



Regression Testing

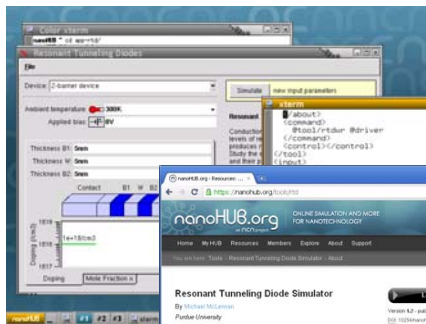
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You've published it!

Build the tool...

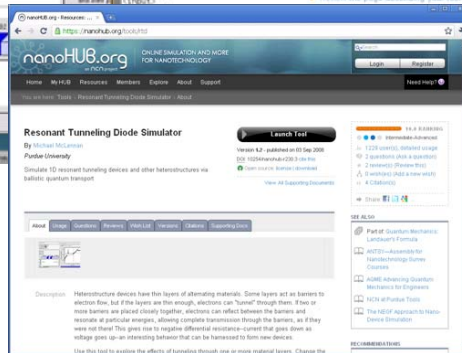


Install, approve...

What's next?

Your latest code is installed and ready on nanoHUB.org. Please test your tool by clicking the button below to make sure that everything is working properly, as well as verify that the page describing your tool is created and displays correct information:

- Test your application: [Launch test](#)
- Review the page describing your tool: [Review page](#)



is working properly, click here to
d in your latest fixes, click here to
the latest version for testing and

Published!

Usually doesn't end there...

Allow download of 3d simulation data +7 0 +5 Wishes
 Proposed by Golam Rabbani on 31 May 2009, 2 Comments

257439 [When I launch this tool, it crashes right away and collapses down to a...](#) open Bugs
 by Michael McLennan ([mmc](#))

$$\frac{m^*_{emit} a^2}{2} \approx \hbar \omega_{phonon}(opt.) \quad \mu = m^*_{emit} \frac{2E}{W} \frac{1}{C_i}$$
 New physics

```

Color xterm
real hbar, hbar2, kb, n0, eVtoJ, pi, q
real ks, mtoom
parameter ( hbar=6.58216e-16,
+ hbar2=hbar**2,
+ kb=8.61738e-5,
+ n0=9.1095e-31,
+ eVtoJ=1.60218e-19,
+ pi=3.141592654,
+ q=eVtoJ,
+ ks=12.846,
+ mtoom=100.0 )
DEFINITIONS --
ltor ... electrons traveling left to right
rtol ... electrons traveling right to left
  
```

What's next?

Your tool has been published and is now open to the public. Users will find out about your tool by reading the following page. Be sure to keep this information up to date:
<http://nanoHUB.org/tools/rtd>

Your options:

- > I've made changes [Please install the latest code for testing and approval.](#)

Versions

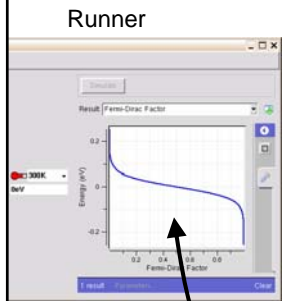
Version	Released	DOI Handle	Published
3.01	03 Dec 2010	10254/nanohub-1307.7	✔
3.0	03 Nov 2010	10254/nanohub-1307.6	✘
2.1	17 Jul 2009	10254/nanohub-1307.5	✔
2.02	25 Sep 2008	10254/nanohub-1307.4	✘
2.0.1	08 May 2008	10254/nanohub-1307.3	✘

You can publish multiple versions and keep more than one active



Create test cases

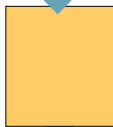
1 Run the desired test case...



tool.xml



driver1



Your Program



run12703129102.xml

2 Move into tests directory

```
Color xterm
$ ls
docs spiro.m tool.xml
$ mkdir tests
$ unset SESSIONDIR
$ rapture
$ ls
docs run12703129102.xml spiro.m te
$ mv run12703129102.xml tests
$
```

Results are moved out of the current working directory to the "results" directory unless you unset SESSIONDIR



~/data/results/\$SESSION

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Label test cases

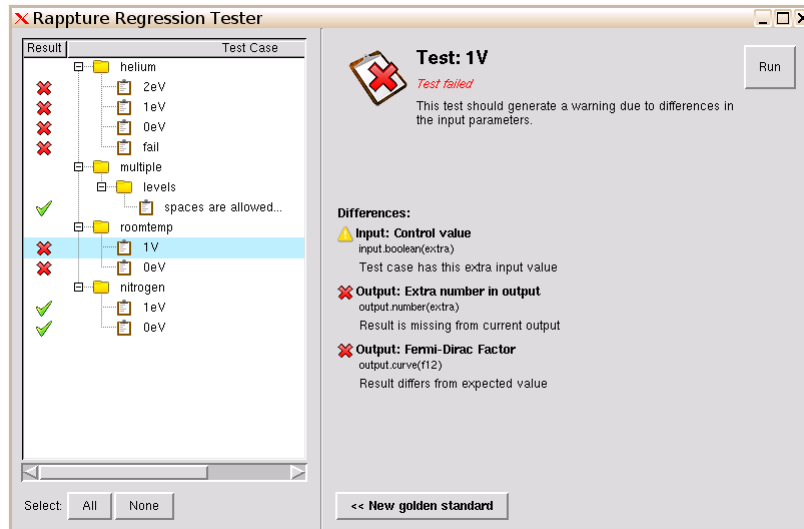
3 Add label/description to each test

```
Color xterm
$ vi tests/run12703129102.xml
```

```
<?xml version="1.0"?>
<run>
  <test>
    <label>roomtemp|0eV</label>
    <description>Should work at room temperature and 0eV.</description>
  </test>
  <tool>
    <about>Press Simulate to view results.</about>
    <command>tcl sh @tool/fermi.tcl @driver</command>
  </tool>
  <input>
    <number id="temperature">
      <about>
        <label>Ambient temperature</label>
        <description>Temperature of the environment.</description>
      </about>
    </number>
  </input>
</run>
```

separator for test folders

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Demo >>

Output results:

- ✘ Output value has changed
- ✘ Output value is missing
- ✘ Output value is extra (not supposed to be there)

Input values:

- ✘ Input value has changed--label, units, etc.
- ✘ Input value is missing from test case
- ✘ Input value is extra (not supposed to be there)

Fix the tool



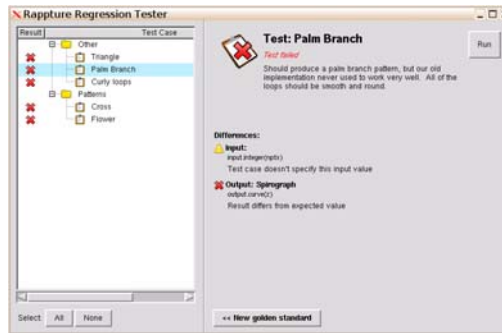
Fix the test





Exercise #5: Make this tool run properly

```
wget http://hubzero.org/resources/380/download/ex5.tgz  
tar xvzf ex5.tgz  
cd ex5  
rappture -tester
```



- Add a test case for (-3, -11, 19) and put it in a group called "New Tests"
- Fix all other tests until they run cleanly
- Shouldn't have to regoldenize more than 2 tests (just once, if you're lucky)