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

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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.
username

Step 3: Import the experiment. Download the rspec from
`http://alis0nc.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.

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[1]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: 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.*[2])

In Flack, select "View → 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 didn't exist yet.

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
_{username}
message to that effect in the terminal.

Now run `omni.py createsliver -a ig-gpo _____lab2omni`
_{username}
`_____`. 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`.
_{username}

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
_{username}
"Completed deletesliver".

Acknowledgement

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