



Chemistry Packages at CHPC

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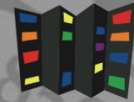
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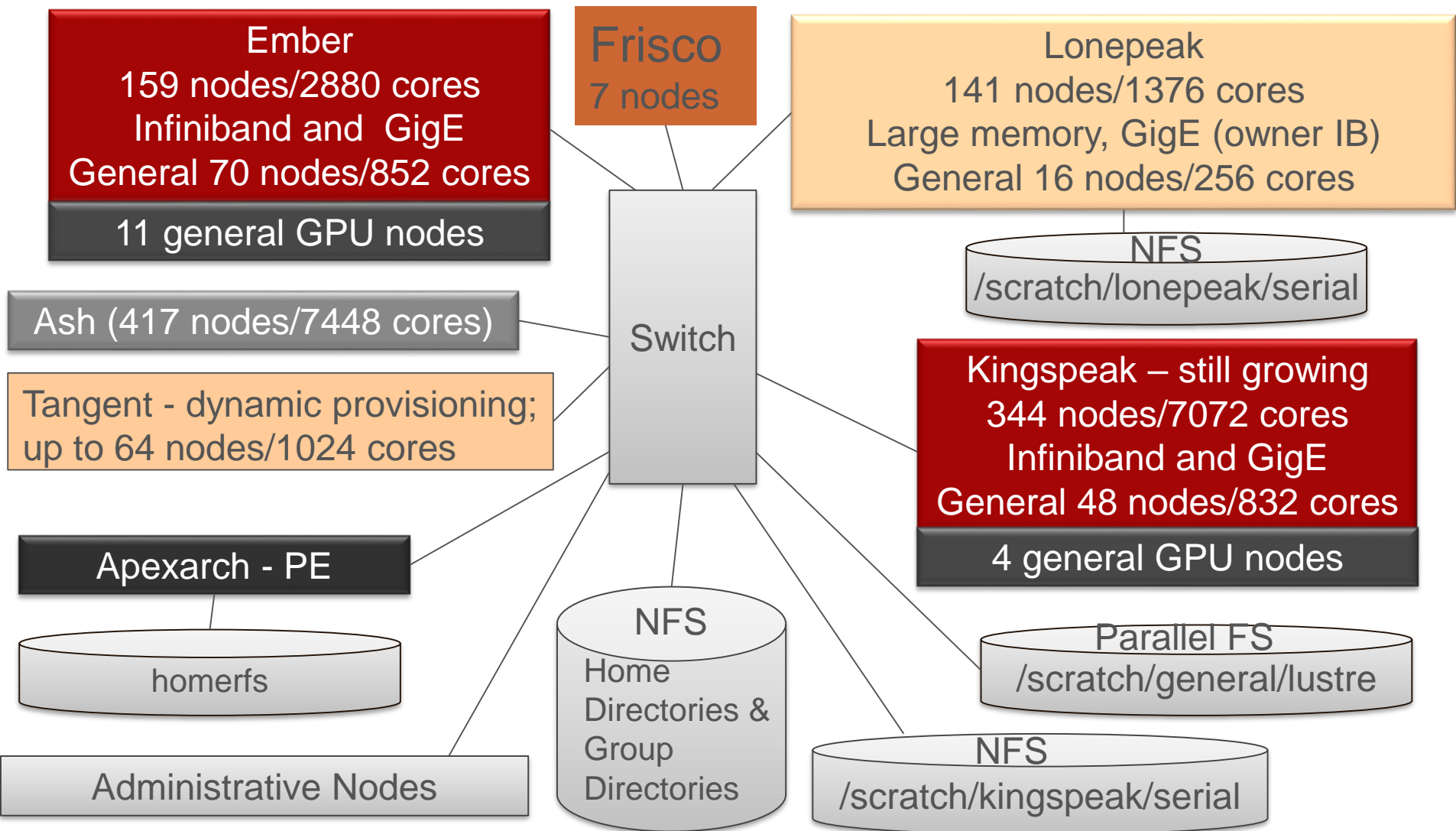
Purpose of Presentation

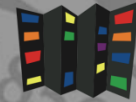
- Identify the computational chemistry software and related tools currently available at CHPC
- Present brief overview of these packages
- Present how to access packages on CHPC
- Information on usage of Gaussian09



Survey about Presentation

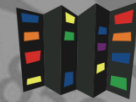
- <https://www.surveymonkey.com/r/8CKKY3C>





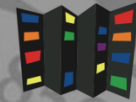
Brief Overview CHPC Resources

- *Computational Clusters*
 - kingspeak, ember – general allocation and owner-guest on owner nodes
 - lonepeak – both general and owner nodes, runs without allocation
 - tangent – only general nodes, variable number of nodes, runs without allocation
 - ash – can run as smithp-guest
- *Home directory* – NFS mounted on all clusters
 - /uufs/chpc.utah.edu/common/home/<uNID>
 - Default is 50GB with no backup unless your group purchases home directory space
- *Scratch systems*
 - /scratch/general/lustre – all clusters – 700 TB
 - /scratch/kingspeak/serial – all clusters but lonepeak – 175 TB
 - /scratch/lonepeak/serial – lonepeak only – 33 TB
 - /scratch/local on compute nodes, varying sizes
- *Applications*
 - /uufs/chpc.utah.edu/sys/pkg & /uufs/chpc.utah.edu/sys/installdir
 - /uufs/**\$UUFSCELL**/sys/pkg where **\$UUFSCELL** = kingspeak.peaks, ember.arches, ash.peaks, for cluster specific builds (mostly due to infinband interconnect)



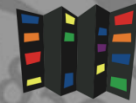
Getting Started at CHPC

- Account application – *an online process*
 - https://www.chpc.utah.edu/apps/profile/account_request.php
- Username is your unid with password administrated by campus
- Interactive nodes
 - two CHPC owned nodes per cluster (**cluster**.chpc.utah.edu) with round-robin access to divide load (on ash, use ash-guest.chpc.utah.edu)
- CHPC login scripts – in account when created –
- Now using modules
 - <https://www.chpc.utah.edu/documentation/software/modules.php>
- Getting started guide
 - www.chpc.utah.edu/docs/manuals/getting_started
- Problem reporting system
 - <http://jira.chpc.utah.edu> or email to issues@chpc.utah.edu



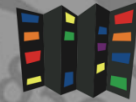
Sources of Useful Information

- Getting Started Guide
 - <https://www.chpc.utah.edu/documentation/gettingstarted.php>
- CHPC policies
 - <https://www.chpc.utah.edu/documentation/policies/index.php>
- Cluster Usage Guides
 - <https://www.chpc.utah.edu/documentation/guides/index.php>
- Application Documentation
 - <https://www.chpc.utah.edu/documentation/software/index.php>
- Programming Guide
 - <https://www.chpc.utah.edu/documentation/ProgrammingGuide.php>



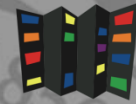
Interactive Node Usage

- Interactive nodes for prepping/testing of input files, analyzing results, compilations, debugging, data transfer, etc
 - no running of jobs
 - 15 min **MAX** cpu
 - no jobs of **ANY** time length that negatively impact ability of other users to get work done (e.g., heavy cpu, memory usage and/or i/o)
- <https://www.chpc.utah.edu/documentation/policies/2.1GeneralHPCClusterPolicies.php#Pol2.1.1>



Batch System -- SLURM

- Used to access compute nodes
 - <https://www.chpc.utah.edu/documentation/software/slurm.php>
 - example scripts, basic commands, information on SLURM environmental variables and directives
- Walltime limits
 - 72 hours (long qos by request) on all clusters except ash which is 24 hours



Access to Interactive Nodes

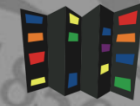
- FastX is the best option
- Server installed on all cluster interactive nodes as well as the seven frisco nodes
- Client can be downloaded and used on any university owned OR personal machine
- Clients exist for windows, mac and linux
- See instructions on how to download at <https://www.chpc.utah.edu/documentation/software/fastx2.php>



Computational Chemistry Packages

- Molecular Mechanics/Dynamics
- Semi Empirical
- Electronic Structure Calculations
 - HF, DFT, MPn, CI, CC, multi-reference methods, etc
- Solid state/Materials Modeling packages
 - Plane Wave Pseudopotential based packages

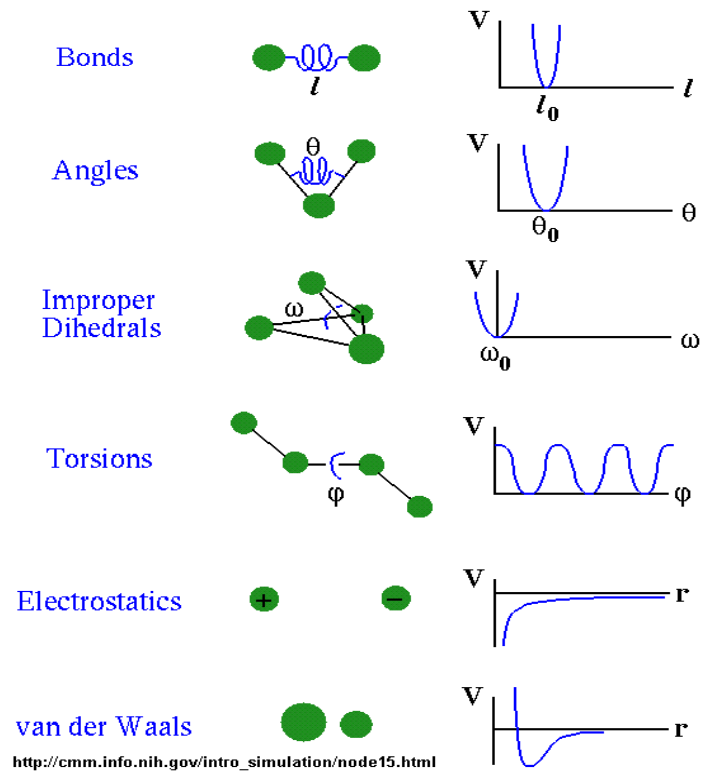
Calculation type & level of theory used depends on a number of factors – the information you are after, system being studied, size of system, computational resources. Often consider accuracy versus computational cost



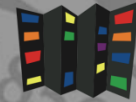
Molecular Mechanics/Dynamics

- Amber
 - <http://ambermd.org>
- Gromacs
 - <http://www.gromacs.org/>
- NAMD
 - <http://www.ks.uiuc.edu/Research/namd/>
- LAMMPS
 - <http://lammps.sandia.gov/>
- Charmm
 - <http://www.charmm.org/>
 - licensed by group

Empirical Potential Energy Function

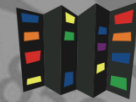


Note – Gaussian and NWChem also have some MM capabilities



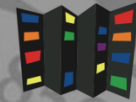
MM/MD packages

- Latest Versions:
 - Amber15 (Amber14 with AmberTools15)
 - *module spider amber/15*
 - Gromacs 5.0.4 (single and double precision builds)
 - *module spider gromacs/5.1.1*
 - Lammps – 10Aug15 version
 - *module spider lammps/7Dec15*
 - HOOMD
 - *module spider hoomd/2.0.0.s*
 - *module spider hoomd/2.0.0.d*
 - NAMD
 - *module spider namd/2.10.ibverbs*
- Basic information on getting started:
 - <https://www.chpc.utah.edu/documentation/software/amber.php>
 - <https://www.chpc.utah.edu/documentation/software/gromacs.php>
 - <https://www.chpc.utah.edu/documentation/software/lammps.php>



Semi-Empirical Packages

- These are based on the Hartree-Fock formalism of electronic structure methods, but make many approximations and obtain some parameters from empirical data
- MOPAC2012 is the only stand alone semi-empirical only package installed at CHPC
- To use:
 - *module load mopac*
 - *mopac input.mop*
- Note – mopac only runs on a single core
- Sample scripts
 - `/uufs/chpc.utah.edu/sys/pkg/mopac/etc/test.slurm`
 - `/uufs/chpc.utah.edu/sys/pkg/mopac/etc/test.slurm` and `my.conf`
- Gaussian, GAMESS also has some semi-empirical capabilities

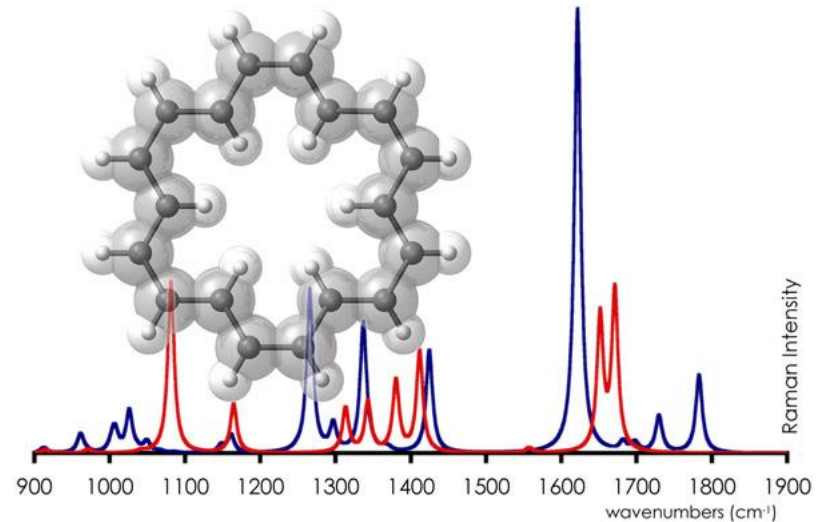


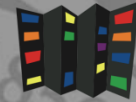
Quantum (Mainly) Packages

- Gaussian09
- Orca
- NWChem (6.3)

There are other packages not currently installed available free of charge, e.g.,

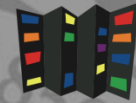
- GAMESS - <http://www.msg.ameslab.gov/gamess/> (general purpose, properties)
- Psi4 – <http://www.psicode.org/> (general purpose, properties)
- CFOUR – <http://www.cfour.de/> (coupled cluster)
- SIESTA – <http://departments.icmab.es/leem/siesta/> (DFT, linear scaling)





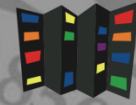
Gaussian09

- Commercial electronic structure package
 - <http://www.gaussian.com> for information and User's Guide
- Version D01 of G09 installed
 - /uufs/chpc.utah.edu/sys/pkg/gaussian09/EM64T (on all but lonepeak)
 - /uufs/chpc.utah.edu/sys/pkg/gaussian09/EM64TL (for lonepeak)
 - Also have AMD64 and legacy AMD64 builds
- For information on accessing the CHPC installation
 - <https://www.chpc.utah.edu/documentation/software/gaussian09.php>



NWChem

- Package developed at PNNL to work on massively parallel systems
- <http://www.nwchem-sw.org>
- Goal: Computational chemistry solutions that are scalable with respect to both chemical system size and MPP hardware size
- Has quantum mechanics, molecular mechanics/dynamics, and quantum molecular dynamics, plane waves for periodic systems
- Version 6.3 (**NOT** with Python support) – working on 6.6 install
 - `/uufs/chpc.utah.edu/sys/pkg/nwchem/nwchem-6.3/bin/LINUX64`
 - `/uufs/ember.arches/sys/pkg/nwchem/nwchem-6.3/bin/LINUX64`
 - `/uufs/kingspeak.peaks/sys/pkg/nwchem/nwchem-6.3/bin/LINUX64`
 - `/uufs/chpc.utah.edu/sys/pkg/nwchem/nwchem-6.3/bin/LINUX64`
- To run:
 - Load appropriate modules – do “*module spider nwchem*” for information
- More information and example batch script at
 - <https://www.chpc.utah.edu/documentation/software/nwchem.php>



Solid State/Materials Packages

Plane wave codes for the study of systems under periodic boundary conditions (PBC)

- NWChem has some functionality
- Quantum Espresso - <http://www.quantum-espresso.org/>
 - Understands crystal space groups
 - Has GIPAW module to do NMR calculations
 - J-ICE and XCrysDen to view
- Wien2K - <http://www.wien2k.at/>
 - Licensed per research group
- VASP – <http://cms.mpi.univie.ac.at/vasp/>
 - Ab initio QM/MD
 - Licensed per research group



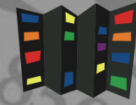
Support Packages

- Molecular Viewers
 - Gaussview
 - Molden
 - VMD
 - Chimera
- Babel (Openbabel)
- Docking
 - Dock
 - AutoDock (and Autodock Vina)
- Cambridge Structural Database
- ECCE (mostly for NWChem)
 - Special case - Talk to me first if you want to use



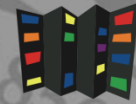
GaussView

- Molecular builder and viewer for Gaussian input/output files
- CHPC provides campus license for linux version
- Chemistry Department has campus license for GaussView for windows; can buy into license
- Access with
 - *module load gaussian09*
 - *gv &*
- **DO NOT** submit jobs from within GaussView – instead create and save input file and use batch system
- Examples of how to use to show MO's, electrostatic potentials, NMR tensors, vibrations given on Gaussian's web page
<http://faculty.ycp.edu/~jforesma/educ/>



Molden

- Another program for viewing molecular/electronic structures; version 4.7
- Works with Gamess, Gaussian, Molpro
- Supports plots of electronic density, MOs, etc
- More information at <http://www.cmbi.ru.nl/molden/molden.html>
- How to use at CHPC:
 - *module load molden*
 - *molden &*



Chimera

- For information on package and usage
<https://www.cgl.ucsf.edu/chimera/>
- Version 1.10.1 installed
- /uufs/chpc.utah.edu/sys/installdir/chimera/1.10.1/bin/chimera
- Access by
 - *module load chimera*
 - *chimera &*

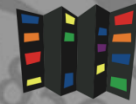
VMD

- Visualization, mainly for MM/MD
- latest version (1.9.2) installed
- Reads a number of different file formats
- Information at <http://www.ks.uiuc.edu/Research/vmd>
- Can install on own desktop (windows/mac/linux versions available)
- To use:
 - *module load vmd*
 - *vmd &*
 - *vglrun -c proxy vmd &* (for nodes with vgl capability (frisco6/7))
- *Can use for 3D viewing on CHPC's vis wall*



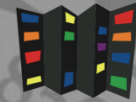
OpenBabel

- Tool to interconvert structure files between a number of formats used in molecular modeling
- See openbabel.org for more information
- To run:
 - *module load openbabel*
 - *babel -i < input-type > < infile > -o < output-type > < outfile >*
 - *babel -H* to see format for usage, options, and input/output file-types



Dock/AutoDock

- Programs to look at binding of a small molecule within the active site of a receptor, usually a macromolecule
- Dock
 - version 6.6 installed
 - get info at: <http://dock.compbio.ucsf.edu>
 - ***module load gcc/4.7.2 mpich2/3.0.4.g dock***
 - ***dock6.mpi*** to start (needs arguments)
- Autodock
 - version 4.2.5.1
 - info available at <http://autodock.scripps.edu>
 - ***module load autodock***
 - ***autodock4*** (with proper arguments) or ***autogrid4***
 - autodocktools, a GUI interface, installed – start with ***adt &***
 - Autodock Vina – multicore performance and enhanced accuracy – start with ***vina*** (needs arguments)



Cambridge Structural Database

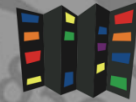
- Moved from library to CHPC summer 2006 – additions to the database are made every 3-4 months; package updated annually
- www.ccdc.cam.ac.uk for information
- Need CHPC account to use
- From PC need Xterm/Xwindowing software (Putty/XMing work well) to start session on any of the interactive nodes
 - ***module load csd***
 - ***cq &*** <- to start conquest (search engine)
 - ***mercury &*** <- to start crystal structure viewer
 - The first time you use it on a given computer you will be asked to confirm licensing
 - need to provide site/license codes (840/6CD8FF)



Integrated Molecular Platform

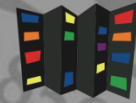
Schrodinger Suite

- Commercial package geared for chemical modeling and simulation in the pharmaceutical field, specifically drug discovery
- <http://www.schrodinger.com/>
- Interface – Maestro (free for academia)
- Calculation code includes Jaguar (Quantum), Macromodel (MM), Qsite (QM/MM)
- Interfaces with Desmond for MD (installed)
- Tools for structure based drug design
 - Docking, ligand design, binding affinities, screening libraries
- Year to Year licensing
 - Token based, so limited in number of concurrent uses
 - Currently owned by single group



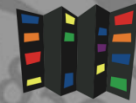
Finally.....

- Let us know if there is some other package that does something that our current packages do not; we can look into the possibility of getting it.
 - Factors: cost, hardware/OS requirements, licensing issues, usage needs
- Any questions – contact me
 - anita.orendt@utah.edu
 - Phone: 801-231-2762
 - Office: 422 INSCC



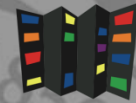
Using Gaussian09

- Gaussian users must be in Gaussian users group
 - *groups* will show you the groups your are in
 - If **g05** is listed, then you are in gaussian users group
- Program website www.gaussian.com
- CHPC Documentation at <https://www.chpc.utah.edu/documentation/software/gaussian09.php>
- Sample script `g09-module.slurm` in `/uufs/chpc.utah.edu/sys/pkg/gaussian09/etc/`
- New – now have `nbo6` installed to use with G09
 - **Pop=NPA6**, **Pop=NBO6**, **Pop=NBO6Read** and **Pop=NBO6Delete** keywords
- Use Gaussview to build molecular system and to create input files
 - *module load gaussian09*
 - *gv &*



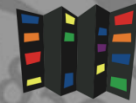
G09 Script

- Two sections for changes:
#SBATCH --partition=lonepeak
#SBATCH --account=youraccount
#SBATCH --time=72:00:00
##SBATCH --constraint=c20
#SBATCH --nodes=1
#SBATCH -o slurm-%j.out-%N
- And:
setenv WORKDIR **\$HOME/g09/project**
setenv FILENAME **input**
setenv SCRFLAG **LOCAL**
setenv NODES **1**



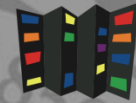
Scratch Choices

- **LOCAL** (/scratch/local)
 - Hard drive local to compute node
 - 400GB on ember; 337 -800 GB on KP
 - Fastest option - recommended **IF** this is enough space for your job
 - Do not have access to scratch files during run but log/chk files written to \$WORKDIR/\$SLURM_JOB_ID/\$UUFSCCELL
 - Automatically scrubbed at end of job
 - Will not have access to rwf, needed for restarts of some jobs
- **KPSERIAL** (/scratch/kingspeak/serial)
 - NFS mounted on all clusters (interactive and compute) EXCEPT lonepeak
 - 175 TB
- **LPSERIAL** (/scratch/lonepeak/serial)
 - Only on lonepeak
 - 33 TB
- **GENERAL** (/scratch/general/lustre)
 - NFS mounted on all clusters (interactive and compute)
 - 700 TB



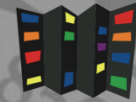
Input File Structure

- *Filename.com*
- Free format, case insensitive
- Spaces, commas, tabs, forward slash as delimiters between keywords
- ! Comment line
- Divided into sections (in order)
 - Link 0 commands (%)
 - Route section – what you want calculation to do
 - Title
 - Molecular specification
 - Optional additional sections



Number of Processors

- %nprocs – number of processors on one node
 - ember – 12
 - kingspeak – 16, 20 or 24, 28
 - lonepeak 8, 12 or 20
 - ash – 12 or 20
 - tangent – 16



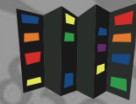
Memory Specification

- Memory usage: default is 6MW or 48MB – all nodes have much more than this!
- If you need more use %mem directive
 - Units : words (default), KB, KW, MB, MW, GB, GW
 - Number must be an integer
- Methods to estimate memory needs for select applications given in Chapter 4 of User's Guide
- %mem value must be less than memory of node
 - Ember general nodes have 24GB; a few owners with 498, 192 or 256GB
 - Kingspeak – most have 64GB; there are some owner nodes with 32 or 128GB, a few with 1TB; 4 general with 384GB
 - Lonepeak – 12 core have 96GB; 20 core have 256GB, owner mixed
 - Ash – 12 core have 24GB; 20 core have 64GB; 24 core have 256GB



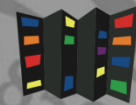
Input - Route Specification

- Keyword line(s) – specify calculation type and other job options
- Start with # symbol
 - for control of the print level in the output file use #n, #t, #p for normal, terse, or more complete output
 - #p suggested as it monitors job progress; useful for troubleshooting problems
- Can be multiple lines
- Terminate with a blank line
- Format
 - keyword=option
 - keyword(option)
 - keyword(option1,option2,...)
 - keyword=(option1,option2,...)
- User's Guide provides list of keywords, options, and basis set notation
http://www.gaussian.com/g_tech/g_ur/l_keywords09.htm



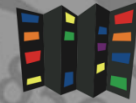
Input - Title Specification

- Brief description of calculation - for user's benefit
- Terminate with a blank line



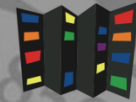
Input – Molecular Specification

- 1st line charge, multiplicity
- Element labels and location
 - Cartesian
 - label x y z
 - Z-matrix
 - label atom1 bondlength atom2 angle atom3 dihedral
- If parameters used instead of numerical values then variables section follows
- Default units are angstroms and degrees
- Again end in blank line



Parallel Nature of Gaussian

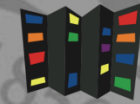
- All runs make use of all core per node with nprocs
- Only some portions of Gaussian run parallel on multiple nodes (includes most of the compute intensive parts involved with single point energies/optimizations for HF/DFT)
- If time consuming links are not – job WILL NOT benefit from running on more than one node
- Not all job types are restartable, but more are restartable in G09 than were G03 (e.g., frequencies and NMR) – see **restart** keyword
 - Requires rwf from previous run
 - Still restart optimizations and single point energies the old way
- CHPC does allow for jobs over standard walltime limit if needed – but first explore using more nodes or restart options
- CHPC also has a few nodes outside of these clusters which have more memory and no wall time limits – talk to me if you think you need to use



Timings of G09 scratch system

Scratch setting	LOCAL	KPSERIAL	
time	1.75 hrs	1.75 hrs	

***depends strongly on amount of I/O and on other jobs usage on shared scratch systems



Scaling G09

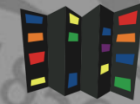
B3PW91;650 bf; 8 opt steps; time in hours

# ember nodes	wall time	# KP 16 core nodes	wall time
1	3.25	1	1.5
2	1.5	2	<1



DFT Frequency of same case

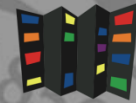
# ember nodes	wall time	# KP 16 core nodes	walltime
1	3.25	1	1.25
2	1.75	2	0.75



Scaling G09 MP2 Opt (Freq)

8 opt steps 338bf; time in hours (w/ freq)

# ember nodes	wall time	# KP 16 core nodes	wall time
1	1 (7.5)	1	30min (3.75)
2	<1 (7)	2	24min (3.75)



RWF Sizes – Choice of Scratch

- For a DFT optimization with 462 basis functions
 - 150mb RWF
- For a DFT freq of above structure
 - 1.1gb RWF
- For a MP2 optimization with 462 bf
 - 55gb RWF AND 55gb SCR file
- For a MP2 frequency of above structure
 - 247gb RWF