

- http://networkx.github.com
- graph.degree(node)
- graph.edge[newNode][successor]["disconnected"] = True
- output: various graph formats (e.g. GML, GraphML, dot)
- However, interactive usage would be handy...





### xdot - exactly what I needed

- http://code.google.com/p/jrfonseca/wiki/XDot
- an interactive viewer for graphs written in Graphviz's dot language
- can be used either as a standalone application from command line, or as a library embedded in your python application





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Features

- Since it doesn't use bitmaps it is fast and has a small memory footprint
- Arbitrary zoom, Keyboard/mouse navigation
- Supports events on the nodes with URLs
- Animated jumping between nodes
- Highlights node/edge under mouse



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## Sample code and clickable nodes

```
def __init__(self):
    xdot.DotWindow.__init__(self)
    self.widget.connect('clicked', self.on_url_clicked)
def on_url_clicked(self, widget, url, event):
    dialog = gtk.MessageDialog(
            parent = self.
            buttons = gtk.BUTTONS_OK,
            message_format="%s clicked" % url)
    dialog.connect('response', lambda dialog,
                            response: dialog.destroy())
    dialog.run()
    return True
```





#### xdot:

self.emit("clicked", unicode(url.url), event)





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self.emit("clicked", unicode(url.url), event)

#### AMEBA:

```
self.splitRatioGraph.node[node]["URL"] = node
[...]
self.widget.connect("clicked", self._node_clicked)
```





## AMEBA: Advanced MEtabolic Branchpoint Analysis







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- Interactively visualizes metabolic networks and display flux distributions
- Easily configurable to produce high-quality figures
- Available online, GPLv3, http://metano.tu-bs.de/ameba





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#### Thank your for your attention! r.rex@tu-bs.de



