High-Speed Networking and Distributed Applications Lab Exercise 2: Introduction to GCF and Install Scripts

CS491 Summer 2013

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.¹

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.
- Step 3: Import the experiment. Download the rspec from http://alisOnc.github.io/cs491/lab2/lab2.rspec, select "Import → Import from file" in Flack, and navigate to that rspec you saved. Specify that you want to use the GPO InstaGENI aggregate manager, instageni.gpolab.bbn.com.cm. Don't hit Submit; you shouldn't actually reserve resources in this step.

¹If 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: Click on the info button for each node and add an install service. Supply the install url http://alisonc.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.*²)

In Flack, select "View \rightarrow Preview request document(s)" and save the request rspec file. Examine it in 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.

While you're examining the rspec, make sure the <install> tag comes before the <execute> tag within the <services> section of each node. When I added the install and execute services, Flack put the <execute> tag first for some reason, so it was trying to execute something that wasn't installed yet.

Step	6: We're switching from Flack to the command line omni tool now. In a terminal,
	run omni.py createslicelab2omni. This should succeed with a
	message to that effect in the terminal.
	Now run omni.py createsliver -a ig-gpolab2omni
	This takes a while, but after a few minutes you should path to rspec you saved in step 5
	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-gpo 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-gpo 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

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