[Updated course schedule](#)

Windows users should download [Mobaxterm](#) - we'll use this to ssh to Amazon. Mac and Linux users will use the built-in ssh client (there is nothing extra to download).

Everyone should download [Cyberduck](#). We'll use this to sftp files to and from Amazon.

Logging into the AWS instances:

```
ssh -i path/to/key.pem ubuntu@ip-address
```

Where `path/to/key.pem` is the path to the key file that you downloaded above, and `ip-address` is replaced with one of the following:

1. 54.167.124.62
2. 54.91.90.4
3. 54.205.65.67
4. 54.82.150.238 (instructor's instance, please don't use)

Workshop commands (for hands-on portions of the workshop):

Day 1: [Microbial Community Diversity (Illumina Tutorial)](#)
Day 2:
- [Working with OTU tables](#)
- Working with alternative marker genes (e.g., [ITS](#), [shotgun read processing](#); file formats)
- Predicting metagenomes with PICRUSt ([tutorial](#); [paper](#); [method summary](#); [method performance](#))

Getting help with QIIME scripts:
http://qiime.org/scripts/index.html

Other useful QIIME links:
http://www.qiime.org
http://qiime.org/tutorials/unix_commands.html
http://qiime.org/tutorials/working_with_aws.html

Interested in using QIIME with StarCluster and IPython? See here:
http://qiime.org/home_static/nih-cloud-apr2012/

The IPython and StarCluster tutorials are invaluable for this:
 http://ipython.org/ipython-doc/rel-0.13/index.html
 http://web.mit.edu/star/cluster/

Interested in using AWS for research or education? AWS grants are available:
 http://aws.amazon.com/education/

Getting started with the unix shell (command line):
 http://software-carpentry.org/v5/novice/shell/index.html

Important links:
 http://www.qiime.org
 http://qiime.org/tutorials/working_with_aws.html
 http://qiime.org/tutorials/tutorial.html

Alternatives to rarefaction: Waste Not, Want Not paper