Oscar

Oscar is Brown's high-performance computing cluster managed by the Brown Center for Computation and Visualization (CCV). Long-term visitors to ICERM with a Brown sponsored ID are provided with an exploratory account on Oscar upon arrival. Oscar access may also be requested by short-term visitors on a request-basis with advance notice.

Overview of Oscar

Long-term visitors to ICERM who receive a Brown ID are provided with an exploratory account on the Oscar high performance computing cluster maintained by Brown's Center for Computation and Visualization. Oscar access may also be provided to short-term visitors on request-basis with *advance notice*.

If you are coming for a short-term visit and would like to request Oscar access, please contact ICERM IT staff no later than three weeks before your planned visit to ensure enough time to process a sponsored ID and enable Oscar access.

Oscar can be used via SSH terminal or via the Oscar VNC client. The Oscar VNC client is preinstalled and available on the thin clients in all ICERM 10th floor offices and the graduate student workspace in the 10th floor lobby.

Using Oscar

Oscar provides both command line (SSH) access and virtual desktop (VNC) access to the computing cluster. All Oscar accounts are capable of using both interfaces, so you should choose the method that will work best for what you are trying to accomplish.

Oscar accounts are tied to Brown Shibboleth accounts, so you must have an ICERM Sponsored Brown ID to use Oscar. Once Oscar access is enabled for your Brown account, you can log in to SSH and VNC using your Brown Shibboleth username and password.

SSH Usage

Oscar's SSH interface provides a standard command line shell for interacting with the cluster. This is the best option for using simple command line scripts and submitting scripts for batch job processing. See the SSH Login Instructions for information on how to connect and basic usage. It's important to note that you should never run complex scripts or computations within the SSH login nodes. Computations should either be submitted as batch jobs or run in an interactive compute session using the `interact` command.

Open OnDemand

Oscar's OOD s a web portal to the Oscar computing cluster. This is the easiest way to access Oscar and navigate around. Once logged in you effortlessly be able to access active jobs, use MATLAB or Mathematica, and even use the Oscar Shell CLI. See the OOD Login Instructions for information on how to get started with the web portal.

VNC Usage

Oscar's VNC client provides a standard Linux graphical desktop using virtual network computing. If you'd like to use applications with a GUI, such as MATLAB or Mathematica, this is the best way to do so. Oscar's VNC sessions run within the scheduling system directly on a compute node, similar to the `interact` command, so you can run computations directly in the VNC session. See the VNC Login Instructions for information on how to get started with the VNC client.

Available Software

Oscar maintains a large library of software packages for use on the HPC cluster. Some of the most commonly used mathematical applications and languages available include:

- MATLAB
- Mathematica
- Sage
- Julia
- R
- Python
- Maple
- Magma

To see the most up to date list of available software, log in to your Oscar account and run the terminal command `module avail`.

Loading Software Modules

Oscar has a large library of software available on the cluster, but only a few apps are pre-loaded in to your sessions. The commands below will allow you to list all available modules, search the list of modules, and load/unload software packages. When using Oscar over VNC, you must open the Terminal Emulator to run these commands.

- To view all available software packages, type `module avail`.

- To search the list of available packages, type `module avail <package>`.
- For example, to search for all available versions of mathematica: `module avail mathematica`. Many packages, like Mathematica, have multiple versions available. This command lets you see all available versions of the package you searched for.
- To load a package into your session, type `module load <package/version>`.
- For example, `module load mathematica/11.0`. This will load the Mathematica 11.0 into your session and make it available for use.
- To unload a package you are no longer using, type `module unload <packagename>`

Module-specific Guides

- Oscar: Mathematica
- Oscar: MATLAB
- Oscar: Sage

Running Jobs

Oscar supports two main methods of running jobs: **batch jobs** and **interactive sessions**.

- Batch jobs are pre-scripted and can be submitted to the cluster's scheduler via the `sbatch` command.
- Interactive jobs are command-line sessions run directly on a compute node via the `interact` command that can be used in real time.

The Running Jobs page of the Oscar User Manual provides the most detailed and up-to-date instructions on scripting and submitting jobs.

Important Notes About the Oscar Cluster

- **Please do not run any computations or simulations on the login nodes, as they are shared with other users. Use SLURM to submit a batch job to the queue for computations or start an interactive session on one of the compute nodes with the command `interact`.**

- The full Oscar User Manual is available on the CCV website.
- Oscar uses SLURM for managing batch jobs and interactive sessions on the cluster.

  Detailed instructions on submitting jobs is available on the Running Jobs page of the Oscar User Manual.
- CCV has a large library of software already installed on the cluster. For a full list of available software, run the command `module avail`. More information about Oscar's software packages are available in the Oscar User Manual. If you require a software package that is not currently available on the Oscar cluster, please contact ICERM's IT staff and we will work with CCV to get the software installed.
- Users can install sub-packages for some modules (like Sage and Python) to their home folders on their own by using the `–user` as an option in the install command. For example, with Sage, the command would be something like `sage -i <package name> –user`.
- The Oscar VNC Client is a Java application that can be installed on most laptops with Java installed. If you wish to install the client on your own laptop, please make sure to download the latest version of CCV VNC Client 2.0+ to ensure proper support and compatibility.

If you have questions about these instructions or require further assistance, please contact the ICERM IT staff by dropping by the administrative offices or emailing support@icerm.brown.edu.

Open OnDemand Access to Oscar

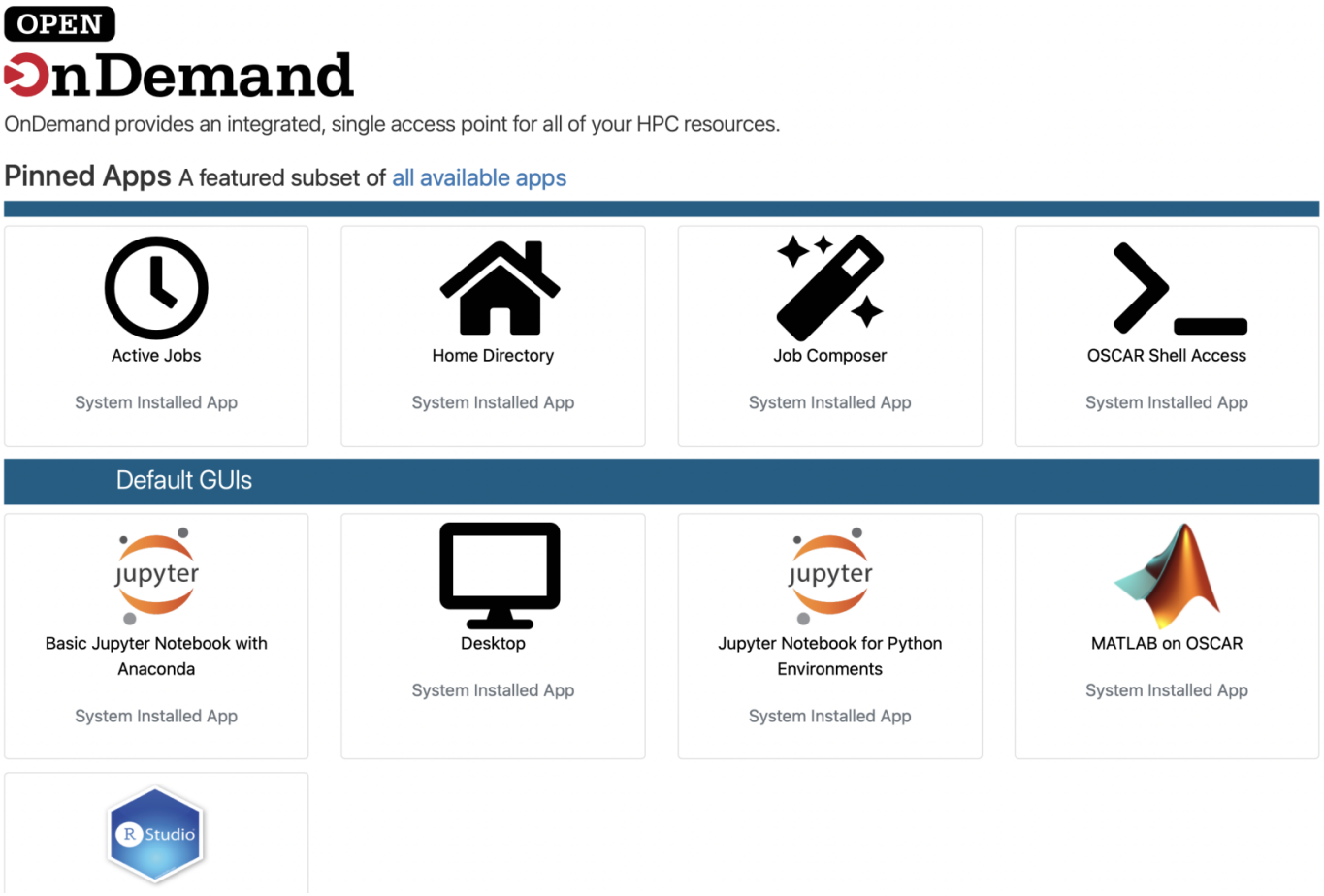
Open OnDemand (OOD) is a web portal to the Oscar computing cluster. **An Oscar account is required to access Open OnDemand.** Visit this link in a web browser and sign in with your Brown username and password to access this portal.

Benefits of OOD:

- No installation needed. Just use your favorite browser!
- No need to enter your password again. SSH into Oscar in seconds!
- No need to use two-factor authentication multiple times. Just do it once, when you log into OOD.
- Use it with, or without, VPN. Your workflow remains the same.

- Just a good time over all □□

Once logged in you'll see a landing page that looks similar to the photo below:



Guides to help you figure your way out once logged in:

Using File Explorer on OOD

Web-based Terminal App

Interactive Apps on OOD

Using Python or Conda environments in the Jupyter App

SSH Access to Oscar

1. Open a terminal prompt. On the ICERM thin clients, enter the username `user` and the password `icerm` to log in to the terminal.

2. In the terminal, type `ssh <your ccv username>@ssh.ccv.brown.edu`. If you are asked to verify the authenticity of the host 'ssh.ccv.brown.edu', type `yes`.

3. You will now be prompted for your password. Enter your password (nothing will show up when you type in the terminal password prompt) and press enter.

4. Once logged in, you should see a “Welcome to Oscar!” message. This means you're now connected to one of the login nodes, which you can use to manage your files and submit batch jobs.

Please DO NOT run any computations directly on the login nodes. Use the batch system to submit your computations to the queue to be processed on the computation nodes or start an interactive session on one of the compute nodes with the command `interact`.

See CCV's Oscar Documentation page on Running Jobs for detailed instructions on batch jobs and interactive sessions.

Oscar Software Modules

List and instructions for software modules available on the Oscar cluster.

Currently Available Modules

If you require a software package that is not currently available on the Oscar cluster, please contact ICERM's IT staff and we will work with CCV to get the software installed.

This list is current as of November 10, 2021. To see the most up to date list of software modules, log into your Oscar account and run the command `module avail`.

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category:
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
bxh_xcede_tools/1.11.14  confocal/1.0            potfit/20201014
cesm_post_process/Oct18  pigz/2.4
~~~~~~~~~~~~~~~~~~~~~~~~ category:  Microstructure modeling ~~~~~~~~~~~~~~~~~~~~~~~~
oof2/2.1.17
~~~~~~~~~~~~~~~~~~~~~~~~~~~ category:  access controlled ~~~~~~~~~~~~~~~~~~~~~~~~~~~
Molpro/2012.1.15
Molpro/2015_gcc
Molpro/2015_serial
Molpro/2018.2_ga
Molpro/2019.2
Molpro/2019.2_ga
Molpro/2020.1
Molpro/2020.1_ga
Molpro/2020.1_openmpi_4.0.5_gcc_10.2_slurm20
gaussian/g09
gaussian/g09-D01
gaussian/g09-D01-TEST
vasp/5.4.1
vasp/5.4.1_debug
vasp/5.4.1_mvapich2-2.3.5_intel_2020.2_slurm20
vasp/5.4.4
vasp/5.4.4_intel
vasp/5.4.4_mvapich2-2.3.5_intel_2020.2_slurm20
vasp/5.4.4_openmpi_4.0.5_gcc_10.2_slurm20
vasp/5.4.4a
vasp/6.1.1_ompi405_yqi27
```

vasp/6.1.1_openmpi_4.0.5_intel_2020.2_yqi27_slurm20
vasp/6.1.1_yqi27
~~~~~~~~~~~~~~~~~~~~~~~~~ category: graph partitioning ~~~~~~~~~~~~~~~~~~~~~~~~~
metis/5.1.0   parmetis/4.0.3 scotch/6.0.4
~~~~~~~~~~~~~~~~~~~~~~~~~ category: image processing
~~~~~~~~~~~~~~~~~~~~~~~~~
multinest/3.10   openslide/3.4.1 pstokes/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: libraries
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
astropy/3.2.1   cudnn/7.4   flann/1.8.4   lapack/3.7.0
astroquery/3.0.9 cudnn/7.6   hnn/1.0   mumps/5.0.2
blas/3.7.0   cudnn/7.6.5   horovod/0.16   mumps/5.0.2-seq
cudnn/5.1   cudnn/8.1.0   horovod/0.19.5   pcl/1.9.1
cudnn/6.0   cudnn/8.2.0   lapack/3.4.2   pcl/1.9.1_nurbs
cudnn/7.0   dlib/19.17   lapack/3.6.0   scalapack/2.0.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: library
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
openslide-python/1.1.1
~~~~~~~~~~~~~~~~~~~~~~~~~ category: machine learning
~~~~~~~~~~~~~~~~~~~~~~~~~
keras/2.0.9   keras/2.1.3_py3 nccl/2.8.4
keras/2.1.1   nccl/2.4.7
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: math
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
gsl/1.15 gsl/2.3   gsl/2.5
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: package
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
subread/1.6.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: software
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
mriconvert/2.1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: utility
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
mriconvert/2.1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: visualization
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
mayavi/4.6.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: (none)
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
HiC-Pro/2.7.8   jo/1.4   repeatmasker/4.1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

HiC-Pro~/2.10.0 libsodium/1.0.17 repeatmodeler/1.0.11
awscli/1.0 mumax/3.9.3 sdl2/2.0.12
basilisk/1.0 ncl/6.4.0 siesta/3.2
canu/1.7.1 neuron/7.5 siesta/4.1
dropest/0.86 neuron/7.7 skewer/0.2.1
fiji/2017-java6 neuron/7.7_mpi squashfs/4.3
fiji/2020 nvidia-driver/440.33.01 tmux/2.8
fmri/20.0.0 pdflib/7.0.5 topcat/4.7
fv/5.5 pypy/6.0.0_2.7 transrate/1.0.3
gcm-core/2.0.498 pypy/6.0.0_3.5 vscode/1.22
grads/2.2.0 pypy/7.3.0_3.6 zstd/1.5.0
hotnet/1.0 repeatmasker/4.0.7
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Applied Maths
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
oof2/2.1.17
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Astrophysics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
polychord/1.0 polychord/2.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Bioinformatics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
MultiQC/1.0 muscle/3.8.31
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: CAD
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
freecad/0.18 librecad/2.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Chemistry
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dalton/2018.0
dalton/2018.0_mvapich2-2.3.5_intel_2020.2_slurm20
~~~~~~~~~~~~~~~~~~~~~~~~ category: Computer Architecture ~~~~~~~~~~~~~~~~~~~~~~~~
risc/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: EDA tools
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cadence/IC06.18.090 cadence/IC6.1.8.33 incisive/15.20.085
~~~~~~~~~~~~~~~~~~~~ category: Executable for ceckpointings ~~~~~~~~~~~~~~~~~~~~
dmtcp/2.6.0
~~~~~~~~~~~~~~~~~~~ category: Flag for CMAKE for fast build ~~~~~~~~~~~~~~~~~~~
ninja/1.9.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: GENETEICS
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
eigensoft/6.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Genomic
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Genrich/0.5 mcscanx/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Genomic Library
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
redundans/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Genomics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
baypass/2.2   beast/2.5.2   kissplice/2.5.1
beast/1.10.4   kissplice/2.5.0
~~~~~~~~~~~~~~~~~~~~ category: Genomics Sequencing Alignment ~~~~~~~~~~~~~~~~~~~~
qualimap/2.2.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Graphics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
beagle/1.0.0
~~~~~~~~~~~~~~~~~~~~~~~~~ category: Helper function type ~~~~~~~~~~~~~~~~~~~~~~~~~
datamash/1.3
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: I/O
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cdo/1.9.8
cdo/1.9.9
hdf5/1.10.0
hdf5/1.10.1_mvapich2-2.3.5_gcc_10.2_slurm20
hdf5/1.10.1_parallel
hdf5/1.10.5
hdf5/1.10.5_fortran
hdf5/1.10.5_mvapich2-2.3.5_intel_2020.2_slurm20
hdf5/1.10.5_openmpi_3.1.3_gcc
hdf5/1.10.5_openmpi_3.1.6_gcc
hdf5/1.10.5_openmpi_4.0.0_gcc
hdf5/1.10.5_openmpi_4.0.5_gcc_10.2_slurm20
hdf5/1.10.5_parallel
hdf5/1.10.7_hpcx_2.7.0_intel_2020.2_slurm20
hdf5/1.10.7_openmpi_4.0.5_gcc_10.2_slurm20
hdf5/1.10.7_openmpi_4.0.5_intel_2020.2_slurm20
hdf5/1.12.0_hpcx_2.7.0_intel_2020.2
hdf5/1.12.0_hpcx_2.7.0_intel_2020.2_slurm20
hdf5/1.12.0_openmpi_4.0.5_intel_2020.2_slurm20
jasper/1.900.1-intel
nco/4.6.6

nco/4.8.2

nco/4.9.3

netcdf/3.6.3

netcdf/4.4.1.1_gcc

netcdf/4.4.1.1_intel

netcdf/4.4.1.1_pgi

netcdf/4.7.0_intel2019.3

netcdf/4.7.4_gcc8.3

netcdf/4.7.4_gcc_10.2_hdf5_1.10.5

netcdf/4.7.4_intel_2020.2_hdf5_1.12.0

sqlite/3.25.2

sqlite/3.31.1

udunits/1.12.11

udunits/2.2.24

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: IDE

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

meshlab/20190129_qt59 spyder/3.3.5

~~~~~~~~~~~~~~~~~~ category: Image processing and visualization ~~~~~~~~~~~~~~~~~~

opencv-python/4.1.0.25

~~~~~~~~~~~~~~~~~~~~~~~~ category: Library for optimizer ~~~~~~~~~~~~~~~~~~~~~~~~

numbbo/2.3_python2 numbbo/2.3_python3

~ category: Material sceince: https://icet.materialsmodeling.org/overview.html ~

icet/0.3

~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Medical imaging

~~~~~~~~~~~~~~~~~~~~~~~~~~~~

mricrogl/1.0   mricrogl/1.2.20210317

~~~~~~~~~~~~~~~ category: Multifunctional Wavefunction Analyzer ~~~~~~~~~~~~~~~~

multiwfn/3.3.9

~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Numerical Library

~~~~~~~~~~~~~~~~~~~~~~~~~~

ngsolve/6.2.1901

~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Numerical Solver

~~~~~~~~~~~~~~~~~~~~~~~~~~~

dedalus/2.1810

dedalus/2.1905

dedalus/2.1905_openmpi_4.05_gcc_10.2_slurm20

dedalus/Sep2019

nektar++/4.5.0

~~~~~~~~~~~~~~~~~~~~~~~~ category: Quantum Monte Carlo

~~~~~~~~~~~~~~~~~~~~~~~~
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```
casino/2.13
~~~~~~~~~~~~~~~~~~~~ category: Tool for Image Manipulation ~~~~~~~~~~~~~~~~~~~~
netpbm/10.47.71
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: Utility
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
globus/1.11
~~~~~~~~~~~~~~~~ category: Visualization Package Qt's Python API ~~~~~~~~~~~~~~~~
pyqt/4.12.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: X
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
turbovnc/2.1.1   turbovnc/2.2.1   turbovnc/2.2.6   turbovnc/2.2.b1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: astronomy
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
ares/0.1              iraf/2.16              sextractor/2.8.6
ares/0.5              iraf/2.16.1+2018.11.01  supermongo/2.4.34
ccfits/2.5            lsst/14.0              swarp/2.38
cfitsio/3.450          planck_likelihood/3.0   theli/1.9.5
cfitsio/3.48           planck_likelihood/3.01  wcstools/3.9.5
ds9/7.6               scamp/2.0.4
galfit/3.0.5           sextractor/2.19.5
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: astrophysics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fiat/Oct2019
~~~~~~~~~~~~~~~~~~~~~~~~~~ category: astropy computing
~~~~~~~~~~~~~~~~~~~~~~~~~~
astropy/3.2.1
~~~~~~~~~~~~~~~~~~~~~~~~~ category: astroquery computing
~~~~~~~~~~~~~~~~~~~~~~~~~
astroquery/3.0.9
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: benchmark
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
elbencho/2.0-1
~~~~~~~~~~~~~~~~~~~~~~ category: binary for genome studies ~~~~~~~~~~~~~~~~~~~~~~
bedGraphToBigWig/1.04
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: bio
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
SNAP/2013-11-29                    mira/4.0.2
abyss/2.1.1                        mne/0.17.0
ale/20140120                        moseq2/0.1.2
aliview/1.25                       moseq2/0.2.0
```

amplisat/20170208
angsd/0.920
anvio/5.2
anvio/5.5
anvio/6.1
anvio/7
arb/6.0.6
augustus/3.3
bamcleave/Oct2018
bamtools/2.3.0
bamtools/2.4.1
bbmap/38.23
bbtools/38.12
bcftools/1.10.2
bcftools/1.13
bcftools/1.9
bcl2fastq/2.20.0
bedops/2.4.35
bedtools/2.25.0
bedtools/2.26.0
beeline/1.0
biolite/1.0.0
biomed/1.0
biopython/1.66
biopython/1.73
bismark/0.20.0
blast/2.2.30+
blast/2.6.0+
blast/2.7.1+
blast/2.8.1+
blast/2.9.0+
blat/36x2
bowtie/1.2.0
bowtie/2.4.1
bowtie2/2.3.0
bowtie2/2.3.5.1
bowtie2/2.4.2
braker/2.1.0
busco/3.0.2
bwa/0.7.15
mothur/1.39.5
mrbayes/3.2.6
mriqc/0.15.2
msmc/1.0.0
msmc/1.1.0
msmc/2.1.2
msprime/0.7.0
msprime/0.7.2
msprime/0.7.4
mummer/4.0.0.beta2
namd/2.11-multicore
namd/2.13b1-multicore
nda-tools/1.0
nextclip/1.3.1
nextgenmap/0.5.2
nipype/1.5.0
nseg/20181012
nvtop/1.1.0
obitools/1.2.12
octopus/0.7.4
oligotyping/2.0
omero/5.6.2
opera/2.0.6
orthomcl/2.0.9
paml/4.8
pandaseq/2.11
paris/1.1.3
paup/4.0a157
paup/4.0a166
paup/4.0a168
pbsuite/15.8.24
pcangsd/0.98
picard-tools/2.17.11
picard-tools/2.9.2
pilon/1.22
pilon/1.24
plink/1.07
plink/1.90
plink/2.00
polyphen/2.2.2

cabana/1.0
cabana/1.1_hpcx_2.7.0_gcc_10.2_slurm20
cantera/5.9.7
ccp4/7.0
circlator/1.5.5
conn/16b
conn/18a
conn/18b
conn/18b_runtime
conn/18b_standalone
conn/19c
conn/20b
conn/20b_standalone
connectome_workbench/1.3.1
connectome_workbench/1.3.2
connectome_workbench/1.4.2
cpac/1.0.1
cpac/1.5.0
cufflinks/2.2.1
cutadapt/1.14
dada2/1.4.1
dada2/1.8
dbg2olc/Sep2018
dendropy/4.2.0
diamond/0.9.12
diamond/0.9.24
diamond/2.0.8
dida/1.0.1
diffreps/1.55.6
dlcpar/1.1
edge-pro/1.3.1
eems/1.0
emboss/6.6.0
entap/0.8.1-beta
entap/0.8.4-beta
exonerate/2.2.0
fastme/2.1.5
fastqc/0.11.5
fastsimcoal/2
fasttree/2.1.10
poolparty/0.8
popoolation2/1.201
prinseq/0.20.4
prodigal/2.6.3
psmc/0.6.5
psmc/0.6.5a
pymol/2.2b
qctool/2.0
qiime/1.9.1
quast/5.0.0
raremetal/4.14.1
raxml/8.2.10
raxml-ng/0.9.0
recon/1.08
repeatscout/1.0.5
revbayes/1.0.5
revbayes/1.0.6
rmblastn/2.10.0
rmblastn/2.6.0
rsem/1.3.1
salmon/0.11.3
salmon/0.8.2
salmon/1.0.0
salmon/1.2.0
salmon/1.3.0
samblaster/0.1.24
samtools/0.1.18
samtools/1.10
samtools/1.12
samtools/1.13
samtools/1.2
samtools/1.3.1
samtools/1.4.1
samtools/1.9
schrodinger/2017-3
schrodinger/2020-1
schrodinger/2020-3
schrodinger/2021-1
schrodinger/2021-3
selscan/1.2.0a

fasttree/2.1.11
fastuniq/1.1
fastx-toolkit/2.6
fgap/1.8.1
fgbio/0.6.1
figtree/1.4.4
flashpca/2.0
freebayes/1.1.0
freebayes/1.2.0
garlic/1.1.6
gatk/4.0.9.0
gatk/4.1.6.0
gatk/4.2.2.0
gdcclient/1.4.0
genemark/4.33
guppy/4.0.11
guppy/4.2.2
guppy/5.0.7
hapbin/1.3.0
hisat2/2.1.0
hmmer/3.1b2
homer/4.10
hotnet2/1.2.1
htseq/0.11.1
htseq/0.9.1
idba/1.1.3
idemp/20180928
ilash/1.0.0
ilash/1.0.2
interproscan/5.26-65.0
interproscan/5.27-66.0
interproscan/5.28-67.0
interproscan/5.32-71.0
interproscan/5.33-72.0
iq-tree/1.6.7
iq-tree/2.0.6
jellyfish/1.1.11
jellyfish/2.2.10
kneaddata/0.6.1
kraken/2.0.7-beta
seqkit/0.10.1
seqtk/1.3
sga/0.10.15
sift/6.2.1
sift4g/2.0.0
sjaracne/0.2.0
skesa/1.68
slicer/4.10.0
slim/3.1
slim/3.2.1
slim/3.3
snippy/Oct2017
spades/3.10.1
spades/3.13.0
span/0.10.0.4787
spm/spm12
spm/spm12_7771
sprint/0.1.8
sratoolkit/2.10.5
sratoolkit/2.11.0
sratoolkit/2.8.2-1
stacks/2.2
stampy/1.0.32
star/2.6.1b
star/2.7.2a
star/2.7.3a
starfusion/1.7.0
starfusion/1.8.1
stringtie/1.3.3b
stringtie/1.3.4d
tabix/0.2.6
tablemaker/2.1.1
taxonkit/0.3.0
tophat/2.1.1
transabyss/2.0.1
transindel/20181017
trf/4.09
trimal/1.4
trimgalore/0.5.0
trimmomatic/0.36

kraken/2.0.9-beta trinity/2.11.0
kraken/2.1.2 trinity/2.4.0
last/956 trinity/2.8.4
macs/2.1.1 usearch/5.2.32
macs/2.2.6 usearch/8.1.1861
mafft/7.310-with-extensions varscan/2.3.9
maker/2.31.10 vcftools/0.1.16
marsbar/0.42 velvet/1.2.10
maxbin2/2.2.5 velvet/1.2.10a
megahit/1.1.3 vep/101
meraculous/2.2.6 vep/104
metabat/2.12.1 viennarna/2.4.9
metaphlan/2.6.0 vmd/1.9.3
metavelvet/1.2.01 vsearch/2.11.1
migrate/3.6.11 weblogo/2.8.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: bio packages
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
bwameth/0.10
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: bioinformatics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
umitools/1.0.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: biology
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
haplostrips/1.2.1 htslib/1.9 meme/5.0.5 mmsplice/0.2.7
htslib/1.13 libBigWig/0.4.4 meme/5.3.0 wiggletools/1.2.3
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: build tool
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
scons/3.0.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: cave
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
gigapixelviewer/alpha minvr/dev_ben vrg3d/265_compat
minvr/0.3master planetaryviewer/alpha vrg3d/265_demos
minvr/0.4 scalable/20150828 vrpn/7.33
minvr/beta scalable/opengl32+
minvr/beta-bleeding vrg3d/265
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: chemistry
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Molpro/2012.1.15
Molpro/2015_gcc
Molpro/2015_serial

Molpro/2018.2_ga

Molpro/2019.2

Molpro/2019.2_ga

Molpro/2020.1

Molpro/2020.1_ga

Molpro/2020.1_openmpi_4.0.5_gcc_10.2_slurm20

ambertools/amber16

ambertools/amber16-gpu

ambertools/amber17

ambertools/amber17_lic

ambertools/amber21

ase/3.13.0

ase/3.19.1

ase/3.8.1

bagel/1.2.2

cp2k/7.1

cp2k/8.1.0

crossrate/2016.3.23

dacapo/2.7.16_mvapich2_intel

dice/1.0

elk/5.2.14

gaussian/g09

gaussian/g09-D01

gaussian/g09-D01-TEST

gaussview/14Aug20

gromacs/2016.6

gromacs/2018.2

gromacs/2018.2_gpu

gromacs/2018.2_hpcx_2.7.0_gcc_10.2_slurm20

gromacs/2020.1

gromacs/2020.1_hpcx_2.7.0_gcc_10.2_slurm20

gromacs/2020.4_gpu

gromacs/2020.4_gpu_hpcx_2.7.0_gcc_10.2_slurm20

gromacs/2020.4_hpcx_2.7.0_gcc_10.2_slurm20

hande/1.1.1

hande/1.1.1_64

hande/1.1.1_debug

hotbit/10mar17

lammps/11Aug17_serial

lammps/29Oct20_openmpi_4.0.5_gcc_10.2_slurm20

medea/3.2.3.0

molden/5.7

mrcc/2014-intel

mrcc/2014-intel-threaded

mrcc/2018-intel

mrcc/2018-intel-threaded

mrcc/2020

n2p2/1.0.0

n2p2/2.0.0

n2p2/2.0.0_hpcx

nbo/7.0

nwchem/6.8-openmpi

nwchem/7.0

nwchem/7.0.2_mvapich2-2.3.5_intel_2020.2_slurm20

openbabel/2.4.1

openbabel/3.0.0

openmolcas/18.09.617

orca/4.0.1.2

orca/4.1.1

orca/4.2.1

orca/5.0.0

orca/5.0.1

prophet/augustegm_1.2

pyscf/1.4.7

pyscf/1.6.3

qchem/5.0.2

qchem/5.0.2-openmpi

qmcpack/3.10.0_openmpi_4.0.5_intel_2020.2_slurm20

qmcpack/3.7.0

qmcpack/3.9.1

qmcpack/3.9.1_openmpi_3.1.6

qmcpack/3.9.2_hpcx_2.7.0_gcc_10.2_slurm20

qmcpack/3.9.2_intel_2020

qmcpack/3.9.2_openmpi_4.0.0_gcc_8.3_slurm20

qmcpack/3.9.2_openmpi_4.0.0_gcc_8.3_slurm20_complex

qmcpack/3.9.2_openmpi_4.0.1_gcc

qmcpack/3.9.2_openmpi_4.0.4_gcc

qmcpack/3.9.2_openmpi_4.0.5_intel_2020.2_slurm20

quantumespresso/6.1

quantumespresso/6.3

quantumespresso/6.4
quantumespresso/6.4.1
quantumespresso/6.4_openmpi_4.0.0_gcc_8.3_slurm20
quantumespresso/6.4_openmpi_4.0.5_intel_2020.2_slurm20
quantumespresso/6.4_openmpi_4.0.5_intel_slurm20
quantumespresso/6.5
quantumespresso/6.5_openmpi_4.0.5_intel_slurm20
quantumespresso/6.6
quantumespresso/6.6_openmpi_4.0.5_intel_2020.2_slurm20
rotd/2014-11-15_mvapich2
schrodinger/2017-3
schrodinger/2020-1
schrodinger/2020-3
schrodinger/2021-1
schrodinger/2021-3
sharc/2.0
sharc/2.1.1
sharc/2.1.1_intel
vasp/5.4.1
vasp/5.4.1_debug
vasp/5.4.1_mvapich2-2.3.5_intel_2020.2_slurm20
vasp/5.4.4
vasp/5.4.4_intel
vasp/5.4.4_mvapich2-2.3.5_intel_2020.2_slurm20
vasp/5.4.4_openmpi_4.0.5_gcc_10.2_slurm20
vasp/5.4.4a
vasp/6.1.1_ompi405_yqi27
vasp/6.1.1_openmpi_4.0.5_intel_2020.2_yqi27_slurm20
vasp/6.1.1_yqi27
xcrysden/1.5.60
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: class
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
class/1435
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: clients
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
aspera/3.8.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: climate
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cesm/1.2.1 cesm/2.1.1 esmf/8.0.0 esmf/8.1.0b11
cesm/1.2.2 esmf/7.1.0r esmf/8.0.0b esmf/8.1.9b17

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: compilers
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Xvfb/1.20.12 gcc/10.2 java/8u111
clang/3.9.1 gcc/4.5.4 java/jdk-11.0.11
clang/7.0.0 gcc/4.7.2 java/jdk-12.0.2
clang/7.1.0 gcc/4.9.4 kokkos/3.3.1
cuda/10.0.130 gcc/5.4 kokkos/3.4.1
cuda/10.1.105 gcc/6.2 llvm/11.0.1
cuda/10.2 gcc/6.3 llvm/3.8.1
cuda/11.1.1 gcc/7.2 llvm/4.0.0
cuda/11.1.1_intel_2020 gcc/8.3 llvm/6.0.1
cuda/11.3.1 intel/2011.11.339 llvm/7.1.0
cuda/7.5.18 intel/2013.1.106 nag/6.2
cuda/8.0.61 intel/2017.0 nag/mbl6i25dnl
cuda/9.0.176 intel/2018.1 pgi/16.7
cuda/9.1.85.1 intel/2019.3 pgi/2019
cuda/9.2.148 intel/2020.2 swig/3.0.10
~~~~~~~~~~~~~~~~~~~~~~~~~ category: computer architecture ~~~~~~~~~~~~~~~~~~~~~~~~~
llvmOpenmp/1.0 llvmOpenmp/2.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: containers
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
singularity2/2.5.2
~~~~~~ category: cross webbrowser web application development environment ~~~~~~
chromedriver/2.46
~~~~~~~~~~~~~~~ category: data analysis(http://www.mega-nerd.com/) ~~~~~~~~~~~~~~~
libsnd/1.0.28
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: data science
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
catboost/0.8.1 manureadr/1.0 pandas/py_3.6.6
catboost/0.8.1_py3 pandas/py_3.5.2
~~~~~~~~~~~~~~~~~~~~~~~~ category: data structure library ~~~~~~~~~~~~~~~~~~~~~~~~
dcm2bids/2.1.4
~~~~~~~~~~~~~~~~~~~~~~~ category: debugging and profiling ~~~~~~~~~~~~~~~~~~~~~~~
forge/18.2.3 forge/19.1.2 forge/21.0.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: dev
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
googletest/1.8.0 qemu/4.1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: devel
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
bazel/0.23.0 glew/1.13.0 opengl/nvidia-375.66
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

```
bazel/0.25.2          glew/2.1.0            opengl/nvidia-390.30
bazel/0.4.4           opengl/mesa-12.0.6    opengl/nvidia-410.72
bazel/0.5.4           opengl/mesa-18.3.3    protobuf/3.4.1
bazel/1.2.1           opengl/nvidia         protobuf/3.6.0_gcc5.4
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: editor
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
emacs/26.3    neovim/0.4.4
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: engineering
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
abaqus/2017               comsol/5.6
abaqus/2021               mentor-calibre/2020.1_36.18
abaqus/2021.1             spectre/191
abaqus/2021.1_intel17     su2/7.0.2
abaqus/6.12sp2            synopsys/2018.06
ansys/18.1                synopsys/2020.06
assura/04.16.107          synopsys/L_2016.03-SP2
comsol/5.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: fMRI
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
brainiak/Feb2018
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: fonts
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
freetype/2.7.1
~~~~~~~~~~~~~~~~~~~~~~~~~ category: gene and species tree ~~~~~~~~~~~~~~~~~~~~~~~~~
phyldog/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: genetics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
megacc/10.1.8
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: genomic
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
admixture/1.3.0          glactools/1.0.7          pybigwig/0.3.15
deeptools/3.2.1          partitionfinder/2.1.1    pysam/0.15.2
deeptoolsintervals/0.1.7 py2bit/0.3.0             pyslim/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: genomics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cellranger/3.1.0      cellranger/arc-1.0.1  faststructure/1.0
cellranger/5.0.1      chromopainter/0.0.4   relernn/6Dec2019
cellranger/6.0.0      clustal_omega/1.2.4
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: graphics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

```
campari/3.0        gnuplot/5.2.3      inkscape/Sep-2019
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: image
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
c3d/1.0.0          imagej/1.52a       leptonica/1.79.0   openexr/2.2.1
ffmpeg/3.2.4       imagemagick/7.0.7  libgd/2.2.5
ffmpeg/4.0.1       isis/3.5.1         libgit/1.1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: image converter
~~~~~~~~~~~~~~~~~~~~~~~~~~~
mriconvert/2.1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: image processing
~~~~~~~~~~~~~~~~~~~~~~~~~~
libgif/5.1.9           libjpeg-turbo/2.0.2     openjpeg/2.3.1
libjpeg/9.0            mayavi/4.6.0            openslide-python/1.1.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: languages
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
R/3.3.2              julia/1.0            miniconda/4.10
R/3.4.0              julia/1.0.2          perl/5.16.0
R/3.4.3              julia/1.1.0          perl/5.18.2
R/3.4.3_mkl          julia/1.2.0          perl/5.24.1
R/3.4.4              julia/1.4.1          perl/5.30.0
R/3.5.2              julia/1.4.2          perl/5.8.9
R/3.6.0              julia/1.5.0          python/2.7.12
R/3.6.3              julia/1.5.1          python/2.7.12_clean
R/4.0.0              julia/1.5.2          python/2.7.16
R/4.0.3              julia/1.5.3          python/3.5.2
R/4.0.5              julia/1.5.4          python/3.6.6
R/4.1.0              julia/1.6.0          python/3.6.6_test
anaconda/2-4.3.0     julia/1.6.1          python/3.6.8_gcc8.3
anaconda/2-5.3.0     julia/1.6.2          python/3.7.4
anaconda/2020.02     julia/1.6.3          python/3.8.12_gcc8.3
anaconda/3-4.3.0     lua/5.3.4            python/3.9.0
anaconda/3-5.2.0     maple/16             qt/3.3.8b
golang/1.15.6        maple/20             qt/3.3.8b-51
golang/1.16.6        materialstudio/2020  qt/5.10.1
golang/1.17.1        mathematica/10.3.1   qt/5.12
idl/8.5.1            mathematica/11.0     qt/5.12.0
idl_DEEPS/8.7.2      mathematica/12.0     qt/5.13.1
java/8u111           matlab/R2016a        qt/5.14.2
java/jdk-11.0.11     matlab/R2017a        qt/5.7.0
java/jdk-12.0.2      matlab/R2017b        qt/5.9.0
```

julia/0.5.1 matlab/R2018a ruby/2.4.0

julia/0.6.1 matlab/R2018b rust/1.45.1

julia/0.6.4 matlab/R2019a rust/1.50.1

julia/0.7.0 matlab/R2021a scala/2.12.2

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: lib

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

lftp/4.8.4

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: libraries

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

Xvfb/1.20.12

acml/5.2.0-gfortran

agalma/1.0.0

armadillo/9.200.4

assimp/4.1.0

assimp/5.0.0

blast-legacy/2.2.26

boost/1.44.0

boost/1.49.0

boost/1.55

boost/1.57

boost/1.62.0-intel

boost/1.63.0

boost/1.68

boost/1.69

boost/1.75.0_openmpi_4.0.5_intel_2020.2_slurm20

boost/1.76.0_hpcx_2.7.0_gcc_10.2_slurm20

boost/1.76.0_hpcx_2.7.0_intel_2020.2_slurm20

bzip2/1.0.2

c-blosc/1.16.3

cdhit/4.6.8

cuda/10.0.130

cuda/10.1.105

cuda/10.2

cuda/11.1.1

cuda/11.1.1_intel_2020

cuda/11.3.1

cuda/7.5.18

cuda/8.0.61

cuda/9.0.176

cuda/9.1.85.1

cuda/9.2.148

ea-utils/1.04.807

fabm/1.0.2

fastq-tools/0.8

fftw/2.1.5

fftw/2.1.5-double

fftw/3.3.6

fftw/3.3.8

fftw/3.3.8a

freeglut/3.0.0

geos/3.4.2

geos/3.7.1

geos/3.8.1

gerris/1.0

global_arrays/5.6.1

global_arrays/5.6.1_i8

global_arrays/5.6.1_openmpi_2.0.3

global_arrays/5.8_openmpi_4.0.5_gcc_10.2_slurm20

gmp/6.1.2

gsl/1.15

gsl/2.3

gsl/2.5

igraph/0.7.1

keras/2.0.9

keras/2.1.1

keras/2.1.3_py3

lemon/1.3.1

leveldb/1.20

libcutensor/10.2

libflint/2.7.1

libint/2.5.0

libpng12/1.2.57

libspatialindex/1.9.3

libtiff/4.0.10

libxc/4.3.4

libzip/0.9-3.1.el6

lp_solve/5.5.2.5

metis/5.1.0

mpfr/3.1.5

mpfr/4.0.2

mpi4py/3.0.1_py3.6.8

mxnet/1.3.0

node.js/14.16.0

node.js/6.10.3

occa/1.2

openblas/0.2.19

openblas/0.2.8

openblas/0.3.7

opencv/3.2.0

opencv/3.4.1

parmetis/4.0.3

pcre2/10.35

phylobales/1.8b

proj/4.9.3

proj/5.2.0

proj/7.0.0

pytorch/1.3.1

sparsehash/2.0.2

suiteparse/4.5.4

sysstat/12.5.4

tensorflow/1.1.0_cpu

tensorflow/1.1.0_gpu

tensorflow/1.13.1_cpu_py3

tensorflow/1.13.1_gpu

tensorflow/1.13.1_gpu_keras

tensorflow/1.13.1_gpu_py3

tensorflow/1.14.0_gpu_py36

tensorflow/1.4.1_cpu

tensorflow/1.4.1_cpu_py3

tensorflow/1.4.1_gpu

tensorflow/1.4.1_gpu_py3

tensorflow/1.4.1_gpu_py3_cuda9.1

tensorflow/1.5.0_cpu_py3

tensorflow/1.5.0_gpu

tensorflow/1.5.0_gpu_py3

tensorflow/2.0.0_cpu_py37

tensorflow/2.0.0_gpu_py37

theano/1.0.1_py3

transdecoder/5.4.0

v8/3.14.5

voro++/0.4.6
vrpn/7.33
whatshap/Sep2018
xeyes/1.0
xz/5.2.4
yaml-cpp/0.6.2
yaml-cpp/0.6.2_intel2019.3
yaml-cpp/0.6.3_intel_2020.2
zlib/1.2.11
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: library
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
catch2/2.3 matplotlib/2.2.4 pmclib/1.1
dcmtk/3.6.6 multinest/3.10 pstokes/1.0
dotnet/5.0.202 nccl/2.4.7 sprng/5.0
easydict/1.7 nccl/2.8.4 statsmodels/0.9.0
fastq_screen/0.13.0 openslide/3.4.1
gsutil/350 p7zip/16.02
~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: machine learning
~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1/1.01 py-faster-rcnn/July2018
1/2.03 rapidjson/1.1.0
attend2u/20180216 scikit-learn/0.19.1
cudnn/5.1 scikit-learn/0.21.2
cudnn/6.0 sciml_class/pytorch-21.06
cudnn/7.0 tensorflow/1.1.0_cpu
cudnn/7.4 tensorflow/1.1.0_gpu
cudnn/7.6 tensorflow/1.13.1_cpu_py3
cudnn/7.6.5 tensorflow/1.13.1_gpu
cudnn/8.1.0 tensorflow/1.13.1_gpu_keras
cudnn/8.2.0 tensorflow/1.13.1_gpu_py3
deeparg/Jan2019 tensorflow/1.14.0_gpu_py36
deeparg/Oct2018 tensorflow/1.4.1_cpu
deeplabcut/1.01 tensorflow/1.4.1_cpu_py3
deeplabcut/2.03 tensorflow/1.4.1_gpu
deeplabcut/2.1.4 tensorflow/1.4.1_gpu_py3
deeplabcut/2.1.9 tensorflow/1.4.1_gpu_py3_cuda9.1
deeplabcut/2.2 tensorflow/1.5.0_cpu_py3
dlib/19.17 tensorflow/1.5.0_gpu
flann/1.8.4 tensorflow/1.5.0_gpu_py3
hnn/1.0 tensorflow/2.0.0_cpu_py37

horovod/0.16 tensorflow/2.0.0_gpu_py37

horovod/0.19.5 tf-horovod/1.0

pcl/1.9.1 xgboost/1.3.3

pcl/1.9.1_nurbs

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: math

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

atlas/3.10.3 lapack/3.7.0 ripser/0.5.3

blas/3.7.0 macaulay2/1.12-1 rss/1.0

cgal/3.14.1 magma/V2.23-10 sage/8.7

fenics/2017.1 magma/V2.25-5 sage/9.0

fenics/2018.1.0 magma/V2.25-5-gpu scalapack/2.0.2

gap/4.9.1 magma-gpu/2.4.0 sympy/1.4

gmsh/3.0.1 magma-gpu/2.5.4_volta trlan/2010.09

lapack/3.4.2 nlopt/2.5.0

lapack/3.6.0 numpy/intel_1.15.1

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: misc

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

mark/Dec18 mysql/8.0.13

mysql/5.7.28 netcdf4-python/4.1.4.2

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: ml

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

bonito/0.3.1

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: model

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

gotm/5.0_qingli gotm/5.3

~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: molecular dynamics

~~~~~~~~~~~~~~~~~~~~~~~~~~~~

mdanalysis/0.19.2

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: mpi

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

mpi/cave_mvapich2_2.3b_gcc

mpi/cave_mvapich2_2.3b_intel

mpi/cave_mvapich2_2.3rc2_gcc

mpi/hpcx_2.7.0_gcc_10.2_slurm20

mpi/hpcx_2.7.0_intel_2020.2_slurm20

mpi/mpich3.3a3_intel_2020.2

mpi/mvapich2-2.3.5_gcc_10.2_slurm20

mpi/mvapich2-2.3.5_intel_2017.0_slurm20

mpi/mvapich2-2.3.5_intel_2020.2_slurm20

mpi/openmpi_2.0.3_intel_2020.2_slurm20

mpi/openmpi_3.1.6_gcc
mpi/openmpi_3.1.6_gcc_10.2_slurm20
mpi/openmpi_4.0.0_gcc
mpi/openmpi_4.0.1_gcc
mpi/openmpi_4.0.4_gcc
mpi/openmpi_4.0.4_gcc_8.3_slurm20
mpi/openmpi_4.0.5_gcc_10.2_slurm20
mpi/openmpi_4.0.5_intel_2020.2_cuda_9.1.85_slurm20
mpi/openmpi_4.0.5_intel_2020.2_slurm20
mpi/openmpi_4.1.1_gcc_10.2_slurm20
osu-mpi/5.3.2
osu-mpi/5.6.2_mvapich2-2.3a_gcc
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: mri
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

afni/17.1.00	freesurfer/6.0.0
afni/18.2.06	freesurfer/6.0.0_rh7
afni/19.0.17	freesurfer/6.0.0_rh7-30-Nov-2018
afni/19.3.08	freesurfer/7.1.1
afni/19.3.10	fsl/5.0.10
afni/20.0.03	fsl/6.0.0
afni/20.1.06	fsl/6.0.3
afni/21.2.04	mmvt/2020-06
ants/2.1.0	mricron/05-2016
ants/2.3.1	mricron/12-2012
ants/2.3.4	mricron/2019-09
dsi/april2019	tortoise/3.1.0

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: neuro
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

dtitk/2.3.1	qit/1.0	qit/2.0	qit/Jun21

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: neuroscience
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
sct/4.2.2
~~~~~~~~~~~~~~~~~~~~~~~~~ category: numerical optimization ~~~~~~~~~~~~~~~~~~~~~~~~~
bayop/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: other
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
sbt/1.2.3
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: package
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ffte/6.0	ffte/6.0/mpi
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: performance
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
ior/2.10.3 ipm/2.0.6_r
ior/3.0.1 osu-mpi/5.3.2
ior/3.2.1 osu-mpi/5.6.2_mvapich2-2.3a_gcc
ipm/2.0.6 papi/5.4.3
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: physics
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
casa/5.1.2
geant/4.10.04.p01
geant/4.10.3
geant/4.10.5
geant/4.9.4.p04
gpaw/0.10.0
gpaw/1.2.0
gpaw/1.2.0_hpcx_2.7.0_gcc
gpaw/1.2.0_mvapich2-2.3a_gcc
gpaw/20.10.0_hpcx_2.7.0_intel_2020.2_slurm20
gpaw/20.10_hpcx_2.7.0_intel_2020.2_slurm20
gpaw/21.1.0_hpcx_2.7.0_gcc_10.2_slurm20
gpaw/21.1.0_openmpi_4.0.5_gcc_10.2_slurm20
gpaw/21.1.0a_openmpi_4.0.5_gcc_10.2_slurm20
hoomd/2.9.0
jdftx/1.4.2
lumericalfdtd/8.16.982
mcx/20180525
mcxlab/2017.7
mujoco-py/1.50.1.23
pymultinest/2.9
root/6.10
~~~~~~~~~~~~~~~~~~~~~~~~ category: profiling and debugging ~~~~~~~~~~~~~~~~~~~~~~~~
cube/4.3.4 ncdu/1.14
ddd/3.3.12 scalasca/2.3.1_intel
gdb/7.12.1 scorep/3.0_intel_mvapich2
gperftools/2.5 valgrind/3.12.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: python
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numpydoc/0.9.1 pytables/3.5.2 six/1.12.0
plotly/3.9.0 python_igraph/0.7.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: python library

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wx/1.0
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annovar/2018Apr16 orthofinder/2.2.7 orthofinder/2.3.3
~~~~~~~~~~~~~~~~~~~~~~~~~~ category: software management
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maven/3.2.2 maven/3.8.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: solvers
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eigen/3.2.2
eigen/3.3.2
eigen/3.4.0
mcl/12.135
mineos/1.0
mumps/5.0.2
mumps/5.0.2-seq
openfoam/4.1
openfoam/4.1a
openfoam/7.0_hpcx_2.7.0_gcc_10.2_slurm20
pari/2.11.2
pastix/5.2.3
petsc/3.14.2_hpcx_2.7.0_gcc_10.2_slurm20
petsc/3.14.2_hpcx_2.7.0_intel_2020.2_slurm20
petsc/3.14.2_mpich3.3a3_intel_2020.2
petsc/3.7.5
petsc/3.7.7
petsc/3.8.3
polyrate/17C
scotch/6.0.4
suiteparse/4.5.4
trilinos/12.12.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: stat
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seaborn/0.10.0
~~~~~~~~~~~~~~~~~~~~~~ category: statistical analysis package ~~~~~~~~~~~~~~~~~~~~~~
glmnet/1.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: statistics
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JAGS/4.2.0   R/3.6.3   caffe/1.0_with_cudnn

JAGS/4.3.0 R/4.0.0 mallet/2.0.8rc3
R/3.3.2 R/4.0.3 rstudio/1.0.44
R/3.4.0 R/4.0.5 rstudio/1.1.463
R/3.4.3 R/4.1.0 rstudio/1.4.1103
R/3.4.3_mkl SAS/9.4M6 stata/14
R/3.4.4 SAS/9.4b stata/15
R/3.5.2 caffe/1.0 wfu_pickatlas/3.0.5b
R/3.6.0 caffe/1.0_CPU_ONLY
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: sys
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dos2unix/7.4.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: system
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wayland/1.18.0 xfce/4.10 xfce/4.16
wayland-protocols/1.20 xfce/4.12
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: tex
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pandoc/2.9.2.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: text editing
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texstudio/2.12.16
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: tool
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dcm2niix/25.0
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: tool kit
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subread/1.6.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: tools
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idr/2.0.2 omero/5.6.2
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: utilities
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atom/1.19.3 git/2.10.2
bamaddrg/20180928 git/2.20.2
binutils/2.29.1 git/2.29.2
binutils/2.31 h4cf/1.2
chrome/55.0 h5py/2.9.0
chrome/73.0 intltool/0.51.0
cmake/3.10.1 itstool/2.0.4
cmake/3.15.4 json_cpp/1.9.4

cmake/3.20.0 json_fortran/8.1.0
cmake/3.6.3 kallisto/0.46.1
cmake/3.8.0 libevent/2.1.8
colordiff/1.0.18 libwnck/3.24.1
comsol/5.2 mercurial/5.1
comsol/5.6 ncurses/6.2
cppunit/1.14.0 pdftk/2.02
curl/7.61.1 perf-tools/2.7
cvs/1.11.23 rclone/1.51.0
depot_tools/Jan2019 rsync/3.1.3
engineering/19.10.237 spfft/0.9.12
engineering/calibre2020.1_36 sublime/2.0.2
express/1.5.1 svn/1.8.17
fileZilla/3.10.0 svn/1.9.5
firefox/56.0.2 texinfo/4.13a
firefox/59.0.2 texlive/2018
firefox/66.0.3 vim/8.1
firefox/68.0 vim/8.1_py3
firefox/87.0 vnc-apps/7.2
ghostscript/9.21 xxdiff/4.0.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: utility
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redis/6.2.4
~~~~~~~~~~~~~~~~~~~~ category: version record for large files ~~~~~~~~~~~~~~~~~~~~
gitlfs/2.7.1
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: vision
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opencv/3.2.0 scikit-image/0.13.1 tesseract/3.05.00
opencv/3.4.1 scikit-image/0.15.0 tesseract/4.00.00
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: visualization
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atomeye/3.0
basemap/1.2.0
blender/2.78
blender/2.79
blender/2.90.1
cartopy/0.16.0
cartopy/0.17.0
cave-demo/yurt
cave-utils/yurt
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caviar/1.0

ferret/7.1

gdal/2.1.3

gdal/2.4.0

gdal/3.0.4

gephi/0.9.2

gimp/2.8.22

gimp/2.9.6

glm/0.9.9

glm/0.9.9.5

grace/5.1.25

graphviz/2.40.1

minvr/0.3master

minvr/0.4

minvr/beta

minvr/beta-bleeding

minvr/dev_ben

ncview/2.1.7

openscad/2015.03-3

openscenegraph/3.4.0

osgearth/2.7

ovito/2.8.2

ovito/2.9.0

paraview/5.1.0

paraview/5.1.0_yurt

paraview/5.4.1

paraview/5.6.0_no_scalable

paraview/5.6.0_yurt

paraview/5.8.0

paraview/5.8.0_mesa

paraview/5.8.0_release

paraview/5.8.1_openmpi_4.0.5_intel_2020.2_slurm20

paraview/5.9.0

photoscan/1.3.0

pyshp/2.0.1

shapely/1.6.4

tecplot/2017

tecplot/2017R3

tecplot/2018R2

tecplot/2019R1

unity/Unity-2017.3.0b1

unity/unity-editor-2017.2.0f3

visit/2.13.2

visit/2.7.2

vmd/1.9.3

vrg3d/265

vrg3d/265_compat

vrg3d/265_demos

vtk/5.6.1

vtk/7.1.1

vtk/7.1.1a

vtk/8.1.0

xcrysden/1.5.60

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: vizualization

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metashape/1.5.4

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: weather

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wrf/3.6.1

wrf/4.2.1_hpcx_2.7.0_intel_2020.2_slurm20

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ category: workshop

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workshop/1.0 workshop/3.0

Oscar: Sage

Loading and Launching Sage

1. Open the Terminal and use the following commands at the command line.

2. `module load sage/9.0` to load Sage. This command will return confirmation "*module: loading 'sage/9.0'*".

3. Sage on Oscar usually has dependent modules. These will be output to your terminal when you load the Sage module similar to the example below.

```
[username@node ~]$ module load sage/9.0
module: loading 'sage/9.0'
module: sage: To use: module load gcc/8.3
```

4. Load any other dependent modules for Sage that were output in the above steps. These modules must be loaded in the specific order specified by the system when the Sage module is loaded. Loading them in a different order may cause Sage to throw errors.

For Sage 9.0: `module load gcc/8.3`

For Sage 8.7: `module load gcc/8.3 sqlite/3.25.2 perl/5.24.1 libgd/2.2.5 mpfr/3.1.5 ffmpeg/4.0.1 imagemagick/7.0.7 texlive/2018`

5. `sage` to launch the Sage console within your Terminal window.

Sage on VNC

The Sage install may not always work properly on Oscar's VNC nodes due to the VNC nodes running older chipsets. The easiest way to remedy this issue is to run sage in an interactive job via the terminal in your VNC session.

Use the interact command with parameters for your specific job to start the interactive session, then load your modules and run the sage binary (steps 2-4 above).

```
interact -n 2 -m 32g -t 04:00:00 -f 'haswell|broadwell|skylake'
```

Installing Sage Packages Locally with --user

It is possible to install most Sage packages locally to your home folder by passing the `–user` parameter at the end of your install command. See below for example steps to install the Sage packages “surface_dynamics” and “sage-flatsurf”. In this example, we are loading both packages from git repositories, so we need to load the git module.

1. `module load git`

2. `sage -pip install git+https://gitlab.com/videlec/surface_dynamics –user`

3. `sage -pip install git+https://github.com/videlec/sage-flatsurf –user`

Using Sage with Batch Scripts

Thanks to Trevor Hyde from Summer@ICERM 2019 for these instructions.

One method for running computations with Sage on Oscar is to write a script and use the slurm batch scheduler to have Oscar run your script. This requires two pieces:

1. A shell script to configure and submit your batch job to the cluster.
2. Your Sage code/program you'd like to run.

Example Batch Script

sage-batch.sh

```
#!/bin/bash


#SBATCH -J test_program
#SBATCH --array=0-9
#SBATCH -t 1:00:00
#SBATCH --mem=8G
```

```
#SBATCH -e data/<oscar-username>/test_output/test%a.err
#SBATCH -o data/<oscar-username>/test_output/test%a.out

module load sage/8.7
module load gcc/8.3 sqlite/3.25.2 perl/5.24.1 libgd/2.2.5 mpfr/3.1.5 ffmpeg/4.0.1 imagemagick/7.0.7
texlive/2018

sage test_program.sage $SLURM_ARRAY_TASK_ID
```

- `#!/bin/bash` tells the system this is a bash (shell) script.
- `#SBATCH -J test_program` sets the name of the job which appears when you check the status of your jobs.
- `#SBATCH –array=0-9` is an easy way of doing parallel computations. In this case it says our job will run on 10 different nodes, each node will be passed a parameter and we have specified that the parameters will take the values 0 through 9. You can specify several ranges or even list individual parameters if you prefer.
- `#SBATCH -t 1:00:00` specifies a time limit in `HH:MM:SS` for each node. Once this time runs out your program will stop running on that node. Be careful setting the time limit too high as doing so may make it take a long time for your job to get scheduled to run. Before starting a big computation try to do some smaller tests to see how long you expect to need.
- `#SBATCH –mem=8G` specifies how much memory each node gets. Standard exploratory accounts get 123GB total to use at any one time. So if you allocate too much per job, fewer jobs will run at once. On the other hand, if you allocate too little and a computation needs more than it has, then it will terminate. If this happens an “out of memory” error will show up in the `.err` file for that node.
- `#SBATCH -e data/<ccv-username>/test_output/test%a.err` and `#SBATCH -o data/<ccv-username>/test_output/test%a.out` specify where the error messages and output for each computation should be sent. You should store these files in your user folder, not on the submit node. We each have a folder inside the `data` directory which you can see from the submit node. In this example I have created a folder titled `test_output` where I’m putting both of these files. **You need to make these folders before you run the computation otherwise the output will be dumped into the void!** The `%a` will get replaced with the array parameter. So for example, since we set our array parameters to be `0-9` there will be 10 nodes running and each of them gets a number between 0 and 9; this node corresponding to the parameter 7 will create two files `test7.err` and `test7.out`.
- `module load sage/8.7` loads the sage module into the node.
- `module load gcc/8.3 sqlite/3.25.2 perl/5.24.1 libgd/2.2.5 mpfr/3.1.5 ffmpeg/4.0.1 imagemagick/7.0.7 texlive/2018` loads the dependency packages for the sage module.

Everything after this in the script happens as if you typed it yourself onto the command line.

- In our example, we want to run sage code, so the line `sage test_program.sage $SLURM_ARRAY_TASK_ID` runs our example sage program `test_program.sage`.
- The file needs to have the `.sage` extension.
- You should write this file in a text editor, not in a Jupyter notebook (although you can first write and test your program in a Jupyter notebook and then copy and paste it into a new file when it’s ready).
- This program is written to accept one input and I have passed it `$SLURM_ARRAY_TASK_ID` which is the array parameter passed to each node. You can use this parameter to select which input parameters to run your program on.

Example Sage Program

test_program.sage

```
import sys


def fun_math(message):
    print message
    sys.stdout.flush()


job_id = int(sys.argv[1])
fun_math('hi this is a test')
fun_math('my job id is' + str(job_id))
```

- In the Sage program, you first define all of your functions and then you include the code you want to run.
- Import `sys` so you can access the array parameter passed to your function from the node. This is accessed in this case by `sys.argv[1]`. Make sure you explicitly coerce to be an integer if you want to use it as an integer; it's a string by default.
- The output of the `print` command is appended to the `.out` file for this node as a new line.
- Notice the line `sys.stdout.flush()` included in the function. This makes the program immediately send whatever output it has to the output file when called. Otherwise the program won’t output **anything** until it has completely finished running. If each node is running 100 potentially long computations and it finishes the first 99 but then times out on the 100th computation, and you don’t include any `sys.stdout.flush()` commands, everything will be lost when time runs out.

Submitting the Batch Job

- To run this batch program go back to the submit node and type `sbatch <NAME_OF_BATCH_FILE>`. In our example here, our batch file is called `sage-batch.sh`, so we simply type `sbatch sage-batch.sh` Slurm will return a line that tells you your job has been submitted together with a job id number.
- To check the progress of your jobs type `myq` from anywhere on Oscar. This will show you what jobs you have running, how much time they have left, and which jobs are still waiting to run. Be patient, sometimes it takes a minute for things to get started.
- If you realize your code is never going to finish or that you've made some terrible mistake, you can cancel a batch job by typing `scancel <JOB_ID>`. You can specify a single node or just put the general job id for the whole run and cancel everything.

Oscar: MATLAB

Loading and Launching MATLAB

1. Open the Terminal and use the following commands at the command line.

2. `module avail matlab` to list all the available matlab versions.

3. `module load matlab/R2018a` to load matlab. This command should return the confirmation "*module loaded*".

4. `matlab` to launch the MATLAB app.

Installing MATLAB Packages such as YALMIP

MATLAB script packages, such as YALMIP, can be installed directly by the user on their Oscar account. These instructions assume you are using Oscar via the VNC client.

1. Open the Terminal on your VNC session.

2. Navigate to your home folder by typing `cd ~`

3. `mkdir -p MATLAB`

4. `wget -O yalmip.zip https://github.com/yalmip/yalmip/archive/master.zip`

5. `unzip yalmip.zip`

6. In MATLAB, add the YALMIP-master directory to your path.

    1. In the MATLAB file browser, navigate to the MATLAB folder you created in your home folder. `cd ~/MATLAB`
    2. Right click on the YALMIP-master folder.

3. Select Add to Path > Selected Folders and Subfolders. This adds the YALMIP folders to your path.

7. To save your MATLAB path, use the savepath command in the MATLAB command prompt. `savepath ~/MATLAB/pathdef.m`

YALMIP also requires a solver like SDPT3. The steps below add SDPT3 to MATLAB.

1. Open the Terminal.

2. `cd ~/MATLAB`

3. `wget -O sdpt3.zip https://github.com/sqlp/sdpt3/archive/master.zip`

4. `unzip sdpt3.zip`

5. In MATLAB, add the sdpt3 directory to your path.

1. In the MATLAB file browser, navigate to the MATLAB folder you created in your home folder. `cd ~/MATLAB`
2. Right click on the sdpt3-master folder.
3. Select Add to Path > Selected Folders and Subfolders. This adds the SDPT3 folders to your path.

6. To update/save your MATLAB path, use the savepath command in the MATLAB command prompt. `savepath ~/MATLAB/pathdef.m`

Oscar: Mathematica

Loading and Launching Mathematica

1. Open the Terminal and use the following commands at the command line.

2. `module avail mathematica` to list all the available mathematica versions.

3. `module load mathematica/11.0` to load mathematica. This command should return the confirmation "*module loaded*".

4. `mathematica` to launch the Mathematica app.