

# Hummingbird Computational Cluster

Overview and Introduction

Hummingbird Support

Team [hummingbird@ucsc.edu](mailto:hummingbird@ucsc.edu)



# Hummingbird Etiquette

**The DOs and DON'Ts of using the Hummingbird Cluster**

# Software - the module system

```
[rkrparson@hb ~]$ module av
----- /opt/ohpc/pub/moduledeps/gnu-openmpi -----
adios/1.12.0  fftw/3.3.7  imb/2018.1  netcdf-cxx/4.3.0  netcdf/4.5.0  phdf5/1.10.1  scalasca/2.3.1  scorep/3.1  superlu_dist/4.2  trilinos/12.12.1
boost/1.66.0  hypre/2.13.0  mumps/5.1.2  netcdf-fortran/4.4.4  petsc/3.8.3  scalapack/2.0.2  scipy/0.19.1  sionlib/1.7.1  tau/2.27
----- /opt/ohpc/pub/moduledeps/gnu -----
gsl/2.4 (D)  hdf5/1.10.1 (D)  metis/5.1.0  mpich/3.2.1  numpy/1.12.1  openblas/0.2.20  openmpi/1.10.7 (L)  pdtoolkit/3.25  superlu/5.2.1
----- /hbopt/software/moduledeps/languages -----
julia/julia-1.1
----- /hbopt/software/moduledeps/gpu-toolkits -----
cuda/cuda-9.0  cuda/cuda-9.1  cuda/cuda-10.1 (D)  motioncor2/mcor2-1.2.0
----- /hbopt/software/moduledeps/python -----
miniconda2Bio  miniconda3  python-2.7.15  python-3.6.2 (L)  python-3.6.5  python-3.6.5GPU  python-3.6.5dev  python-3.7.6GPU
----- /hbopt/software/moduledeps/gnu-software -----
OpenFOAM/OFM-5.x  bowtie/bowtie1-2.1.1  bowtie/bowtie2-2.3.2  (D)  gsl/gsl-2.4  parallel/para20200122
R/R-3.5.0  bwakit/bwa-0.7.15  hdf5/hdf5-1.10.2  pari-gp/parigp-2.11.4
R/R-3.6.1Bio  cadence/cadence  hisat/hisat2-2.1.0  plink/gnu-1.09
R/R-3.6.1Mpi  (D)  cellranger/cr-2.2  hmmer/hmmer-3.2.1  pnetcdf/pnetcdf-1.10.0
R/R-3.6.1  cfitsio/3.48  imageMagick/imagem-7.0.8  proj4/proj4-6.1.1
SMRTLink/smrt-7.0.1  (D)  jags/jags-4.3.0  qe/qe-6.1
SMRTLink/smrt-8.0.0  clustal.OBSneedsrecompile/clustal-omega-1.2.4  java/java-8  samtools/samtools-1.5
XBeach/23.5527  cp2k/cp2k-4.1  lapack/lapack-3.8.0  samtools/samtools-1.10 (D)
angsd/gnu-930  fastqc/fastqc-0.11.7  lftp.OBSneedsrecompile/lftp-4.8.3  singularity/singularity-2.5.2
apbs-pdb2pqr/apbs3.0pd2  fffpeg/ffpeg-4.0  matlab/2017b  spades/SPAdes-3.11.1
armadillo/armadillo-9.300.2  flappie/flappie-1.0.0  matlab/2018b  (D)  sratoolkit/sratoolkit-2.8.2-1
bbtools/bbmap-38.79  gatk/gatk-4.0.11.0  mercurial/mercurial-3.7.3-1  stacks2/stacks-2.2
bcftools/bcftools-1.5  gatk/gatk-4.1.8.1  migrate/migrate-3.6.11  star/star2-2.5.3a
bcftools/bcftools-1.10.2  (D)  gaussian/gaussian-09.D1.01  minimap2/m2-2.17  stata/stata-15.0.0
bclfastq2/bcl-20.0  gdal/gdal-2.4.2  mkl2019/mkl-2019  structure/structure-2.3.4
beagle/beagle-2.1  gdal/gdal-2.4.3  (D)  multinet/mnest-3.10  swig/swig-4.0.2
beast/beast-0  gdal/gdal-3.0.2  namd/namd-2.12  tetoolkit/tetoolkit-2.0.3
beast/beast-2  (D)  gromacs/gromacs-5.1.4  gromacs/gromacs-2016.3  trimomatic/trimomatic-0.38
bedtools/bedtools-2.26.0  gromacs/gromacs-2016.3  (D)  opencv/opencv-3.4.1  trinity/trinity-2.4.0
blast/blast-2.7.1  gromacs/gromacs-2019.2GPU  orca/orca-2.4.1  vg/vg-1.12.1
----- /hbopt/software/modulefiles -----
hb-gnu (L)  hb-gnu7  hb-pgi
```

# Using the cluster - Scheduling

# Template SLURM scripts

Premade templates for your convenience. Just make a copy to your working directory and edit to meet your needs

```
[rkparson@hb scripts]$ pwd
/hb/software/scripts
[rkparson@hb scripts]$ ls
CUDA                               gmx.README                       openmpi-job.slurm                structure.slurm
g09.slurm                          gpu-example.slurm                R-3.3.2.slurm                   trinity.slurm
gmx-514.1node.instruction.slurm    java.slurm                       samtools.slurm                   single-cpu-job.slurm
gmx-514.1node.intel.slurm          matlab.slurm                     singularity.slurm
```

If you have a template that is useful to more than just yourself, let us know and we can include it here.

# Anatomy of a basic SLURM Script

Name of Partition to use



Name to give your run



Name for output/error logs  
(use for troubleshooting)



Number of nodes to request



Number of tasks your  
program will require



Amount of RAM requested  
for your program



Time limit for the run (!!!)



Get status emails about your job



```
#!/bin/bash
#SBATCH -p 128x24
#SBATCH -j example_job
#SBATCH -o job.%j.out
#SBATCH -e job.%j.err
#SBATCH -N 1
#SBATCH -n 24
#SBATCH --mem=600mb
#SBATCH --time=00:05:00
#SBATCH --mail-type=ALL
#SBATCH --mail-user=rkparson@ucsc.edu

module load python-3.6.5

export EXMP_VAR="foo"

python my_python_script.py
```

# Anatomy of a basic SLURM Script

Any modules your program  
requires in order to run

Any system variables your  
program might require

The program to run

```
#!/bin/bash
#SBATCH -p 128x24
#SBATCH -j example_job
#SBATCH -o job.%j.out
#SBATCH -e job.%j.err
#SBATCH -N 1
#SBATCH -n 24
#SBATCH --mem=600mb
#SBATCH --time=00:05:00
#SBATCH --mail-type=ALL
#SBATCH --mail-user=rkparson@ucsc.edu

module load python-3.6.5

export EXMP_VAR="foo"

python my_python_script.py
```

# Submitting your job

```
sbatch your_job_script.slurm
```

# Verifying your job's settings

```
scontrol show job <jobid>
```

```
[rpkarson@hb project]$ scontrol show job 88174
JobId=88174 JobName=6_first_occurrence
  UserId=blufox(12431) GroupId=ucsc_p_all_usr(100000) MCS_Label=N/A
  Priority=4294886988 Nice=0 Account=(null) QOS=(null)
  JobState=RUNNING Reason=None Dependency=(null)
  Requeue=1 Restarts=0 BatchFlag=1 Reboot=0 ExitCode=0:0
  RunTime=17-18:40:21 TimeLimit=62-00:00:00 TimeMin=N/A
  SubmitTime=2020-11-15T17:02:41 EligibleTime=2020-11-15T17:02:41
  AccrueTime=2020-11-15T17:02:41
  StartTime=2020-11-15T17:02:41 EndTime=2021-01-16T17:02:41 Deadline=N/A
  PreemptTime=None SuspendTime=None SecsPreSuspend=0
  LastSchedEval=2020-11-15T17:02:41
  Partition=128x24 AllocNode:Sid=hb:82983
  ReqNodeList=(null) ExcNodeList=(null)
  NodeList=hbcomp-024
  BatchHost=hbcomp-024
  NumNodes=1 NumCPUs=1 NumTasks=1 CPUs/Task=1 ReqB:S:C:T=0:0:*:*
  TRES=cpu=1,mem=125G,node=1,billing=1
  Socks/Node=* NtasksPerN:B:S:C=0:0:*:* CoreSpec=*
  MinCPUsNode=1 MinMemoryNode=125G MinTmpDiskNode=0
  Features=(null) DelayBoot=00:00:00
```

That's a lot of details!



# A view into what's running - `queue`

```
[rkparson@hb ~]$ queue -l
Wed Dec  2 13:15:07 2020
```

JOBID	PARTITION	NAME	USER	STATE	TIME	TIME_LIMI	NODES	NODELIST(REASON)
88174	128x24	6_first_	blufox	RUNNING	16-20:12:26	62-00:00:00	1	hbcomp-024
88297	128x24	mapping_	jharenca	RUNNING	12-02:44:22	UNLIMITED	3	hbcomp-[012-014]
88370	128x24	7_first_	blufox	RUNNING	7-21:54:56	62-00:00:00	1	hbcomp-020
88493	128x24	8_first_	blufox	RUNNING	1-00:48:10	62-00:00:00	1	hbcomp-025
88498	128x24	PMZ7bi2	vroger	RUNNING	21:38:24	20-20:00:00	1	hbcomp-006
88499	128x24	P7iunfre	vroger	RUNNING	21:35:09	20-20:00:00	1	hbcomp-007
88501	128x24	P7cunfre	vroger	RUNNING	21:28:56	20-20:00:00	1	hbcomp-009
88507	128x24	75898_3p	amstahl	RUNNING	20:07:49	INVALID	3	hbcomp-[010-011,018]
88511	128x24	extsemim	gross	RUNNING	5:01:56	20-10:00:00	3	hbcomp-[015-017]

Much easier to parse!

# Hummingbird is NOT a SUPERCOMPUTER!

- Hummingbird does NOT use a high speed backplane, thus it is not suitable for highly parallelized jobs requiring many cores/nodes acting synchronously (FEM, FDTD, etc...)
- Humming IS good for serialized style processing (Monte Carlo, batch processing, etc...)
- Users are limited to using three nodes for a single job (a maximum of 72 cores)
- Most nodes only have 128 GB of RAM
- Hummingbird works on First-In, First-Out with Backfilling
- We don't *enforce* a MaxTime, so you *should*

# A quick way to check the cluster - `sinfo`

Some queues are restricted and are not for general use

```
[rkparson@hb ~]$ sinfo
PARTITION  AVAIL  TIMELIMIT  NODES  STATE NODELIST
Instruction*  up    4:00:00    3  idle hbcomp-[000,004-005]
Course       up    4:00:00    2  idle hbcomp-[001-002]
256x44      up    infinite    1  idle hbcomp-003
128x24      up    infinite    1  down* hbcomp-008
128x24      up    infinite    9  mix  hbcomp-[010-014,018,020,024-025]
128x24      up    infinite    6  alloc hbcomp-[006-007,009,015-017]
128x24      up    infinite    3  idle hbcomp-[019,023,026]
96x24gpu4   up    infinite    1  idle hbcgpu-021
1024x28     up    infinite    1  idle hbcomp-028
```

We have four NVIDIA GPUs, and are setup for CUDA and TensorFlow!

# Knowing your Hummingbird variants

## hb.ucsc.edu

- Cluster login node
- Used for:
  - Compiling your code
  - Checking the status on your submitted jobs



"Violet-tailed Sylph resting on a branch in northwestern Ecuador"  
[https://en.wikipedia.org/wiki/File:Violet-tailed\\_Sylph\\_2\\_ICB.jpg](https://en.wikipedia.org/wiki/File:Violet-tailed_Sylph_2_ICB.jpg)

## hbfeeder.ucsc.edu

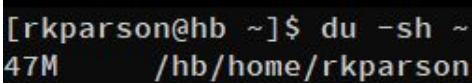
- Cluster storage node
- Used for:
  - Accessing your data when you don't need the cluster
  - Transferring your data to or from the cluster



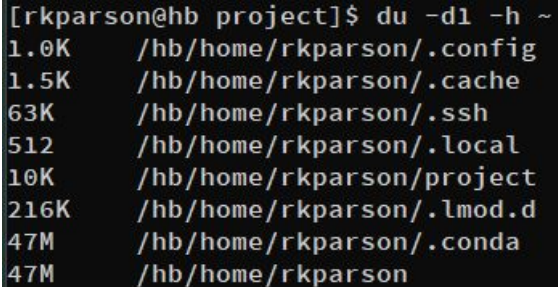
Male Anna's Hummingbird  
<https://en.wikipedia.org/wiki/File:AnnashummingbirdPaloAltoNorvig.jpg>

# How much space are you using?

- Everyone is limited to 1TB of storage in their home folders.
- If you exceed this, your jobs won't run correctly.
- How to check:

- `du -sh ~` 

total used space summary

- `du -d1 -h ~` 

used space per-folder (one-layer deep)

# Key points to take away

- ✓ DO Check the Message of the Day for useful updates
- ✓ DO Check in the modules before you ask for software
- ✓ DO Use the scheduler when submitting jobs
- ✗ DON'T Use the cluster for heavily parallel style workflows
- ✓ DO Set time limits on your jobs
- ✗ DON'T Overprovision when submitting a job
- ✓ DO regularly check your disk space usage
- ✗ DON'T Leave data in Scratch long-term
- ✓ DO Reach out for help!

# Reaching out for help!

Open a ticket!

<https://ucsc.service-now.com/ess/>

Come to our weekly open-hours sessions!

Find the link in our Message of the Day on the Hummingbird login node:

```
Do you have questions? Need help? Want to speak to an expert?  
Join the Hummingbird Zoom-in Help Clinic Thursdays at 1pm  
https://ucsc.zoom.us/j/98567158305?pwd=emZhYzB1N0tqeS9UbVpYd1lpchAYdz09 (UCSC log-in required)  
[rkparson@hb ~]$
```

Check out the website for more information!

<https://www.hb.ucsc.edu/>

Please take a moment and fill out our  
post-session survey

[https://docs.google.com/forms/d/e/1FAIpQLSeaLMqv3yPcgxy3-sfwZsnCLu5PHvyXg4i60rYnSRxJVVEZog/viewform?usp=sf\\_link](https://docs.google.com/forms/d/e/1FAIpQLSeaLMqv3yPcgxy3-sfwZsnCLu5PHvyXg4i60rYnSRxJVVEZog/viewform?usp=sf_link)