

# Introduction to GaussView and Gaussian

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- Description of Both Programs
- How to Create Input Files (with GaussView)
- How to Submit Calculations
- How to Visualize Output

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Description • Input • Submit • Visualize



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## Gaussian 03:

an electronic structure package capable of predicting many properties of atoms, molecules, and reactive systems

*e.g.*

- Energies
- Structures
- Vibrational frequencies

utilizing *ab initio*, density functional theory, semi-empirical, molecular mechanics, and hybrid methods.

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# GaussView:

graphical interface for Gaussian 03

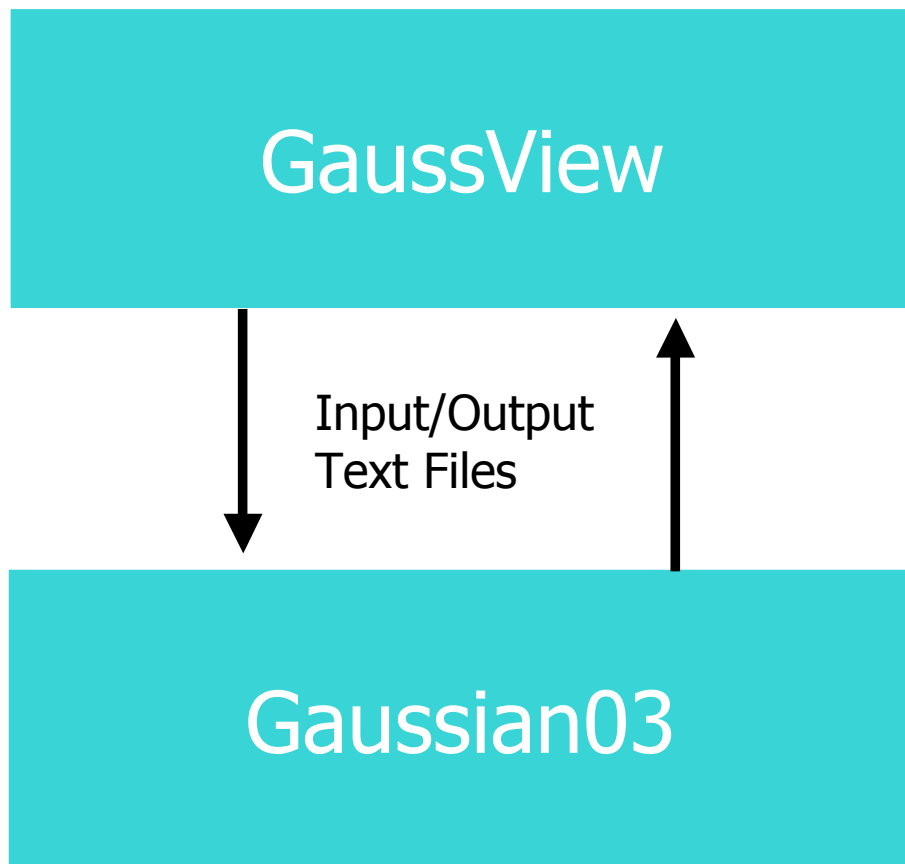
- build molecules or reactive systems
- setup Gaussian 03 input files
- graphically examine results

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Visualization

Electronic Structure Calculations

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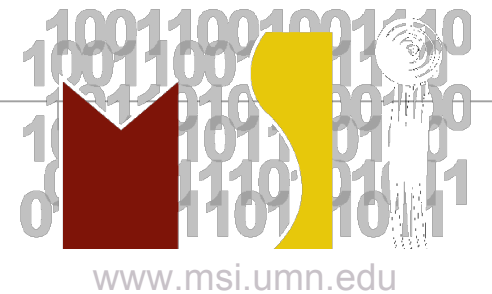


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# Calculations with Gaussian

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# Types of Calculations

- single point energy and properties (electron density, dipole moment, ...)
- geometry optimization
- frequency
- reaction path following

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## Levels of Theory Available:

- semi-empirical  
AM1, PM3, MNDO, ...
- density functional theory  
B3LYP, MPW1PW91, ...
- *ab initio*  
HF, MP2, CCSD, CCSD(T), ...
- hybrid  
G2, G3, ...

The level of theory is the set of underlying approximations used to describe the chemical system. Higher levels of theory are often more accurate however they come at much greater computational cost.

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## Basis Sets Available:

- Pople-type  
3-21G, 6-31G, 6-311G(d,p), ...
- Dunning  
cc-pVDZ, aug-cc-pVTZ, ...
- Huzinaga and Others  
MIDIX, ...
- User-defined

Basis sets are used for most calculations in Gaussian. They are a set of functions that are used to describe electronic wavefunctions.

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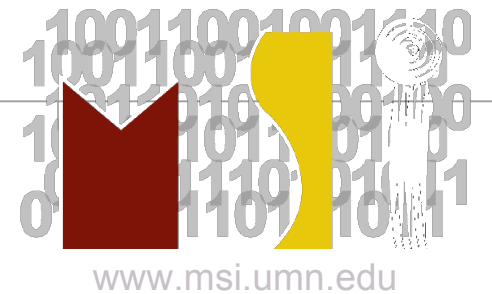


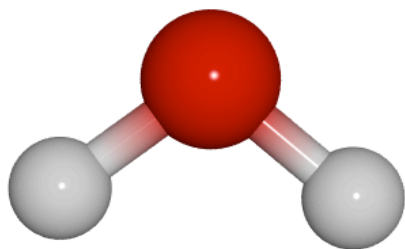
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# Creating Input Files for Gaussian

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## Water Optimization Input File

```
%mem=32mb
```



**system resources**

```
#p hf/6-31g opt
```



**computational model  
type of calculation**

```
hf/6-31g optimization of water
```



**title**

```
0 1
```



**charge & multiplicity**

```
o
```

```
h 1 oh
```

```
h 1 oh 2 ahoh
```



**structure definition  
(z-matrix)**

```
oh=0.9
```

```
ahoh=104.0
```



**variable values**

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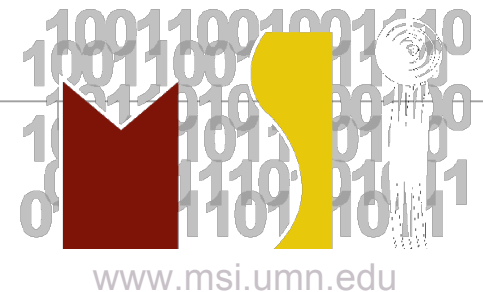
Spin multiplicity:

$$\text{multiplicity} = n + 1$$

where  $n = \#$  of unpaired electrons

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## Building with GaussView:

- Instead of typing all the coordinates, theory, basis set, etc., we can use GaussView.
- The calculation is specified by pointing and clicking to build the molecule, and using pull-down menus to select the calculation type, level of theory and basis set.
- GaussView generates the Gaussian input file, and can run Gaussian without ever returning to the Unix prompt.
- GaussView can also be used to read Gaussian output files and visualize the results.

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# Getting Started with GaussView:

- Login remotely

```
ssh -X sp.msi.umn.edu
```

- Load Gaussian/GaussView module

```
module add g03
```

- Launch GaussView

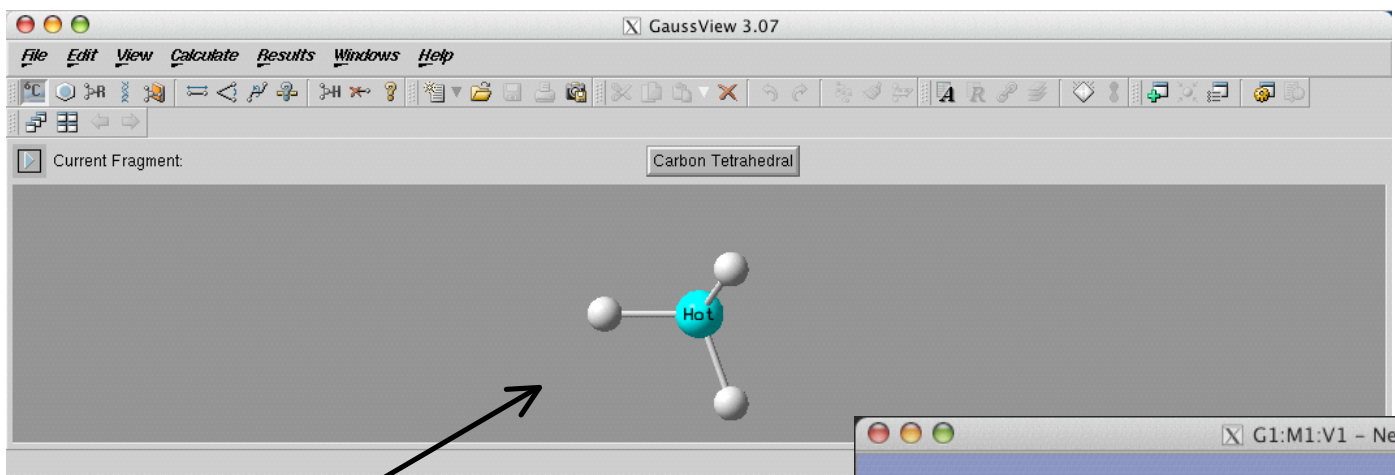
```
gv
```

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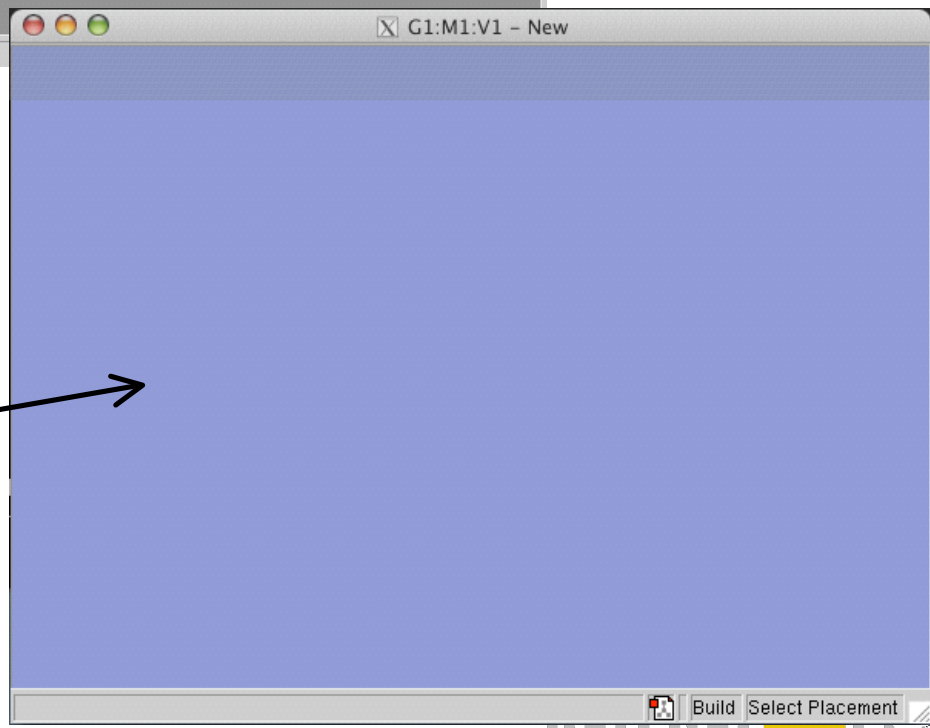


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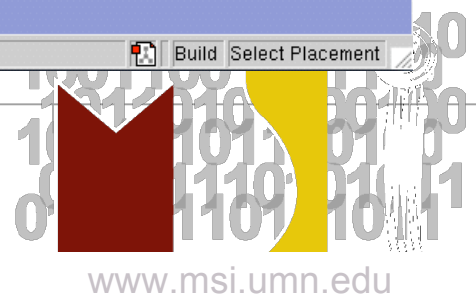


Builder

Viewer



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<b>Mouse Button</b>	<b>Action</b>	<b>Function</b>
<b>Left</b>	Click	Selects or inserts item
	Drag Left/Right	Rotates about Y-axis
	Drag Up/Down	Rotates about X-axis
<b>Center/Left-Right</b>	Drag	Translation of molecule
<b>Right</b>	Drag Left/Right	Rotates about Z-axis
	Drag Up/Down	Zooms in and out
<i>Note:</i> Holding down the Tab key limits mouse action to the closest distinct fragment.		

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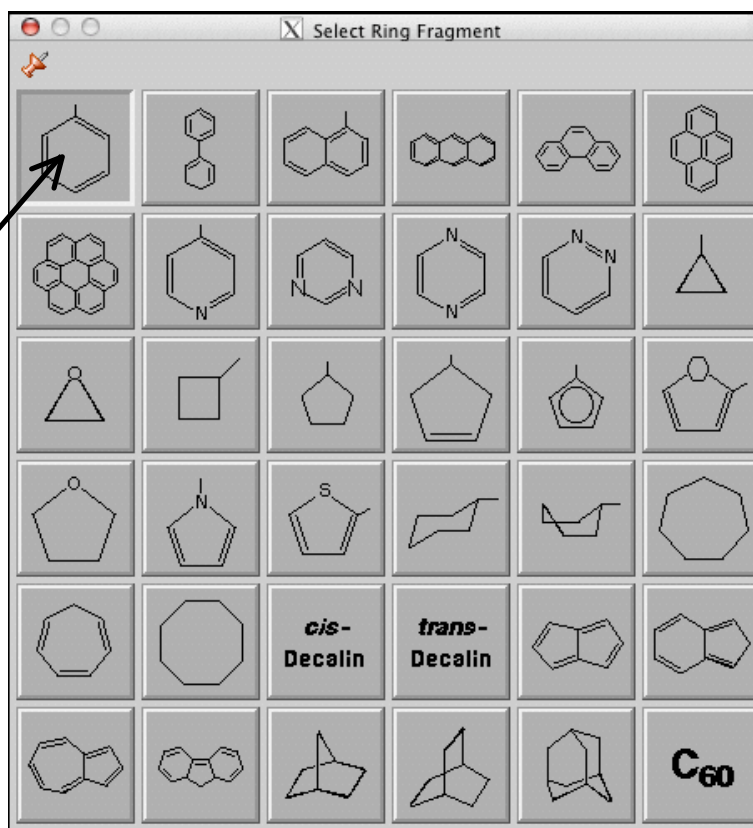
Description • [Input](#) • Submit • Visualize



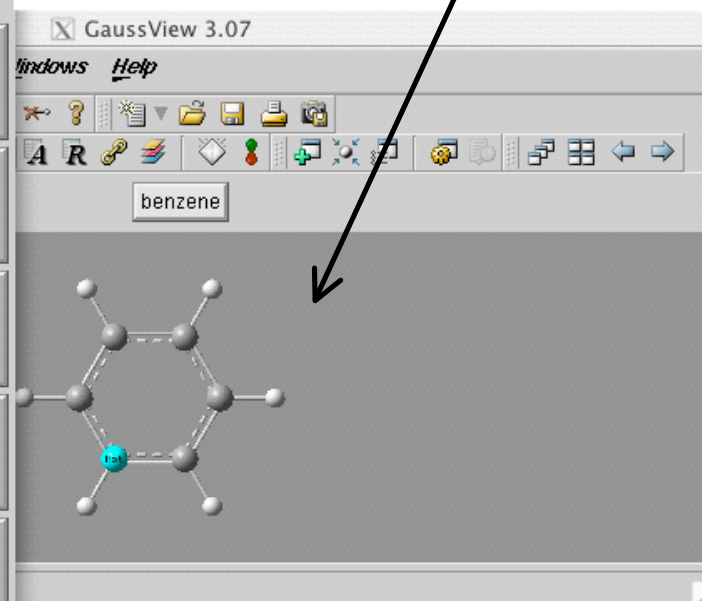


# Molecule Building

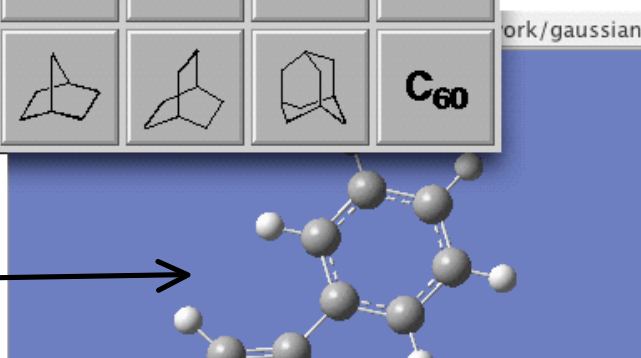
Fragments are Selected



Selected fragments Are previewed here



Molecule is put together Here

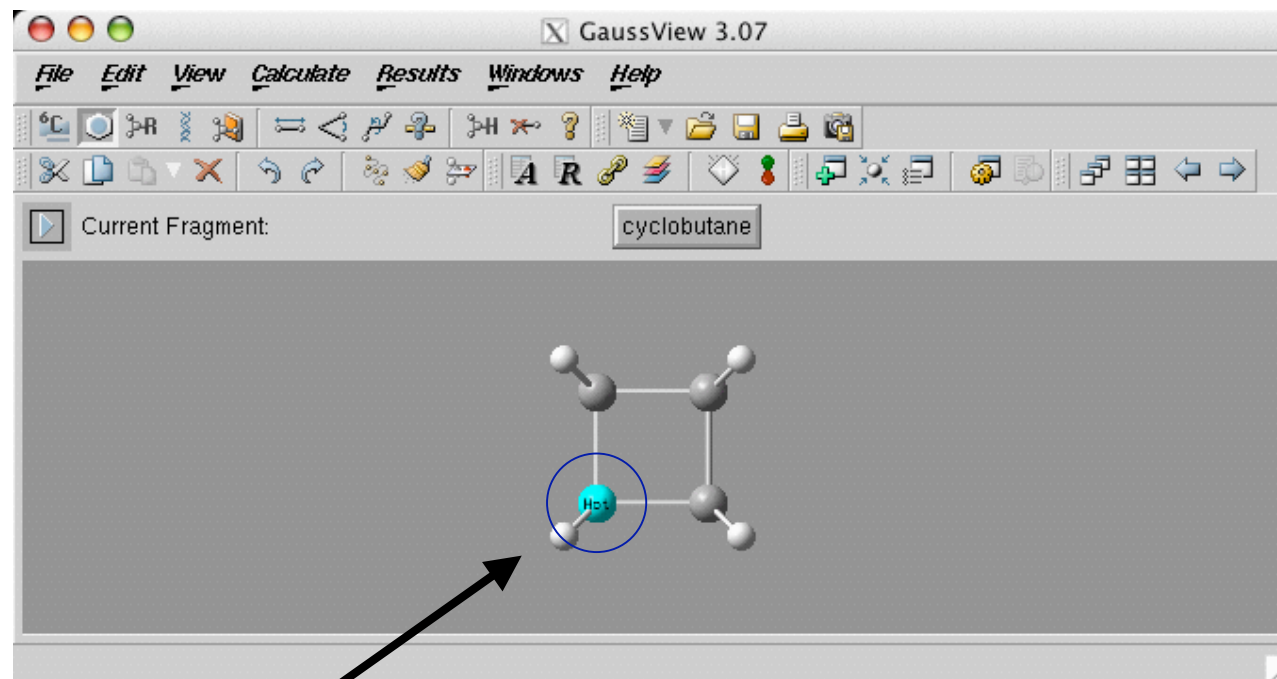


Description • [Input](#) • Submit • Visualize

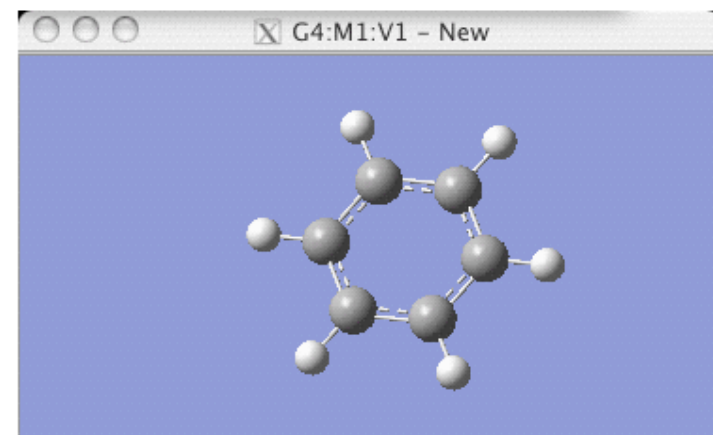


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# Molecule Building



The atom labeled "Hot" is where the fragment will attach to the system you are building.



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# Steps to Building

- Choose an atom or fragment
- Choose the location of the fragment that will attach to your molecule in the builder window
- Select/add the fragment to your molecule in the viewer window
- repeat



Result

Select Element

H X Bq He

Li Be B C N O F Ne

Na Mg Al Si P S Cl Ar

K Ca Sc Ti V Cr Mn Fe Co Ni Cu Zn Ga Ge As Se Br Kr

Rb Sr Y Zr Nb Mo Tc Ru Rh Pd Ag Cd In Sn Sb Te I Xe

Cs Ba La Hf Ta W Re Os Ir Pt Au Hg Tl Pb Bi Po At Rn

Fr Ra Ac Rf Db Sg Bh Hs Mt

Ce Pr Nd Pm Sm Eu Gd Tb Dy Ho Er Tm Yb Lu

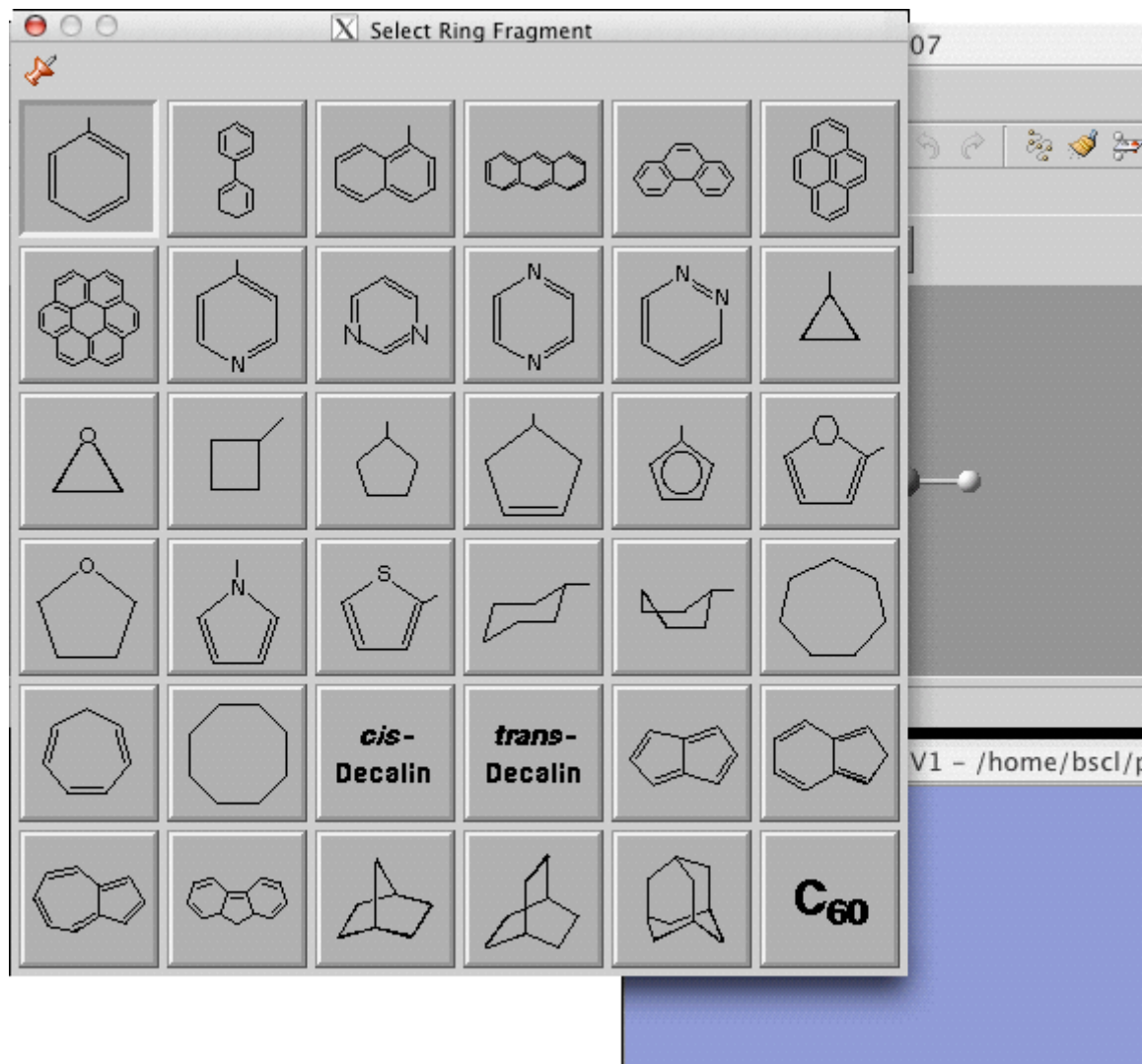
Th Pa U Np Pu Am Cm Bk Cf Es Fm Md No Lr

Select Carbon Fragment:

C Atom  $\text{—C}\equiv$   $\text{=C=}$   $\text{=C}$   $\text{—C}$   $\text{C}$

Elements:

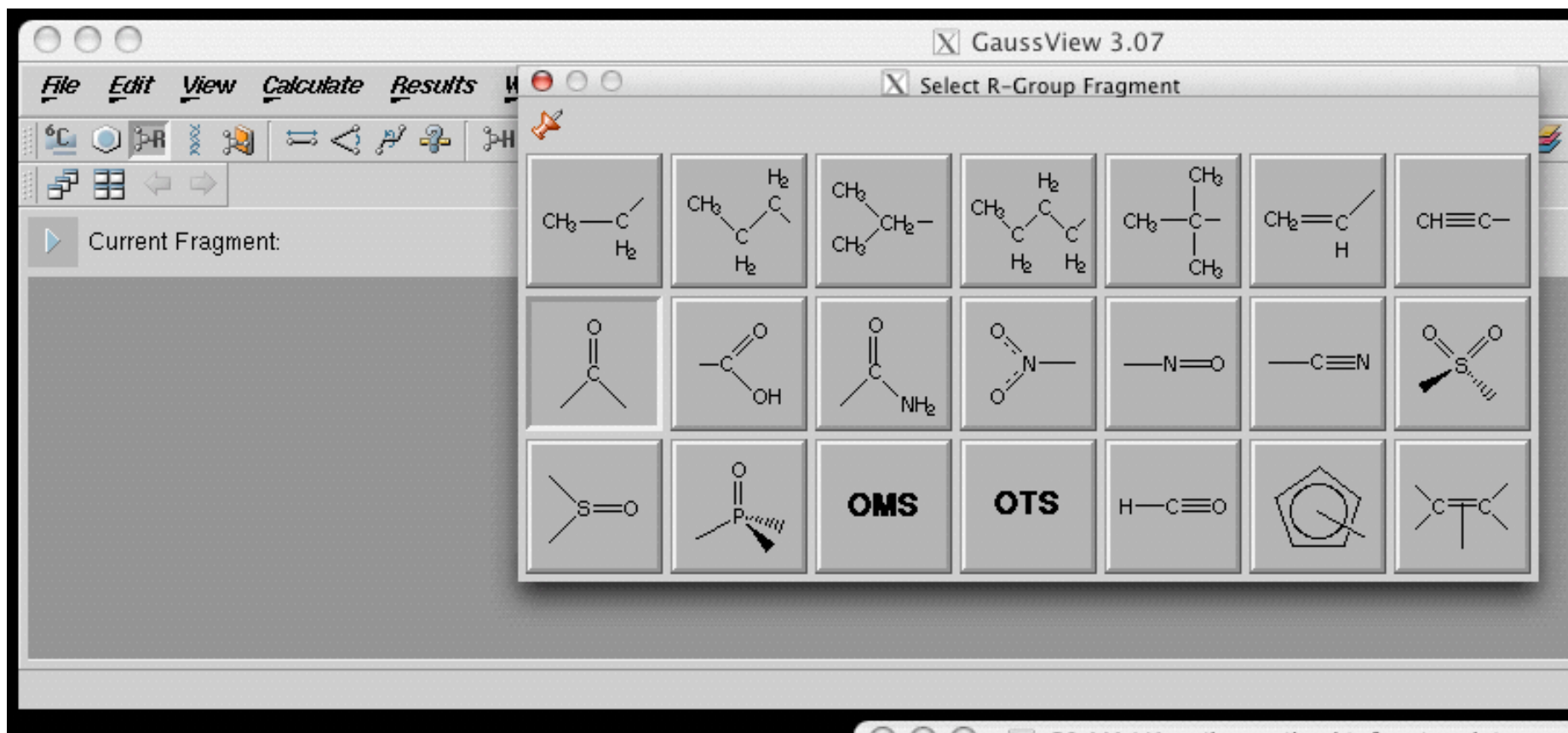
Description • [Input](#) • Submit • Visualize



## Ring Fragments:

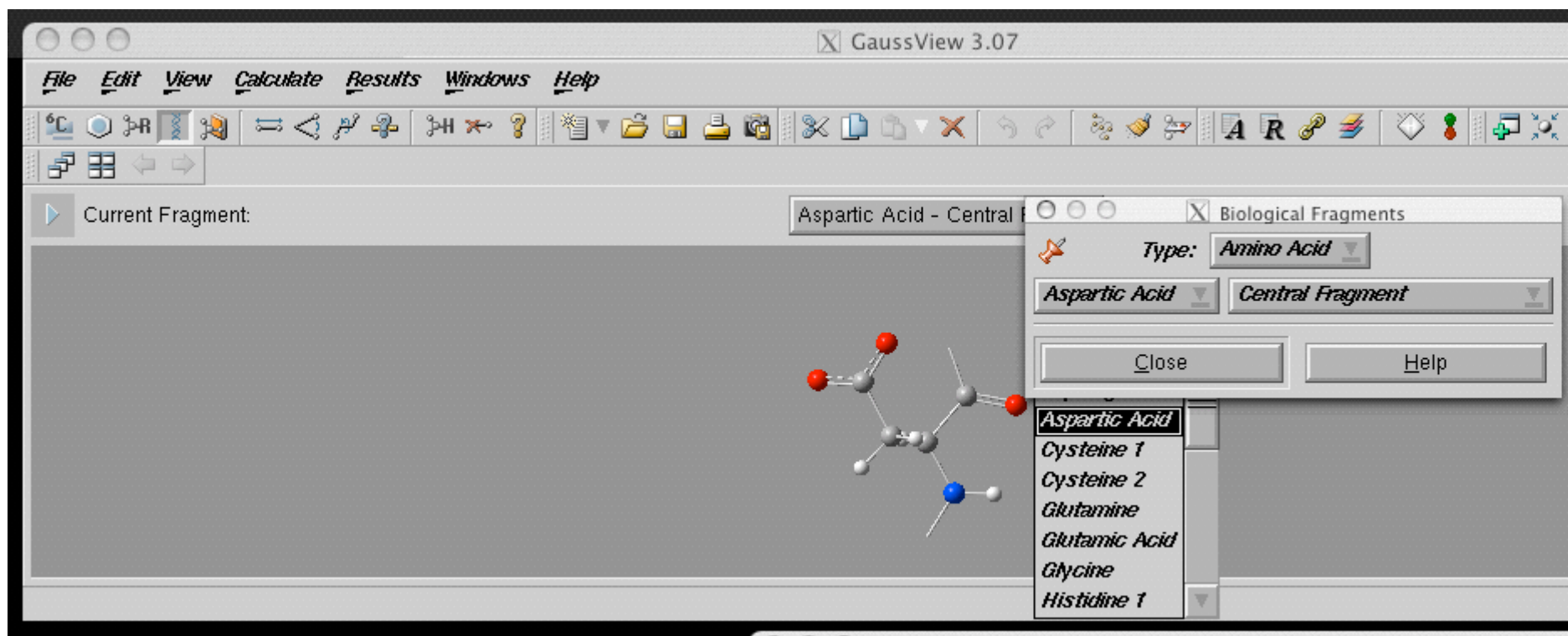
Description • [Input](#) • Submit • Visualize

# R-Group Fragments:



Description • [Input](#) • Submit • Visualize

# Biological Fragments:



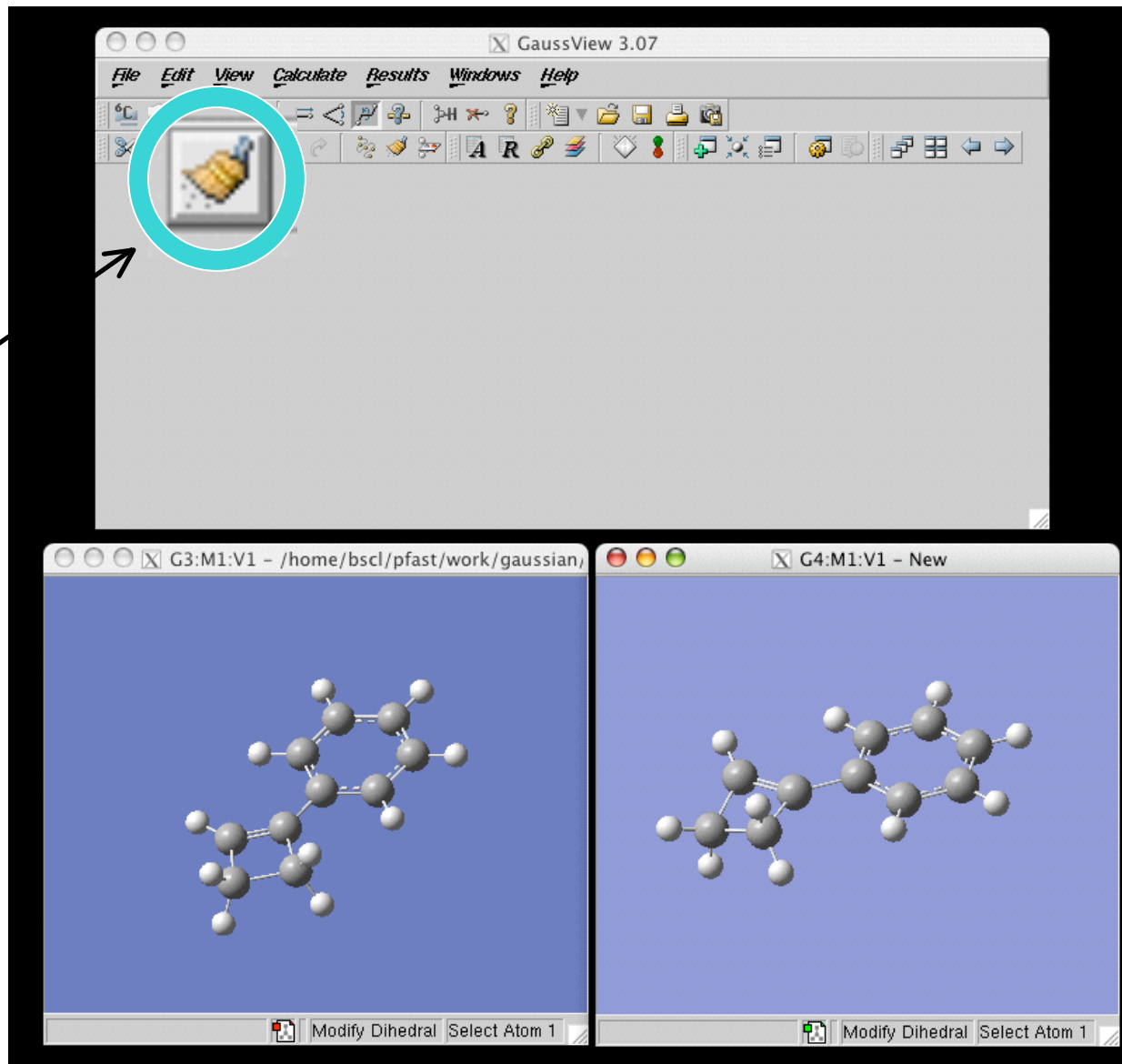
Description • **Input** • Submit • Visualize



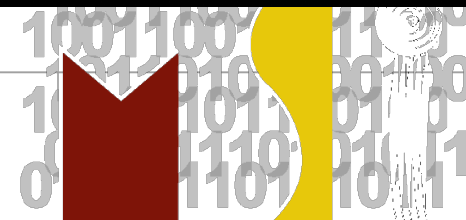
# Molecule Building

clean up

This option will use a MM calculation to optimize the geometry (very fast).



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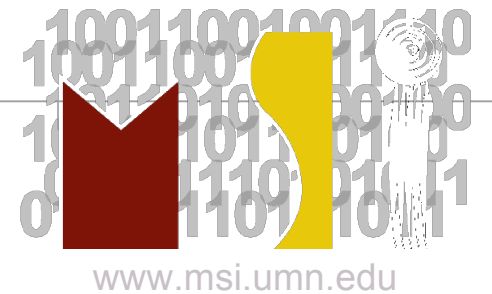
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# Submitting Calculations

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## Interactive:

### Command:

```
g03 < input_file > output_file
```

### Notes:

- 1) input and output files can use absolute or relative pathnames
- 2) Gaussian temporary files can be redirected by setting the GAUSS\_SCRDIR environment variable.

```
setenv GAUSS_SCRDIR /scratch/pfast
```

- 3) BE CAREFUL how long you run interactively

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# Batch:

## Command:

**qg03 [-options] input\_file**

## Options:

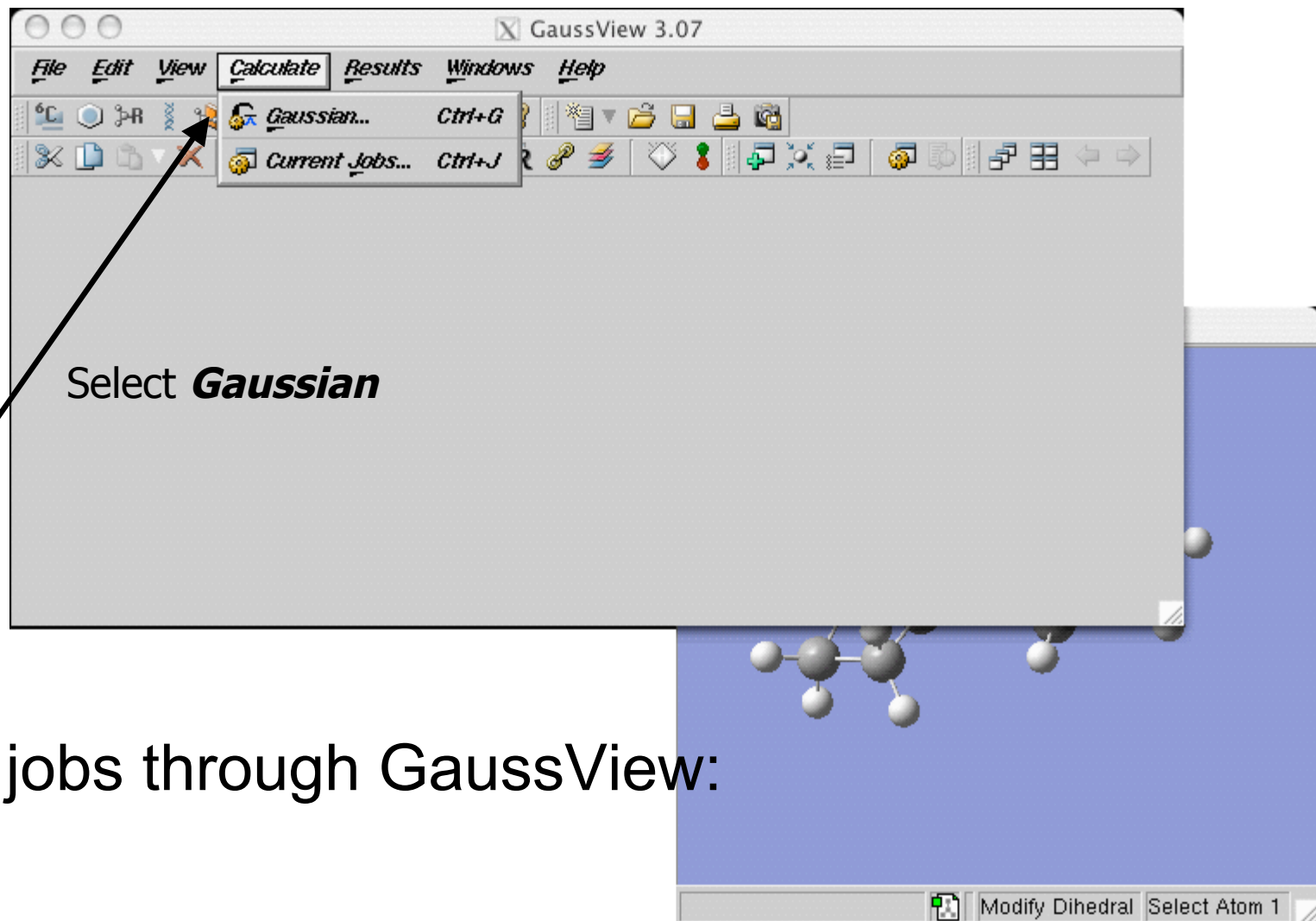
- h help, display a usage list and the defaults
- e email notification
- m total amount of memory
- n node, choose the particular processor
- p number of processors
- r run?
- s scratch space
- t amount of wallclock time

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Description • Input • **Submit** • Visualize

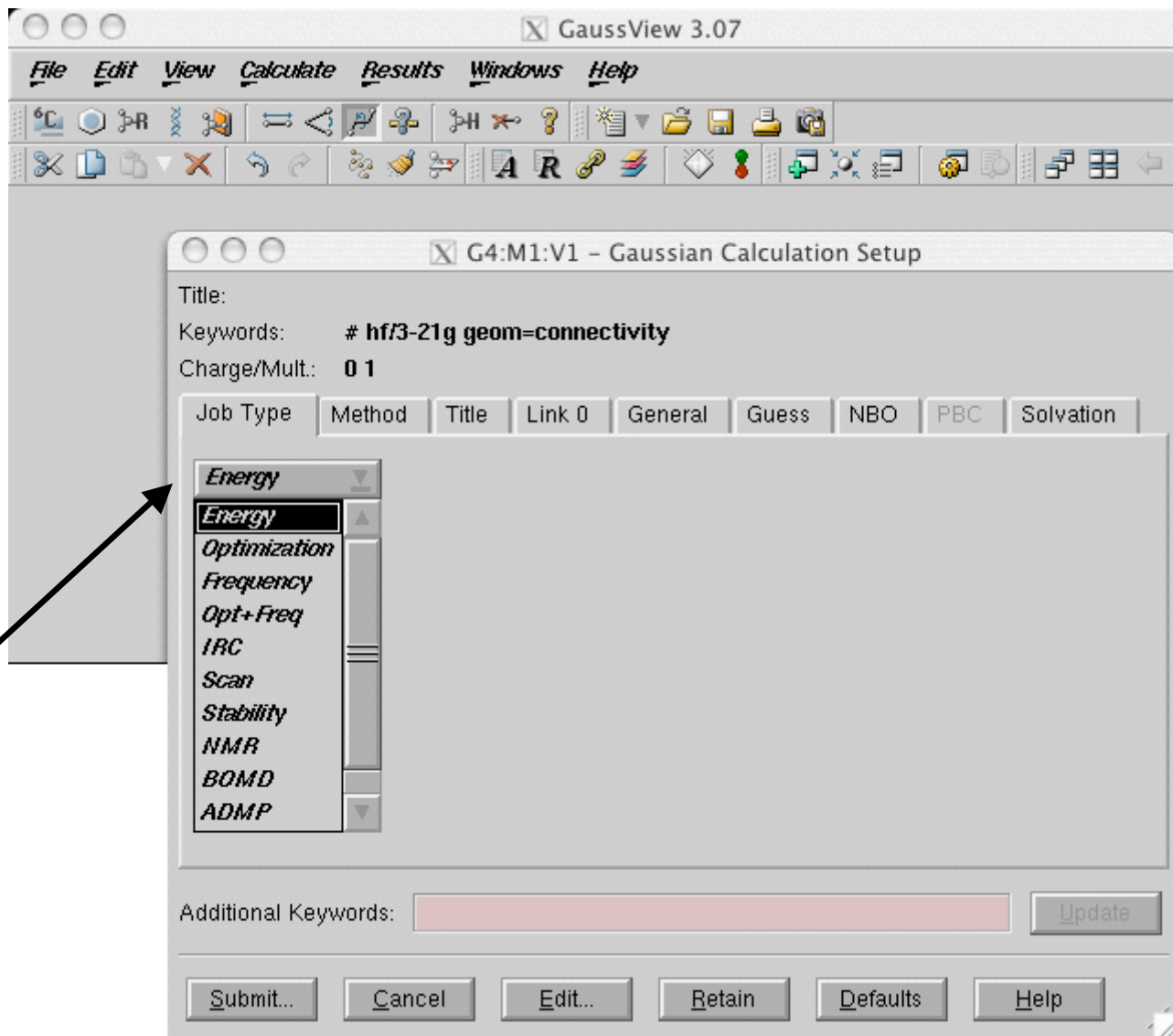


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Submitting jobs through GaussView:

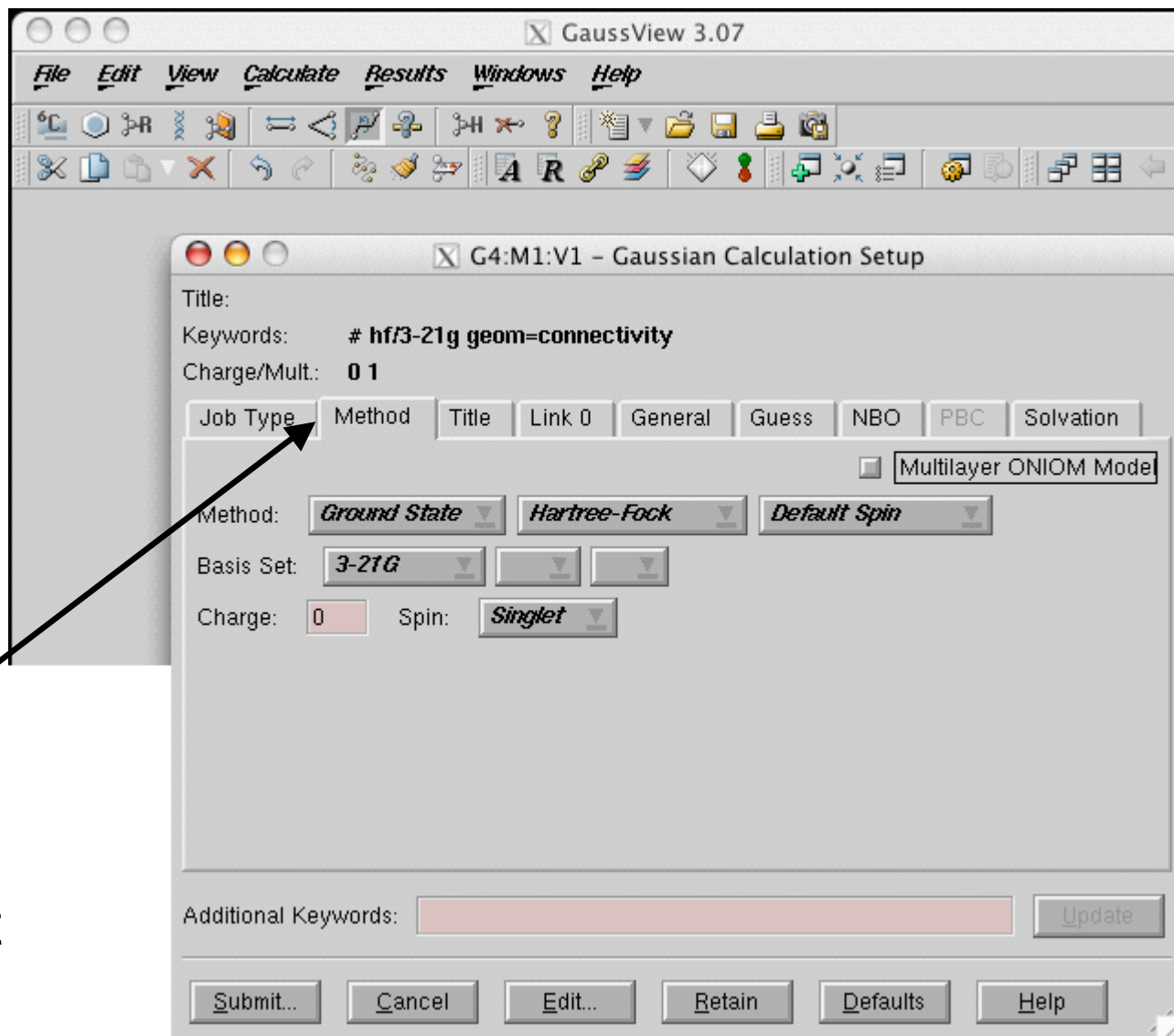
Description • Input • **Submit** • Visualize



Choose Job Type

Description • [Input](#) • Submit • Visualize

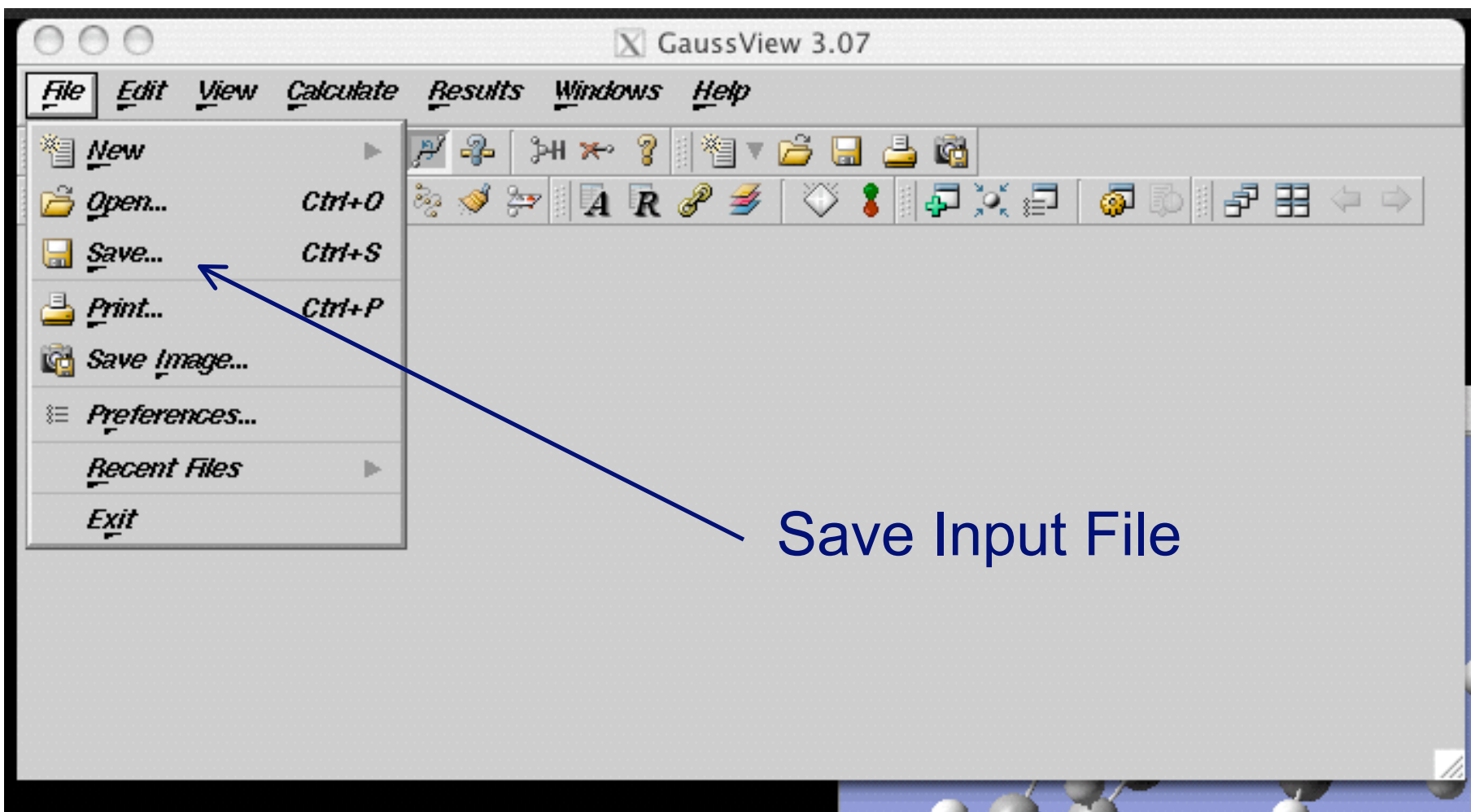




Method & Basis Set

Description • [Input](#) • Submit • Visualize

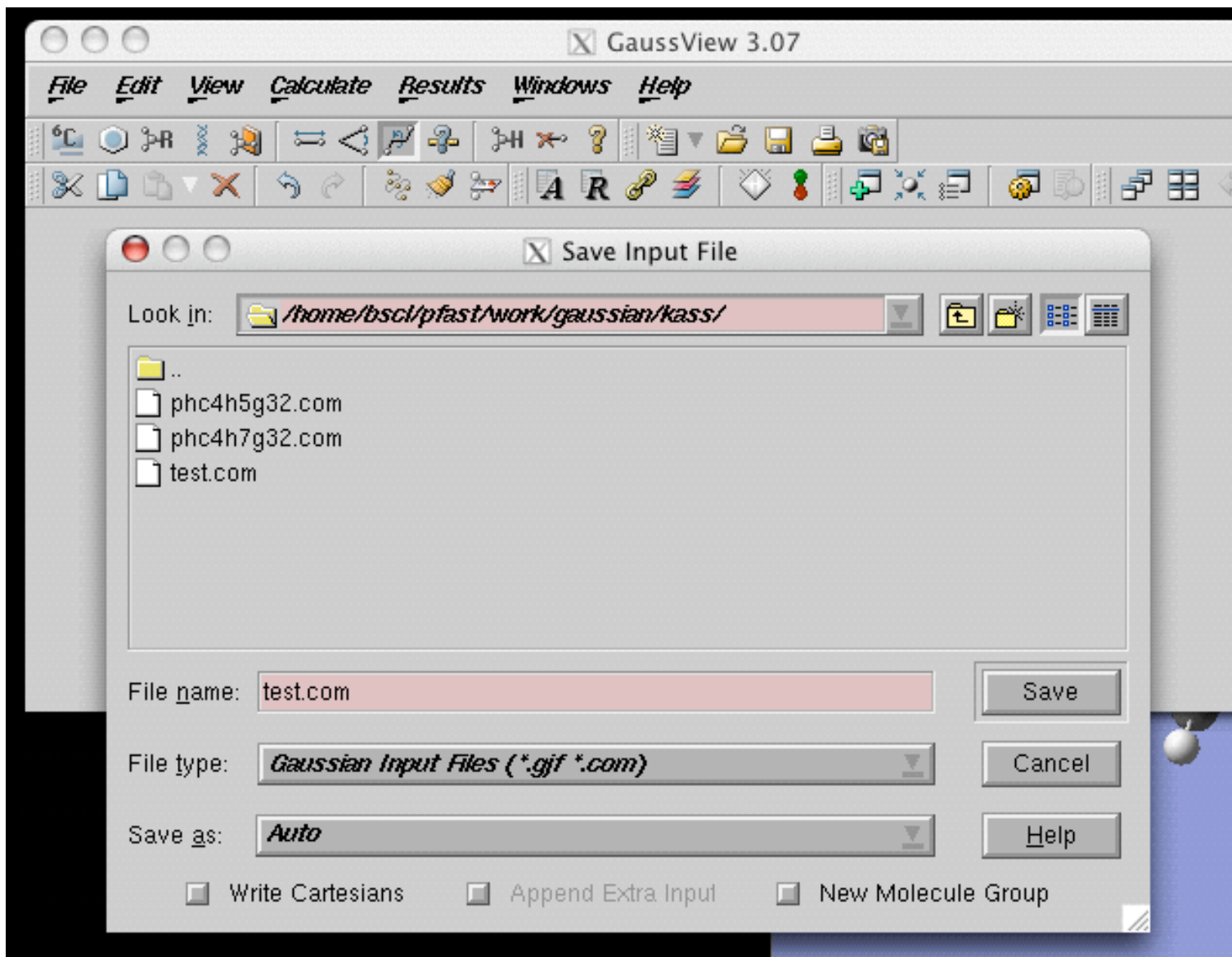




Save Input File

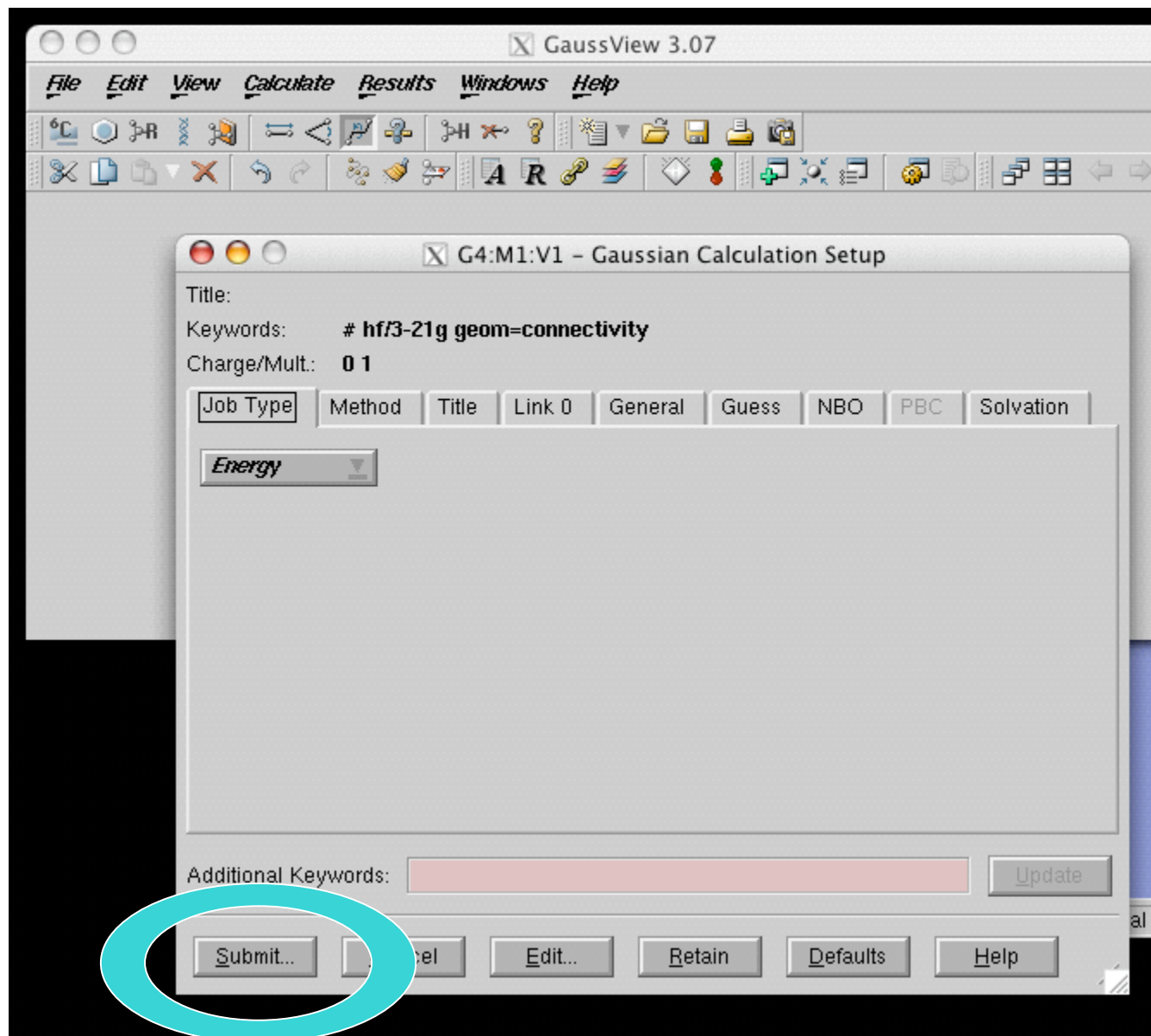
Description • **Input** • Submit • Visualize



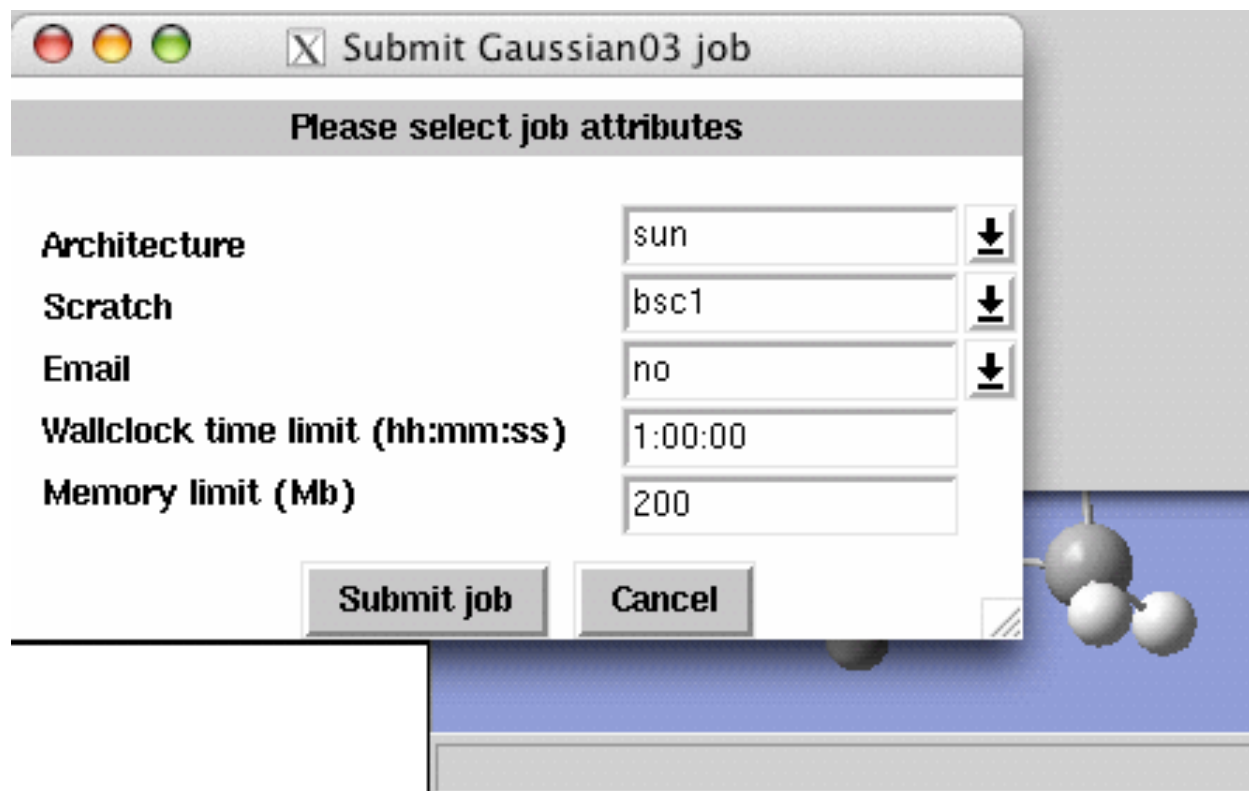


Description • [Input](#) • Submit • Visualize





Description • Input • **Submit** • Visualize



The submission dialogue box will appear a little different depending on which machine you are running GausView on.

Description • Input • **Submit** • Visualize



# Submitting your Gaussian job

If you haven't saved your input file yet, Gaussview will Prompt you to save your input file.

You will name the input file, and then submit the calculation.

When Gaussian is finished running, you will receive a message in Gaussview.

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# How to Visualize

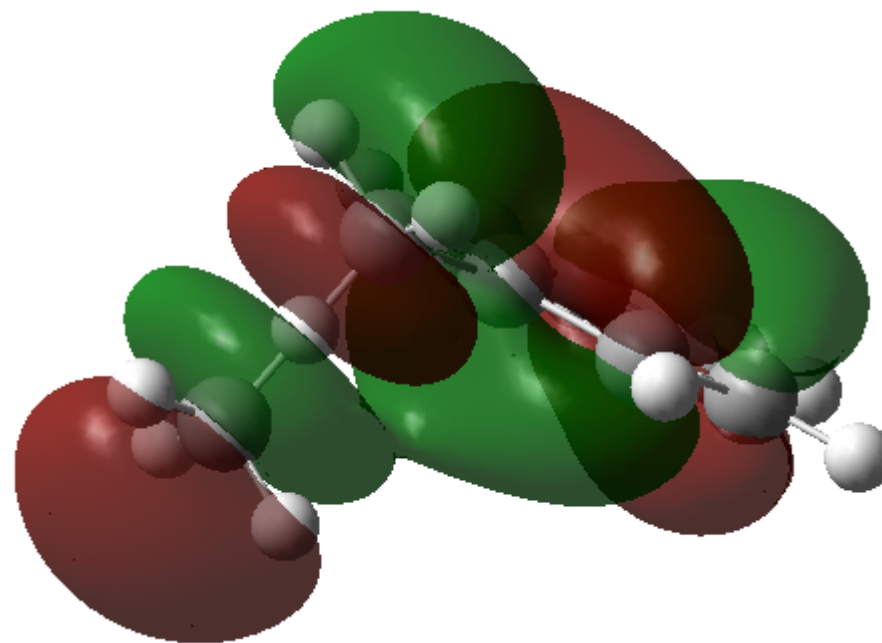
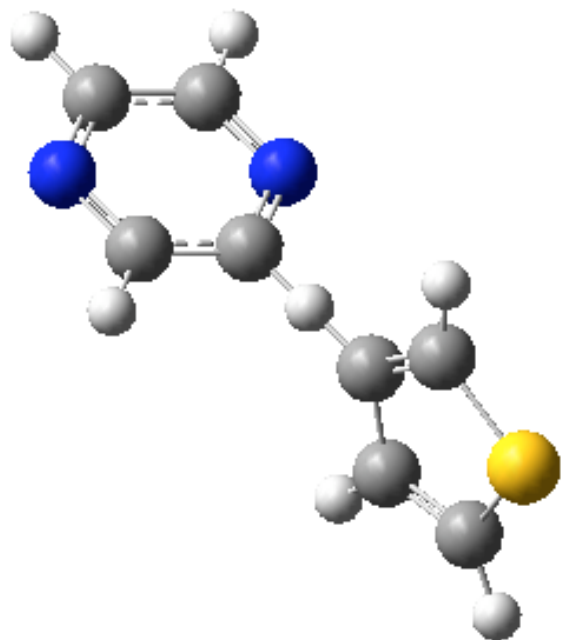
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# Visualization Features



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# How to view your output

- Your submitted calculation will run in the background.
- When it is complete, Gaussview will inform you and ask you if you wish to view an output file.
- From the list of files, you can pick your output (something.chk)



# How to view your output

- If you ever want to open an output file again, you can go to:

File → Open

In the GaussView menus to open any output file.

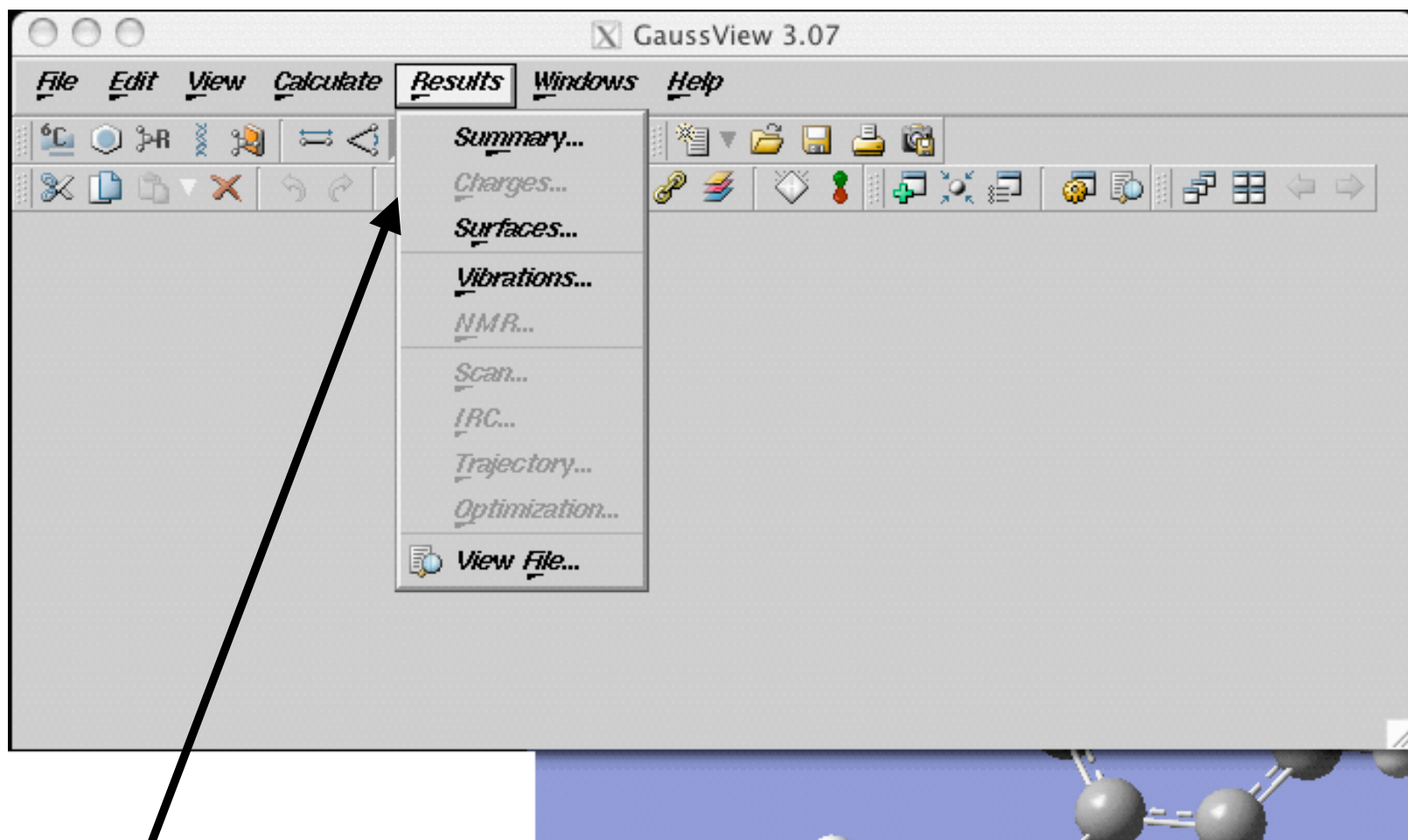


# Output that can be visualized

- Geometry
- Vibrations
- Orbitals
- Electron density
- Electrostatic potential







Main results menu

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G2:M1:V1 - Display Vibrations

#	Freq	Infrared	Raman	Depolar-P	Depolar-U
20	1065.45	5.515	5.1725	0.3761	0.5466
21	1084.76	0.3698	43.4916	0.2113	0.3489
22	1126.59	0.9363	2.654	0.3501	0.5186
23	1127.71	0.3781	0.7197	0.3948	0.5661
24	1134.54				
25	1141.54				
26	1160.71				
27	1167.97				
28	1182.59				
29	1227.29				
30	1273.62				

Frames / Cycle:

Displacement:

Show Displacement Vectors

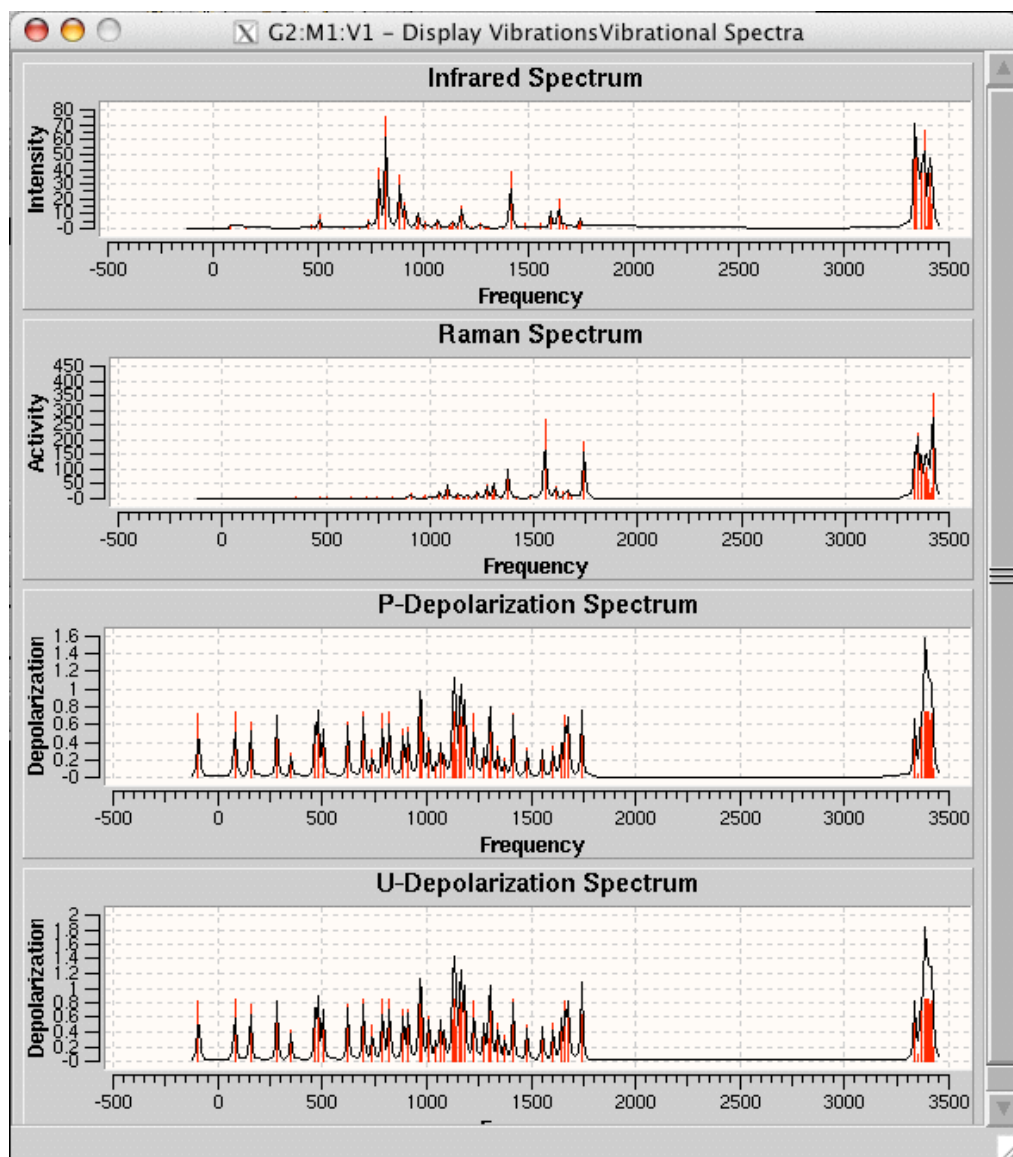
Show Dipole Derivative Unit

G2:M1:V1 - /home/bscl/pfast/work/gaussian/kass/test.chk

Read Only Read Only

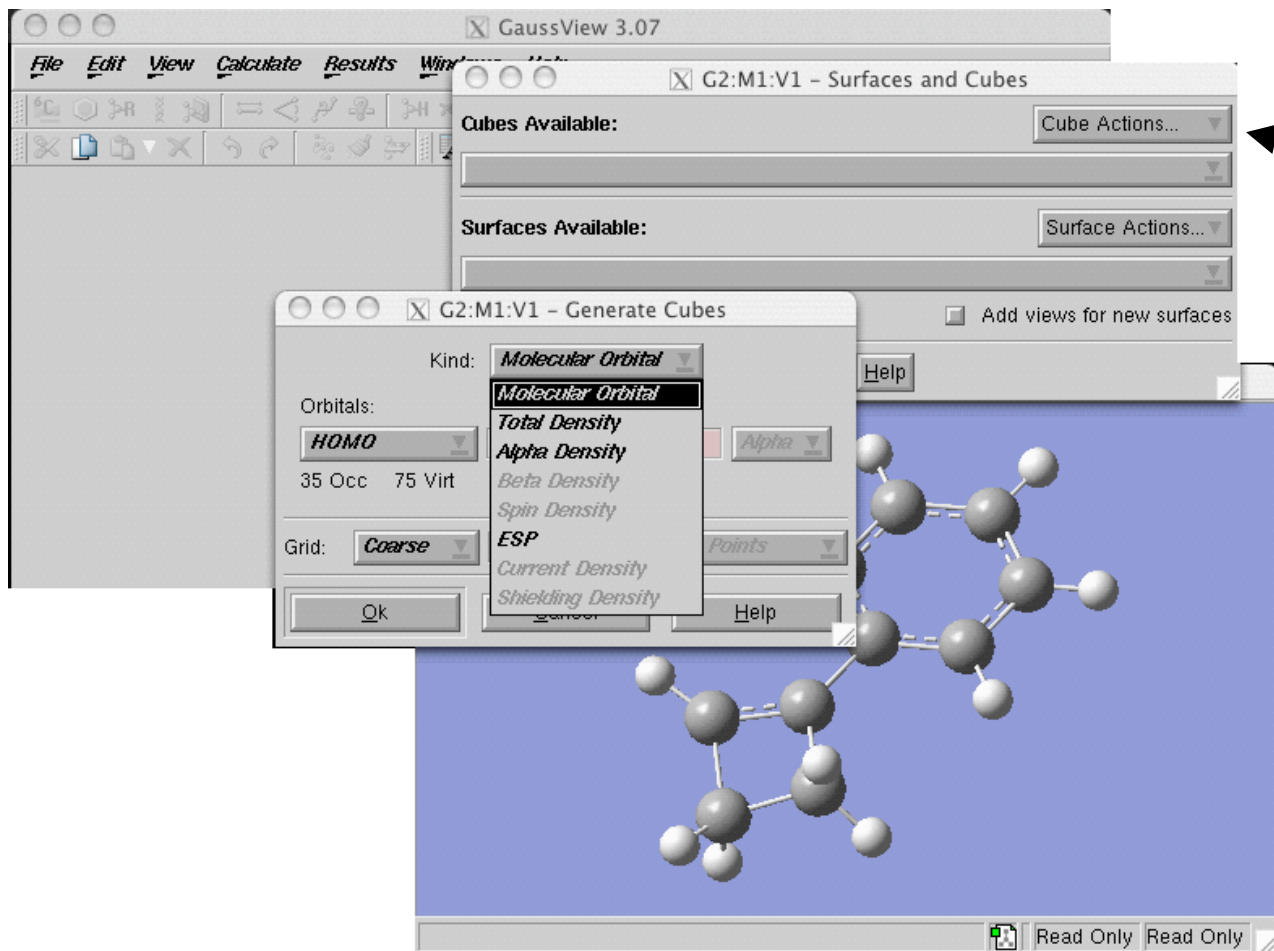
## Frequencies

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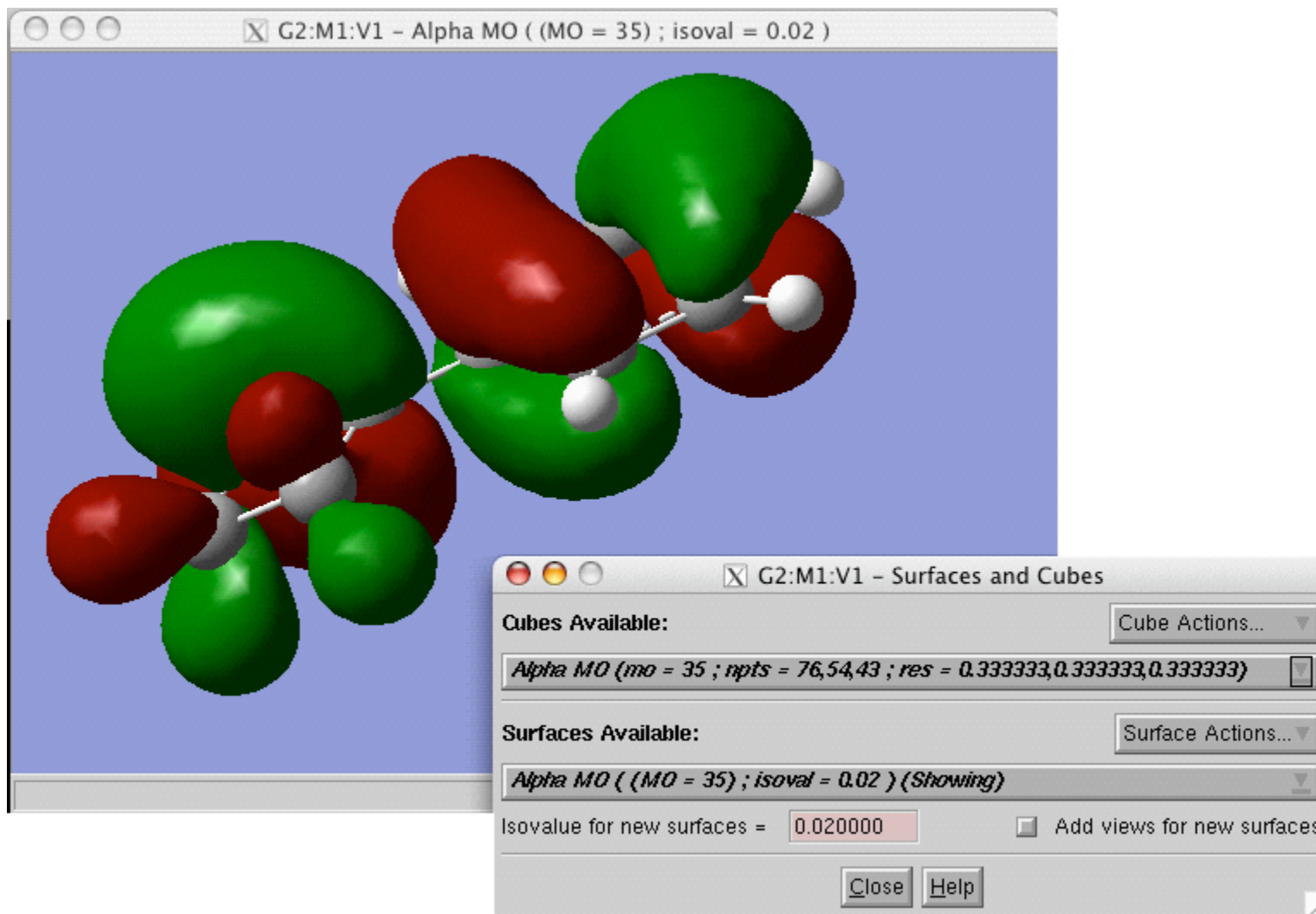
Spectra

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A cube file is a format of 3-D data that can be plotted.

You can generate a cube file to display orbitals, electron densities, electrostatic potentials, etc.



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# Questions?

**<http://www.gaussian.com>**

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[audette@chem.umn.edu](mailto:audette@chem.umn.edu)  
[help@msi.umn.edu](mailto:help@msi.umn.edu)

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