Jupyter Notebooks for Performing & Sharing Bioinformatics Analyses

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https://github.com/ljdursi/glbio-jupyter-workshop





The plan for this morning

- Run Jupyter notebooks on your laptop, in R and Python
- How to perform interactive analyses in a web browser using Jupiter
- How does it all work?
- Using markdown and latex to format notebooks nicely
- "Port" an R bioinformatics workflow from scripts into a Jupyter notebook
- Sharing a Jupyter notebook online:
 - SageMathCloud
 - GitHub and git; nbviewer
 - <u>mybinder.org</u>





The plan for this morning

Perfectly reasonable and interesting things to discuss that we won't be talking about today:

- Combining R and Python: cool and possible but requires a little setup
- IPython magics (probably)





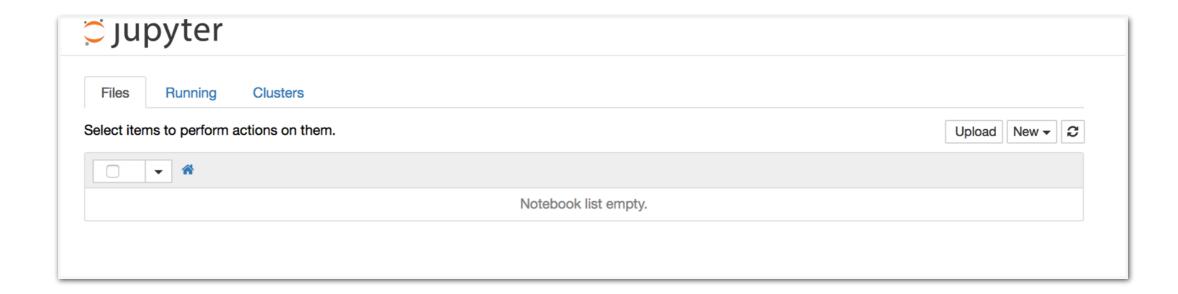
- Make a Notebooks directory and start from there
- Command Line: Linux, Mac

```
coredump:~ ljdursi$ mkdir ~/Desktop/Notebooks
coredump:~ ljdursi$ cd ~/Desktop/Notebooks/
coredump:Notebooks ljdursi$ jupyter notebook
[I 12:56:20.381 NotebookApp] The port 8888 is already in use, trying another random port.
[I 12:56:20.390 NotebookApp] Serving notebooks from local directory: /Users/ljdursi/Desktop/N
otebooks
[I 12:56:20.391 NotebookApp] Ø active kernels
[I 12:56:20.391 NotebookApp] The Jupyter Notebook is running at: http://localhost:8889/
[I 12:56:20.391 NotebookApp] Use Control-C to stop this server and shut down all kernels (twi
ce to skip confirmation).
```





- Make a Notebooks directory and start from there
- Command Line: Linux, Mac
- Browser should open (or go to localhost:8888)





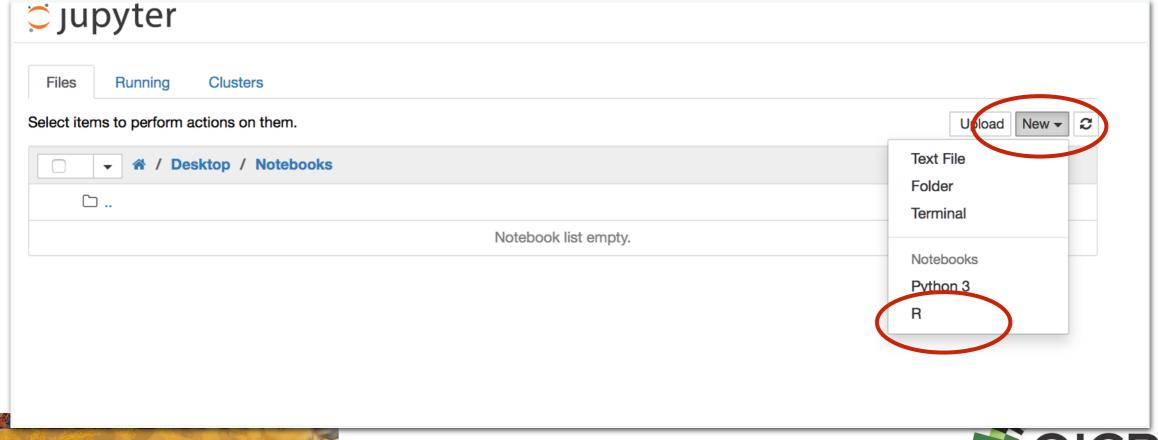


 Or you can start from home (eg, launch from start menu:Win) and navigate folders, and create new folders:





• Let's start up an R notebook



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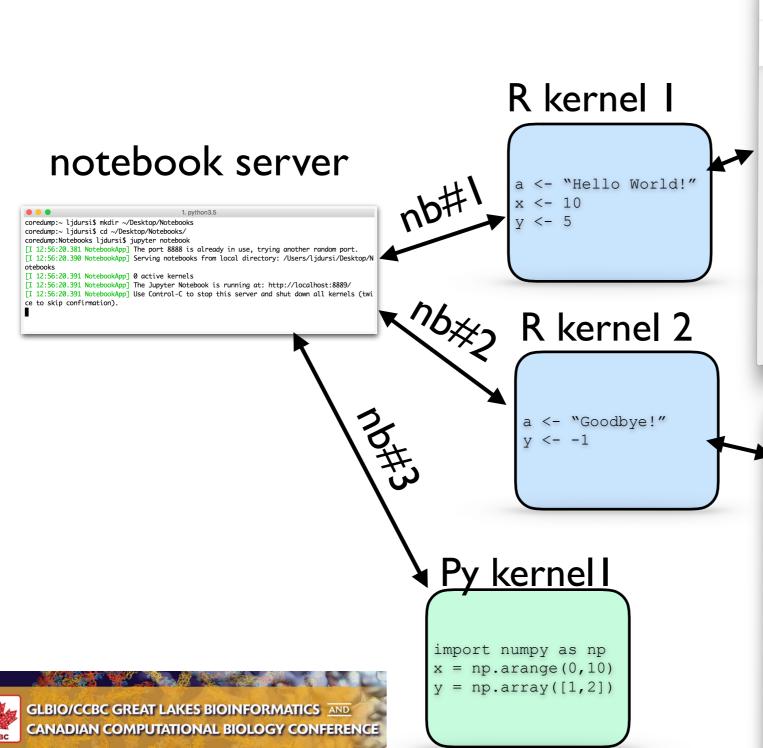


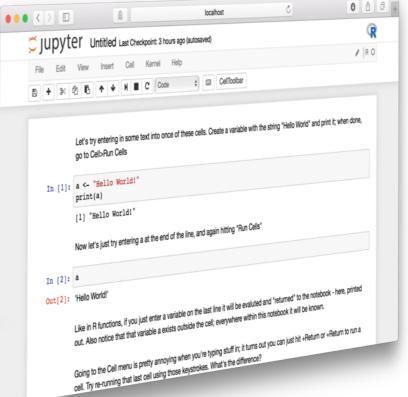
Demo - starting notebook

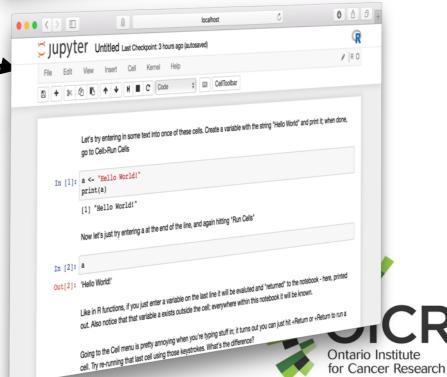




How does this all work?

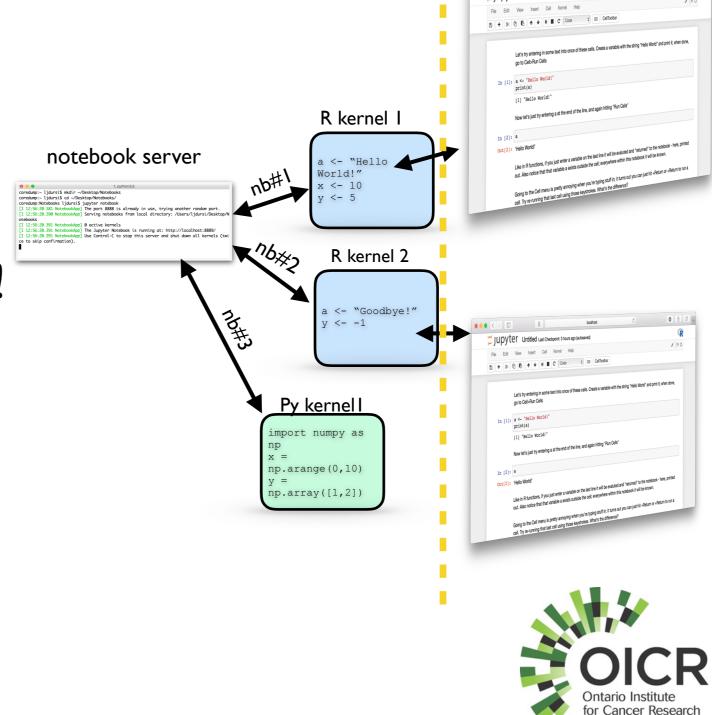






How does this all work?

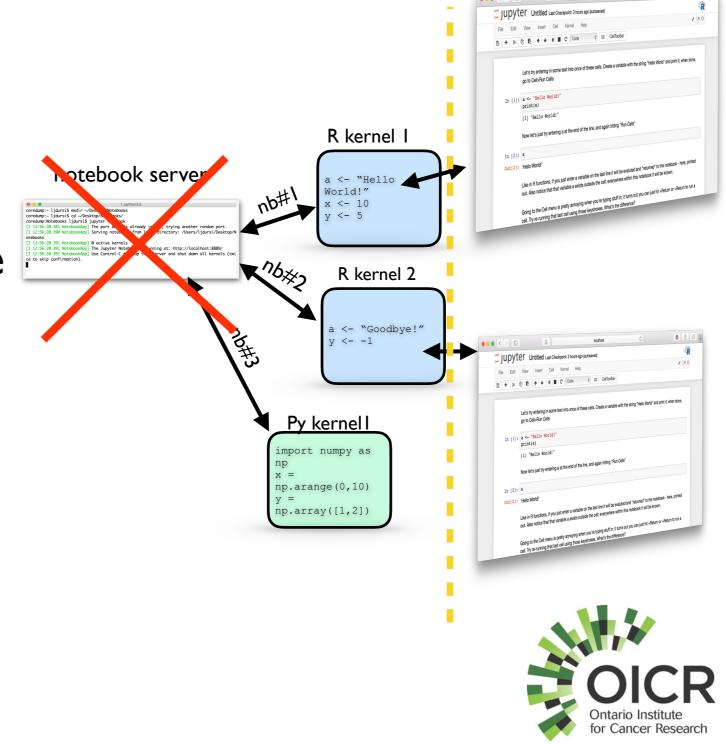
- There's no rule that says the notebook server/kernels has to be on same machine as browser!
- Can be running on remote server (or cluster)
- AWS demo





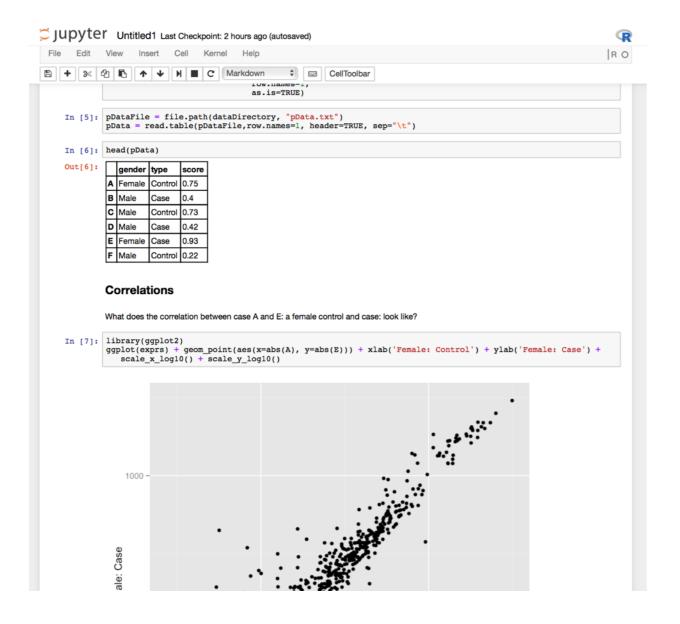
How does this all work?

- AWS demo...
- What happens if the notebook server dies?
- Demo





All input+output in ipynb file



```
"cells": [
  "outputs": [],
  "source": [
   "data <- read.csv('http://dursi.ca/content/images/GSE37704_featurecounts.csv')\n",
   "metadata <- read.csv('http://dursi.ca/content/images/GSE37704_metadata.csv')"
 },
  "outputs": [
     "name": "stdout",
    "output_type": "stream",
     "text": [
      ''data.frame':\t19808 obs. of 8 variables:\n",
     " $ ensgene : Factor w/ 19808 levels \"ENSG000000000003\",..: 15488 19676 19628 19554 19334 15792 16078 15
867 15778 15793 ...\n",
      " $ length : int 918 718 1982 939 939 3214 5539 3395 2833 3424 ...\n",
      " $ SRR493366: int 0 0 23 0 0 124 1637 120 24 4 ...\n",
     " $ SRR493367: int 0 0 28 0 0 123 1831 153 48 9 ...\n",
     " $ SRR493368: int 0 0 29 0 0 205 2383 180 65 16 ...\n",
     " $ SRR493369: int 0 0 29 0 0 207 1226 236 44 14 ...\n",
     " $ SRR493370: int 0 0 28 0 0 212 1326 255 48 16 ...\n",
     " $ SRR493371: int 0 0 46 0 0 258 1504 357 64 16 ...\n"
  "outputs": [
     "data": {
     "image/png":
     "iVBORw0KGgoAAAANSUhEUgAAA0gAAANICAYAAAD958/bAAAEDWlDQ1BJQ0MgUHJvZmlsZQAA0
     I2NVV1oHFUUPrtzZyMkzlNsNIV0qD8NJQ2TVjShtLp/3d02bpZJNtoi6GT27s6Yyc44M7v9oU9
     FUHwx6psUxL+3gCAo9Q/bPrQvlQol2tQgKD60+INQ6Ium65k7M5lpurHeZe58853vnnvuuWfvB
```

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All the input+output is located in the .ipynb file

