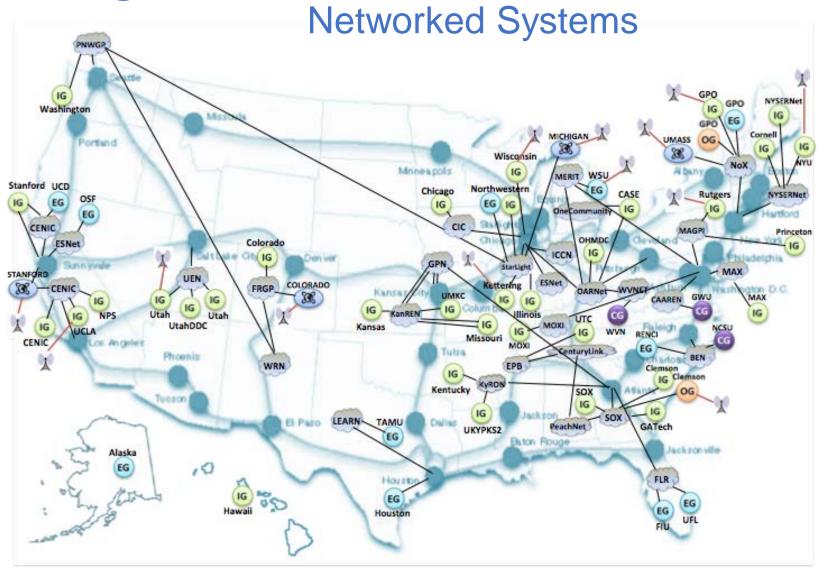


# Running Workflows on Educational Clouds Part 1: ExoGENI

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Background - ExoGENI: National Infrastructure for Next-Gen



- GENI Racks at 50+ campuses around the US
- OpenFlow switches for software defined networking





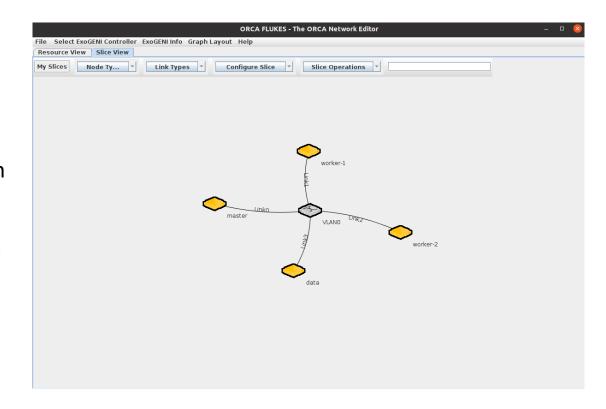






## **Background** – ExoGENI

- ExoGENI is and NSF funded project that provides open infrastructure for networking, distributed systems research and education.
- It allows you to create "slices" that provide network isolation to your transfers
- A Slice is an entity that encapsulates the information of your topology.
  - It contains the compute nodes, OS and node configuration (usually virtual machines)
  - The network links between them and network configuration



Reference: <a href="https://www.geni.net/">https://www.geni.net/</a>













### **ExoGENI** – Getting Started (Login)

Visit the GENI portal and login using your USC account:

#### https://portal.geni.net/



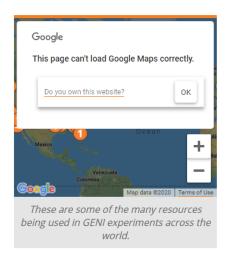
#### Welcome to GENI

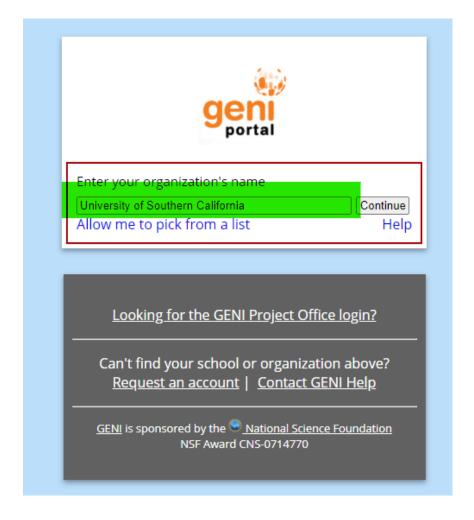
<u>GENI</u> is a new, nationwide suite of infrastructure supporting "at scale" research in networking, distributed systems, security, and novel applications. It is supported by the <u>National Science Foundation</u>, and available without charge for research and classroom use.



#### Find out more about using GENI:

- New to GENI?
- Information for GENI experimenters
- Published research that used GENI resources
- Get help using GENI







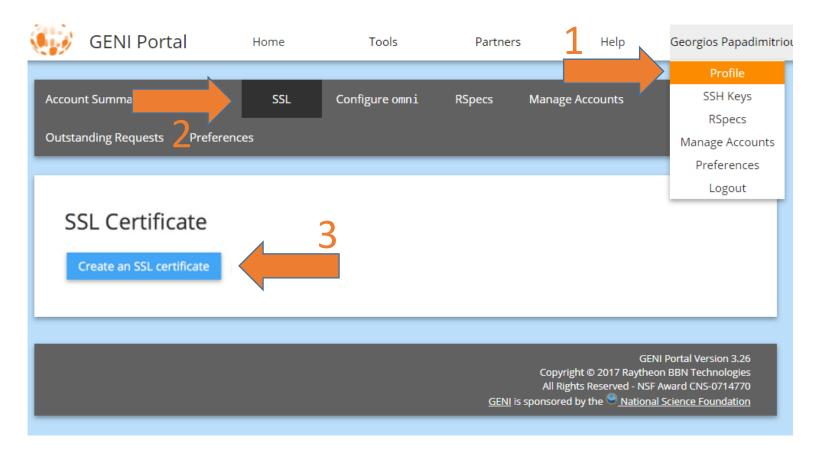












After you login, go to your profile, click on the SSL tab and hit the "Create an SSL certificate" button.













#### **GPO Member Authority**

#### **GENI Certificate Renewal**

In order to use some GENI tools (like omni) you need a signed SSL user certificate.

There are two options for renewing a certificate:

- 1. Have it generated for you. This is the easiest option. If in doubt, use this option.
- Have the SSL certificate generated for you based on a private key you keep locally. This is the most secure option. For advanced users only.

# Simple Option: Have the SSL certificate 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.) Remember, in order to use this, you will need to have the downloaded combination certificate/private key file. Show Advanced Option Close

GENI is sponsored by the National Science Foundation

Click on the "Generate Combined Certificate and Key" button.











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#### **GPO Member Authority**

#### **GENI Certificate Management**

**Download Your Portal Generated Certificate and Private Key:** 

Download Your Portal Generated Certificate and Private Key



Close

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Click on the "Download" button. Save the file to a known location (E.g., ~/.ssl/geni-papadimi.pem)



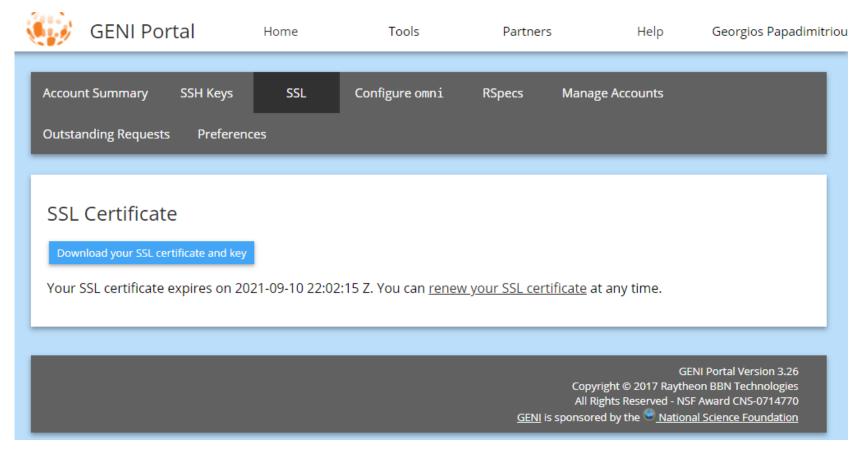












You can find the generated SSL certificate and key if you go back to your profile, under the SSL tab!











ssh-keygen -b 4096 -f ~/.ssh/exogeni\_rsa

If you don't have already, generate an SSH key (with or without password protection)!











#### **ExoGENI** – Getting Started (Install Oracle's Java)

- Download latest Java from Oracle https://www.java.com/en/download/linux\_manual.jsp
- 2) Untar the file into your preferred location E.g., tar -xzvf jre-8u261-linux-x64.tar.gz -C ~/Software/Java/
- 3) Add Java bin to your PATH env variable E.g., echo "export PATH=/home/papajim/Software/Java/jre1.8.0\_261/bin:\\$PATH" >> ~/.bashrc









#### **ExoGENI** – Getting Started (Download Flukes)

- 1) Download latest Flukes (gui to interact with ExoGENI) <a href="http://geni-images.renci.org/webstart/flukes-0.7.4.zip">http://geni-images.renci.org/webstart/flukes-0.7.4.zip</a>
- 2) Unzip the file into your preferred location E.g., cd ~/Software/flukes && unzip flukes-0.7.4.zip
- 3) Update flukes.jnlp codebase location E.g., sed —i 's/.\*codebase.\*/ codebase="file:\/\/\/home\/papajim\/Software\/flukes"/g' flukes.jnlp
- 4) Update bcprov.jnlp codebase location E.g., sed —i 's/.\*codebase.\*/ codebase="file:\/\/\/home\/papajim\/Software\/flukes"/g' bcprov.jnlp





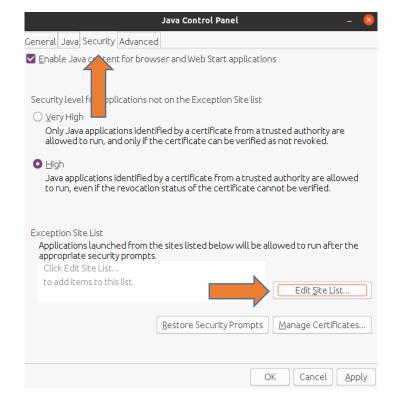


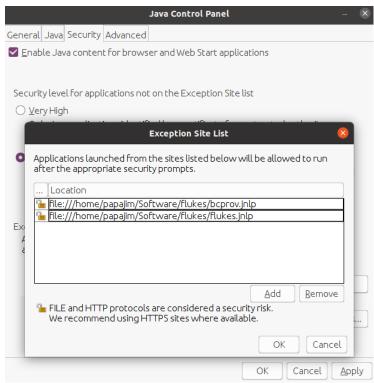




### **ExoGENI** – Getting Started (Add Flukes Exception to Java Secutiry)

- 1) Execute the command "javaws –viewer"
- 2) Click on the Security Tab
- 3) Click on Edit Site List
- 4) Add exceptions for both
  - flukes.jnlp
  - bcprov.jnlp

















#### **ExoGENI** – Getting Started (Add Flukes Properties)

In your home directory (E.g., /home/georgpap) create a file ".flukes.properties" with the following content.

orca.xmlrpc.url=https://geni.renci.org:11443/orca/xmlrpc user.certfile=/home/papajim/.ssl/geni-papadimi.pem user.certkeyfile=/home/papajim/.ssl/geni-papadimi.pem enable.modify=true ssh.key=~/.ssh/exogeni\_rsa # SSH Public key to install into VM instances ssh.pubkey=~/.ssh/exogeni\_rsa.pub # Path to XTerm executable on your system xterm.path=/opt/X11/bin/xterm





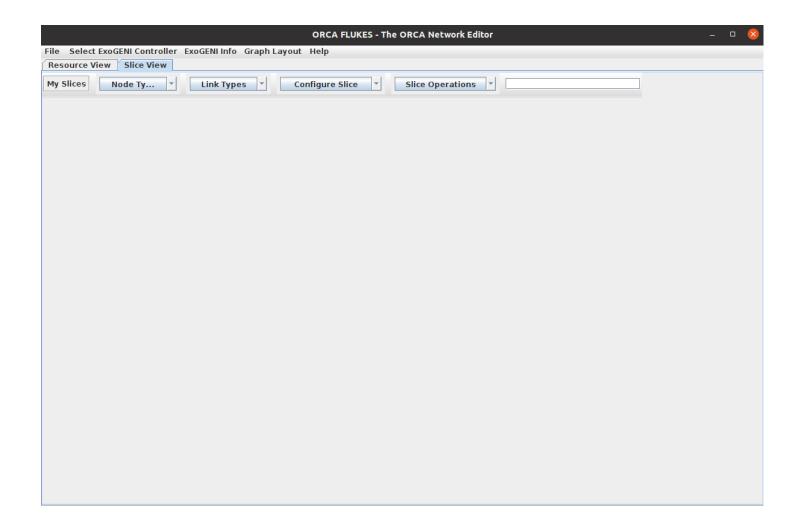






#### **ExoGENI** – Getting Started (Run Flukes)

Execute: "javaws flukes.jnlp"













#### **ExoGENI** – Getting Started (Creating a Slice)

# Demo

Scripts: <a href="https://github.com/papajim/exogeni">https://github.com/papajim/exogeni</a>











#### **ExoGENI** – Limit Network Speeds

```
#!/bin/bash
```

```
interface="ens6" bandwidth="1000"
```

```
tc qdisc add dev $interface root handle 1: htb default 11
tc class add dev $interface parent 1: classid 1:1 htb rate ${bandwidth}mbit
tc class add dev $interface parent 1:1 classid 1:11 htb rate ${bandwidth}mbit
tc qdisc add dev $interface parent 1:11 handle 20: sfq perturb 10
timestamp=$(date '+%d/%m/%Y %H:%M:%S');
echo "[$timestamp] Upload bandwidth limited to $bandwidth Mbits (IF: $interface)"
```

#tc qdisc del dev \$interface root

https://github.com/papajim/exogeni/blob/master/limit\_network.sh











# **Network Monitoring - TSTAT**

To execute TSTAT use the following:

sudo tstat -s /home/panorama/tstat-logs/ -i ens6 -l











# **ExoGENI** — Adding Anomalies

Interference	Command
CPU	stress -c THREAD_NUM e.g., stress -c 2
HDD	stress -d THREAD_NUMhdd-bytes BYTES e.g., stress -d THREAD_NUMhdd-bytes 50M
Network Loss	tc qdisc add dev DEV root netem loss LOSS e.g., tc qdisc add dev ens6 root netem loss 1%
Network Reordering	tc qdisc add dev DEV root netem delay DELAY reorder REORDER CORRELATION e.g., tc qdisc add dev ens6 root netem delay 10ms reorder 25% 50%













### Panorama360 Monitoring - Prerequisites

- HTCondor 8.6+:
  - https://research.cs.wisc.edu/htcondor/downloads/
- Pegasus Panorama:
  - Compile from source: <a href="https://github.com/pegasus-isi/pegasus/tree/panorama">https://github.com/pegasus-isi/pegasus/tree/panorama</a>
  - Pre-compiled binaries: <a href="http://download.pegasus.isi.edu/pegasus/4.9.3panorama/">http://download.pegasus.isi.edu/pegasus/4.9.3panorama/</a>
- Docker 17.02+:
  - https://docs.docker.com/install/
- Docker Compose:
  - https://docs.docker.com/compose/











# How to Deploy: Monitoring Backend (RabbitMQ, ELK Stack)

- On a host that has Docker and Docker Compose installed, clone https://github.com/Panorama360/data-collection-arch
- Change to the cloned directory and execute the following command:

docker-compose up -d

#### • Example:

```
georgpap@iris:~/GitHub/panorama360/data-collection-arch$ docker-compose up -d Creating network "panorama_net" with driver "bridge"
Creating panorama-rabbitmq ... done
Creating panorama-elasticsearch ... done
Creating panorama-kibana ... done
Creating panorama-logstash ... done
georgpap@iris:~/GitHub/panorama360/data-collection-arch$
```









# How to Deploy: Checking Services (RabbitMQ, ELK Stack)

Now the host should have RabbitMQ, Elasticsearch, Logstash, and Kibana running as Docker containers with their service ports exposed. Try to access them...

- RabbitMQ: http://<hostname or ip>:15672
- Elasticsearch: <a href="http://<hostname.or.ip>:9200">http://<hostname.or.ip>:9200</a>
- Logstash: <a href="http://<hostname.or.ip>:9600">http://<hostname.or.ip>:9600</a>
- Kibana: <a href="http://<hostname.or.ip>:5601">http://<hostname.or.ip>:5601</a>











### How to Deploy: Enabling Stampede Events

- In order to get pegasus-monitord to publish <u>all</u> of its events to an AMQP endpoint in JSON format, <u>3 properties</u> must be specified in the workflow's properties file (eg. "pegasus.properties").
  - pegasus.monitord.encoding = json
  - pegasus.catalog.workflow.amqp.url = amqp://[username:password]@<hostname>[:port]/<exchange\_name>
  - pegasus.catalog.workflow.amqp.events = stampede.\*

#### • Example:

```
# Monitord Events
pegasus.monitord.encoding=json
pegasus.catalog.workflow.amqp.url=amqp://panorama:panorama@amqp.isi.edu:5672/panorama/monitoring
pegasus.catalog.workflow.amqp.events = stampede.*
```

More about stampede events: <a href="https://pegasus.isi.edu/documentation/stampede">https://pegasus.isi.edu/documentation/stampede</a> wf events.php











# How to Deploy: Enabling Transfer Events

- In order to get pegasus-transfer to publish transfer statistics from the Globus Transfer Service to an AMQP endpoint in JSON format, 2 profiles must be specified in the workflow's sites catalog (eg. "sites.xml"), under the site where pegasus-transfer is going to be invoked (eg. "local").
  - env.PEGASUS\_TRANSFER\_PUBLISH = 1
  - env.PEGASUS\_AMQP\_URL = amqp://[username:password]@<hostname>[:port]/<exchange\_name>

#### • Example:

```
<!-- The local site contains information about the submit host -->
       <site handle="local">
         <directory type="shared-scratch" path="${PWD}/work/scratch">
           <file-server operation="all" url="go://georgepap#exo-master/${PWD}/work/scratch"/>
         </directory>
         <directory type="local-storage" path="${PWD}/work/outputs">
10
11
           <file-server operation="all" url="go://georgepap#exo-master/${PWD}/work/outputs"/>
12
         </directory>
13
         <!-- These profiles tell pegasus-transfer to publish stats to an AMQP endpoint -->
         file namespace="env" key="PEGASUS TRANSFER PUBLISH">1
14
         15
       </site>
```









### How to Deploy: Enabling Kickstart Online Traces

- In order to get pegasus-kickstart to publish traces of resource usage statistics to an AMQP endpoint in JSON format, <a href="2">2 profiles</a> must be specified in the workflow's sites catalog (eg. "sites.xml") under the compute site.
  - pegasus.gridstart.arguments = -m <interval in seconds>
  - env.KICKSTART\_MON\_URL =
     rabbitmq://[USERNAME:PASSWORD]@<hostname>[:port]/api/exchanges/<exchange\_name>/publish

#### • Example:

 Alternatively if we want to customize the monitoring interval per computational task we can specify the profile in the workflow's transformation catalog (eg. "tx.txt")











# How to Deploy: Enabling Kickstart Online Traces (MPI Jobs)

- Usually MPI jobs are not launched by Pegasus-Kickstart. Thus, adding the gridstart.arguments profile doesn't have any effect.
- We can work around this by using a wrapper script for the MPI job, that invokes directly pegasus-monitor.
- We still need to specify **KICKSTART\_MON\_URL** in the sites catalog.

#### • Example:

```
#!/usr/bin/env bash

cd $PEGASUS_SCRATCH_DIR

mpirun pegasus-monitor -i 10 /shared/software/NAMD_2.12_Linux-x86_64-MPI/namd2 $0
6
```













# How to Deploy: Enabling Darshan Logs (MPI Jobs)

- In case your MPI application wasn't compiled and statically linked with Darshan's library, we need to set a profile in the transformation catalog, adding the path of the library to LD\_PRELOAD.
- We launch the application using a wrapper script, and as post job steps:
  - Build the darshan log path from the environmental variables
  - Invoke pegasus-darshan with the files as input

```
tr namd {
    site local-slurm {
        pfn "/shared/software/wrappers/namd_wrapper_slurm.sh"
        arch "x86_64"
        os "LINUX"
        type "INSTALLED"
        profile pegasus "exitcode.successmsg" "End of program"
        profile pegasus "memory" "2500M"
        profile globus "jobtype" "single"
        profile env "LD_PRELOAD" "/shared/software/darshan-3.1.6/lib/libdarshan.so"
        }
        Transformation Catalog
```

```
#!/usr/bin/env bash
      cd $PEGASUS SCRATCH DIR
      mpirun pegasus-monitor -i 10 /shared/software/NAMD 2.12 Linux-x86 64-MPI/namd2 🖇 6
      #post job parse darshan output
      DAY=$ (date '+%d')
      DAY=$ { DAY##0 }
      MONTH=$ (date '+%m')
      MONTH=${MONTH##0
      YEAR=$ (date '+%Y')
12
13
14
      darshan base=/shared/darshan-logs/${YEAR}/${MONTH}/${DAY
      darshan_file=${darshan_base}/${SLURM_JOB_USER} namd2_id${SLURM_JOB_ID} *.darshan
15
16
17
      for f in $darshan file; do
18
         $PEGASUS HOME/bin/pegasus-darshan -f "$f"
                                                                Wrapper Shell Script
19
      done
```











# How to Deploy: Enabling Darshan Logs (MPI Jobs)

- pegasus-darshan will output in stdout a monitoring payload, that will be picked by pegasus-monitord, which in its turn will publish it to the AMQP endpoint.
- This can also be used as a generic way of adding new tools to this architecture.

```
@@@MONITORING PAYLOAD - START@@@
      "monitoring event": "darshan.perf",
      "payload": [
         " POSIX module data": {
           " agg perf by cumul ": 14.667417,
          " agg perf by open": 14.667417,
           " agg perf by open lastio": 14.667417,
           " agg perf by slowest": 14.667417,
           " shared files ": {
            " time by cumul io only ": 0.0,
12
            " time by cumul meta only ": 0.0,
13
            " time by open ": 0.0,
            " time by open lastio ": 0.0,
            " time by slowest ": 0.0
           " total bytes ": 403761,
           "unique files": {
19
            " slowest rank ": 0.0,
20
            " slowest rank io time ": 0.026253,
21
22
            " slowest rank meta only time ": 0.023997
23
26
      " ts ": 1552878285
28
29
    @@@MONITORING PAYLOAD - END@@@
```













# Thank you!

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