

Background

Some background from the Gaussian web site:

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

GaussView5 links:

<https://www.d.umn.edu/~psiders/courses/chem5650/gaussviewtutorial/tutorial.html>

<https://www.mtholyoke.edu/courses/jwijngaa/PS/Gaussview2.pdf>

Principles

1. Variation Principle

$$\int \Psi_{approx}^* H \Psi_{approx} dV = E_{approx} \geq E_{\text{exact ground state}}$$

The Hamiltonian is always “exact”

The wavefunction is always approximate, and is **varied** to reach the lowest possible ground state energy with the type of function **chosen**

More exact if:

- 1) Larger, more detailed **basis set** of atomic orbitals
- 2) More electron-electron **correlation (dodging)**

Specific Objectives:

- 1. Create an input file for water. Compute its equilibrium energy and structure, and examine its molecular orbitals.**
- 2. Compute the geometry and energy of a pair of H-bonded waters.**
- 3. Compute and compare vibrational frequencies for N₂O, and CO₂ at different levels of accuracy and make assignments to observed spectra.**
- 4. Create and examine benzene MOs and vibrations, including benzene-d1.**

GaussView lets you examine the results of Gaussian calculations using a variety of graphical techniques.

Gaussian results that can be viewed graphically include the following:

- ❖❖ **Optimized molecular structures.**
- ❖❖ **Molecular orbitals.**
- ❖❖ Electron density surfaces from any computed density.
- ❖❖ Electrostatic potential surfaces.
- ❖❖ Surfaces for magnetic properties.
- ❖❖ Surfaces may also be viewed as contours.
- ❖❖ **Atomic charges and dipole moments.**
- ❖❖ **Animation of the normal modes corresponding to vibrational frequencies.**
- ❖❖ IR, Raman, NMR, VCD and other spectra.
- ❖❖ Molecular stereochemistry information.
- ❖❖ Animation of geometry optimizations, IRC **reaction path following**, potential energy surface scans, and ADMP and BOMD trajectories. Two variable scans can also be displayed as 3D plots.
- ❖❖ Plots of the total energy and other data from the same job types as in the previous item.

Outline

374-18 Exp 7 Thur 8mar18

1. wiki.crc.nd.edu/wiki/images/d/d7/Gaussview-5-ref.pdf
2. Login with netid, password
3. find a work directory **c:\users\your netid**
and go to it
4. find the GaussView icon under **All programs GaussView 5.0 icon**
open
click help --- just to see what is there, including **tutorials**
5. File -> Preferences : **choose: launch directory**
notice Display format
find the **Gaussian 09W icon** and open it
File-> Preferences: **choose: launch directory**
6. Look at *Gaussview-5-ref.pdf*
what can be done
typographic conventions

Menu items = blue

Buttons =green

Dialog names = Black. Gaussian

keywords and options like Opt=QST2 = Purple

7. Main Interface Control Panel

Current fragment

Various Tool Bars (detachable, moveable

View windows

Dialogs

Preferences

Main Interface: Control Panel

Tool Bars

Current Fragment

The screenshot displays the GaussView 5 software interface. At the top is the main control panel with a menu bar (File, Edit, View, Calculate, Results, Windows, Help) and a toolbar. Below the toolbar is the 'Builder Fragment' section, which shows the current fragment as 'Nitrogen Trivalent (A-A-LP)'. The central area is a 3D view window showing a ball-and-stick model of a nitrogen atom with three bonds. Below this is a 'G1:M1:V1 - New' window showing a ball-and-stick model of a benzene ring with a nitrogen atom. To the right are two fragment selection toolbars: 'R-Group Fragments' and 'Element Fragments'. The 'R-Group Fragments' toolbar shows various organic groups like methyl, ethyl, propyl, and vinyl. The 'Element Fragments' toolbar shows a periodic table of elements. At the bottom right, there is a 'Select Nitrogen Fragment' section with options for different nitrogen bonding environments: a nitrogen atom, a nitrogen atom with a triple bond, a nitrogen atom with a double bond, and a nitrogen atom with a single bond and a lone pair.

a View Window

2 of the "Tools"

**Hovering the MOUSE over
an icon will tell its
function**

**in the lower left corner of
screen**

Outline -2

Tool bars and Icons

hovering over icon & look lower left

8. View Builder

5 items for creating “molecules”

UNDO = ctrl-z

REDO = ctrl-y

Positioning

bond length

angle

dihedral

options to know about

inquire

add valence

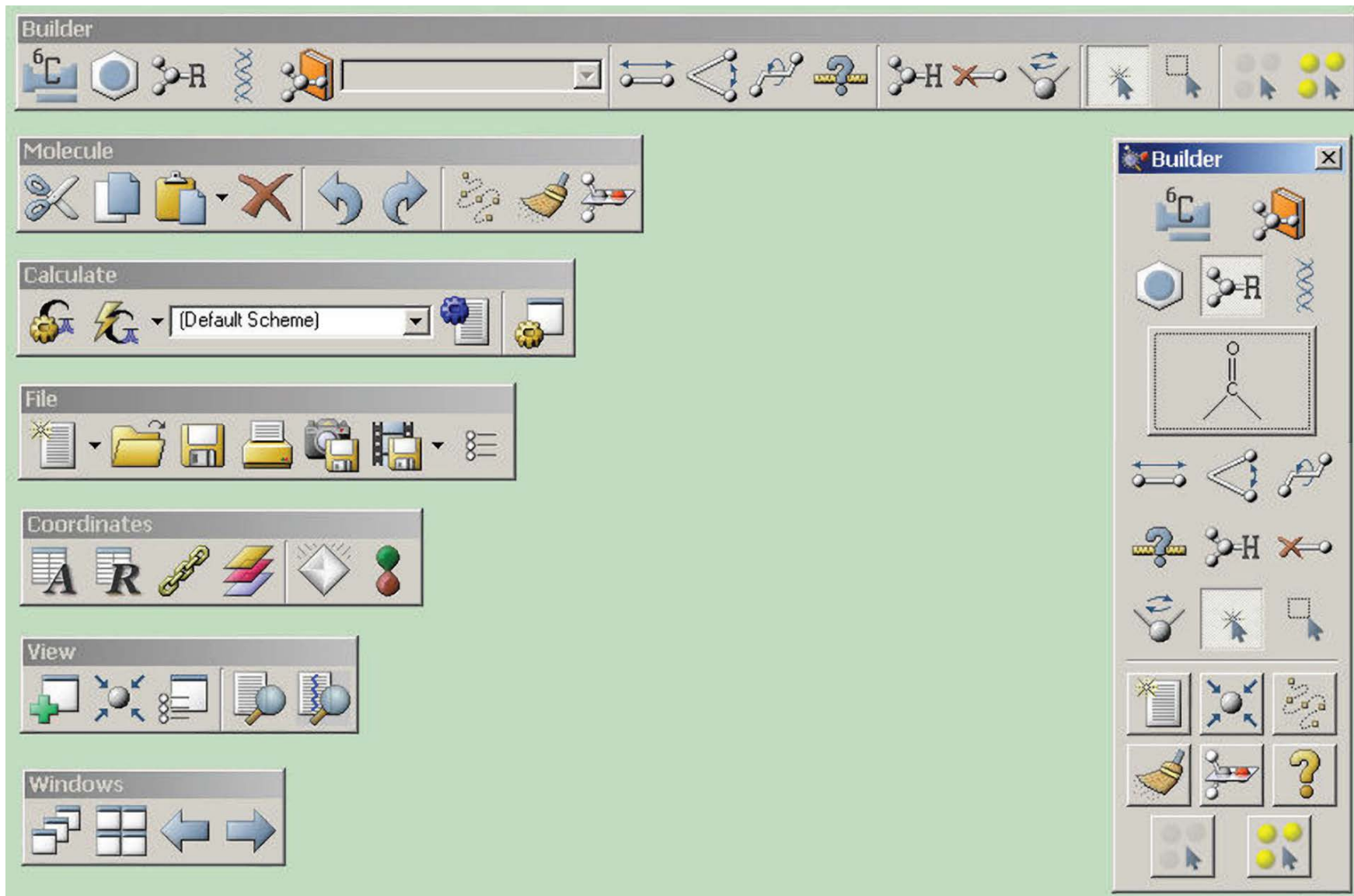
delete atom

selecting

clean

symmetrize

All of the Tool Bars:



5 tools for constructing a molecule

get forms any element by clicking
on any atom

pick one of an assortment of rings

pick one of an assortment common small groups

protein and nucleic acid components

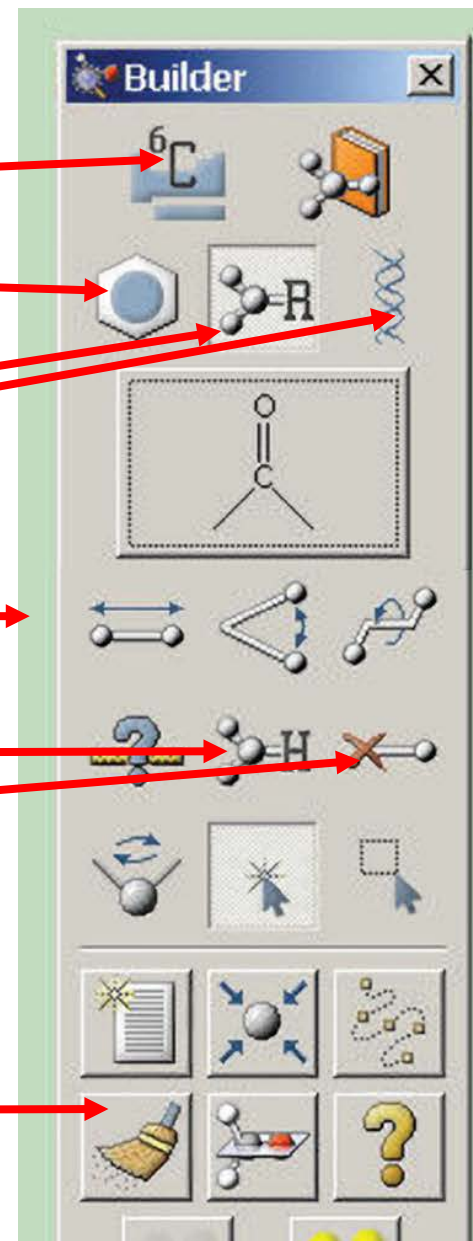
measuring and changing:

bond lengths, angles, and dihedrals

Add a valence (H atom):

delete an atom:

“Clean”: will roughly optimize the structure you
have made



UNDO = control-z

REDO = control-y

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The essential ingredients of this file come in the following order: the *route section* (or “**route card**”) begins with #, and contains the method/basis (e.g., hf/6-31g) and other key words (separated by any number of spaces, in any order, case insensitive (non-ambiguous abbreviations are allowed)). The route section may contain any number of lines, terminated by a blank line.

Example input file for H₂O: h2o-1.gjf

```
%chk=mydirectory/h2o-1.chk
```

```
# hf/3-21g opt pop=full
```

```
Title info
```

```
0 1
```

```
o 0. 0. 0.
```

```
h 1. 0. 0.
```

```
h 0. 1. 0.
```

← blank lines mark the different sections of input

Next is the *net charge and multiplicity*. (multiplicity = degeneracy of the total electron spin state = $2S + 1$. Total **ANY** angular momentum squared = $S(S+1)(h/2\pi)^2$. For a singlet state (closed shell ground state is always singlet) $S=0$, $2S+1 = 1$. For a doublet, $S=1/2$, i.e., (1 unpaired electron), $2S + 1 = 2$; and for triplet $2S+1 = 3$ (2 unpaired electrons with z component electron spin quantum numbers, $m_s = -1, 0, 1$).

Next is a list of *atom symbols or atomic numbers and coordinates* given as either a set of x,y,z values or by a *Z-matrix*. Important: numerical coordinates **must have decimal points**, with spaces between. Exact positioning does not matter.

The list of atoms and coordinates **must end with a blank line**

“Optimizing” geometry, keyword = opt

This means the program will do a series of variation calculations, compute the force on each atom and move the atoms accordingly a little bit, and repeat the process until *forces are essentially zero* on each atom.

Will this process find the lowest energy geometry for a molecule???

Outline -3

8. Display MOs

9. Vibrations

Examples

create GFP

benzene normal modes

PBC