



CS 4001/7001 Cloud Computing
Spring 2015

Lab # 1 – GENI Account Setup and Services Overview

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1. Purpose of the Lab

Setup your GENI account, and use it to reserve an experiment environment a.k.a. “slice” that features 2 compute nodes communicating over a Layer 2 connection. Run a “Hello GENI” experiment with GUI (Flack) and Command-line (Omni) tools in your reserved slice by automatic installation and execution of software to perform basic bandwidth measurement tests between the nodes.

2. References to guide Lab work

- [1] Chapter 1, Distributed and Cloud Computing, Hwang, Fox & Dongarra
- [2] GENI Terminology/Architecture: <http://groups.geni.net/geni/wiki/GeniNewcomersWelcome>
- [3] GENI Tutorial Paper:
<http://www.sigcomm.org/sites/default/files/ccr/papers/2012/January/2096149-2096161.pdf>
- [4] GENI Omni Tool: <http://trac.gpolab.bbn.com/gcf/wiki/Omni>
- [5] GENI Flack Tool: <http://www.protogeni.net/ProtoGeni/wiki/FlackManual>
- [6] GENI Understanding Aggregate Manager exercise:
<http://groups.geni.net/geni/wiki/GENIEducation/SampleAssignments/UnderstandAMAPI/Procedure>

3. Lab Steps and output collection guidelines



Figure 1: Lab Steps Overview

The Figure 1 shows the required steps to successfully create an account and setup your environment in the GENI infrastructure. You will need to understand GENI terminology/architecture documentation and get familiar with GUI (Flack) and Command-line (Omni) tools to create your “Hello World” GENI slice. Finally, you will verify that your slice is alive!

3.1 GENI Terminology and Architecture

Take your time in order to understand the [GENI terminology](#) [2], and experiment workflow shown in Figure 1. Go through the GENI wikis to find detailed information of each step of the workflow. Pay special attention to the capabilities of tools such as Flack/Omni and their [integration to setup your GENI environment](#) [3] for experiments.

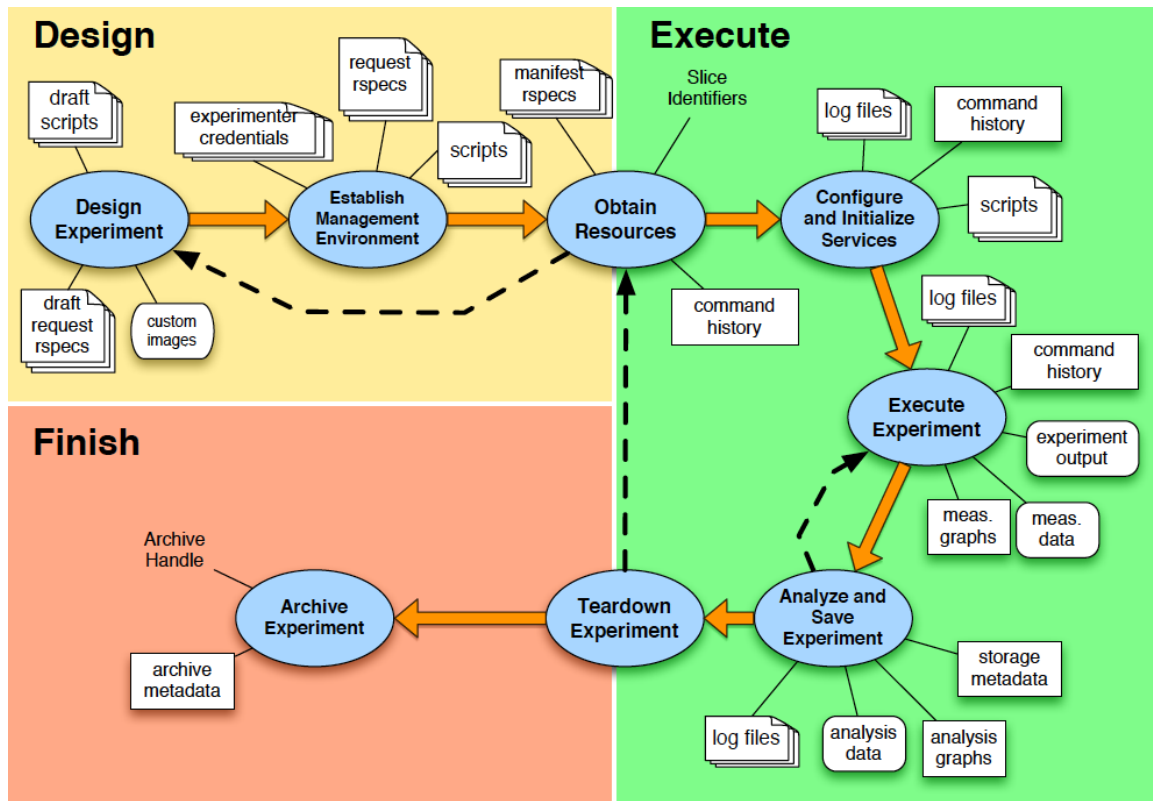


Figure 2: Experiment workflow within GENI architecture [3]

3.2 GENI Account Setup

a) Create your GENI account

Go to GENI portal <https://portal.geni.net> and press the “Use GENI” button. From the Drop Down menu, select your institution. Start typing the name of your institution and see the list become smaller.

You will be transferred to the Pawprint Login Page. Fill in your username and password. Complete the form that appears after you have successfully logged in and press ‘Continue’.



You will be transferred to an Activation Page. Make sure both checkboxes are checked by default and then press Activate. You have successfully created your GENI account!

b) Associate your GENI account with the course

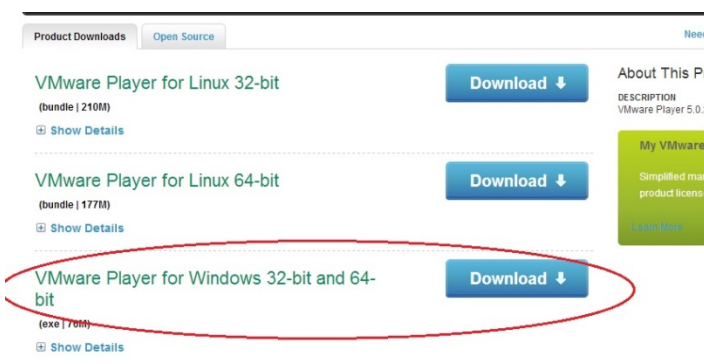
In order to use the portal to reserve GENI infrastructure resources for your lab exercises, you must join the project '[Calyam_UMissouri_Spring2015](#)' by clicking on the "Join a Project" button in the Home page.

3.3 Pre-work for GENI Environment Setup

3.3.1 Install VMware Player (*only for Windows OS users to setup Linux image in VM*)

Download and install VMware Player software for Windows from:

https://my.vmware.com/web/vmware/free#desktop_end_user_computing/vmware_player/5_0



Once the download is complete, run the .exe file to complete the installation.



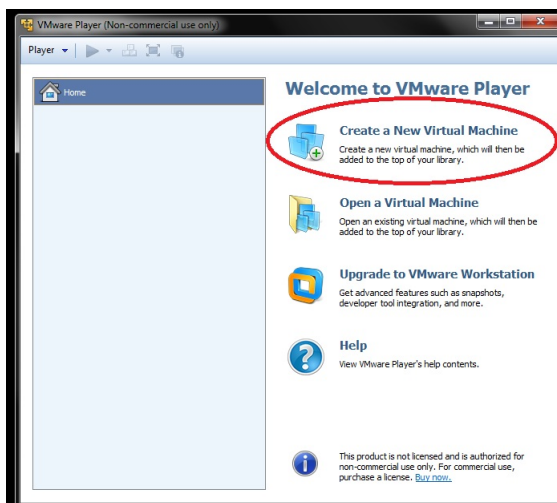
Next, download and install a lightweight Linux image [xubuntu-13.10-desktop-i386.iso](#) from either links <http://cdimage.ubuntu.com/xubuntu/releases/13.10/release/>



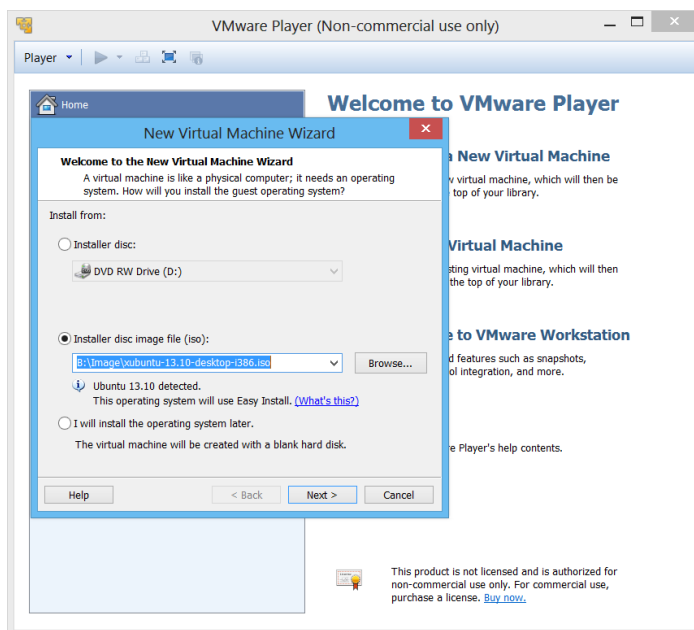
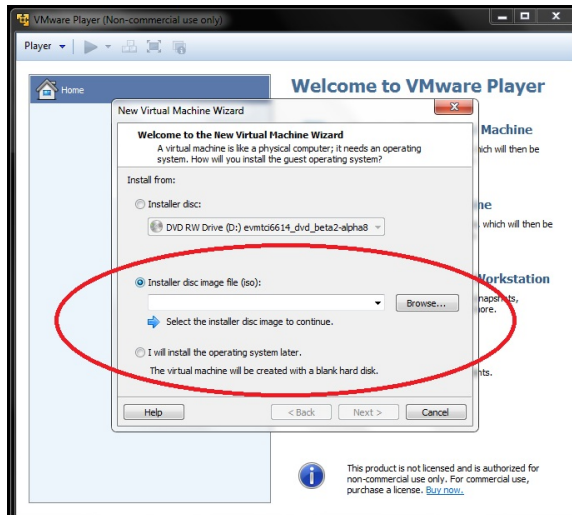
Name	Last modified	Size	Description
Parent Directory		-	
MD5SUMS	17-Oct-2013 10:01	131	
MD5SUMS-metalink	17-Oct-2013 10:01	141	
MD5SUMS-metalink.gpg	17-Oct-2013 10:01	198	
MD5SUMS.gpg	17-Oct-2013 10:01	198	
SHA1SUMS	17-Oct-2013 10:01	147	
SHA1SUMS.gpg	17-Oct-2013 10:01	198	
SHA256SUMS	17-Oct-2013 10:01	195	
SHA256SUMS.gpg	17-Oct-2013 10:01	198	
xubuntu-13.10-desktop-amd64.iso	16-Oct-2013 21:29	842M	Desktop image for 64
xubuntu-13.10-desktop-amd64.iso.torrent	17-Oct-2013 10:00	33K	Desktop image for 64
xubuntu-13.10-desktop-amd64.iso.zsync	17-Oct-2013 10:00	1.6M	Desktop image for 64
xubuntu-13.10-desktop-amd64.list	16-Oct-2013 21:29	4.0K	Desktop image for 64
xubuntu-13.10-desktop-amd64.manifest	16-Oct-2013 21:16	44K	Desktop image for 64
xubuntu-13.10-desktop-amd64.metalink	17-Oct-2013 10:01	1.0K	
xubuntu-13.10-desktop-i386.iso	16-Oct-2013 21:30	834M	Desktop image for PC

Note: If the above links are not accessible through the manual, you can use the Xubuntu Image link provided in 'Assignments' section of Blackboard.

Start the VMware Player and select 'Create a new Virtual Machine'.

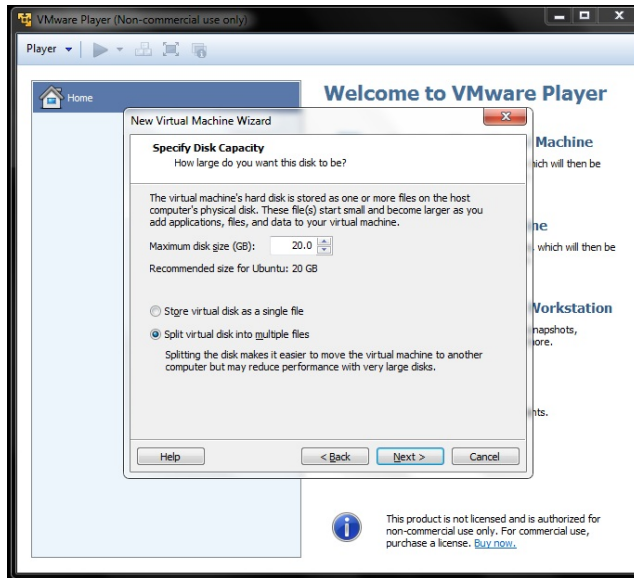


Select the 2nd radio button: Installer disc image file (iso): and browse to your xubuntu-13.10-desktop-i386.iso file which you just downloaded.

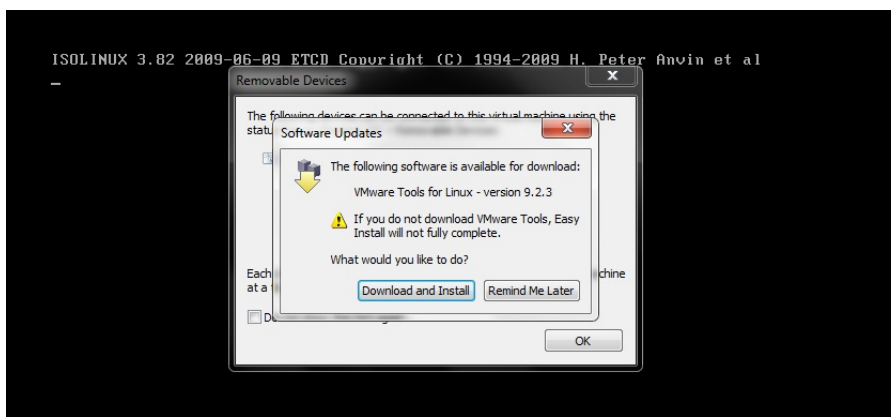


Once you select 'Next', provide your user login information and proceed with the default settings and select the 'Finish' button.

Note: Please make sure you have at least 20 GB of free memory on your disk.



XUbuntu software starts installing, and if you get a window to install VMware tools, select download and install as shown below (**Note:** do not go with 'Remind Me Later' option!)

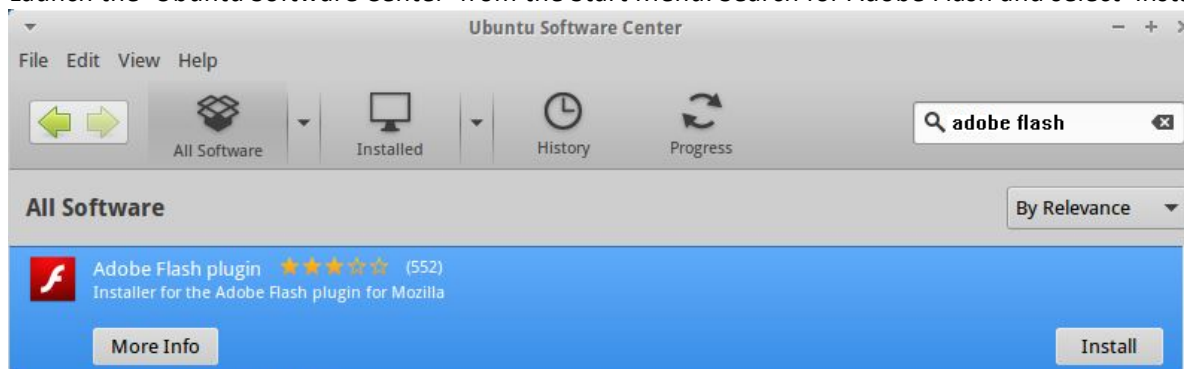


Your installation status should look similar to the below screen shots once the VMware tools are installed; this will take a few moments to get installed, please be patient.



Once the installation is successfully complete, you should get a window to enter your user name and password to login to your Linux Virtual Machine.

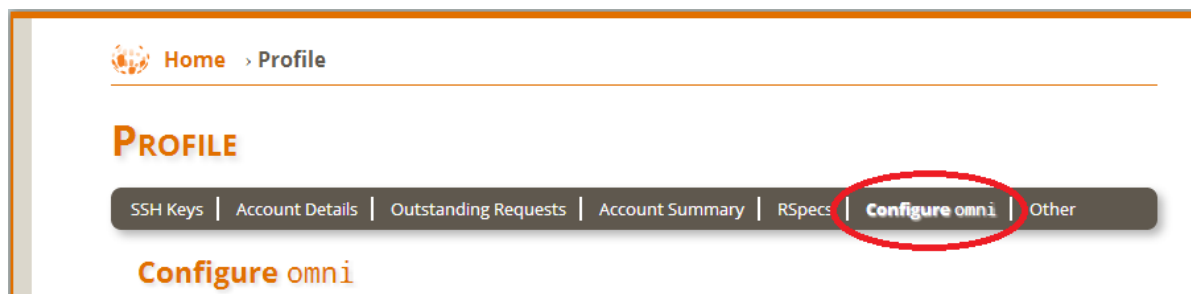
Launch the 'Ubuntu Software Center' from the Start Menu. Search for Adobe Flash and select 'Install'.



You are now ready to run your next steps of GENI experiment in the installed VM!

3.3.2 Install and Configure Omni (*All users need to do this*)

After you are logged in to your VM, open your browser with the GENI Portal page <https://portal.geni.net/>. Login to your GENI portal, select the tab labeled 'Profile' in the upper right corner, and then select the section labeled 'Configure: omni'.





Now look for 'Option 1: Automatic omni configuration'

Option 1: Automatic omni configuration

To automatically configure omni, use the [omni-configure](#) script distributed with omni as described below.

1. In order to use omni you will need to generate an SSL certificate.
2. Download your customized omni configuration data and save it in the default location (~/.Downloads/omni.bundle):

[Download your omni data](#)

3. Run the following command in a terminal to generate a configuration file for omni (omni_config):

```
omni-configure
```

4. Test your setup by running the following command in a terminal:

```
omni -a gpo-ig getVersion
```

The output should look similar to this [example output](#).



Tip Make sure you are running **omni 2.5.3** or newer.

To determine the version of an existing omni installation, run:

```
omni --version
```

If necessary, [download](#) and [install](#) the latest version of omni.

Complete [omni-configure instructions](#) are available.



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If necessary, [download](#) and [install](#) the latest version of omni.

Complete [omni-configure instructions](#) are available.

Click on the 'download' as shown to download the Omni tool. This will take you to a new page shown below. Click on the 'Download' button again (circled below) and in the new page, scroll down, click 'Accept' to start downloading your gcf package.

Welcome to the gcf project wiki

The gcf project provides a reference implementation of the [GENI Aggregate Manager API](#). It consists of:

- **omni** - A command line client for reserving GENI resources via the GENI Aggregate Manager API
- **gcf-am** - A reference implementation of a GENI Aggregate Manager
- **gcf-ch** - A reference implementation of a GENI Clearinghouse

Getting Started

1. **Download** the full software.
 - **Windows** binaries are available for Omni and experimenter tools.
 - **Mac OS X** binaries are available for Omni and experimenter tools.
 - Or get **older versions** or the source.
2. **Install** the software.
 - **Install from source**
 - **Install the Mac binaries**
 - **Install the Windows binaries**
3. Configure the software using one or both of the following:
 - **Configure omni** : For experimenters that want to use the command line tool to reserve resources in GENI.
 - **Configure gcf**: For developers that want to test with or build on top of the reference aggregate and clearinghouse. To actually test gcf you probably also need to [configure omni](#).





Next, go back to the Configure Omni page in the GENI portal and click on the 'install' button.

Option 1: Automatic omni configuration

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[Download your omni data](#)


3. Run the following command in a terminal to generate a configuration file for omni (omni_config):

```
omni-configure
```

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```
omni -a gpo-ig getversion
```

The output should look similar to this [example output](#).



Tip Make sure you are running **omni 2.5.3** or newer.

To determine the version of an existing omni installation, run:

```
omni --version
```

If necessary, [download](#) and [install](#) the latest version of omni.

Complete [omni-configure instructions](#) are available.

This will take you to a new page with steps to install Omni. On that page, follow the Steps from 1 to 3: Step1: 'Create the gcf directory' Step 2: 'Add GCF to your path' and Step 3: 'Install Software Dependencies' as described in the page.

Useful suggestion/tips for Steps 1 - 3:

In Step 1, while executing the commands given in the 3rd bullet point, the terminal will throw the error: rm: cannot remove `gcf`: No such file or directory; (since this will be your first setup). The ln command here is used to create a symbolic link called gcf to your gcf installation directory. This is done to make the process of updating omni easier in future. It's optional not mandatory; ignore the particular command and proceed with rest of commands:

```
$ cd <install-dir>
$ ln -s gcf-2.7 gcf
```

In Step 2 of the Installation Page, the .bashrc file will be located in your home user directory /home/<username>/. You can go directly to the file in your folder structure to edit it. This will be a hidden file; you can use the command Ctrl+H to view it. You could also navigate to the file on your terminal and use the below command:



```
$ vi .bashrc
```

In the `.bashrc` file, make sure you give the absolute path for `gcf` folder, for example:

```
/home/<username>/GENI/gcf-2.7/src
```

```
/home/<username>/GENI/gcf-2.7/examples
```

Now, go back to the ‘Configure Omni’ page in the GENI portal and click on ‘Download your omni data’ in Step 2 of this section.

Option 1: Automatic omni configuration

To automatically configure omni, use the [omni-configure](#) script distributed with omni as described below.

1. In order to use omni you will need to generate an SSL certificate.
2. Download your customized omni configuration data and save it in the default location (`~/Downloads/omni.bundle`):

[Download your omni data](#)

3. Run the following command in a terminal to generate a configuration file for omni (`omni_config`):

```
omni-configure
```

4. Test your setup by running the following command in a terminal:

```
omni -a gpo-ig getversion
```

The output should look similar to this [example output](#).



Tip Make sure you are running **omni 2.5.3** or newer.

To determine the version of an existing omni installation, run:

```
omni --version
```

If necessary, [download](#) and [install](#) the latest version of omni.

Complete [omni-configure instructions](#) are available.

Make sure your default project matches the project name you previously joined for the course i.e., **Calyam_UMissouri_Spring2015**. If not, make that your default.

NOTE: To be able to download Omni bundle, you might need to generate an SSL certificate by clicking on the “Generate Combined Certificate and Key File”.

Recommended Option: Have the objects generated for you

If in doubt, use this option.

[Generate Combined Certificate and Key File](#)

An SSL certificate always has a corresponding SSL private key. This option will generate one file which contains both the signed SSL certificate and the corresponding private key. (This is a new key generated for this SSL certificate and is different from your SSH private key.)



Click 'Download your omni data' and save the file in your Downloads folder. You will get a Warning that SSH key has not been uploaded. Ignore the Warning for now since you will do this later in the Step-1 of your experiment.

[Home](#) → [Profile](#) → [Omni Bundle](#)

Download Omni Configuration Data

Warning

No SSH keys have been uploaded. Please [Upload an SSH key](#) or [Generate and Download an SSH keypair](#) to enable login to nodes.

Use the omni configuration data downloaded from this page, to automatically [configure omni](#). Save the customized omni configuration data in the default location.

Choose a default project to use with omni: [Calyam_UMissouri_Spring2015](#)

Choose the version of omni you are using: [2.5.3 or newer](#)

To determine the version of your omni, run: `omni --version`

[Download your omni data](#) [Cancel](#)

Open a terminal window and type:

```
$: omni-configure.py
```

If your path configuration is correct, the cert and key files you need will be installed in the appropriate folders. In case you get 'omni-configure.py': command not found, please re check your previous steps.

3.3 GENI "Hello World" Experiment

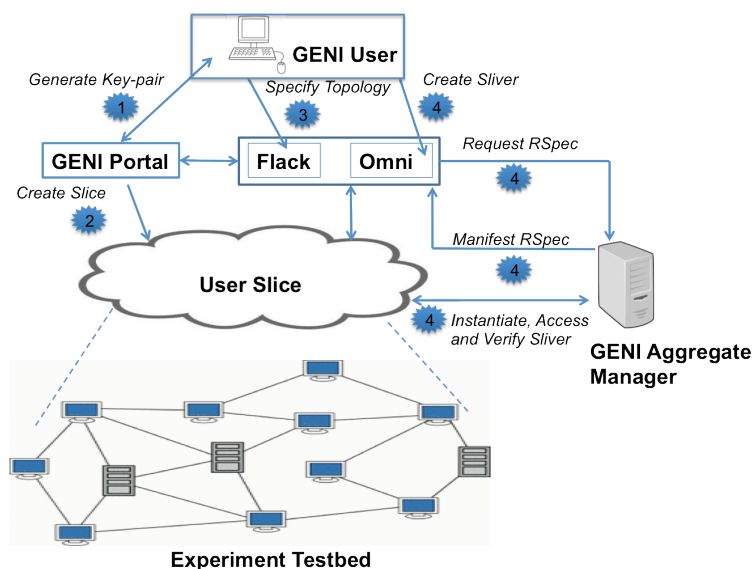


Figure 3: GENI Experiment Testbed Overview



As shown in Figure 3, your “Hello World” experiment will comprise of 4 steps that are described below.

Step-1: Generate Key-pair

Access to your compute resources in GENI through the portal is provided through SSH key-pairs and hence you need to upload your public key to the portal.

In the Profile page ‘SSH Keys’ section, select ‘generate and download an SSH keypair’ button, enter same passphrase twice and click ‘Generate SSH private key’.

Note: Please remember your passphrase as it will be needed again in later part of your lab exercises.

[Home](#) → [Profile](#)

Profile

[Account Summary](#) | [SSH Keys](#) | [SSL](#) | [Configure omni](#) | [RSpecs](#) | [Tools](#) | [Outstanding Requests](#)

SSH Keys

No SSH keys have been uploaded. SSH keys are required to log in to reserved compute resources. You have two options:

- [generate and download an SSH keypair](#) The private key (but not the passphrase that protects it) might be shared with other GENI entities. If you choose this option do not reuse this key pair outside of GENI, or
- [upload an SSH public key](#) , if you have one you want to use. If you only choose this option then some GENI tools might not work properly

If you're not sure what to do, choose [generate and download an SSH keypair](#)

[Home](#) → [Profile](#) → [Generate SSH Keypair](#)

Generate an SSH private key

SSH keys are required to log in to reserved compute resources. On this page, you can generate a new SSH key pair.

Please supply a new passphrase to protect your SSH private key (minimum 5 characters).

Passphrase:

Confirm Passphrase:

[Generate SSH private key](#)

If you already have an SSH key pair that you want to use, you can instead [upload an SSH public key](#) .

If you're not sure what to do, use this page to generate a new key pair.



Profile

Account Summary | **SSH Keys** | SSL | Configure omni | RSpecs | Tools | Outstanding Requests

SSH Keys

Name	Description	Public Key	Private Key	Edit	Delete
id_geni_ssh_rsa 0a:10:e4:44:0b:5a:5e:1c:67:00:9c:43:a7:ea:51:c3	Generated SSH keypair	Download Public Key	Download Private Key	Edit	Delete

Note: You will need your SSH private key on your local machine.

If you generated your SSH keypair on this portal and have not already done so, be sure to:

1. Download your SSH key.
2. After you download your key, be sure to set local permissions on that file appropriately. On Linux and Mac, do

```
chmod 0600 [path-to-SSH-private-key]
```

3. When you invoke SSH to log in to reserved resources, you will need to remember the path to that file.
4. Your SSH command will be something like:

```
ssh -i path-to-SSH-key-you-downloaded [username]@[hostname]
```

[Upload another SSH public key](#)

Next, press the 'Download Private Key' button; Open a terminal and execute the below commands. In case, .ssh folder does not exist, create one by: `mkdir /home/<username>/.ssh`

The ssh-add command will prompt for the passphrase, enter the passphrase you used in the previous step of generating ssh key.

```
$ mv ~/<Download path>/id_geni_ssh_rsa ~/.ssh/.  
$ chmod 0600 ~/.ssh/id_geni_ssh_rsa  
$ ssh-add ~/.ssh/id_geni_ssh_rsa
```

Above commands will allow you to log into your nodes securely without a password.



Step-2: Create Slice

Go to 'Projects' tab, and select 'Create Slice' button under the project Calyam_UMissouri_Spring2015.

[Home](#) → [Projects](#)

GENI Projects

My Projects

[Join a Project](#)
[Ask Someone to Create a Project](#)
[Ask to be a Project Lead](#)

Project Name	Project Lead	Purpose	Slice Count	Create Slice
Calyam_UMissouri_Spring2015	Calyam, Prasad	Course work related labs	0	Create Slice

Choose a slice name with the convention *Lab1<Pawprint>*, leave the description empty and click 'Create slice' button.

[Home](#) → [Project Calyam_UMissouri_Spring2015](#) → [Create Slice in project Calyam_UMissouri_Spring2015](#)

Create New Slice

A GENI slice is a container for reserving and managing a set of GENI resources.

Project name	Calyam_UMissouri_Spring2015	
Slice name	<input type="text" value="Lab1xyz99"/>	-- Required
Slice description	<input type="text"/>	

Note: Slice names must not contain whitespace. Use at most 19 alphanumeric characters or hyphen (no leading hyphen) : "a-zA-Z0-9-".

Note: Slice names are public and must be unique across your project.

[Create slice](#) [Cancel](#)

Step-3: Specify Topology

Download RSpec file from Blackboard (Assignments -> GENI Lab-1 RSpec) and make sure it is saved as 'Lab1.rspec'



Select the 'Flack' button under the tools menu in your slice as shown below:

Home → Project Calyam_UMissouri_Spring2015 → Slice Lab1xyz99

Notice
Created slice Lab1xyz99

GENI Slice: Lab1xyz99

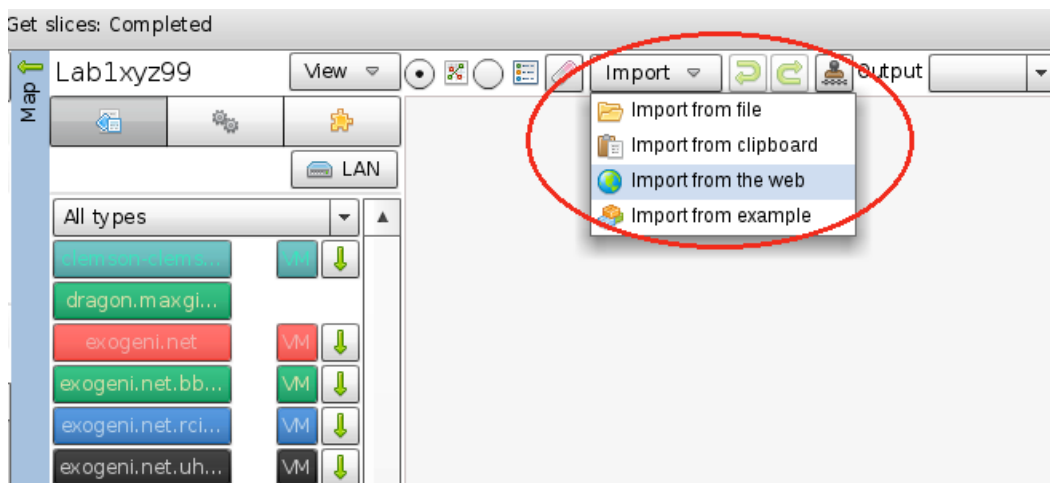
Need help? Look at the [Portal Help](#) or [GENI Glossary](#).

Slice Actions
[Add Resources](#) [Manage Resources](#) [Manage Slice Members](#) [Slice Identifiers](#) [Recent Actions](#)

Renew Slice
Project expires on 2015-06-30 23:59:59 Z
Slice expires on 2015-01-15 07:26:10 Z
Renew ☐ slice only ☒ slice & known resources until 2015-01-15 [Renew](#)

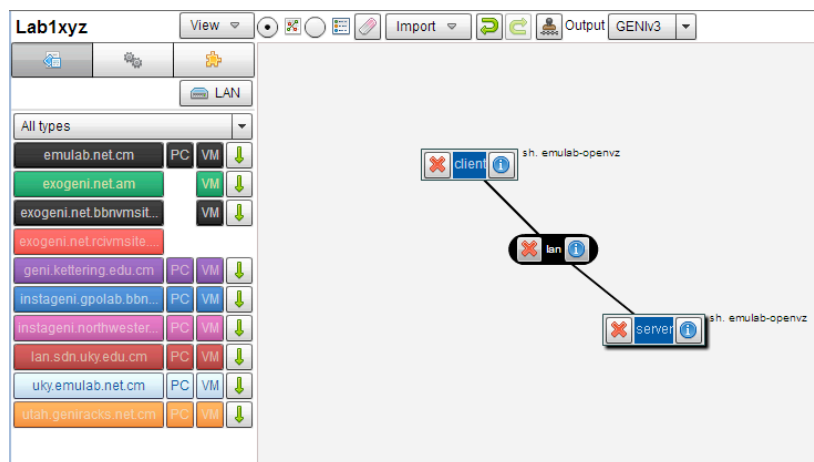
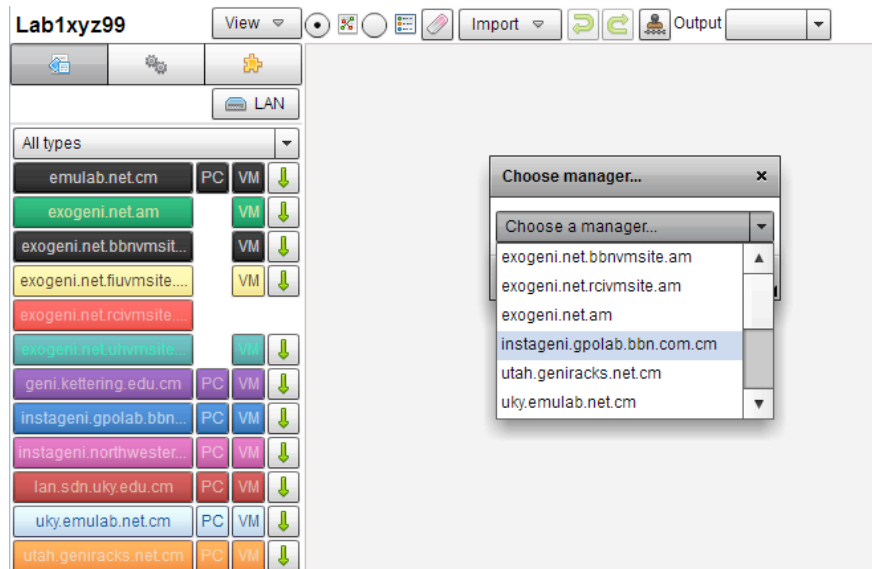
Slice Tools
[Flack](#) [GENI Desktop](#) [LabWiki](#) [Omni](#) [jFed](#) [Slice Jacks \(beta\)](#)

The Flack tool launches in a new page. Once the tool is ready, import an RSpec file of a simple experiment topology in Flack using 'Import from file'.



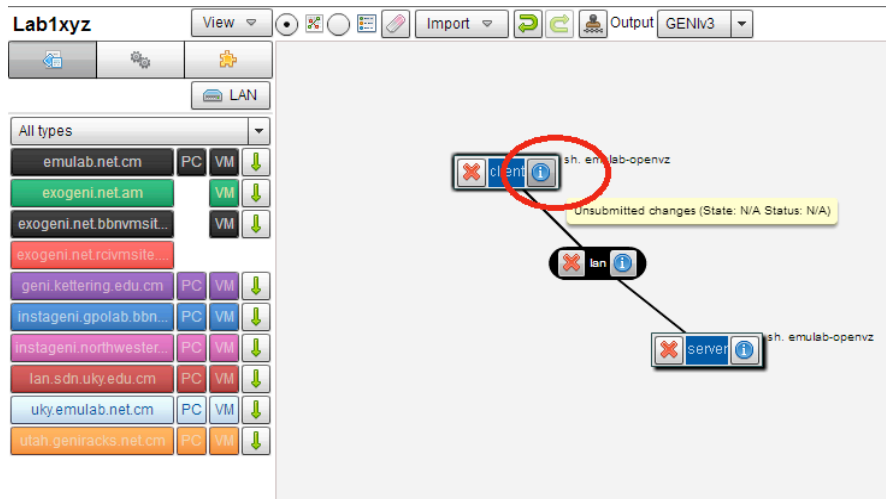
Browse to the location where you downloaded 'Lab1.rspec' from Blackboard and click 'Ok'

Because this file contains a generic description of resources and does not specify any particular aggregate manager, Flack will report "There were resources detected without a manager selected, please select which manager you would like to use." Select 'OK', and then **choose the name of the manager for flack assigned to you**. Then select 'Accept', and a network topology should appear on the canvas.



Next, you will modify the experiment in Flack to automatically install the Iperf tool for network performance testing within your slice.

Modify the 'client' node by clicking on the "i" button shown below.



client

Manager instageni.g... **Binding** ☒ Unbound ☐ Bound to **Sliver Type** emulab-xen ☐ Exclusive?

Disk Image Select advertised image Select a user for user-created disk images Select user-created disk image

☒ Name ☐ URL Select image above, paste URN, or manually type OSID

Version If required, give a disk image version.

Install **Execute** using sh

When you open the node information, you will see options to request installation of custom software and its execution within your experiment for installation and execution of services. Use the '+ Add Execute Service' button to request the appropriate command:

```
sudo apt-get install iperf -y
```

be executed using

```
sh
```

Once the "execute" services is specified, click on the "Interfaces and Links" tab which is the middle tab and type in the IP address for VM:if0 as 10.100.0.2 as shown below



Once you select the server node information as shown below, select the 'Apply' button.

server

Manager instageni.g... **Binding** ☒ Unbound ☐ Bound to **Type...** **Sliver Type** emulab-xen

Disk Image Select advertised image Select a user for user-created disk images Select user-created disk image

☒ Name ☐ URL *Select image above, paste URN, or manually type OSID*

Version *If required, give a disk image version.*

Install **Execute** `sudo apt-get install iperf-y` using sh



server

Interface	Physical	MAC	IP	Mask	Type
VM-0:if0	<input type="checkbox"/> Bound to		10.100.0.3		

☐ Routable Control IP (Emulab only)

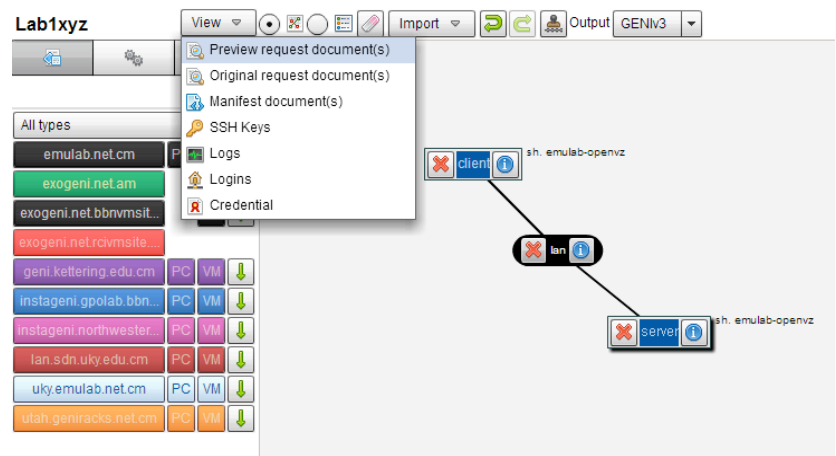
client

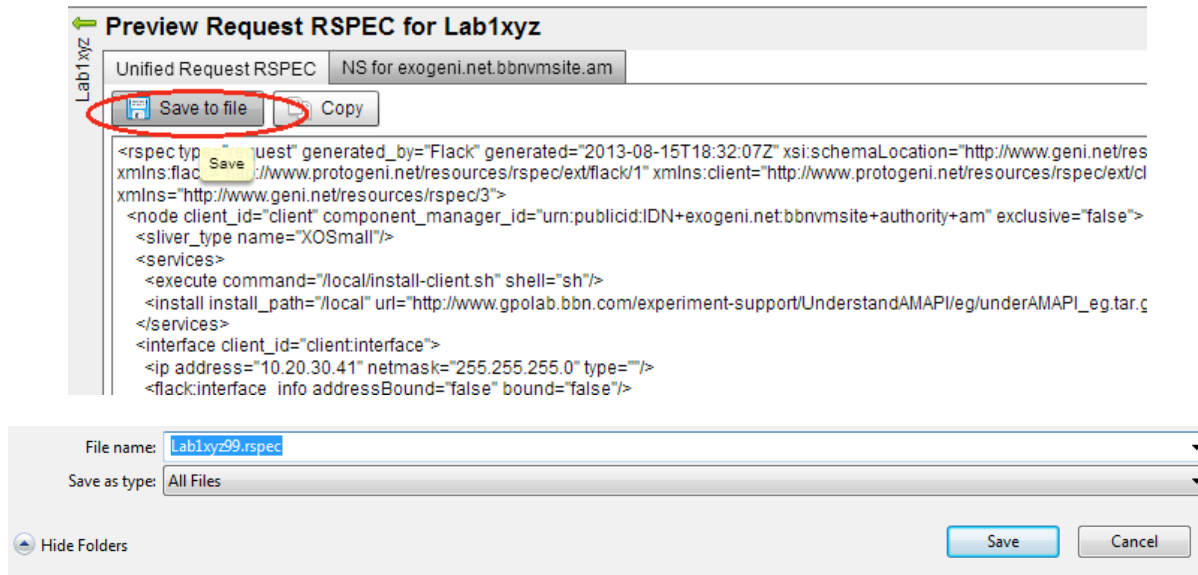
lan0

Next, we will Export the modified request RSpec.

From the 'View' menu, select the 'Preview request document(s)' item. This will bring up a window showing the current RSpec -- please take a moment to inspect it.

Use the 'Save to file' button in the upper left to make a local copy of your RSpec and name it as Lab1<Pawprint>.rspec (*make sure you select the File Type to All Files*). We'll use this in the next step to demonstrate how Omni tool also uses RSpec files to communicate requests to aggregate managers.





Step-4: Create, Access and Verify your Sliver

4.1 From a terminal, enter the below command where:

```
$ omni.py -a AM_NICKNAME createsliver SLICENAME RSPEC_FILE
```

- AM_NICKNAME is the nickname for your assigned aggregate manager as mentioned in the class
- SLICENAME is the name of the slice you created at the portal
- RSPEC_FILE should be replaced with the rspec path you saved previous step

For example: If you selected the InstaGENI BBN as the aggregate manager, your slice name as Lab1xyz, and you saved your RSPEC file in the rspecs folder under the home directory, the command will be as shown below:

```
$ omni.py -a ig-bbn createsliver Lab1xyz99 rspecs/Lab1xyz99.rspec
```

If all is well, Omni should give you a number of informational messages, such as:

```
INFO:omni:Loading config file /home/geni/.gcf/omni_config
```

It should quickly proceed to the point where it makes the request to the remote manager:

```
INFO:omni:Creating sliver(s) from rspec file  
/home/geni/Downloads/experiments.rspec for slice ...
```



This step can sometimes be time-consuming, so please be patient. If it succeeds, within a few minutes Omni should report:

```
INFO:omni: Completed createsliver:
```

and your sliver is complete!

4.2 Now use the command:

```
readyToLogin.py --no-keys -a AM_NICKNAME SLICENAME
```

where (as before) AM_NICKNAME and SLICENAME are your aggregate manager nickname and your slice name.

If the output reports that the sliver is not yet ready (for example, it might say that the status is "changing" or "No information available"), then please wait a minute or two and try again. Once everything is complete, readyToLogin.py will give an output similar to:

```
#=====
#SSH CONFIGURATION INFO for User root
#=====

Host client

  Port 22

  HostName 192.1.242.42

  User root

  IdentityFile /home/xyz/.ssh/geni_key_portal

  IdentityFile /home/xyz/.ssh/geni_cert_portal_key

Host server

  Port 22

  HostName 192.1.242.32

  User root

  IdentityFile /home/xyz/.ssh/geni_key_portal
```



```
IdentityFile /home/xyz/.ssh/geni_cert_portal_key

=====
=====

LOGIN INFO for AM: https://bbn-hn.exogeni.net:11443/orca/xmlrpc

=====
=====

For more login info, see the section entitled:

    'Providing a private key to ssh' in 'readyToLogin.py -h'

User root logs in to client using:

    ssh root@192.1.242.42

User root logs in to server using:

    ssh root@192.1.242.32
```

Note: In case, your ssh client might not be set up to log in with above commands, try re-running `readyToLogin.py` without the `--no-keys` option, and it will give you one or more ssh commands to choose from (which should work, although you might require the key passphrase).

4.3 Open two terminals and log in to client and server nodes. Copy and paste the ssh command line given under the client and server directly into your terminal to log in to the client and server that we will use to run tests.

Note: In case, there are two ssh commands generated for each node, use either of the commands to login. When logging in for the first time, you may be prompted for a passphrase. Please enter the passphrase which you supplied earlier for ssh key generation.

You may get a warning from ssh complaining that the authenticity of the host cannot be established. Say "yes", you do want to continue connecting, and you should see a shell prompt from the remote end:

```
[xyz@client ~]$
[xyz@server ~]$
```

Since Iperf is already installed on both the VMs, we now run the Iperf test between these two nodes. You can do this by entering the following command at server:

```
[xyz@server ~]$iperf -s
```



The server is setup at server now type the following command at client:

```
[xyz@client ~]$iperf -c 10.100.0.3
```

The IPs are the ones we provided earlier in Flack tool. You will get the following outputs from client and server from the Iperf test

```
-----
Client connecting to 10.100.0.3, TCP port 5001
TCP window size: 85.0 KByte (default)
-----
[ 3] local 10.100.0.2 port 44790 connected with 10.100.0.3 port 5001
[ ID] Interval      Transfer    Bandwidth
[ 3] 0.0-10.0 sec  4.09 GBytes 3.51 Gbits/sec
```

```
-----
Server listening on TCP port 5001
TCP window size: 85.3 KByte (default)
-----
[ 4] local 10.100.0.3 port 5001 connected with 10.100.0.2 port 44790
[ ID] Interval      Transfer    Bandwidth
[ 4] 0.0-10.0 sec  4.09 GBytes 3.51 Gbits/sec
```

Take a screenshot of both client and server terminal windows for submission in your lab report

As you can see from the above screenshot you have created a virtual network with VMs with Layer 2 connectivity and have a very high throughput (3.51 Gbps). This concludes the first GENI lab assignment!

5. What to turn in for Grading?

(Report with answers to below questions should be turned in at the beginning of the class on the due date; don't forget to write your name and title (e.g., Lab X) on the reports)

1. Provide a screenshot of the reserved slice resources in your GENI portal account. (Show content by clicking on "Details" under "Action" column in your slices listing page; it should correspond to the navigation path - Home → Project Calyam_UMissouri_Spring2015 → Slice Lab<pawprint> → Resources on Slice Lab<pawprint>). Also provide the screenshot of iperf result on client and server.
2. What would be the added capabilities and benefits in performing an experiment on GENI Future Internet infrastructure versus the commercial Internet infrastructure? (Refer to the GENI wiki, but write in your own words)
3. Define the following terms: (i) slice, (ii) sliver, (iii) aggregate manager and (iv) RSpec (Refer to the GENI wiki, but write in your own words)
4. How does Federated Identity and Access Management in the GENI portal allow you to use your Pawprint and password to login? What are the benefits of this approach? (Refer to GENI Tutorial and <https://spaces.internet2.edu/display/InCFederation/Research+and+Scholarship+Category>)



5. Explain the role of “Experiment Control Tools” such as Omni, jFed and Flack in GENI. What are the advantages of using the Omni command line tool in comparison to using the Flack GUI tool to reserve resources?
6. What is the significance of generating the SSH and SSL keys in your .ssh folder? (Refer GENI wiki, but write in your own words)

NOTE: Release your resources after finishing your lab report by following below steps

The command to use is:

```
omni.py -a AM_NICKNAME deletesliver SLICENAME
```

where AM_NICKNAME is the aggregate manager nickname and SLICENAME is the name of your slice. After a few moments, Omni should respond with:

```
INFO:omni: Completed deletesliver:
```