General Interest Seminar

Gaussian 16 and NBO7 on Graham and Cedar

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Gaussian on CC Clusters

- A licensed software available on Graham and Cedar
- Software are installed as Module packages
- Basic module commands

```
module avail
                                  # to list all available module software
module spider gaussian
                                  # to see what gaussian versions are available
 [jemmyhu@gra-login1 ~]$ module spider gaussian
  gaussian:
   Versions:
     gaussian/g03.d01
     gaussian/g09.e01
     gaussian/g16.b01
     gaussian/g16.c01
```

[jemmyhu@gra-login1~]\$ module load gaussian/g16.c01

Slurm submit/Run script:

- account type (default or RAC account)
- compute resource (cpus, memory, runtime)
- job type (mpi, openmp, serial)
- software (module load, run command)

Several ways to run Gaussian on Graham/Cedar

- by default, Gaussian runs as a serial job on one cpu, good for small molecules
- shared-memory parallel (use multi-cpus/cores on one socket or node,

1 task with multi-threads, cpu ranges from 2 to cpus per node)

```
#!/bin/bash
#SBATCH --account=def-jemmyhu
                                  # PI's group acount
#SBATCH --mem=10G
                                 # memory amount, roughly 2 times %mem
#SBATCH --time=00-03:00
                                  # time (DD-HH:MM)
#SBATCH --cpus-per-task=16
                                 # No. of cpus as defined by %nprocs
#SBATCH --output=g16 test.log
                                  # output file
module load gaussian/g16.c01
                                   # G16 command
G16 g16 test.com
or
g16 < g16 test.com >& g16 test.log # g16 command
```

[~\$] sbatch g16_test.sh

Gaussian Basics

```
Latest version: g16.c01
Resource request (mem, cpu, time)
Gaussian files
file location, .chk
Input sample
Restart
Disk: scratch vs local/tmp
Utilities
```

https://docs.computecanada.ca/wiki/Gaussian

Gaussian Files

```
input file: .com, .gjf
   run script: .sh
   output: .log
   runtime files (unnamed): .rwf, .inp, .d2e, .int, .skr
         G16: /scratch/user/jobid/
          g16: /localscratch/username.jobid.0/
   User can name the .chk and .rwf files
Interactive job (test)
 [~$] salloc --time=2:0:0 --cpus-per-task=16 --mem=10g --account=def-jemmyhu
  (max 3 hrs)
 [~$] module load gaussian/g16.c01
 [~$] G16 g16_test.com
```

G16 simplest input: CO-b3lyp.com

```
//Simplest Input, serial, default memory
                                             //Simplest Input, 16 cpus parallel
#p b3lyp/6-311++g(2df,p) opt freq
                                             %mem=5G
                                             %nproc=16
<< CO-6311++g(2df,p)—B3LYP-Opt-Freq >>
                                             #p b3lyp/6-311++g(2df,p) opt freq
0 1
                                              << CO-6311++g(2df,p)—B3LYP-Opt-Freq >>
C
o 1 co
                                             0 1
                                             C
co=1.1281
                                             o 1 co
(blank line)
                                             co=1.1281
```

Input file with named .rwf: CO-b3lyp-rwf.com

```
//specify a .chk file
%chk=CO-b3lyp
%mem=5G
%nproc=16
                                              %nosave
#p b3lyp/6-311++g(2df,p) opt freq
<< CO-6311++g(2df,p)—B3LYP-Opt-Freq >>
0 1
o 1 co
                                              0 1
                                              C
co=1.1281
                                              o 1 co
```

```
//specify a .rwf file
%rwf=CO-b3lyp
%chk=CO-b3lyp
%mem=5G
%nproc=16
#p b3lyp/6-311++g(2df,p) opt freq
<< CO-6311++g(2df,p)—B3LYP-Opt-Freq >>
co=1.1281
```

The named .chk and/or .rwf files will be created in the current job directory

Checkpointing

- .chk can be used to restart an optimization job used for property (freq, etc) calculation afterwards used for GaussView
- 2. In G16, .rwf can be used to restart a job, particularly to restart a job failed in the freq calculation step

Restart

Restart opt job from .chk

```
%chk=Cu_test.chk
%mem=10g
%nproc=16
#B3LYP/DGDZVP Opt Geom=AllCheck Guess=Read
(one blank line)
```

Restart freq from .rwf

```
%rwf=/scratch/jemmyhu/Cu_test.rwf
%NoSave
%chk=Cu_test.chk
%mem=10g
%nproc=16
#p restart
(one blank line)
```

File structure: scratch (G16) vs localscratch (g16)

	module load gaussian/g16.c01 G16 g16_test.com	module load gaussian/g16.c01 g16 < g16_test.com >& g16_test.log
Runtime files (.rwf, .inp, .d2e, .int, .skr)	\$SCRATCH /scratch/userid/jobid/	\$SLURM_TMPDIR (/localscratch/username.jobid.0/)
Disk size	> 1TB	< 1TB (800-900GB?)
Speed		faster
File life time	Files stay when job failed. Clear up jobid folder yourself	removed right after the job is done
For restart	.rwf left for restart	None. Name .chk and .rwf for possible restart

Job location/folder: .com, .log, .sh; named .chk, .rwf

File structure example: scratch (G16) vs localscratch (g16)

```
[jemmyhu@gra766 g16.c01]$ squeue -u jemmyhu
      JOBID
                                 NAME ST TIME LEFT NODES CPUS TRES PER N MIN MEM NODELIST
            USER
                     ACCOUNT
(REASON)
                    def-jemmyhu cpu g16 nbo7.sh R 2:53:35 1 8 N/A
   57611549 jemmyhu
                                                                   8G gra766 (None)
   57611551 jemmyhu
                    def-jemmyhu cpu G16 test.sh R 2:58:30 1 8 N/A
                                                                  8G gra750 (None)
g16 for job 57611549
   [jemmyhu@gra-login1 ~]$ ssh gra766
   [jemmyhu@gra766 /]$ cd /localscratch
   [jemmyhu@gra766 localscratch]$ cd jemmyhu.57611549.0
   [jemmyhu@gra766 jemmyhu.57611549.0]$ ls
   Gau-28440.inp Gau-28451.d2e Gau-28451.int Gau-28451.rwf Gau-28451.skr
   [jemmyhu@gra766 jemmyhu.57611549.0]$ pwd
   /localscratch/jemmyhu.57611549.0
```

G16 for job 57611551

[jemmyhu@gra766 scratch]\$ ls 57611477 57611551

Disk error

Erroneous write. write 122880 instead of 4239360.

fd = 3

writwa

writwa: File exists

Erroneous write. write -1 instead of 3648000.

fd = 4

writwa

writwa: No space left on device

Solutions:

- 1. If you start the job with g16, /tmp does not have enough space, switch to G16
- 2. If you use G16, one /scratch disk array does not have enough space, configure lfs striping to stripe data over multiple OSTs, e.g., default count is 1, set to be 3:

lfs setstripe -c 3 /scratch/yourname/

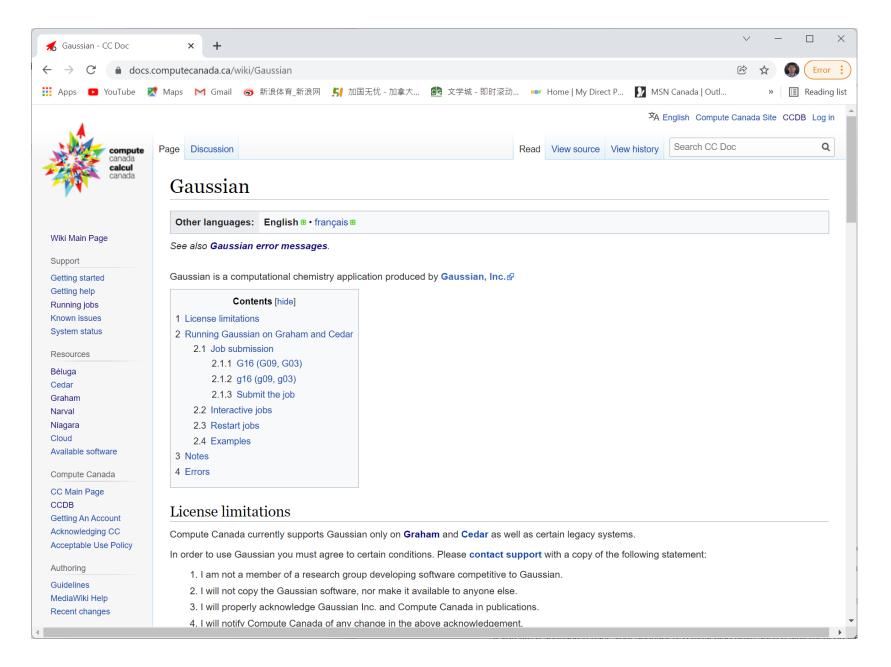
Gaussian Utilities

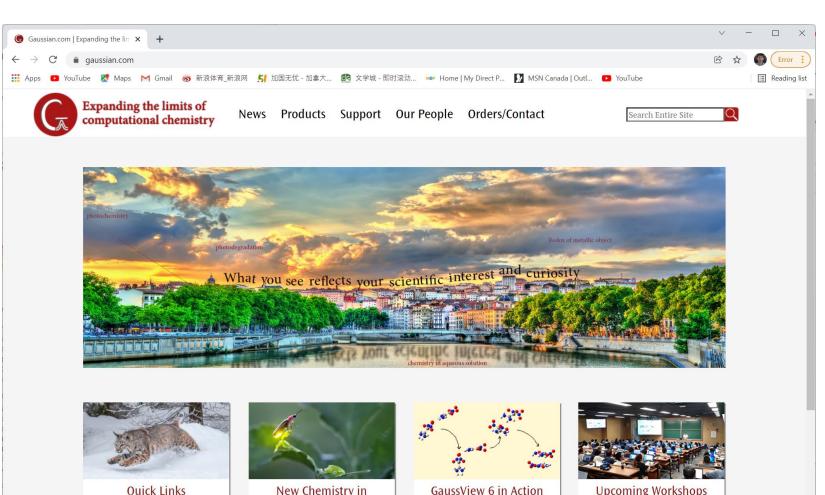
Utilities

formchk cubegen freqchk

•••••

use the same version direct run from command line





Citations • Release Notes Keywords • FAQ/Tips Videos: YouTube English • YouTube Japanese • 优酷 Gaussian频道 Computer Requirements **Prices** Sales Agents Section 508 VPAT

New Chemistry in Gaussian 16

Gaussian 16 expands the range of molecules and types of chemical problems that you can model. More...

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NBO: Natural Bond Orbital

The NBO program performs the analysis of a many-electron molecular wavefunction in terms of localized electron-pair bonding units.

The program carries out the determination of

- NAOs: natural atomic orbitals
- NHOs: natural hybrid orbitals
- NBOs: natural bond orbitals
- NLMOs: natural localized molecular orbitals

and uses these to perform

- NPA: natural population analysis (NPA),
- NBO energetic (deletions) analysis,
- NRT: natural resonance theory
- NCS: natural chemical shielding

and other tasks pertaining to localized analysis of wavefunction properties

What NBO version is in Gaussian package?

Gaussian has built-in NBO-3.1, the default NBO in Gaussian when using keyword pop=nbo

What NBO versions are on Graham and Cedar?

NBO is not installed as an independent package, it's built-in with Gaussian package on the clusters

Versions:

```
gaussian/g03.d01
gaussian/g09.e01 - NBO6
gaussian/g16.b01 - NBO6
gaussian/g16.c01 - NBO7
```

Recommend to use the latest versions

What's new in NBO7?

NEDA for Gaussian

Natural Energy Decomposition Analysis (NEDA) is implemented for Gaussian 16, Rev. C.01

Improved NRT and \$CHOOSE Algorithms

improved "solver" (QPNRT algorithm) for variational optimization of NRT resonance weights and bond orders, a more flexible and robust \$CHOOSE algorithm to obtain the density contribution for each idealized resonance bonding pattern

Natural Poly-electron Population Analysis (NPEPA)

2nd-order Reduced Density Matrix Elements (RDM2)

Resonance Natural Bond Orbitals (RNBO)

input

https://gaussian.com/relnotes/

- •[REV C] NBO version 7 is supported. There are new options to the Population keyword:
- Pop=NPA7, Natural Population Analysis
- Pop=NBO7, full Natural Bond Orbital Analysis
- Pop=NBO7Read, full NBO with NBO input read from the input stream
- Pop=NBO7Delete, NBO analysis of the effects of deletion of some interactions
- Pop=NEDA, Natural Energy Decomposition Analysis

input to the NBO portion consists simply of one or more keywords enclosed in NBO keylists in the ESS input file.

The main NBO keylist (the \$NBO keylist) is of the form:

```
$NBO ...(keywords)... $END
```

Simple examples of such \$NBO keylists are

```
$NBO dipole nrt $END
$NBO file=myjob archive naonbo ncs=0.05 $END
```

Other keylist identifiers include

```
$CORE, $CHOOSE, $NRTSTR, $DEL, and $NPEPA
```

Keylists cannot be nested, and each new keylist must begin on a newline.

The NBO program reads the keywords of each keylist to set various job options, then interrogates the ESS program for information concerning the wavefunction to perform the requested tasks

NBO input is terminated by a blank line. Thus, keylist input may appear as follows:

```
$nbo steric $end
$del
delete 1 element 3 11
$end
<blank line>
```

Example

NBO analysis with geometry optimization

```
# rhf/3-21g opt pop=nbo7
Methylamine...rhf/3-21g optimization
0 1
C
  1 1.47
H 1 1.09 2 109.4712
H 1 1.09 2 109.4712 3 120.0
H 1 1.09 2 109.4712 3 240.0
H 2 1.01 1 109.4712 3 60.0
H 2 1.01 1 109.4712 3 300.0
```

numerical optimization with deletions

```
# rhf/3-21g opt=z-matrix pop=nbo7del
Methylamine...reoptimization with LEWIS deletions
01
C
N 1 CN
H 1 CHa 2 NCHa
H 2 NH 1 CNH 3 -beta 0
CN 1.4712
CHa
    1.0901
alfa
     121.4224
      64.2403
beta
$nbo print=0 nbosum $end
                            ! Turn off all printing but NBO Summary
$choose
                            ! Fix Lewis structure for all geometries
 lone 2 1 end
  bond s 1 2 s 1 3 s 1 4 s 1 5 s 2 6 s 2 7 end
$end
$del lewis $end
                             ! Perform deletions analysis
```

Output

```
NATURAL ATOMIC ORBITAL AND
   NATURAL BOND ORBITAL ANALYSIS
(c) Copyright 1996-2021 Board of Regents of the University of Wisconsin System
  on behalf of the Theoretical Chemistry Institute. All rights reserved.
   Cite this program [NBO 7.0.10 (8-Feb-2021)] as:
   NBO 7.0. E. D. Glendening, J. K. Badenhoop, A. E. Reed,
   J. E. Carpenter, J. A. Bohmann, C. M. Morales, P. Karafiloglou,
   C. R. Landis, and F. Weinhold, Theoretical Chemistry Institute,
   University of Wisconsin, Madison, WI (2018)
Filename set to /scratch/jemmyhu/57734053/Gau-2187
Job title: Methylamine...rhf/3-21g optimization
NATURAL POPULATIONS: Natural atomic orbital occupancies
NAO Atom No lang Type(AO) Occupancy Energy
1 C 1 s Cor(1s) 1.99978 -11.17840
2 C 1 s Val(2s) 1.08927 -0.19713
3 C 1 s Ryd(3s) 0.00071 1.95478
4 C 1 px Val(2p) 1.21779 -0.06924
```

```
NATURAL BOND ORBITALS (Summary):
                        Principal Delocalizations
    NBO
                Occupancy Energy (geminal, vicinal, remote)
Molecular unit 1 (CH5N)
----- Lewis -----
 1. CR (1) C 1 1.99978 -11.17840 18(g)
 2. CR (1) N 2 1.99984 -15.42894 22(g)
 3. LP (1) N 2 1.97257 -0.40269 11(v),12(v),13(v)
 4. BD (1) C 1- N 2 1.99876 -0.80619
 5. BD (1) C 1- H 3 1.99852 -0.65507 20(v)
 6. BD (1) C 1- H 4 1.99370 -0.65295 14(v)
 7. BD (1) C 1- H 5 1.99370 -0.65295 15(v)
 8. BD (1) N 2- H 6 1.99539 -0.77276 12(v)
 9. BD (1) N 2- H 7 1.99539 -0.77276 13(v)
----- non-Lewis -----
 10. BD*(1) C 1- N 2 0.00009 0.57358
```

Examples on Graham in

/home/jemmyhu/tests/test Gaussian/g16/g16.c01/NBO7

