

### Linux commands

cd	Change directory
mkdir	Create directory
rmdir	Remove directory
rm	Remove file
cp	Copy file
ls	List of content of current directory

Exemple: `cp he.inp he3216.inp`

This will copy the file he.inp and rename the copy as he3216.inp

### The studied atom/molecule

Multiplicity (n number of unpaired electron)	n+1 (n number of unpaired electron)
Charge	+/-/0

### Run gamess

he.inp	name of the input script
he.out	name of the output script
rungms	run gamess

Exemple : `rungms he>he.out`

Will run gamess with the script he.inp, and give you the output in the file he.out

### Output file

How to see if my calculation worked?

Look density converged in the output file

Where to see the final energy (HF) ?

Right after the message density converged the Hartree Fock energy calculation is provided  
 FINAL RHF ENERGY IS=

Where to see the final energy (MP2/CCSD) ?

Look for a message E (MP2/CCSD) =

How to see the number of basis fonction?

Beginning of the output script there is a recap of the input script, and search for Nb of cartesian basis fonction=

⚠ RHF final energy is always provided even if you don't do HF calculation.

### Input in \$BASIS

STO-nG	GBASIS=	NGAUSS=n
	S=STO	
n-21G	GBASIS=	NGAUSS=n
	S=N21	
n-31G	GBASIS=	NGAUSS=n
	S=N31	
n-311G	GBASIS=	NGAUSS=n
	S=N311	

cc-PVnZ GBASIS=C- !  
 Cn ISPHERE=1  
 in \$CONTROL

x shell NxFUNC=n- x=p, d, f  
 polarisation umber of  
 function set

Semi GBASIS=MNDO  
 empirical methods

GBASIS=AM1

GBASIS=PM3

Exemple:

- ▶ Calculation with 6-31G\* Basis set for He  
 GBASIS=N31 NGAUSS=6 NPFUNC=1
  - ▶ Calculation with 6-31G\*\* Basis set for He  
 GBASIS=N31 NGAUSS=6 NPFUNC=2
- Use P because He is full on s, not on p



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### Input in \$DATA

1. title/details
2. symmetry point group, usually C1
3. empty line, unless symmetry different than C1
4. Atomic coordinates
  - ▶ COORDS=CART
 atome name / nuclear charge / X / Y / Z  
 H 1 0.0 0.0 0.0  
 C 6 1.1 0.0 0.0
  - ▶ COORDS=ZMT
 atom / l / distance / J / angle / K / torsion  
 H 1 1.1 2 125.0 3 180.0
  - ▶ COORDS=ZMTMPC
 atom / distance / l / angle / l / torsion / l / J / K  
 H 1.1 1 125.0 1 180.0 1 2 3

⚠ For COORDS=ZMT and COORDS=ZMTMPC, only put the required data !

Atom 1 : only name

Atome 2 : name + distance

Atome 3 : name + distance + angle

Atome 4 and + : all data

### Input in \$CONTRL

Method/Wave function choice	Close Shell System	SCFTY= P=RHF default
	Open Shell System	SCFTYP= UHF
		SCFTYP= ROHF
		SCFTY= P=GVB
		SCFTYP= MCSCF
Electron correlation method	Mollera-P-lesseta MPn	MPLV= L=n
	DFT	DFTYP= word
	coupled-cluster CC	CCTYP= word
	configuration interaction CI	CITYP= word
	valence bond VB	VBYP= word
	TDDFT	TDDFT= word

### Input in \$CONTRL (cont)

Other	Charge <i>n</i> of molecule	ICHARG= <i>n</i>
	Multiplicity <i>n</i> of molecule	MULT= <i>n</i>
	Format of geometry in \$DATA	COORDS= word

DFT method's words: VWN/BP86/BLYP . . .  
 CC method's words: CCD/CCSD/CCSD (-T) . . .  
 Words for coordinates: CART/-ZMT/ZMTMPC



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