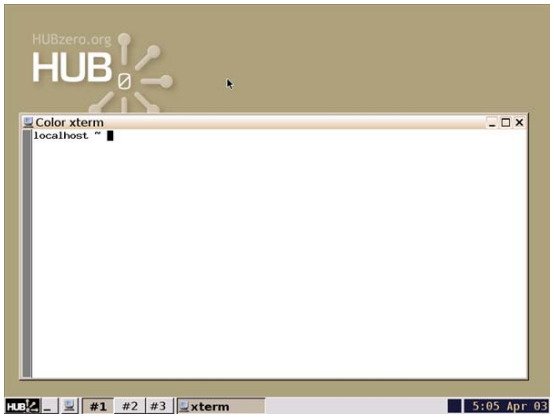
Using Workspaces to Develop Simulation Tools



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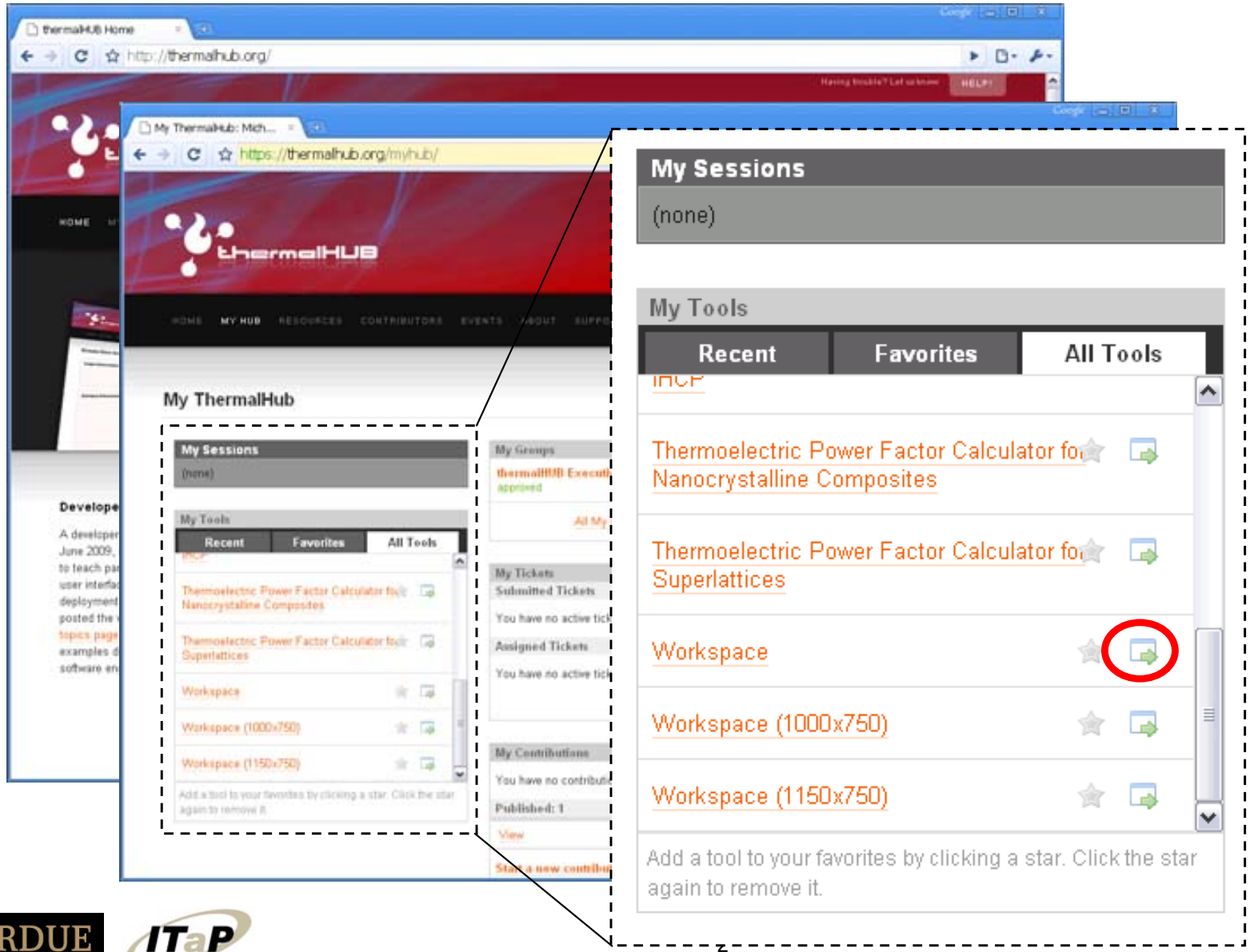
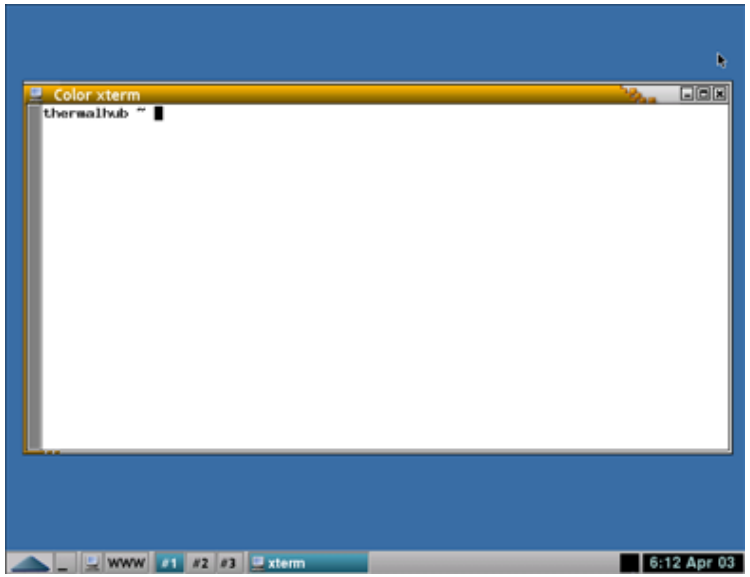
HUBzero™ Platform for Scientific Collaboration

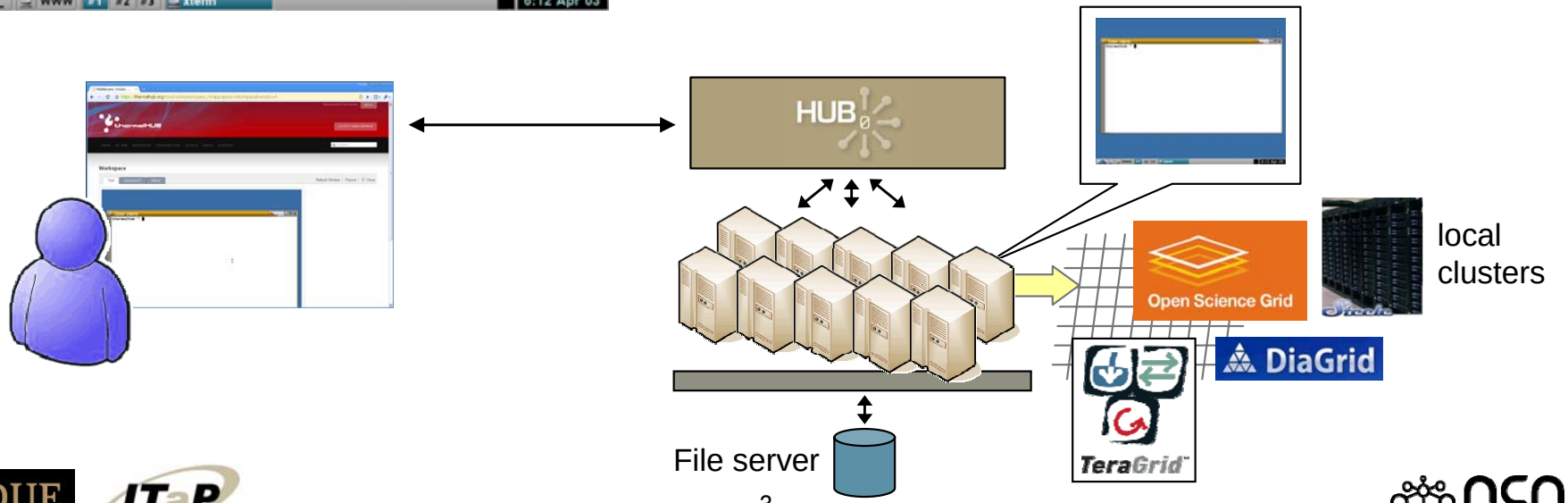
Getting into a Workspace



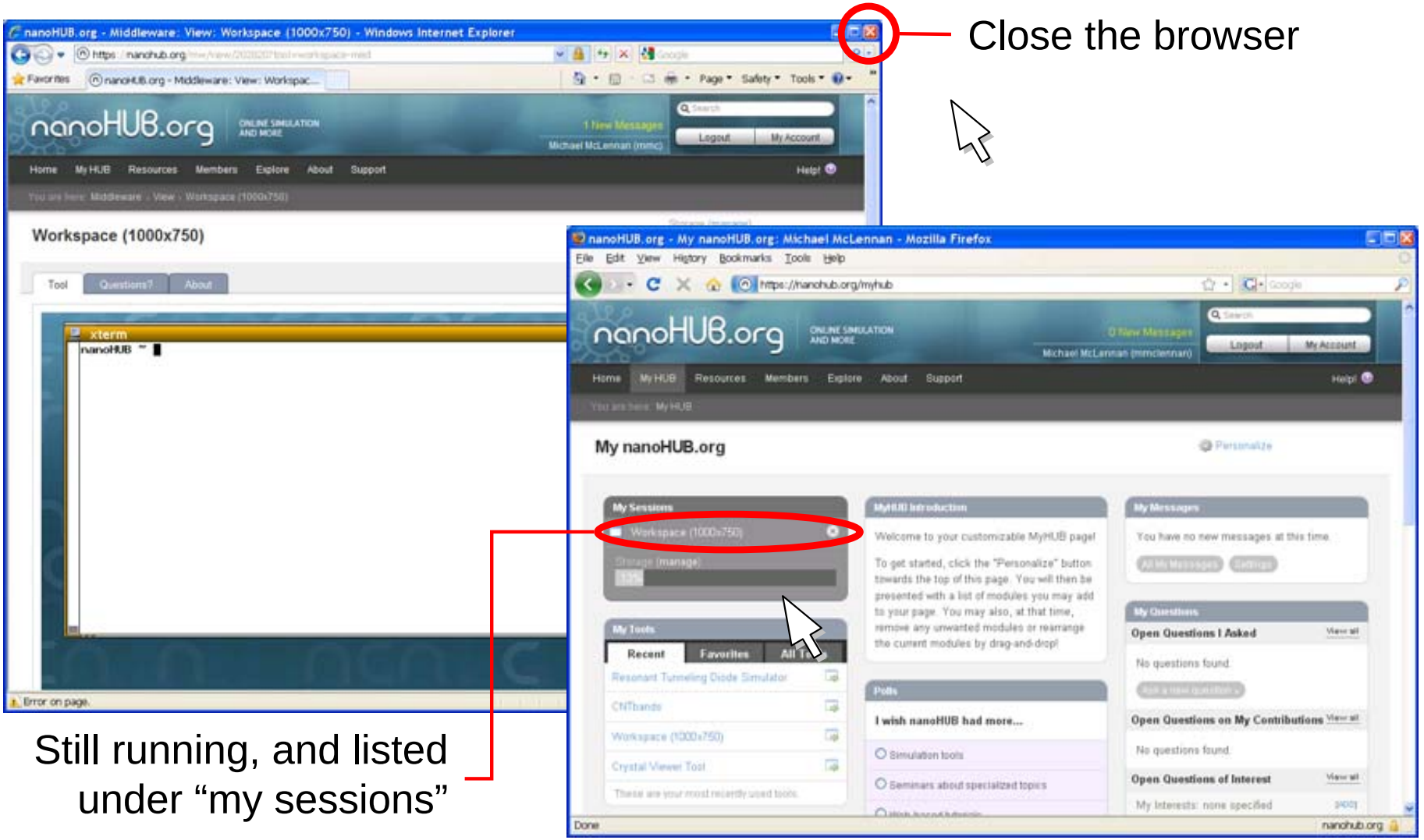
What is a workspace?



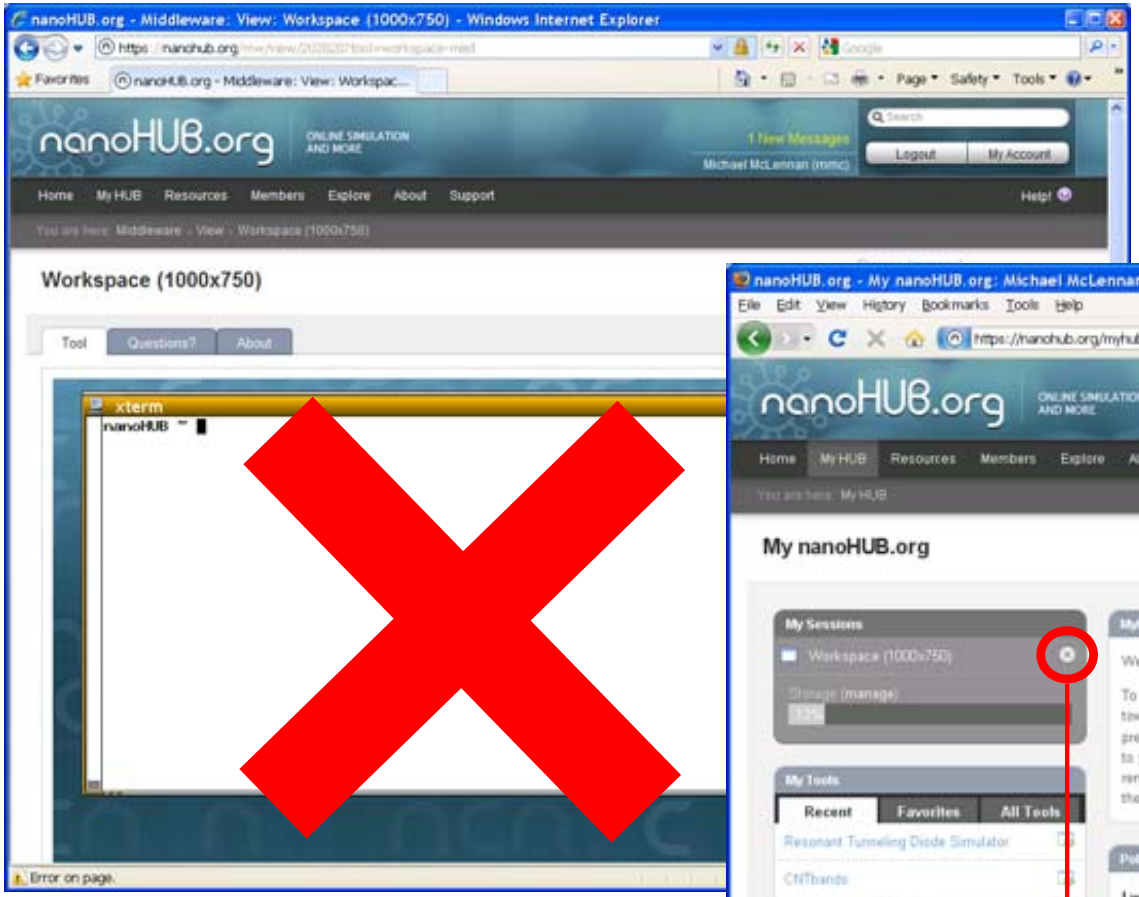
- Full-featured Linux desktop
- For tool developers
- For researchers
- Accessible from any web browser
- Still running after you close your browser
- Access to Grid resources
- File storage provided by the hub



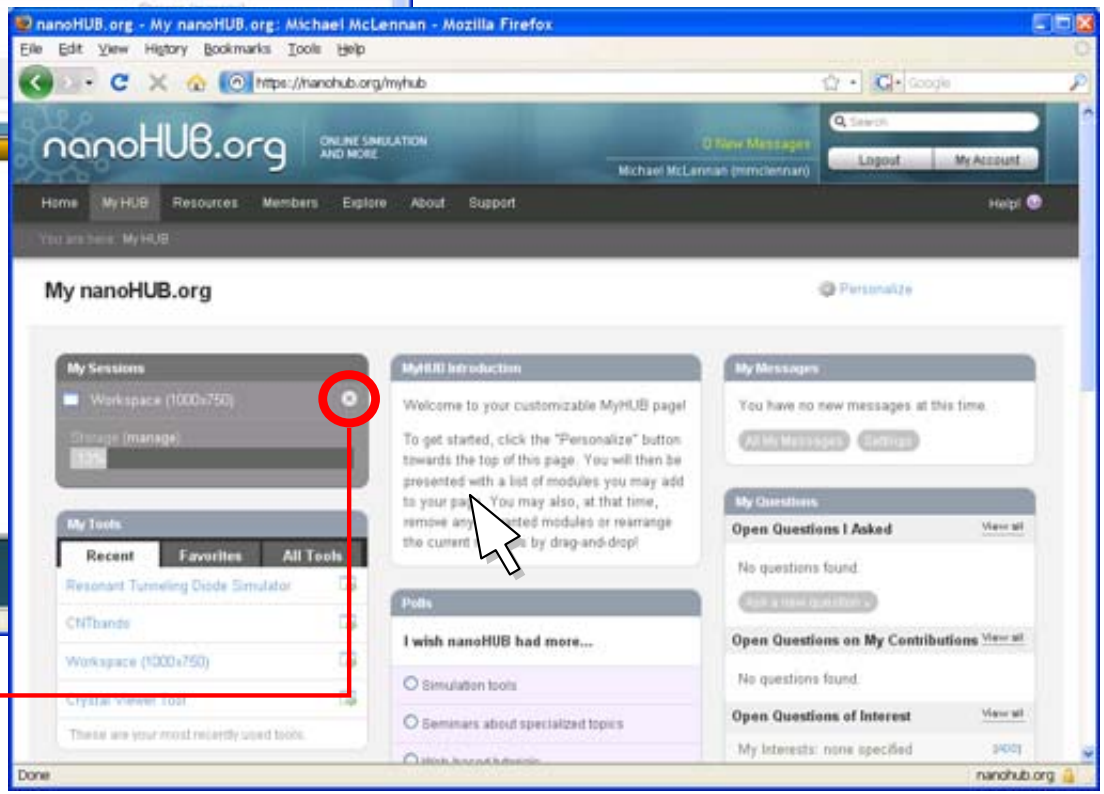
Accessing running workspaces



Closing workspaces

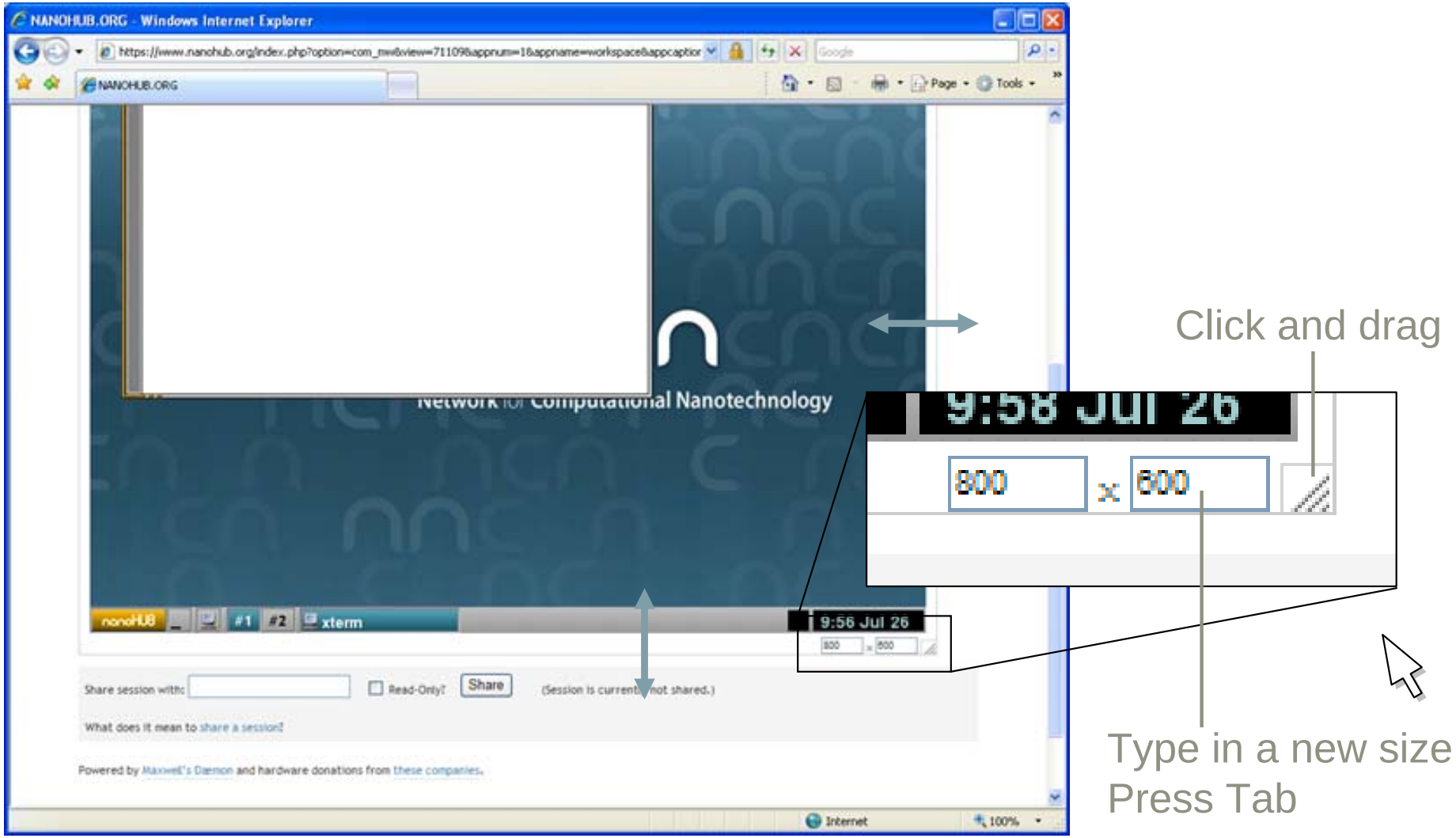


OR

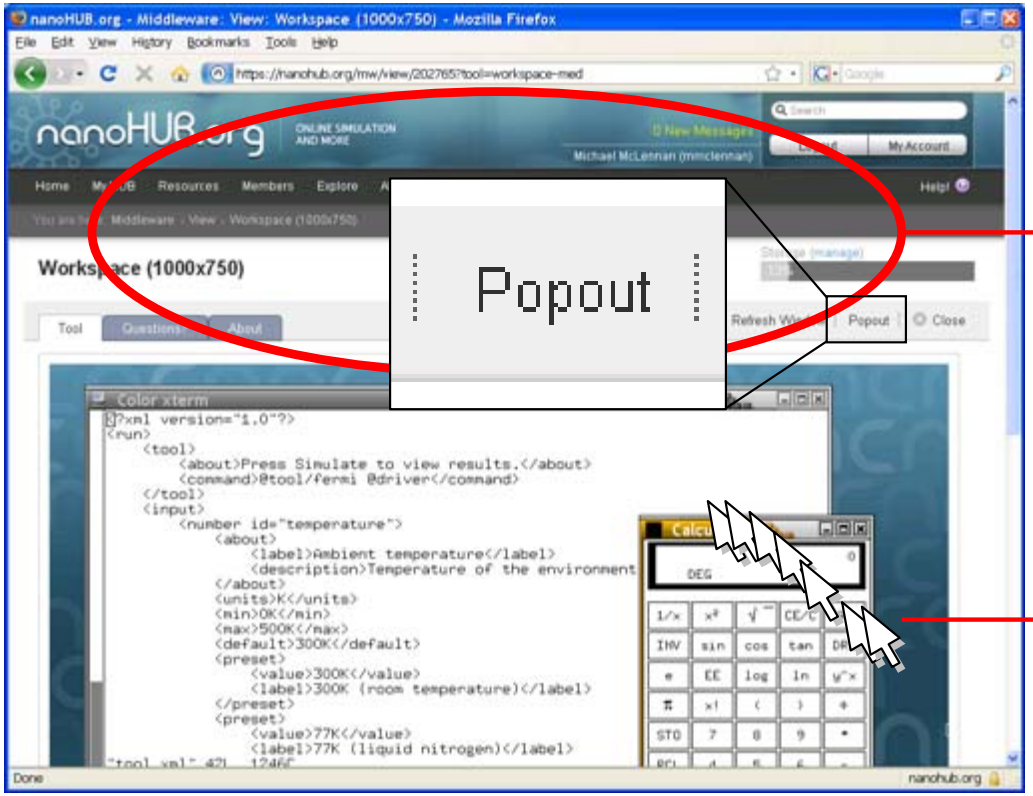


Closes the session

Resize the screen



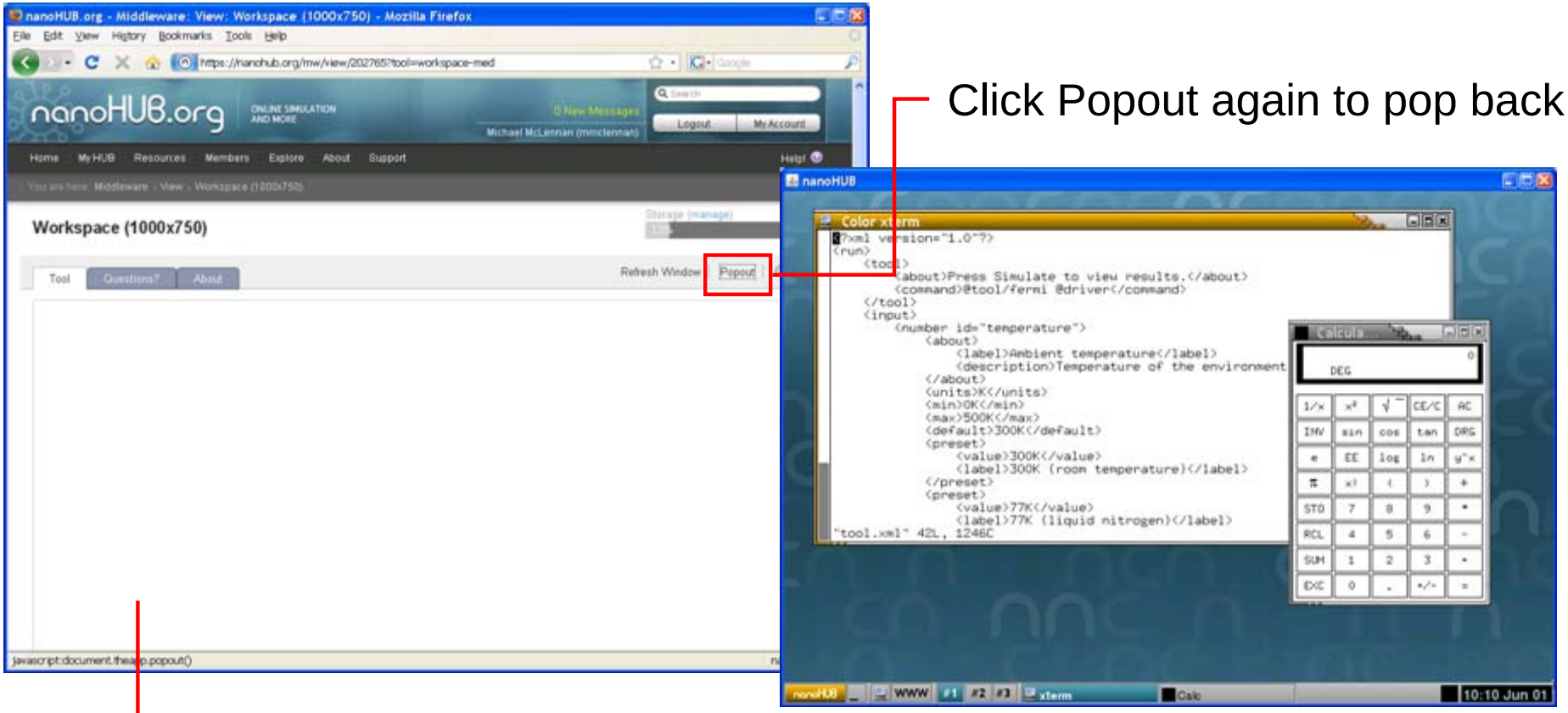
Pop out as a separate window



Get rid of this header and see more of the workspace

Solve problem of mouse trails *e.g.*, MacOSX/Firefox

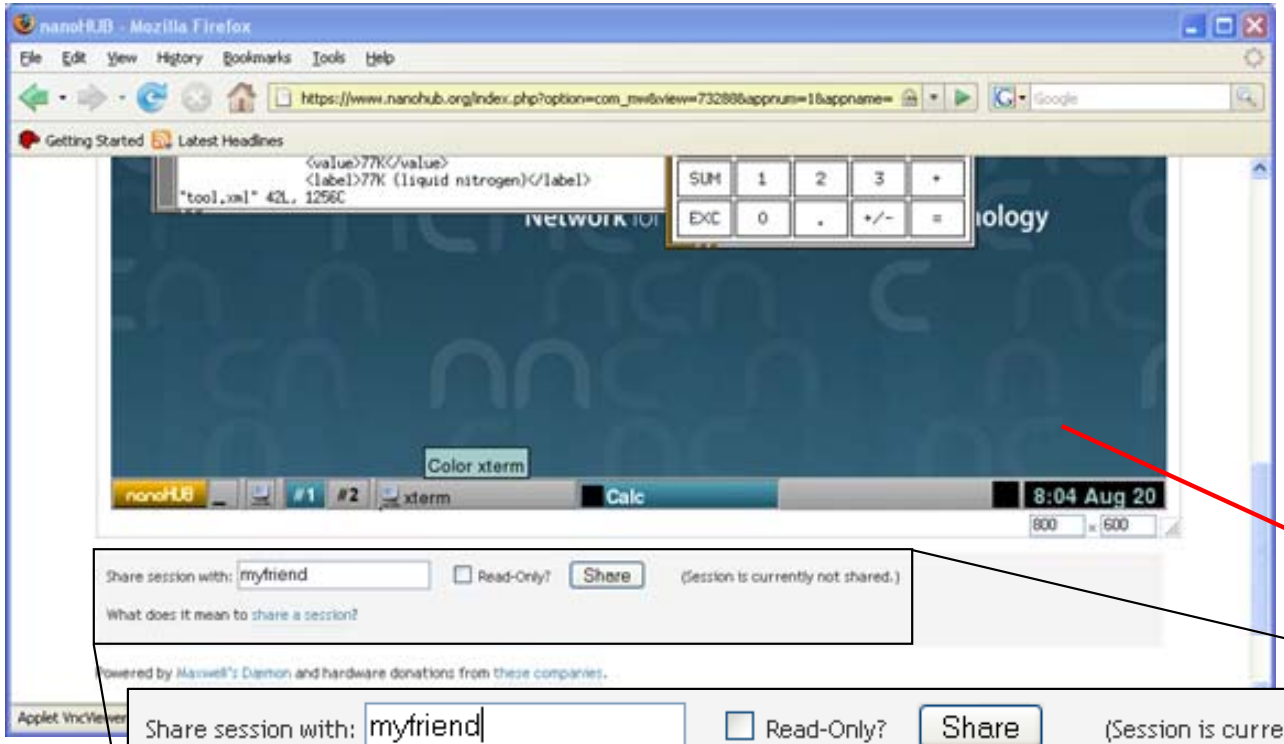
Pop out as a separate window

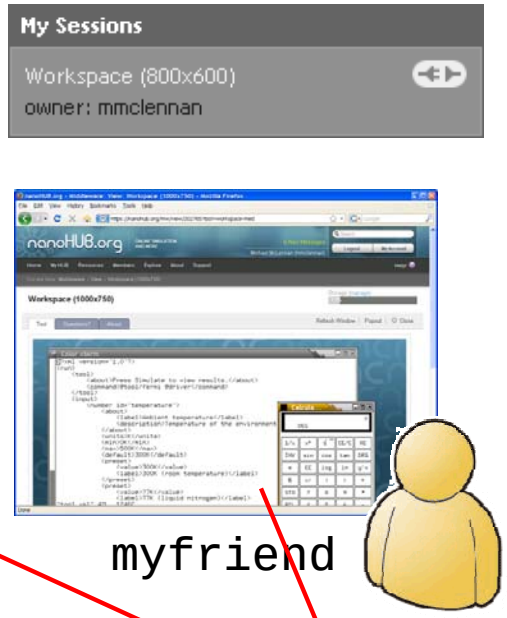


Click Popout again to pop back in

This area goes blank.
Closing this window also closes the popup.

Share your screen

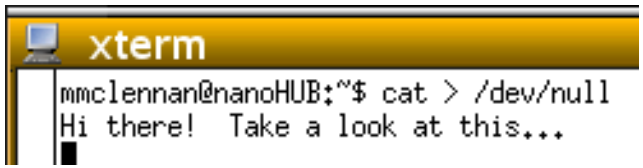




See same screen at same time

Enter the login for your friend

Check this if you don't want to share control



Linux Cheat Sheet

`ls` *pattern* — list files in the current directory
- `ls` — list all files
- `ls *.xml` — list files ending with `.xml`

`mkdir` *name* — make a new directory called *name*
- `mkdir assmt3` — make a new directory called `assmt3`

`cd` *name* — change working directory
- `cd assmt3` — change to directory `assmt3`
- `cd ..` — change to parent directory
- `cd` — change back to home directory (good if you get lost)

`cp` *from to* — copy file *from* to file *to*

```
cp /apps/rappture/current/examples/zoo/number/tool.xml .
cp ../assmt3/tool.xml newtool.xml
```

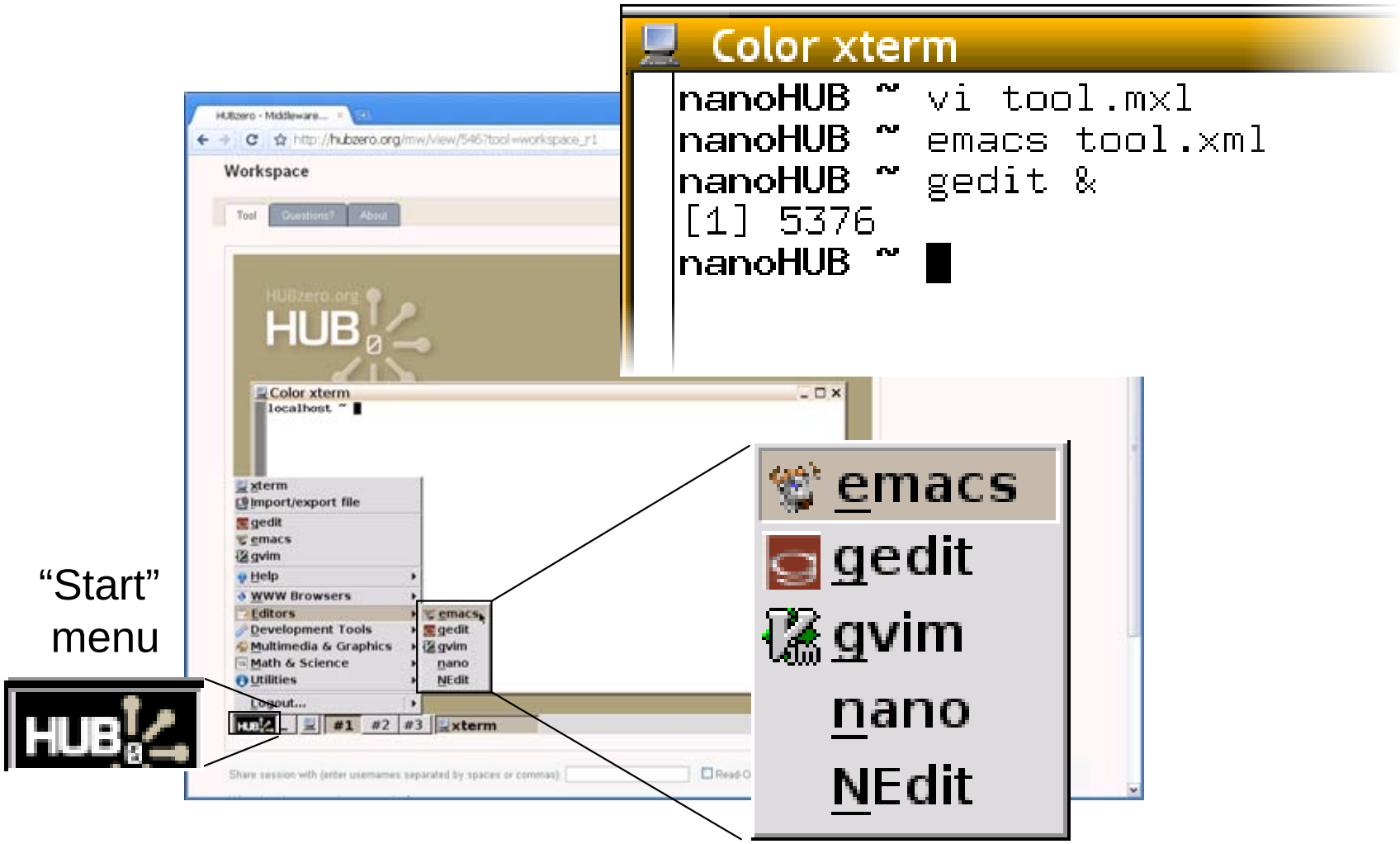
`gedit` *file* — edit the specified file

`rappture` — run Rappture (loads `tool.xml` by default)

```
rappture -tool foo.xml
```

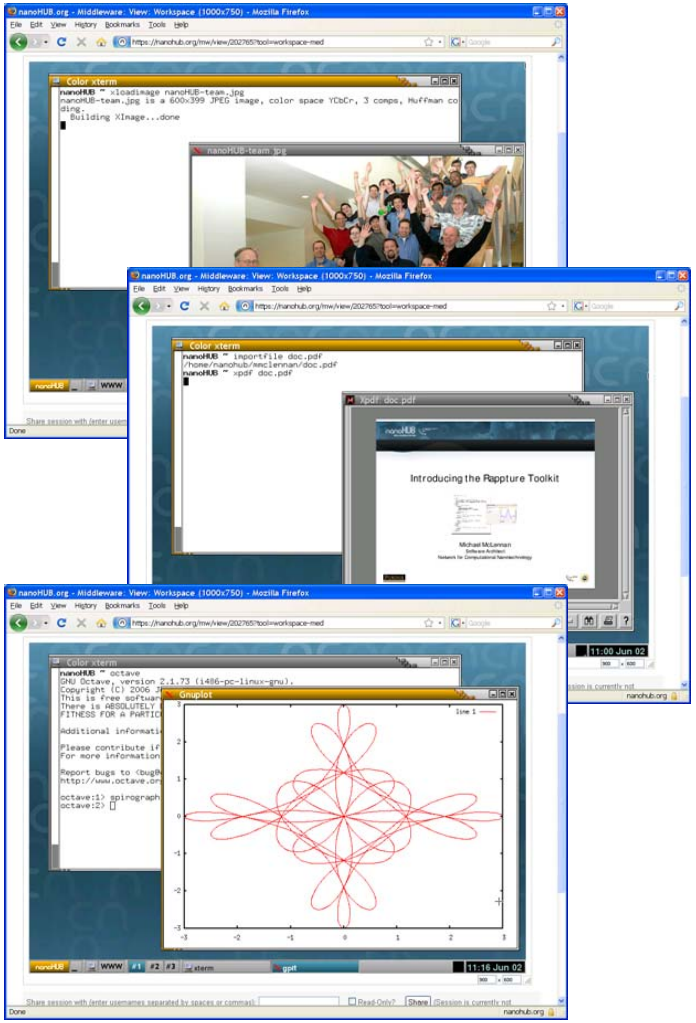
`/`	= separates directories
`.`	= current directory
`..`	= parent directory
`*`	= matches anything
`?`	= matches single char

Editors



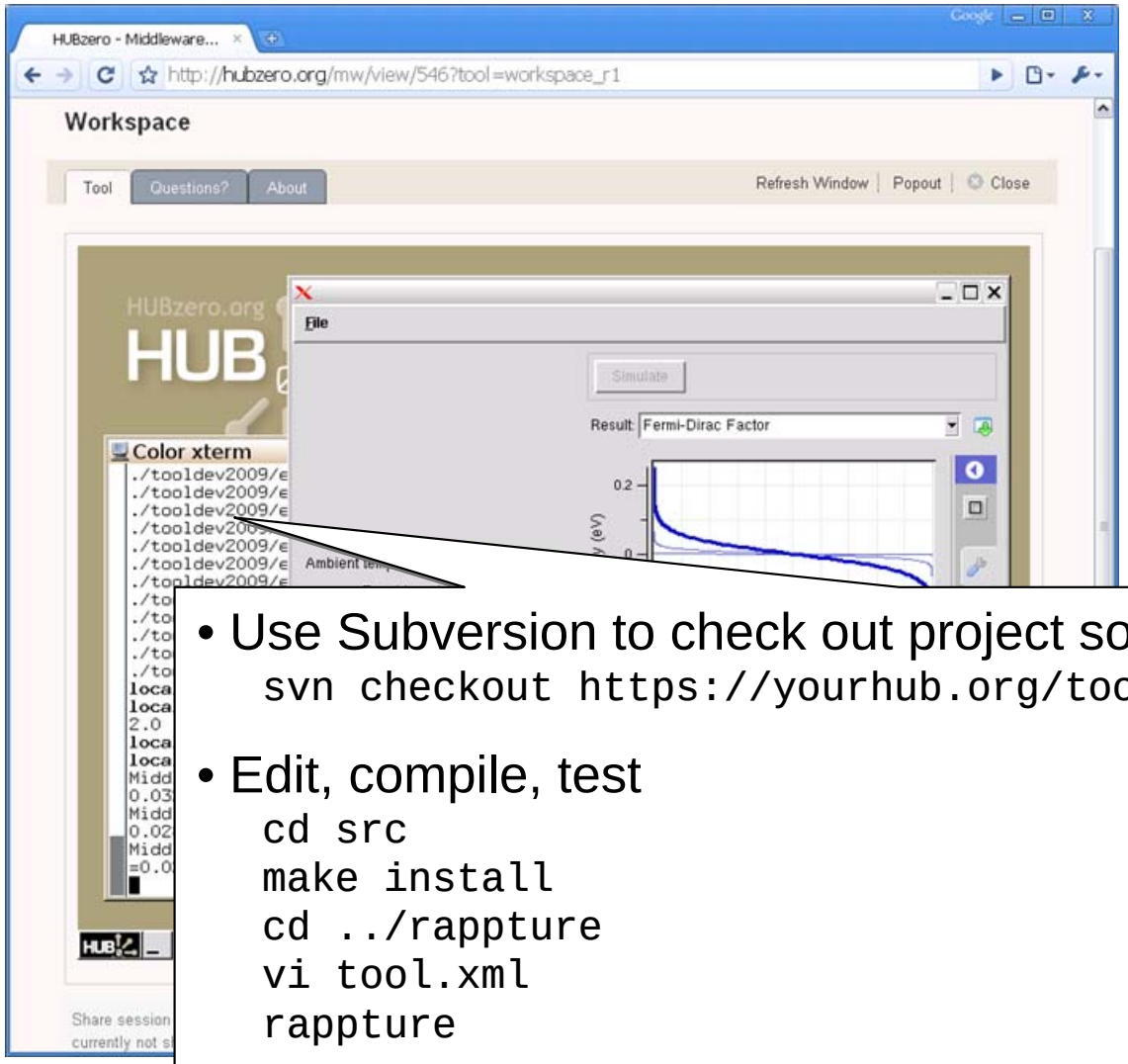
"Start" menu

Other utilities



`xloadimage` *`file`*	view image file
`xpdf` *`file`*	PDF viewer
`gimp &`	image editor
`dx &`	scientific data explorer
`octave &`	MATLAB clone
`xcalc &`	calculator

Developing tools



See instructions:

- in your project area
  at wiki/GettingStarted
- Subversion tutorial
- Rappture tutorial

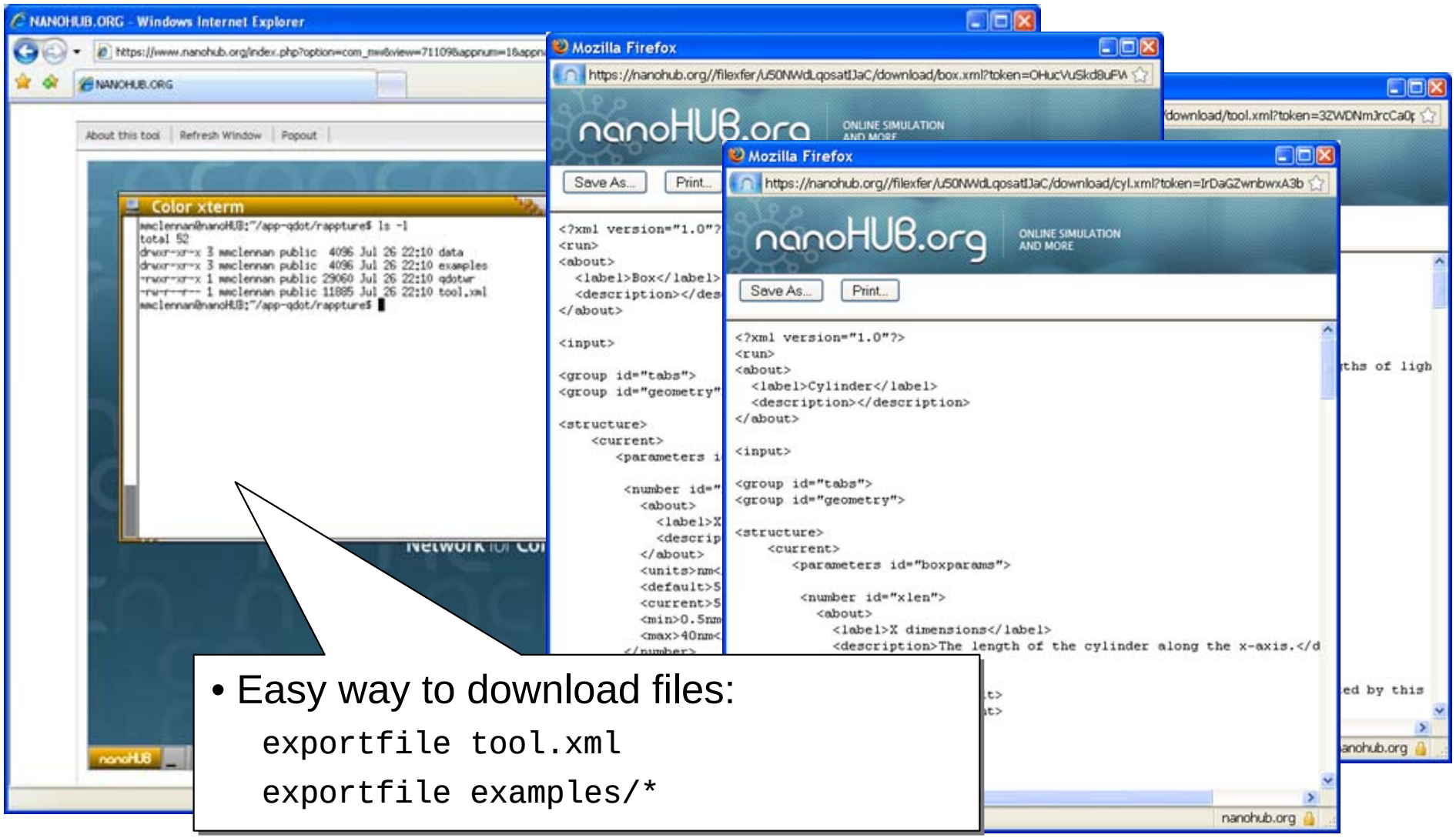
- Use Subversion to check out project source code

```
svn checkout https://yourhub.org/tools/yourtool/svn/trunk yourtool
```

- Edit, compile, test

```
cd src
make install
cd ../rappture
vi tool.xml
rappture
```

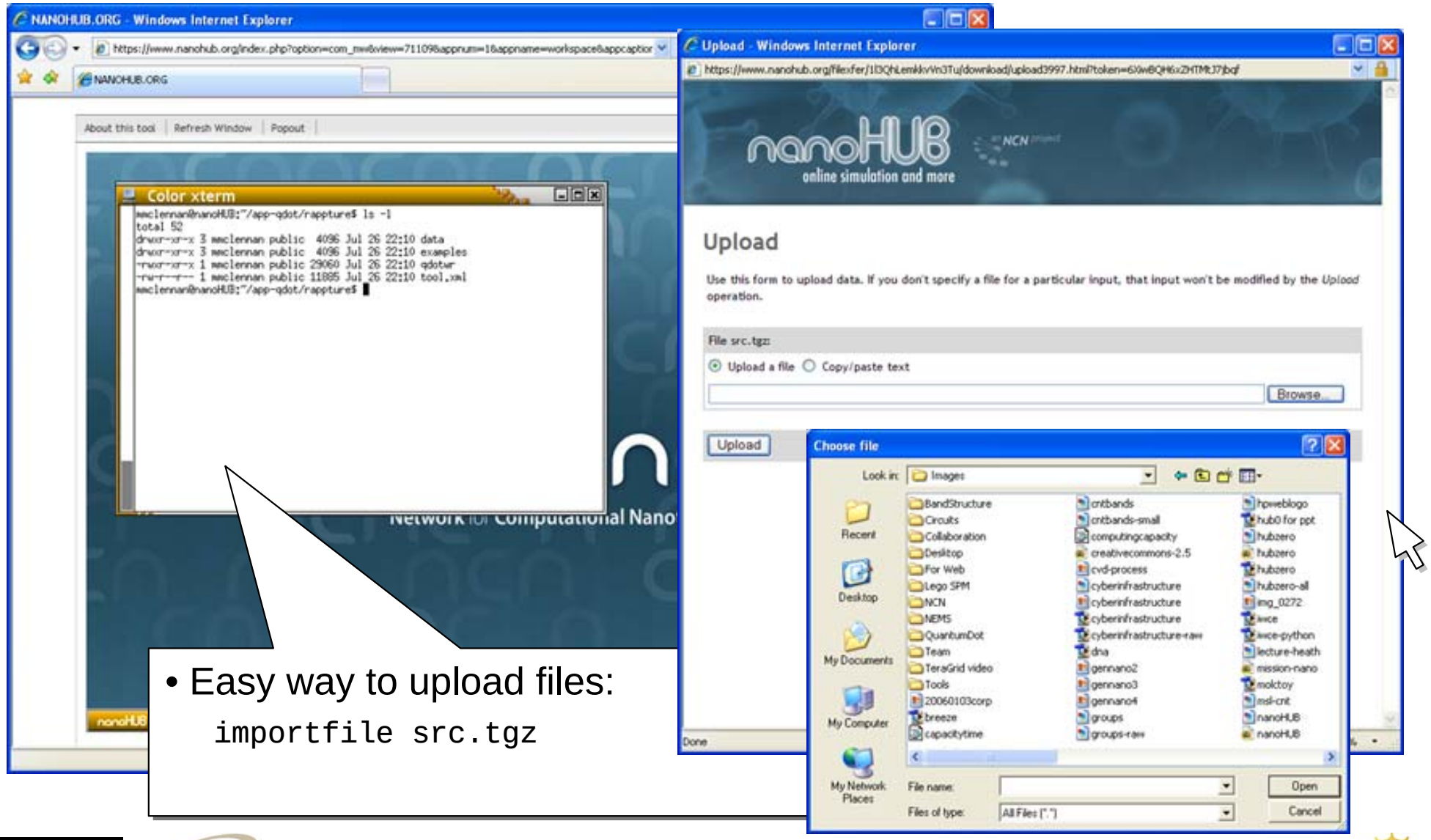
Downloading Files



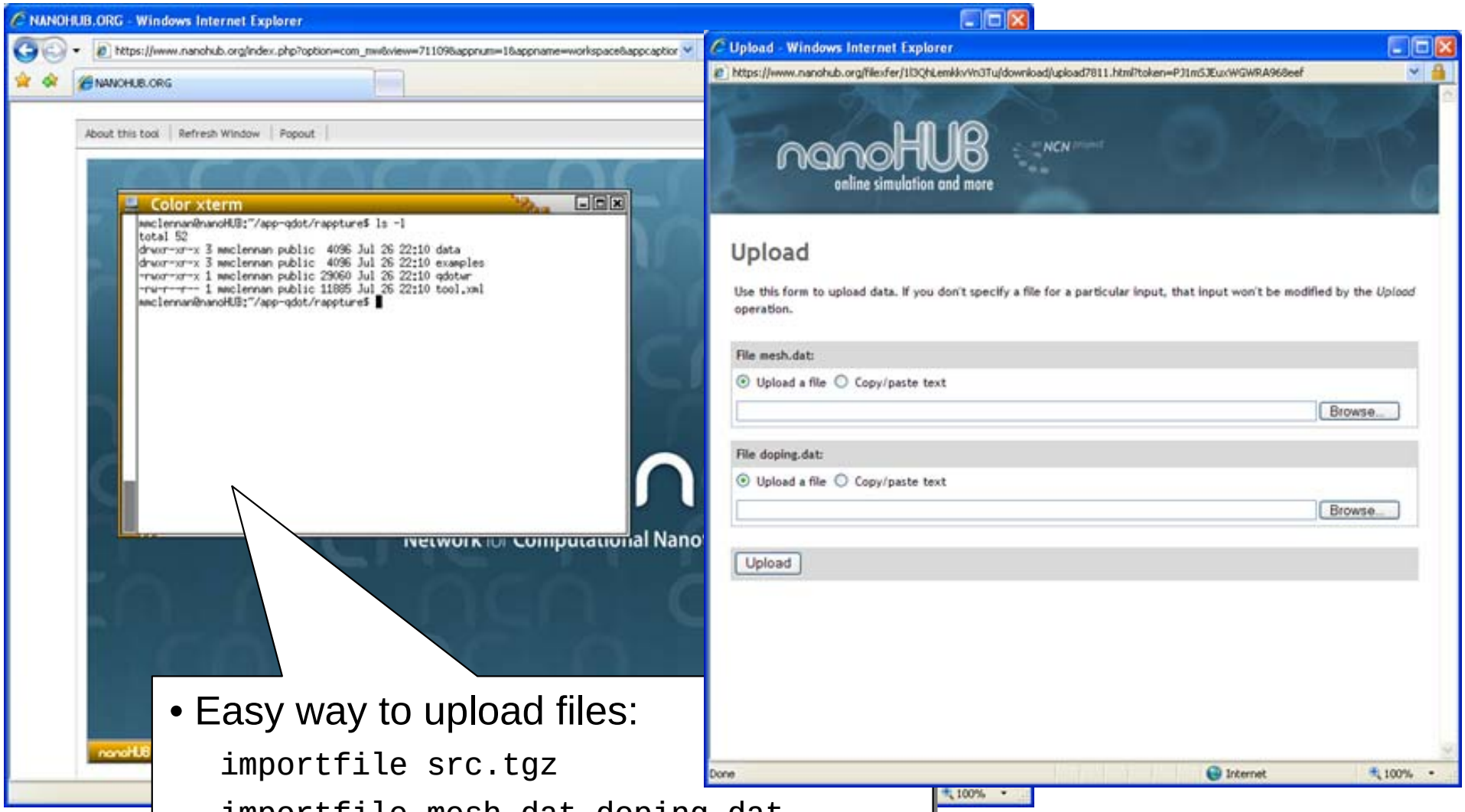
- Easy way to download files:

```
exportfile tool.xml
exportfile examples/*
```

Uploading files



Uploading files

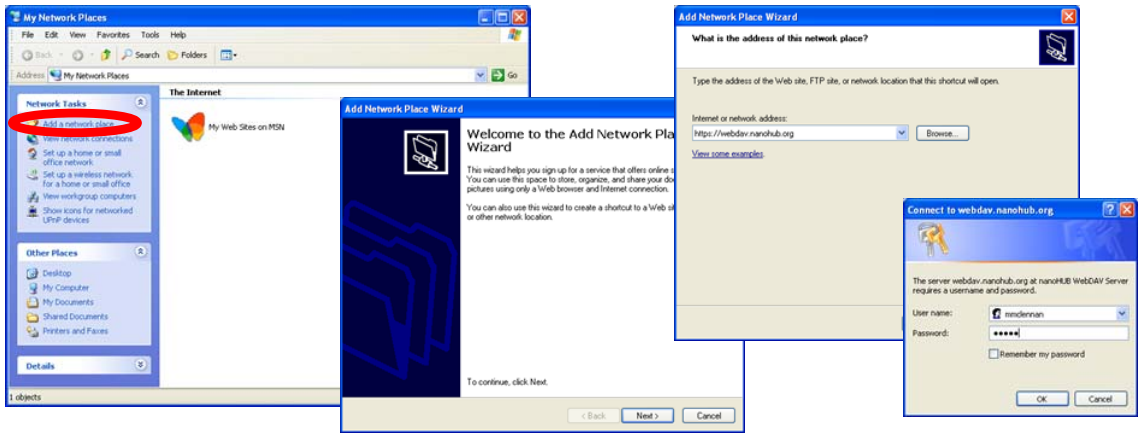


- Easy way to upload files:

```
importfile src.tgz
importfile mesh.dat doping.dat
```

Other ways to transfer files

Drag & drop on the desktop (webdav)

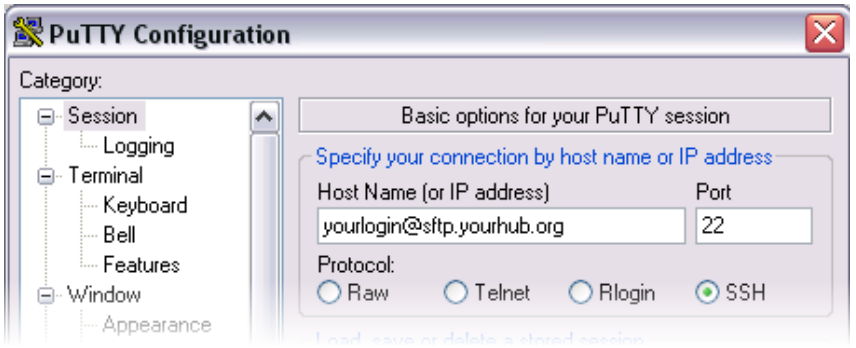


On Microsoft Windows:

- Go to *My Network Places*
- Click *Add a network place*
- Internet or network address:
  `https://nanohub.org/webdav`

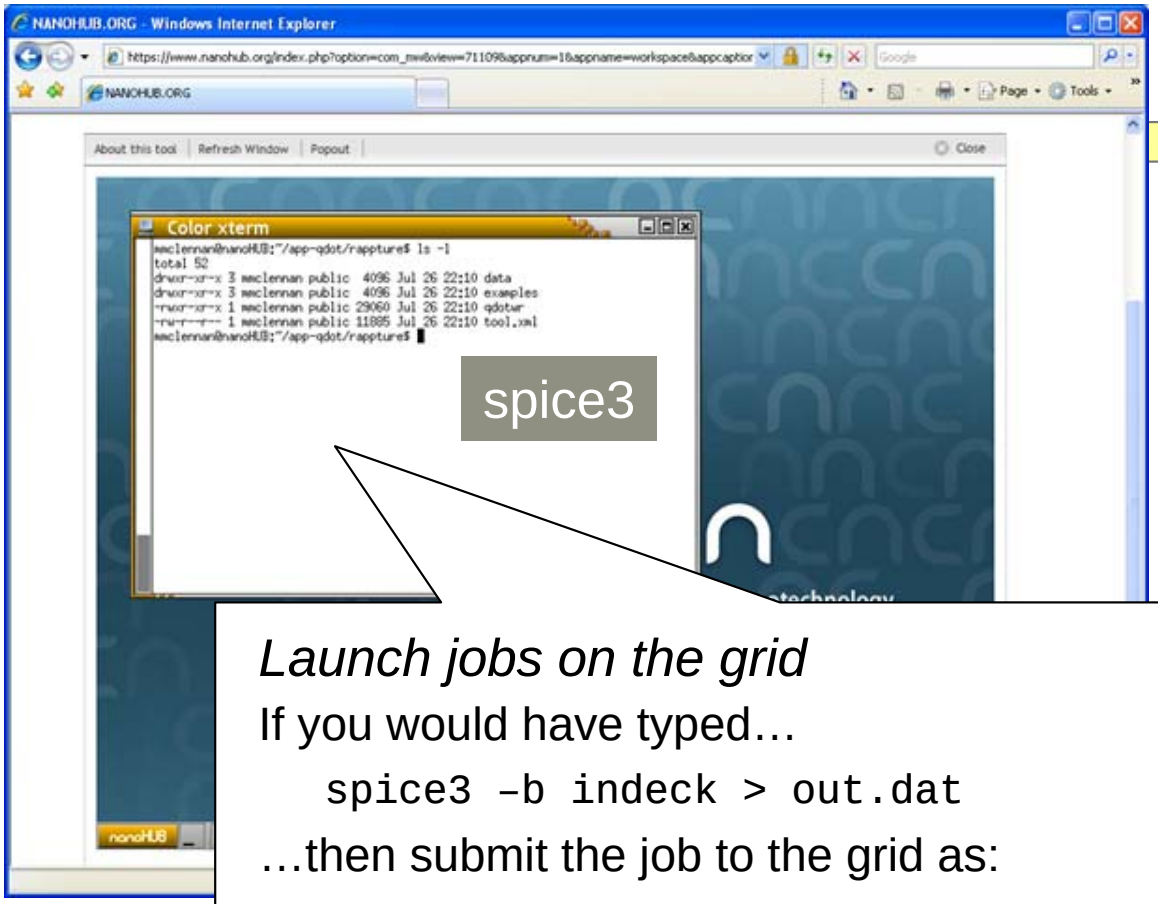
Secure FTP (sftp)

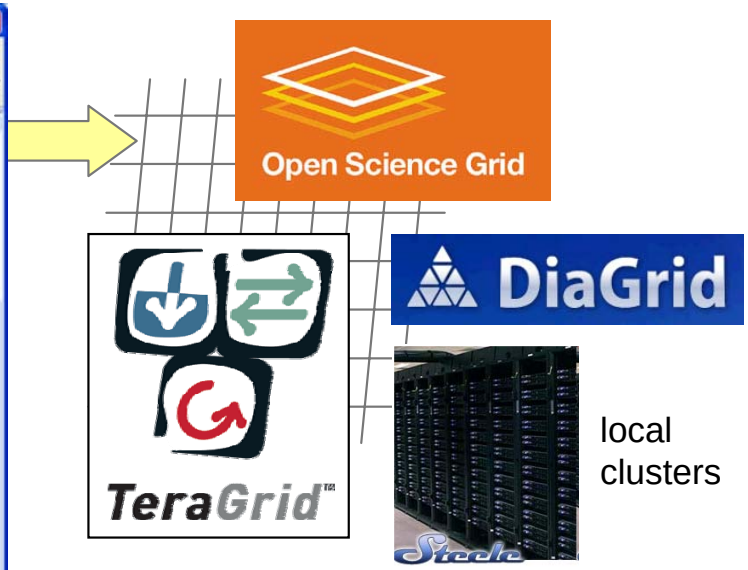
sftp client, such as PUTTY
http://www.putty.org/



`yourlogin@sftp.yourhub.org`

Accessing the Grid





Launch jobs on the grid

If you would have typed…

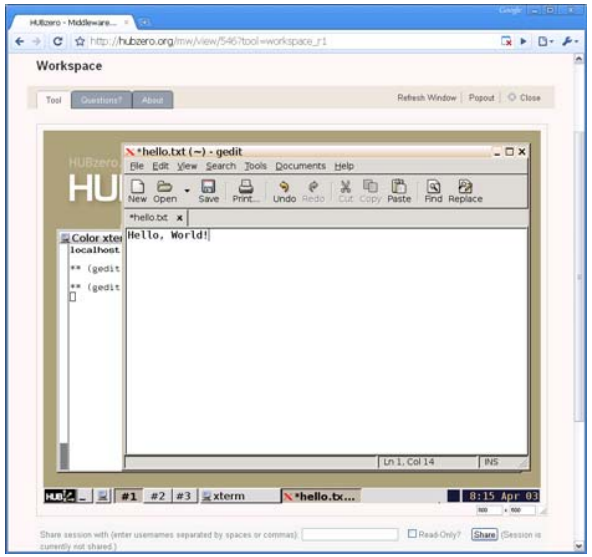
```
spice3 –b indeck > out.dat
```

…then submit the job to the grid as:

```
submit spice3 –b indeck > out.dat
submit --venue steele spice3 –b indeck > out.dat
```

Exercise #1: Using Workspaces

1) Log in and launch a workspace
2) Bring up your favorite editor and create a file called `hello.txt` with the text: `Hello, World!`
3) Export the file to your desktop
4) Import another file back into your workspace



Hint: look at commands…

```
exportfile --help
importfile --help
```