Nano cluster

System Description

Host name: nano.ncsa.illinois.edu

Hardware

- 8x SuperMicro SYS-4028GR-TR
  - X10DRG-O+ CPU motherboard
  - 128 GB DDR4 (8x 16 GB Micron 2133 MHz 36ASF2G72PZ-2G1A2)
  - 8 PCI-E 3.0 ports, switched
  - Mellanox MT27500 Family [ConnectX-3] QDR IB
  - 1x 256 GB Samsung SSD 850
  - NFS-mounted 30TB home (2x 6-drive RAID z2 with 4TB drives)
  - GlusterFS w/ 2-node fault tolerance - 62TB usable

Software

- CentOS 7
- CUDA 9.2/10.0
- PGI 16.10
- Intel ICC 16
- gcc 4.8
- gcc 5.3 via 'scl enable devtoolset-4 bash'

To request access please fill out this form. (Use the link on the confirmation page to sign up for a new account. The same link is also included in the confirmation email.)

Instructions for running Jupyter Notebooks on compute nodes

Usage notes:

- nano (141.142.204.5) is the head node of the cluster, it should not be used for any computations!
- to connect to the cluster, ssh username@nano.ncsa.illinois.edu

- to get access to a particular node for interactive use, use qsub, e.g.,
  - to get one GPU and one CPU core on node 7 for 1 hour for interactive use:
    - qsub -I -l nodes=nano7:ppn=1:gpus=1,walltime=3600
  - to get entire node 1 for 1 hour for exclusive interactive use:
    - qsub -I -l nodes=nano1:ppn=12,walltime=3600

- better yet, do not allocate nodes for interactive use, instead just submit batch jobs, see for example Job Scripts section at https://kb.iu.edu/d/avmy for details. This is a much better way to share computing resources.

- interactive jobs are limited to 12 hours maximum walltime per job.
- batch jobs are limited to 96 hours
- submit request to staff for longer batch jobs (up to 240 hours)
- to see what’s running on the cluster, just run qstat
- this is a shared resource, please keep in mind that other users are using it as well; do not take over the system beyond what you really need.
- home directory is cross-mounted and accessible from all nodes

- Current System Status: https://nano.ncsa.illinois.edu:3000/d3QVrDIFmz/nano-status

DL frameworks

- TensorFlow 1.10

Node configuration (see login message for the exact configuration):

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<tr>
<th>nano1</th>
<th>nano2</th>
<th>nano3</th>
<th>nano4</th>
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