

Xml2jupyter: Mapping parameters between XML and Jupyter widgets

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Software

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Summary

Jupyter Notebooks (Kluyver et al. 2016, Perkel (2018)) provide executable documents (in a variety of programming languages) that can be run in a web browser. When a notebook contains graphical widgets, it becomes an easy-to-use graphical user interface (GUI). Many scientific simulation packages use text-based configuration files (hopefully in some standard format) to provide parameter values. Xml2jupyter is a Python package that bridges this gap. It provides a mapping between configuration files, formatted in the Extensible Markup Language (XML), and Jupyter widgets. Widgets are automatically generated from the XML file and these can, optionally, be incorporated into a larger GUI for a simulation package. Users modify parameter values via the widgets and the values are written to the XML configuration file. Xml2jupyter has been tested using the PhysiCell (Ghaffarizadeh et al. 2018) simulation software and will be used by students for classroom and research projects.

A PhysiCell configuration file defines model-specific user parameters in XML. Each parameter element consists of its name with attributes, defining its data *type* and *units* (optional), and the parameter's default value. The attributes will determine the appearance and behavior of the Jupyter widget. For numeric widgets (the most common type for PhysiCell), xml2jupyter will calculate a delta step size as a function of the default value and this step size will be used by the widget.

To illustrate, we show the following contrived XML example, containing each of the four allowed data types (currently):

```
▼<PhysiCell_settings>
  ▼<user_parameters>
    <radius type="double" units="micron">250.0</radius>
    <threads type="int">8</threads>
    <color type="string">red</color>
    <debug type="bool">True</debug>
  </user_parameters>
</PhysiCell_settings>
```

When we map this into Jupyter widgets, we obtain the following rendered result (left). The middle snapshot shows the updated numeric value after the user does a single delta step (up) on the `radius` (note the step size of 10) and the right snapshot after the user single steps the `threads` value (note the step size of 1).

radius	<input type="text" value="250"/>	micron	radius	<input type="text" value="260"/>	micron	radius	<input type="text" value="260"/>	micron
threads	<input type="text" value="8"/>		threads	<input type="text" value="8"/>		threads	<input type="text" value="9"/>	
color	<input type="text" value="red"/>		color	<input type="text" value="red"/>		color	<input type="text" value="red"/>	
<input checked="" type="checkbox"/> debug			<input checked="" type="checkbox"/> debug			<input checked="" type="checkbox"/> debug		

For a more realistic example, consider the `config_biorobots.xml` configuration file (found in the `config_samples` directory). To demonstrate `xml2jupyter` on this XML file, one would: 1) clone or download the repository, 2) copy the XML configuration file to the root directory, and 3) run the `xml2jupyter.py` script, providing the XML file as a argument.

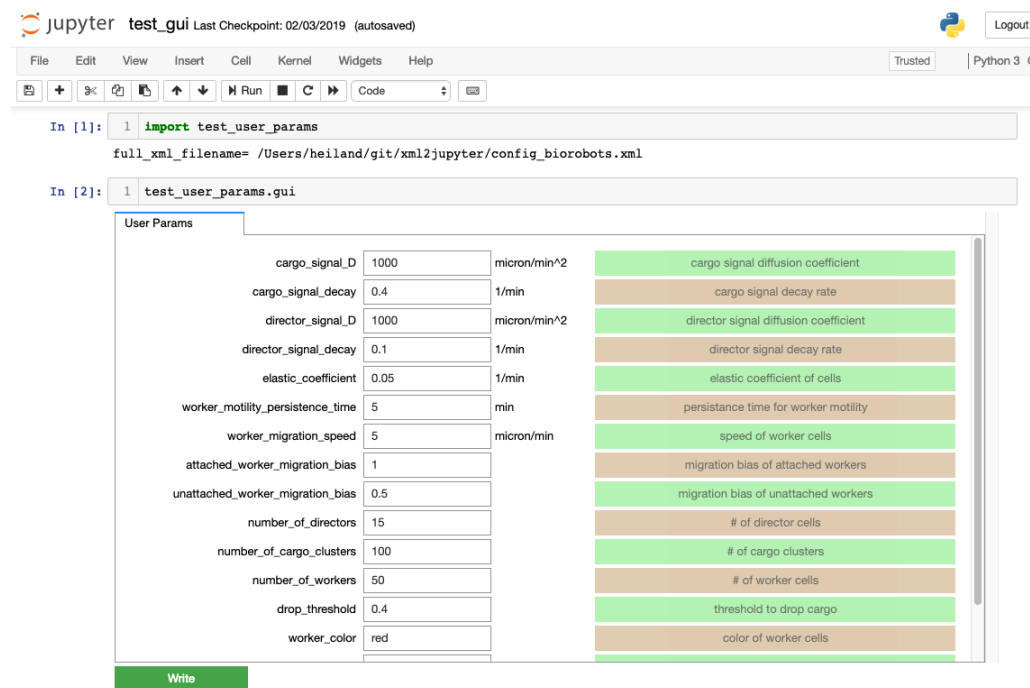
```
$ cp config_samples/config_biorobots.xml .
$ python xml2jupyter.py config_biorobots.xml
```

The `xml2jupyter.py` script parses the XML and generates a Python module, `user_params.py`, containing the Jupyter widgets, together with methods to populate their values from the XML and write their values back to the XML. To “validate” the widgets were generated correctly, one could, minimally, open `user_params.py` in an editor and inspect it.

But to actually see the widgets rendered in a notebook, we provide a simple test:

```
$ python xml2jupyter.py config_biorobots.xml test_user_params.py
$ jupyter notebook test_gui.ipynb
```

This should produce the following notebook in your browser after selecting **Run all** in the **Cell** menu:



Jupyter test_gui Last Checkpoint: 02/03/2019 (autosaved)

File Edit View Insert Cell Kernel Widgets Help Trusted Python 3

```
In [1]: 1 import test_user_params
        full_xml_filename= /Users/heiland/git/xml2jupyter/config_biorobots.xml

In [2]: 1 test_user_params.gui
```

User Params

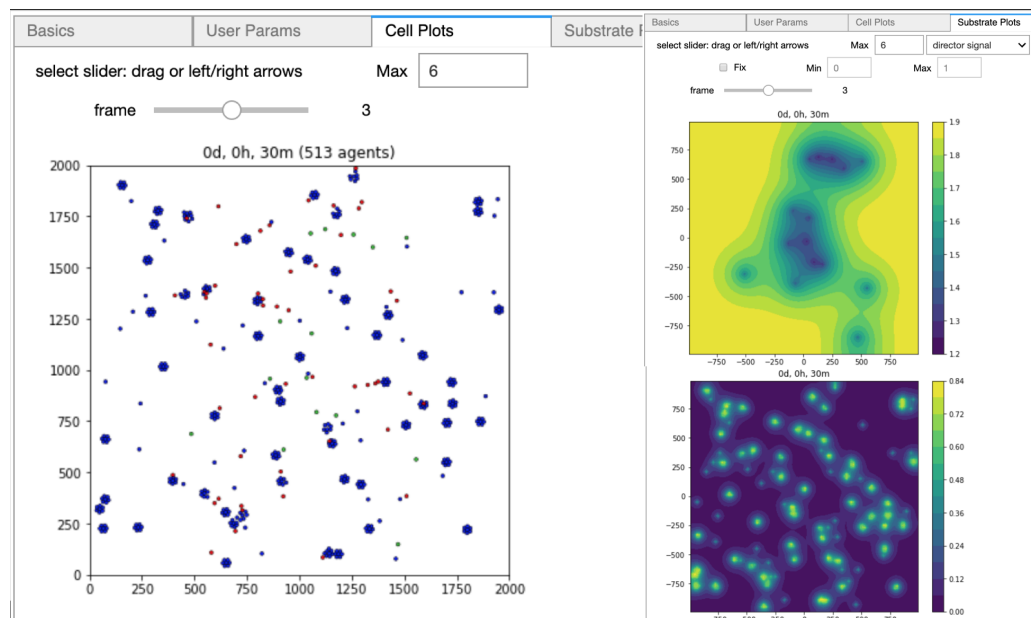
cargo_signal_D	<input type="text" value="1000"/>	micron/min^2	cargo signal diffusion coefficient
cargo_signal_decay	<input type="text" value="0.4"/>	1/min	cargo signal decay rate
director_signal_D	<input type="text" value="1000"/>	micron/min^2	director signal diffusion coefficient
director_signal_decay	<input type="text" value="0.1"/>	1/min	director signal decay rate
elastic_coefficient	<input type="text" value="0.05"/>	1/min	elastic coefficient of cells
worker_motility_persistence_time	<input type="text" value="5"/>	min	persistence time for worker motility
worker_migration_speed	<input type="text" value="5"/>	micron/min	speed of worker cells
attached_worker_migration_bias	<input type="text" value="1"/>		migration bias of attached workers
unattached_worker_migration_bias	<input type="text" value="0.5"/>		migration bias of unattached workers
number_of_directors	<input type="text" value="15"/>		# of director cells
number_of_cargo_clusters	<input type="text" value="100"/>		# of cargo clusters
number_of_workers	<input type="text" value="50"/>		# of worker cells
drop_threshold	<input type="text" value="0.4"/>		threshold to drop cargo
worker_color	<input type="text" value="red"/>		color of worker cells

Write

PhysiCell Jupyter GUI

Our ultimate goal is to generate a fully functional GUI for PhysiCell users. `Xml2jupyter` provides one important piece of this - dynamically generating widgets for custom user parameters for a model. With other Python modules that provide additional components

(tabs) of the GUI, common to all PhysiCell models, a user can configure, run, and visualize output from a simulation. Two tabs that provide visualization of output files are shown below with results from the *biorobots* simulation. Note that some of the required modules are not available in the Python standard library, e.g., Matplotlib (Hunter 2007) and SciPy. We provide instructions for installing these additional dependencies in the repository README.






Extensions and Discussion

We hope others will be inspired to extend the core idea of this project to other text-based configuration files. XML is only one of several data-interchange formats. It just happens to be the one of interest to us for PhysiCell.

While the additional Python modules that provide visualization are specifically tailored to PhysiCell output, they can serve as templates for other file formats and provide similar functionality. We welcome contributions, especially for three-dimensional data.

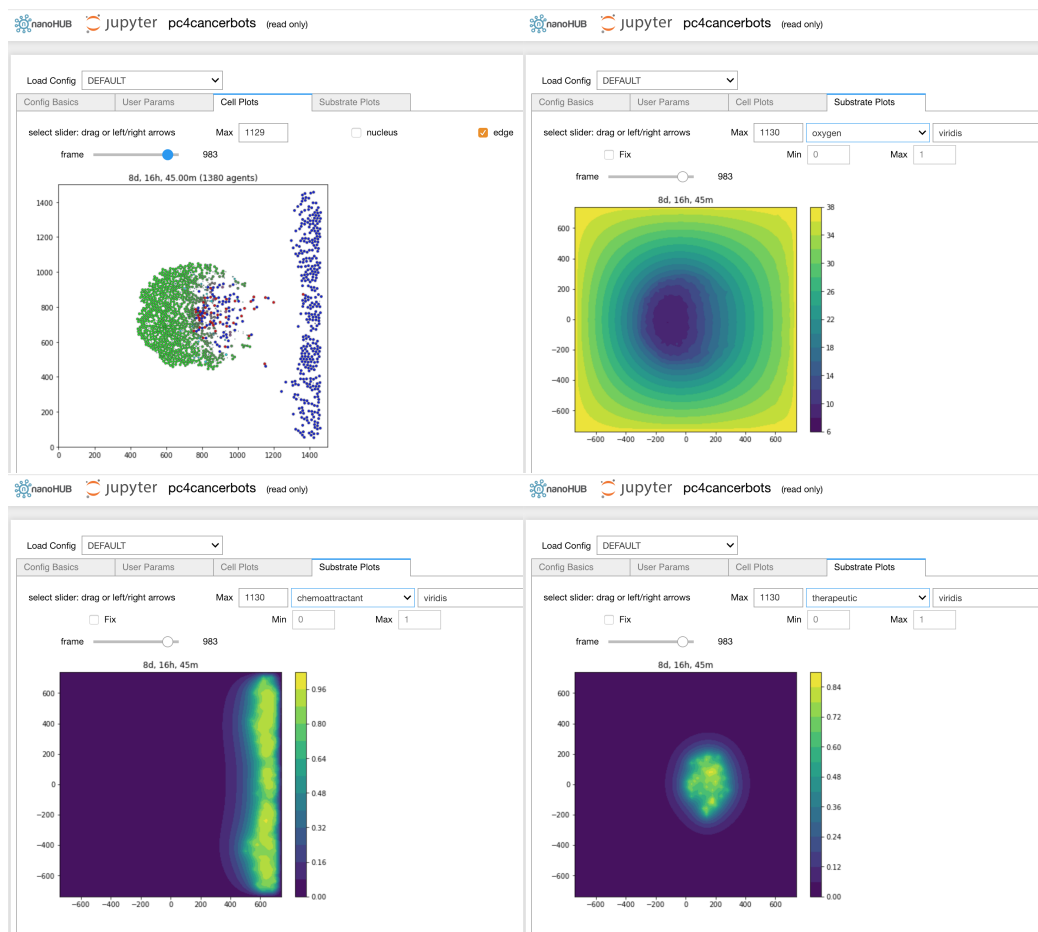
Xml2jupyter has helped us port PhysiCell-related Jupyter tools to nanoHUB (Madhavan et al. 2013), a scientific cloud for nanoscience education and research that includes running interactive simulations. For example, we show screen shots from our [pc4cancerbots](#) tool running on nanoHUB, where the *User Params* tab has been generated using the `xml2jupyter.py` script. Other PhysiCell-related nanoHUB tools that have been created using `xml2jupyter` include [pc4heterogen](#) and [pcISA](#). Readers can create an account on nanoHUB and run these simulations for themselves. We will ask students to create their own nanoHUB tools, using `xml2jupyter`, that can 1) be run and evaluated by the instructor, 2) be shared with others, and 3) become part of a student's living portfolio.



 pc4cancerbots (read only)
 
 Terminate Sess

Load Config: DEFAULT

Config Basics	User Params	Cell Plots	Substrate Plots
	therapy_activation_time: 10080 min		time at which therapy begins
	save_interval_after_therapy_start: 3 min		save (output) interval after therapy begins
	cargo_o2_relative_uptake: 0.1		oxygen uptake for cargo cells
	cargo_apoptosis_rate: 0.00004065 1/min		apoptosis rate for cargo cells
	cargo_relative_adhesion: 0		relative adhesion for cargo cells
	cargo_relative_repulsion: 5		relative repulsion for cargo cells
	worker_o2_relative_uptake: 0.1 1/min		oxygen uptake for worker cells
	worker_apoptosis_rate: 0 1/min		apoptosis rate for workers
	worker_motility_persistence_time: 5 min		motility persistence of workers
	worker_migration_speed: 2 micron/min		migration speed for workers
	attached_worker_migration_bias: 1		migration bias for attached workers
	unattached_worker_migration_bias: 1		migration bias for unattached workers
	worker_relative_adhesion: 0		relative adhesion for workers
	worker_relative_repulsion: 5		relative repulsion for workers
	elastic_coefficient: 0.05 1/min		elastic coefficient of cells

In the four screenshots below, we show the cell plot tab (upper-left) and three different substrate plots. This particular model and simulation is described in this [video](#).



We welcome suggestions and contributions to xml2jupyter. For example, currently, we

arrange the generated parameter widgets in a single column, with (optional) descriptions of the parameters. This is an appropriate layout for an educational setting. But if a GUI will be used by researchers who are already familiar with the parameters, it may be preferable to generate a more compact layout of widgets.

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