

# High-Speed Networking and Distributed Applications

## Lab Exercise 2: Introduction to GCF and Install Scripts

CS491

Summer 2013

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In this lab exercise, you will set up the GENI Control Framework on your computer and work with resource specification (rspec) XML files. You will also load and run software automatically in a GENI node using install script functionality.

### Procedure

**Step 0:** Download `gcf` from

<http://software.geni.net/local-sw/download&software=gcf-2.3.3.tar.gz>  
and follow the instructions at <http://trac.gpolab.bbn.com/gcf/wiki/QuickStart>  
to install it.<sup>1</sup>

Stop right after step 3 “Install software dependencies”, because configuration will be handled through the GENI Portal.

**Step 1:** Go to your GENI Portal account and click the “Profile” link at the top navigation, then click “Configure `omni`”.

Download your customized configuration data, making sure you select KU-CS491 as your default project.

Run `omni-configure.py` in the terminal and `omni` will autoconfigure itself based on the configuration data you downloaded. If it complains that a key already exists, hit `n` to not replace it.

**Step 2:** Create a slice through the GENI Portal and call it                     lab2. Launch Flack.

username

**Step 3:** Import the experiment. Select “Import → Import from Web” in Flack, and supply this URL: <http://alis0nc.github.io/cs491/lab2/lab2.rspec>. Specify that you want to use the Kettering aggregate manager, `geni.kettering.edu.cm`. Wait for your resources to become ready.

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<sup>1</sup>If you’re using a syslab computer, you should copy the `gcf-2.3.3` directory to your home folder because you don’t have root privileges on the box. If you’re using your own laptop, you can copy the directory anywhere you want.

**Step 4:** Once they're ready, click on the info button for each node and add an install service. Supply the install url `http://alis0nc.github.io/cs491/lab2/lab2.tar.gz` and install location `/local`. Add an execute service similarly with command `sudo /local/install-script.sh` to be executed using `sh`.

**Step 5:** We are going to draw back the curtain and see what's going on behind the scenes. (*Pay no attention to that man behind the curtain.*<sup>2</sup>)

In Flack, select "View → Preview request document(s)" and save the request rspec file. Examine it either in the Flack window or your favourite text editor. This xml file contains the specifications for the compute resources (virtual machine nodes) and network links you requested in Flack. This file gets sent to the aggregate manager so that it can give you what you requested.

**Step 6:** We're switching from Flack to the command line `omni` tool now. In a terminal, run `omni.py createslice _____lab2omni`. This should succeed with a message to that effect in the terminal.

Now run `omni.py createsliver -a ig-kettering _____lab2omni`. This takes a while, but after a few minutes you should see a "Completed createsliver" message and now your reserved nodes are ready to log into.

**Step 7:** Follow the instructions at `http://groups.geni.net/geni/wiki/GEC17Agenda/GettingStartedWithGENI_II/ExecuteExperiment` to log into your nodes and look at the experiment results. Use `ig-kettering` for the `AM.NICKNAME` and \_\_\_\_\_lab2omni for the `SLICENAME`.

**Step 8:** Clean up after yourself by deleting your resources. You already know how to do this in Flack. In omni, it's `omni.py -a ig-kettering deletesliver _____lab2omni`. When that command succeeds, you'll see the output of "Completed deletesliver".

## Acknowledgement

Adapted from Wong, G. (2013-07-21). "Getting started with GENI and the GENI Portal, part II". Presented at the *17th GENI Engineering Conference*, Madison, Wisconsin. `http://groups.geni.net/geni/wiki/GEC17Agenda/GettingStartedWithGENI_II`

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<sup>2</sup>The Wizard of Oz, 1939. `www.youtube.com/watch?v=YWyCCJ6B2WE`