

1/23/13

Ok, first log entry, here we go:

I'm trying to figure out why NAS 1 doesn't show up on the Ganglia diagnostic page.

-I found the code for the page by going to the main page on Firefox and just right clicking to "View Page Source"

-There appear to be a few instances in the code that list all the nodes and compute elements that Ganglia outputs and NAS 1 is not included.

-I'm going to try duplicating the code for NAS 0, which is working fine, and put it into the code for the page

So

```
<td><a href="?c=FLTECH&h=nas-0-0.local&m=&r=hour&s=descending&hc=4"></a></td>
```

goes to

```
<td><a href="?c=FLTECH&h=nas-0-1.local&m=&r=hour&s=descending&hc=4"></a></td>
```

And

```
<OPTION VALUE="nas-0-0.local">nas-0-0.local
```

goes to

```
<OPTION VALUE="nas-0-1.local">nas-0-1.local
```

Nevermind... I can't change the code from there, so I need to find the ACTUAL code...

1/26/13

Taking a break from the Ganglia work and creating an account for Dr. Yumiceva.

I'm not being allowed to access the root account, so I asked Jordan.

Turns out he just forgot to add me to root access. We got it all figured out and Dr. Yumiceva's username is yumiceva.

1/28/13

Ok, so back to the Ganglia issue:

I finally got to read the files that Kim sent me in her email.

Specifically, the command 'dbreport gmond <node>', which I believe is supposed to show the values for that node. Running the command with nas-0-1 works, but so does running it with nas-0-2, which I'm not sure is a real node or not. It does appear to be the only other "nas" node to show up, so maybe nas 1 is labeled wrong? I need to find out how gmond communicates with the website and where it

stores it's information.

Possibly helpful?: <http://sourceforge.net/apps/trac/ganglia/wiki/Gmond%203.1.x%20General%20Configuration>

just tried: 'gmond -t' and got an interesting file, but will need to read through in later...

1/30/13

In the sourceforge help page for gmond, there is a section labeled "Access Control", which "allows you to specify exactly which hosts gmond process data from". So does this mean that it determines which nodes to collect data from? And if it does, I most likely need the IP address of nas 1 and to add it into the gmond software through the ACL(access control list). If not, I have no idea what I'm doing...

There are three parameters in the gmond config file: udp_send_channel, udp_rcv_channel, and tcp_accept_channel

The sourceforge website says these parameters can contain an acl but they don't appear to in the default, so maybe I'm barking up the wrong tree. The default has an only "mcast_join", "port", "ttl", and "bind". I don't really see any connection between this and the nodes, so I'm going to try looking else where for now. I should also write an email to Kim, which thanks her and asks questions!

Ok, here's something maybe:

when I did 'dbreport gmond nas-0-1', there were values for the three parameters I found in the gmond config file. They don't appear to be the same as the ones in the default gmond file, which could mean that the default file is not including nas1 or it could mean anything else.

Just got a lesson in how to run the MTS! And I'm out of time again. Sending an email off to Kim, then heading out.

1/31/13

Mostly just searching through all the folders and files in the Ganglia folder for something that can point me towards XML files...

Ok, this directory:

/var/lib/ganglia/rrds/FLTECH

appears to have all the nodes except nas-0-1 in it. Maybe ganglia needs this?

The nas-0-0 directory includes a lot of .rrd files.

2/1/13

This site has been very helpful:

http://sourceforge.net/apps/trac/ganglia/wiki/ganglia_readme

It mentions that the web frontend (e.g. the website I'm trying to fix) gets its information from gmetad and that it's written in PHP, which I knew.

Going to the 'gmetad.conf' is just the port that it is supposed to connect to and that seems to be correct. I hypothesize that Nas1 is missing from the XML tree that gmetad accesses. Need to find those xml files!

Found a large batch of xml files in '/etc/gconf/' directory. They all start with %gconf-tree in the file names but they don't appear to be attached to any specific nodes. They are just labeled alphabetically for something. Oh, they're all in different languages... After finding the one in english, it just appears to be a list of commands, not relating to gmond or ganglia.

'/etc/xml/' is a dead end as well.

So the directory '/' has what appears to be a connection to nas 0 in its entirety. There isn't any nas 1 however. So it's missing in more places than 1 for sure.

2/4/13

I told Jordan about the places that I found nas1 missing and he recommended attempting to create a directory for it and hope that the system fills the directory in. He said it probably wouldn't help much but that it was worth a try. He said to check the permissions of the directories already there and see if they match the one I create. I'm also going to email Kim with my findings since she wasn't here today. Making a directory nas-0-1.local in /var/lib/ganglia/rrds/FLTECH

Ok... so permission was denied to create a directory... Can it do that? I'll have to ask Jordan what that means.

I'm looking through files that all seem to relate to a TTree class. There's documentation on it but I have no idea if it's relevant, except for the fact that I think the XML files I'm looking for are in a tree...

2/6/13

Kim emailed me back. She thinks that the rrd files are part of the key. She told me about a rrdcreate method that is probably used to create the rrd files for the graphs. I need to look for the file that uses that creation function...

2/13/13

Back to work after being stupidly busy. I haven't found anything on the rrdcreate thing and Jordon added that Hohlmann wants me to find out why the Job Queue option isn't working either. It should show any jobs that are running but it doesn't. Maybe it has something to do with condor_q?

I finally got my DOE certs from OSG today!

Using sudo privileges, I created a directory, nas-0-1.local, in /var/lib/ganglia/rrds/FLTECH, so that it would match the one for nas0, but it's missing the files inside and I don't want to copy them without knowing what they are. I can't read them.

Found something that might be relevant to the job queue issue:

/var/lib/condor/spool has a directory called job_queue.local

Other than that, nothing to report on the ganglia issue.

Kim suggested using a line "grep -r rrdcreate *" to find any usages of the rrdcreate function. I checked in /var/lib and found a couple but they generally appear to be binary files I can't read...

2/15/13

Checked on the directory I created but there's still nothing in it, so that's not going to help. I'm deleting it now.

Used "sudo grep -r -l nas1" and now to wait...

While I'm waiting, I'm trying to brush up on linux commands, since I don't really know many.

This website is hugely helpful :<http://ss64.com/bash/>

So I waited 15 minutes but nothing happened so I killed it.

Seriously, I need to figure out this grep command

Tried grep -r -l condor_q in /nas0/condor with no results...

2/20/13

It looks like the update that Jordan just did changed the ganglia view a little but the technical problems remain; no nas 1 and nothing in the job queue.

Found some interesting new files in var/www/wiki that might be relevant to why the wiki isn't working, which I think Jordan asked Kim to look at. I emailed them back to let them know that I found that file.

Trying the grep thing again, specifically "grep -r rrdcreate" in /var/log.

Researching the job queue issue and found someone that had a similar problem. It just turned out that they didn't have the latest install of python ganglia, which in that case was 2.3.2, though that was in

2003... We might have a similar problem however. I'll have to ask Jordan. Ok, sent email to Jordan with those findings.

Still nothing from the grep... I'm beginning to suspect that I'm either using the command wrong, or am simply giving it too large an area to search through. I'll give it another ten minutes but that's it. Ok, I killed but now I'm trying "grep "rrdcreate"" (note the quotation marks) in /var/www/html/ganglia. I'm hoping this is a smaller area to search through? Or I might still be using it wrong...

Ok, I tried using it with a bunch of individual files, in the form of "grep "rrdcreate" file"... Still nothing

2/21/13

Jordan gave me this command to find our edition of ganglia-python:

```
rpm -qa | grep ganglia
```

This will show all software packages installed by rpm, then the grep search finds only the ones with ganglia in them.

We do indeed have a version of ganglia-python, version 5.0-1. I have no idea how to check if this is the right version... Emailed Jordan back with my findings

2/22/13

Not sure what I'm supposed to be doing since I'm meeting with Jordan later but for now I guess I'll keep looking for some file that creates those rrd directories...

I think I may have finally figured out what's wrong with my grep command. I was missing the * at the end of the command to identify which directory I wanted to search in. The * indicates the current directory.

Searching through lots of places, mostly in /var/ but there were way too many results and nothing jumps out. Jordan's going to help me more later.

3/11/13

Ok, the week before spring break I was working on updating the nodes. I completed one with Jordan's help then did compute1-1 and compute1-2 on my own. They should be fully functional now. Then I was on break for a week.

Currently I don't have much in the way of stuff I need to do. Turns out Nas 1 is being funky all around so I'm supposed to leave that alone until Jordan takes a good look at it.

3/18/13

So completely back to the job queue ganglia issue:

I found an html file using the grep command in var/www/html/roll-documentation/service-pack/5.0 called fixes.html. Here's what it says to do if job queue won't show anything:

"The fix is to change the way the ganglia metric gets job queue info from SGE (the old method was 'qstat -f -xml' and the new method is 'qstat -f -u * -xml'. "

My first attempt to find the file I need to change is a grep search but I don't know where to start looking so it will take forever, if it even works. The next thing I should try is looking for the ganglia metric files manually, then searching them for the correct file.

Also, I should check if this even is Rocks 5.0 or if we have something newer.

No such luck on the grep search in about 20 mins.

3/20/13

The cluster's running local jobs again! Woo!

I'm trying to follow the lead from the documentation a couple days ago. I asked Jordan which version of Rocks we have.

Ok, used rocks commands to find the current license, which is for 5.0 actually. The command was

“rocks list license”.

Now that I know that might be the real problem, I'm trying another grep search, this time only in /var. So far nothing. I need a more efficient way of searching...

3/22/13

New responsibilities as maintenance for the group website!

First job: Make windows partition on computer so I can run macromedia program to edit the website!

3/25/13

I tried looking for the file in /opt/ganglia using a grep search as Jordan suggested. I'm also going to start looking into using Wine for the macromedia website editor or a newer website editor. Dr H wants me to look into a newer version with the IT crew

3/29/13

So Jordan got me a bunch of info on the job queue thing. Turns out we never had it set up so I have to go in and add everything! I'm not sure where to start and reading the thread he sent me is a little difficult. The website https://github.com/ganglia/gmetric/tree/master/hpc/sge_jobs seems to have both the files I'm gonna need in it.

So it looks like I need to add the file “sge.sh” to etc/profile.d/ and some php file into

<wwwroot>/ganglia/graphs.d/. I'm not sure what that wwwroot is supposed to be? I just asked Jordan so I'm sure he'll get back to me soon.

In the conf.php file, “#\$optional_graphs = array('packet');” this line needs to be uncommented and then “jobqueue” needs to be added to the array.

Ok, so I added “jobqueue” into the line, making it “\$optional_graphs = array('packet', 'jobqueue');”.

Created file sge.sh in /etc/profile.d/ then copy/pasted the file from the website into it. I'm a bit worried that I need to change something but I'll leave it for now. At least until Jordan gets back to me.

4/8/13

Ok... Well the changes that I made in /profile.d/ messed up the entire system and Jordan had to kill it then restart it, and is still trying to reconfigure our network settings. My job is to find out where it went wrong.

Here's the first bit. The “source” in the first line of the sge.sh code doesn't exist on our cluster. There is no sge directory in /usr/local.

Neither does the path /usr/bin/gmetric, which is either a command or a path?

I'm going to look for the sge directory somewhere other than where it's supposed to be now.

4/19/13

Jordan fixed the cluster late last week but Ganglia is now only showing the frontend, instead of all the nodes. I'm supposed to find out why and fix it but in this case I have no clue. I've tried restarting by doing #service greceptor restart, but it didn't change anything on the page.

I'm not sure what else to do, as Jordan doesn't know and neither do I.

This file is missing /usr/bin/gstat, that's probably bad.

So is /usr/bin/gmetric... Luckily, /usr/sbin/gmond and /usr/sbin/gmetad are still there.

Emailing Jordan now to see if this is important.

Tried running #telnet localhost 8649, which was supposed to spit out an XML file of data on the cluster but the data seems to be missing. Right now, I'm using the ganglia_readme page on sourceforge.net :http://sourceforge.net/apps/trac/ganglia/wiki/ganglia_readme.