(1 July 2016)

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* Section 2 - Input Description *
*                                *
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This section of the manual describes the input to GAMESS. The section is written in a reference, rather than tutorial fashion. However, there are frequent reminders that more information can be found on a particular input group, or type of calculation, in the 'Further Information' section of this manual. Numerous complete input files are shown in the 'Input Examples' section.

Note that this chapter of the manual can be searched online by means of the "gmshelp" command, if your computer runs Unix. A command such as

```
gmshelp scf
```

will display the $SCF input group. With no arguments, the gmshelp command will show you all of the input group names. Type "<return>" to see the next screen, "b" to back up to the previous screen, and "q" to exit the pager. If gmshelp does not work, ask the person who installed GAMESS to fix the 'gmshelp' script, as it is extremely useful.

The order of this section is chosen to approximate the order in which most people prepare their input ($CONTRL, $BASIS/$DATA, $GUESS, and so on). The next few pages contain a list of all possible input groups, grouped in this way. The PDF version of this file contains an index of all group names in alphabetical order.

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name	function	module:routine

Molecule, basis set, wavefunction specification:

$CONTRL	chemical control data	INPUTA:START
$SYSTEM	computer related options	INPUTA:START
$BASIS	basis set	INPUTB:BASISS
$DATA	molecule, geometry, basis set	INPUTB:MOLE
$ZMAT	internal coordinates	ZMATRX:ZMATIN
$LIBE	linear bend coordinates	ZMATRX:LIBE
$SCF	HF-SCF wavefunction control	SCFLIB:SCFIN
$SCFMI	SCF-MI input control data	SCFMI :MIINP
$DFT	density functional theory	DFT :DFTINP
$TDDFT	time-dependent DFT	TDDFT :TDDINP
$CIS	singly excited CI	CISGRD:CISINP
$CISVEC	vectors for CIS	CISGRD:CISVRD
$MP2	2nd order Moller-Plesset	MP2 :MP2INP
$RIMP2	resolution of the identity MP2	RIMP2 :RIDRVR
$AUXBAS	RI-MP2's basis set specification	RIMP2 :RIDRVR
$CCINP	coupled cluster input	CCSDT :CCINP
$EOMINP	equation of motion CC	EOMCC :EOMINP
$MOPAC	semi-empirical specification	MPCMOL:MOLDAT
$GUESS	initial orbital selection	GUESS :GUESMO
$VEC	orbitals (formatted)	GUESS :READMO
$MOFRZ	freezes MOs during SCF runs	EFPCOV:MFRZIN
$DFTB	DFTB input	DFTBLB:INPUT
$DFTBSK	Slater-Koster table input	DFTBSK:SKTAB

Note that MCSCF and CI input is listed below.

Potential energy surface options:

$STATPT	geometry search control	STATPT:SETSIG
$TRUDGE	nongradient optimization	TRUDGE:TRUINP
$TRURST	restart data for TRUDGE	TRUDGE:TRUDGX
$FORCE	hessian, normal coordinates	HESS :HESSX
$CPHF	coupled-Hartree-Fock options	CPHF :CPINP
$CPMCHF	coupled-MR-Hartree-Fock options	MCPCGX:MCPCGX
$MASS	isotope selection	VIBANL:RAMS
$HESS	force constant matrix (formatted)	HESS :FCMIN
$GRAD	gradient vector (formatted)	HESS :EGIN
$DIPDR	dipole deriv. matrix (formatted)	HESS :DDMIN
$ALPDR	alpha polar. der. (formatted)	RAMAN :ADMIN
$VIB	HESSIAN restart data (formatted)	HESS :HSSNUM
$VIB2	num GRAD/HESS restart (formatted)	HESS :HSSFUL
$VSCF	vibrational anharmonicity	VSCF :VSCFIN
$VIBSCF	VSCF restart data (formatted)	VSCF :VGRID
$GAMMA	3rd nuclear derivatives	HESS :GAMMXX
$EQGEOM	equilibrium geometry data	HESS :FFCARX

$HLOWT	hessian data from equilibrium	HESS :FFCARX
$GLOWT	3rd derivatives at equilibrium	HESS :FFCARX
$IRC	intrinsic reaction coordinate	RXNCRD:IRCX
$DRC	dynamic reaction path	DRC :DRCDRV
$MEX	minimum energy crossing point	MEXING:MEXINP
$CONICL	conical intersection search	
$MD	molecular dynamics trajectory	MDEFP :MDX
$RDF	radial dist. functions for MD	MDEFP :RDFX
$GLOBOP	Monte Carlo global optimization	GLOBOP:GLOPDR
$GLBFRG	Monte Carlo atom groups	GLOBOP:GLOPDR
$GRADEX	gradient extremal path	GRADEX:GRXSET
$SURF	potential surface scan	SURF :SRFINP

Interpretation, properties:

$LOCAL	localized molecular orbitals	LOCAL :LMOINP
$TRUNCN	localized orbital truncations	EFPCOV:TRNCIN
$ELMOM	electrostatic moments	PRPLIB:INPELM
$ELPOT	electrostatic potential	PRPLIB:INPELP
$ELDENS	electron density	PRPLIB:INPELD
$ELFLDG	electric field/gradient	PRPLIB:INPELF
$POINTS	property calculation points	PRPLIB:INPPGS
$GRID	property calculation mesh	PRPLIB:INPPGS
$PDC	MEP fitting mesh	PRPLIB:INPPDC
$MGC	mean gradient charges	
$RADIAL	atomic orbital radial data	PRPPOP:RADWFN
$MOLGRF	orbital plots	PARLEY:PLTMEM
$STONE	distributed multipole analysis	PRPPOP:STNRD
$COMP	thermochemical calculation	COMP :COMPX
$RAMAN	Raman intensity	RAMAN :RAMANX
$NMR	NMR shielding tensors	NMR :NMRX
$MOROKM	Morokuma energy decomposition	MOROKM:MOROIN
$LMOEDA	LMO-based energy decomposition	MOROKM:MMOEDIN
$QMEFP	QM/EFP energy decomposition	EFINP :QMEFPAX
$FFCALC	finite field polarizabilities	FFIELD:FFLDX
$TDHF	time dependent HF of NLO props	TDHF :TDHFX
$TDHFX	TDHF for NLO, Raman, hyperRaman	TDX:FINDTDHFX

Solvation models:

$EFRAG	use effective fragment potential	EFINP :EFINP
$FRAGNAME	specifically named fragment pot.	EFINP :RDSTFR
$FRGRPL	inter-fragment repulsion	EFINP :RDDFRL
$EWALD	Ewald sums for EFP electrostatics	EWALD :EWALDX
$MAKEFP	generate effective fragment pot.	EFINP :EFPX
$PRTEFP	simplified EFP generation	EFINP :PREFIN
$DAMP	EFP multipole screening fit	CHGPEN:CGPINP
$DAMPGS	initial guess screening params	CHGPEN:CGPINP
$PCM	polarizable continuum model	PCM :PCMINP

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$PCMGRD  PCM gradient control              PCMCV2:PCMGIN
$PCMCAV  PCM cavity generation             PCM   :MAKCAV
$TESCAV  PCM cavity tesselation            PCMCV2:TESIN
$REORG   solvent reorganization in IEF-PCM REORG :RORGIN
$NEWCAV  PCM escaped charge cavity         PCM   :DISREP
$IEFPCM  PCM integral equation form. data  PCM   :IEFDAT
$PCMITR  PCM iterative IEF input           PCMIEF:ITIEFIN
$DISBS   PCM dispersion basis set          PCMDIS:ENLBS
$DISREP  PCM dispersion/repulsion          PCMVCH:MORETS
$SVP     Surface Volume Polarization model SVPINP:SVPINP
$SVPIRF  reaction field points (formatted) SVPINP:SVPIRF
$COSGMS  conductor-like screening model    COSMO :COSMIN
$SCRF    self consistent reaction field    SCRF  :ZRFINP

Integral, and integral modification options:

$ECP     effective core potentials         ECPLIB:ECPPAR
$MCP     model core potentials             MCPINP:MMPRED
$RELWFN  scalar relativistic integrals     INPUTB:RWFINP
$EFIELD  external electric field           PRPLIB:INPEF
$INTGRL  2e- integrals                     INT2A :INTIN
$FMM     fast multipole method             QMFM  :QFMMIN
$TRANS   integral transformation           TRANS :TRFIN

Fragment Molecular Orbital method:

$FMO     define FMO fragments              FMOIO :FMOMIN
$FMOPRP  FMO properties and convergers     FMOIO :FMOPIN
$FMOXYZ  atomic coordinates for FMO        FMOIO :FMOXYZ
$AFOMOD  capping atom input for FMO
$OPTFMO  input for special FMO optimizer   FMOGRD:OPTFMO
$FMOHYB  localized MO for FMO boundaries   FMOIO :FMOLMO
$FMOBND  FMO bond cleavage definition      FMOIO :FMOBON
$FMOENM  monomer energies for FMO restart  FMOIO :EMINOU
$FMOEND  dimer energies for FMO restart    FMOIO :EDIN
$OPTRST  OPTFMO restart data               FMOGRD:RSTOPT
$GDDI    group DDI definition              INPUTA:GDDINP

Polymer model:

$ELG     polymer elongation method         ELGLIB:ELGINP

Divide and conquer model:

$DANDC   DC SCF input                      DCLIB :DCINP
$DCCORR  DC correlation method input       DCLIB :DCCRIN
$SUBSCF  subsystem definition for SCF      DCLIB :DFLCST
$SUBCOR  subsystem definition for MP2/CC   DCLIB :DFLCST
$MP2RES  restart data for DC-MP2           DCMP2 :RDMPDC
```

```
$CCRES   restart data for DC-CC            DCCC  :RDCCDC

clusters in molecules

$CIMINP  controls clusters in molecules    CIMINF:CIMINP
$CIMATM  fine tune calculation level       CIMINF:CIMINP
$CIMFRG  fine tune atomic fragmentation    CIMINF:CIMPRT

quantum mechanics/molecular mechanics model:

$QUANPO  QuanPol calculation               QUANPO:QUANPOL
$FFDATA  QuanPol coordinates for molecules QUANPO:QUANPOL
$FFDATB  QuanPol coordinates for molecules QUANPO:QUANPOL
$FFPDB   QuanPol coordinates for proteins  QUANPO:QUANPOL


MCSCF and CI wavefunctions, and their properties:

$CIINP   control over CI calculation       GAMESS:WFNCI
$DET     determinant full CI for MCSCF     ALDECI:DETINP
$CIDET   determinant full CI               ALDECI:DETINP
$GEN     determinant general CI for MCSCF  ALGNCI:GCIINP
$CIGEN   determinant general CI            ALGNCI:GCIINP
$ORMAS   determinant multiple active space ORMAS :FCINPT
$CEEIS   CI energy extrapolation           CEEIS :CEEISIN
$CEDATA  restart data for CEEIS            CEEIS :RDCEEIS
$GCILST  general MCSCF/CI determinant list ALGNCI:GCIGEN
$GMCPT   general MCSCF/CI determinant list GMCPT :OSRDDAT
$PDET    parent determinant list           GMCPT :OSMKREF
$ADDDET  add determinants to reference     GMCPT :OSMKREF
$REMDET  remove determinants from ref.     GMCPT :OSMKREF
$SODET   determinant second order CI       FSODCI:SOCINP
$DRT     GUGA distinct row table for MCSCF GUGDRT:ORDORB
$CIDRT   GUGA CI (CSF) distinct row table  GUGDRT:ORDORB
$MCSCF   control over MCSCF calculation    MCSCF :MCSCF
$MRMP    MRPT selection                    MP2   :MRMPIN
$DETPT   det. multireference pert. theory  DEMRPT:DMRINP
$MCQDPT  CSF multireference pert. theory   MCQDPT:MQREAD
$EXCORR  interface to MPQC's R12 program   EXCORR:GETEXC
$CASCI   IVO-CASCI input                   IVOCAS:IVODRV
$IVOORB  fine tuning of IVO-CASCI          IVOCAS:ORBREAD
$CISORT  GUGA CI integral sorting          GUGSRT:GUGSRT
$GUGEM   GUGA CI Hamiltonian matrix        GUGEM :GUGAEM
$GUGDIA  GUGA CI diagonalization           GUGDGA:GUGADG
$GUGDM   GUGA CI 1e- density matrix        GUGDM :GUGADM
$GUGDM2  GUGA CI 2e- density matrix        GUGDM2:GUG2DM
$LAGRAN  GUGA CI Lagrangian                LAGRAN:CILGRN
$TRFDM2  GUGA CI 2e- density backtransform TRFDM2:TRF2DM
$DIABAT  diabatic states                   DIAB:DIABINP
```

```
$TRANST  transition moments, spin-orbit    TRNSTN:TRNSTX

* this column is more useful to programmers than to users.
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$CONTRL group (note: only one "oh"!)

This group specifies the type of wavefunction, the type of calculation, use of core potentials, spherical harmonics, coordinate choices, and similar fundamental job options.

Because this is a very long input group, here is a short list of its most important keywords:
SCFTYP, MPLEVL, CITYP, CCTYP, DFTTYP, TDDFT
RUNTYP, ICHARG, MULT, RELWFN/PP, NZVAR, ISPHER

SCFTYP specifies the self-consistent field wavefunction. You may choose from

= RHF Restricted Hartree Fock calculation (default)

= UHF Unrestricted Hartree Fock calculation

= ROHF Restricted open shell Hartree-Fock. (high spin, see GVB for low spin)

= GVB Generalized valence bond wavefunction, or low spin ROHF. (needs $SCF input)

= MCSCF Multiconfigurational SCF wavefunction (this requires $DET or $DRT input)

= NONE indicates a single point computation, rereading a converged SCF function. This option requires that you select CITYP=ALDET, ORMAS, FSOCI, GENCI, or GUGA, requesting only RUNTYP=ENERGY or TRANSITN, and using GUESS=MOREAD.

The treatment of electron correlation for the above SCF wavefunctions is controlled by the keywords DFTTYP, VBTYP, MPLEVL, CITYP, and CCTYP contained in this group. No more than one of these may be chosen in a single run (except as part of RUNTYP=SURFACE). Scalar relativistic effects may be incorporated using RELWFN for any of these wavefunction choices, correlated or not.

```
DFTTYP = NONE      ab initio computation (default)
       = XXXXXX    perform density functional theory run,
                   using the functional specified.  Many
                   choices for XXXXXX are listed in the
                   $DFT and $TDDFT input groups.

TDDFT  = NONE      no excited states (default)
       = EXCITE    generate time-dependent DFT excitation
                   energies, using the DFTTYP= functional,
                   for RHF or UHF references.  Analytic
                   nuclear gradients are available for RHF.
                   See $TDDFT.
       = SPNFLP    spin-flip TD-DFT, for either UHF or ROHF
                   references.  Nuclear gradients and
                   solvent effects are coded. See $TDDFT.
       = POL       (hyper)polarizability calculation, for
                   RHF only.  See $TDDFT.

                        * * * * *

VBTYP  = NONE      no valence bond calculation (default)
       = VB2000    use the VB2000 program to generate VB
                   wavefunctions, for SCFTYP=RHF or ROHF.
                   Analytic nuclear gradients are not
                   available. A $VB2000 input group is
                   required.  See
                     ~/gamess/vb2000/DOC/readme.GAMESS
                   for info about $VB2000, and see also
                     http://www.scinetec.com/~vb

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MPLEVL =           chooses Moller-Plesset perturbation
                   theory level, after the SCF.  See $MP2,
                   or $MRMP for MCSCF.
       = 0         skip the MP computation (default)
       = 2         perform second order energy correction.
```

MP2 (a.k.a. MBPT(2)) is implemented for RHF, UHF, ROHF, and MCSCF wavefunctions, but not GVB. Gradients are available for RHF, UHF, or ROHF based MP2, but for MCSCF, you must choose numerical derivatives to use any RUNTYP other than ENERGY, TRUDGE, SURFACE, or FFIELD.

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CITYP = chooses CI computation after the SCF, for any SCFTYP except UHF.
- = NONE skips the CI. (default)
- = CIS single excitations from a SCFTYP=RHF reference, only. This is for excited states, with analytic nuclear gradients available. See the $CIS input group.
- = SFCIS spin-flip style CIS, see $CIS input.
- = ALDET runs the Ames Laboratory determinant full CI package, requiring $CIDET.
- = ORMAS runs an Occupation Restricted Multiple Active Space determinant CI. The input is $CIDET and $ORMAS.
- = FSOCI runs a full second order CI using determinants, see $CIDET and $SODET.
- = GENCI runs a determinant CI program that permits arbitrary specification of the determinants, requiring $CIGEN.
- = GUGA runs the Unitary Group CI package, which requires $CIDRT input. Analytic gradients are available only for RHF, so for other SCFTYPs, you may choose only RUNTYP=ENERGY, TRUDGE, SURFACE, FFIELD, TRANSITN.

PMTD1 = For CITYP=ALDET or ORMAS, or for these two CI steps in MCSCF runs, for EFP solvent calculations, this flag enables use of "polarization method 1" for the effective fragments. See also FSTATE in $CIDET or $DET
- = .TRUE. The EFP dipoles will not be re-polarized to the CITYP wavefunction (default)
- = .FALSE. The EFP dipoles will be re-polarized to the CITYP wavefunction

* * * * *

CCTYP chooses a Coupled-Cluster (CC calculation for the ground state and, optionally, Equation of Motion Coupled-Cluster (EOMCC) computation for excited states, both performed after the SCF (RHF or ROHF). See also $CCINP and $EOMINP.

```
 Only CCSD and CCSD(T) for RHF can run in parallel.
 For ROHF, you may choose only CCSD and CR-CCL.

= NONE      skips CC computation (default).
= LCCD      perform a coupled-cluster calculation
            using the linearized coupled-cluster
            method with double excitations.
= CCD       perform a CC calculation using the
            coupled-cluster method with doubles.
= CCSD      perform a CC calculation with both
            single and double excitations.
= CCSD(T)   in addition to CCSD, the non-iterative
            triples corrections are computed, giving
            standard CCSD[T] and CCSD(T) energies.
= R-CC      in addition to all CCSD(T) calculations,
            compute the renormalized R-CCSD[T] and
            R-CCSD(T) energies.
= CR-CC     in addition to all R-CC calculations,
            the completely renormalized CR-CCSD[T]
            and CR-CCSD(T) energies are computed.
= CR-CCL    in addition to a CCSD ground state, the
            non-iterative triples energy correction
            defining the rigorously size extensive
            completely renormalized CR-CC(2,3), also
            called CR-CCSD(T)_L theory, is computed.
            Ground state only (zero NSTATE vector)
            CCTYP=CR-EOM type CR-EOMCCSD(T) energies
            and CCSD properties are also generated.
            For further information about accuracy,
            and A to D CR-CC(2,3) energy types,
            see REFS.DOC.
= CCSD(TQ)  in addition to all R-CC calculations,
            non-iterative triple and quadruple
            corrections are used, to give CCSD(TQ)
            and various R-CCSD(TQ) energies.
= CR-CC(Q)  in addition to all CR-CC and CCSD(TQ)
            calculations, the CR-CCSD(TQ) energies
            are obtained.

     excited state options, note that EOM-CCSD
     is available for RHF or ROHF references,
     but triples corrections only for RHF cases.
= EOM-CCSD  in addition to a CCSD ground state,
            excited states are calculated using the
            equation of motion coupled-cluster
```

```
                method with singles and doubles.
        = CR-EOM    in addition to the CCSD and EOM-CCSD,
                    noniterative triples corrections to CCSD
                    ground-state and EOM-CCSD excited-state
                    energies are found, using completely
                    renormalized CR-EOMCCSD(T) approaches.
        = CR-EOML   in addition to printing all results that
                    CR-EOM obtains, this solves the lambda
                    equations, and gives triples corrections
                    analogous to ground state CR-CCL.

             ionization processes,
        = IP-EOM2   ionized EOMCC with up to 2h1p
                    excitations (i.e., IP-EOMCCSD)
        = IP-EOM3A  ionized EOMCC with all 1h and 2h1p,
                    and active-space 3h2p  excitations
                    (i.e., IP-EOMCCSDt)
        = EA-EOM2   electron-attached EOMCC with up to 2p1h
                    excitations (i.e., EA-EOMCCSD)
        = EA-EOM3A  electron-attached EOMCC with all 1p and
                    2p1h, and active-space 3p2h excitations
                    (i.e., EA-EOMCCSDt).
```

Labels "p" and "h" in the description of IP and EA EOMCC methods refer to particles (unoccupied correlated orbitals) and holes (occupied correlated orbitals). EA and IP runs produce both ground and excited states of systems obtained by attaching an electron to or removing an electron from the underlying CCSD reference ground state, using the EOMCC formalism. Thus, EA and IP runs read $CCINP as well as $EOMINP inputs.

Any publication describing the results of CC calculations obtained using GAMESS should reference the appropriate papers, which are listed on the output of every run, and in chapter 4 of this manual.

Analytic gradients are not available, so use CCTYP only for RUNTYP=ENERGY, TRUDGE, SURFACE, or maybe FFIELD, or request numerical derivatives.

Generally speaking, the Renormalized energies are obtained at similar cost to the standard values, while Completely Renormalized energies cost twice the time. For usage tips and more information about resources on the various Coupled Cluster methods, see Section 4, 'Further Information'.

```
CIMTYP   chooses a Cluster-In-Molecule (CIM) calculation.
       = NONE      skip CIM computation, i.e., perform
                   a canonical calculation (default).
       = SECIM     perform a single-environment CIM (SECIM)
                   computation.
       = DECIM     perform a dual-environment CIM (DECIM)
                   computation.
       = GSECIM    perform a generalized SECIM (GSECIM)
                   computation. The $CIMFRG must be
                   included as well.
See also $CIMINP and, optionally, $CIMFRG and $CIMATM.
If CIMTYP is given, SUBMTD in $CIMINP is required. Only
RUNTYP=ENERGY and SCFTYP=RHF or ROHF work when CIMTYP is
given. See SUBMTD in $CIMINP for more details.

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RELWFN   Selects all-electron scalar relativity treatment.
         See the $RELWFN input group for more information,
         including nuclear derivative availability.
       = NONE use the basic Schrodinger equation (default)
       = LUT-IOTC local unitary transformation modification
            of IOTC, due to H.Nakai, J.Seino, Y.Nakajima.
            This is the fastest and most numerically
            reliable scalar relativity method, so it is
            preferred over RESC, DK, or IOTC.
       = IOTC infinite-order two-component method of
            M. Barysz and A.J. Sadlej.
       = DK   Douglas-Kroll transformation, available at
            the 1st, 2nd, or 3rd order.
       = RESC relativistic elimination of small component,
            the method of T. Nakajima and K. Hirao,
            available at 2nd order only.
       = NESC normalised elimination of small component,
            the method of K. Dyall, 2nd order only.

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RUNTYP             specifies the type of computation, for
                   example at a single geometry point:

       = ENERGY    Molecular energy. (default)
       = GRADIENT  Molecular energy plus gradient.
       = HESSIAN   Molecular energy plus gradient plus
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                second derivatives, including harmonic
                harmonic vibrational analysis.
                See the $FORCE and $CPHF input groups.
                For FMO, use FMOHESS instead of HESSIAN.
        = FMOHESS   the same as HESSIAN, for FMO runs,
                supported only for RHF, R-DFT, UHF,
                U-DFT, and ROHF.
        = GAMMA     Evaluate up to 3rd nuclear derivatives,
                by finite differencing of Hessians.
                See $GAMMA, and also NFFLVL in $CONTRL.

                multiple geometry options:

        = OPTIMIZE  Optimize the molecular geometry using
                analytic energy gradients. See $STATPT.
        = TRUDGE    Non-gradient total energy minimization.
                See $TRUDGE and $TRURST.
        = SADPOINT  Locate saddle point (transition state).
                See $STATPT.
        = MEX       Locate minimum energy crossing point on
                the intersection seam of two potential
                energy surfaces.  See $MEX.
        = CONICAL   Locate conical intersection point on
                the intersection seam of two potential
                energy surfaces.  See $CONICL.
        = IRC       Follow intrinsic reaction coordinate.
                See $IRC.
        = VSCF      anharmonic vibrational corrections.
                See $VSCF.
        = DRC       Follow dynamic reaction coordinate.
                See $DRC.
        = MD        molecular dynamics trajectory, see $MD.
        = GLOBOP    Monte Carlo-type global optimization.
                See $GLOBOP.
        = OPTFMO    genuine FMO geometry optimization using
                nearly analytic gradient.  See $OPTFMO.
        = GRADEXTR  Trace gradient extremal.  See $GRADEX.
        = SURFACE   Scan linear cross sections of the
                potential energy surface.  See $SURF.

                single geometry property options:

        = COMP      composite thermochemistry calculation,
                including G3MP2.  See $COMP input.
        = G3MP2     evaluate heat of formation using the
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                G3(MP2,CCSD(T)) methodology.  See test
                example exam43.inp for more information.
        = PROP  Molecular properties will be calculated.
                Orbital localization can be requested as
                well.  See $ELPOT, etc.
                Converged orbitals must be input in a
                $VEC input, which suffice to reproduce
                the wavefunction only for simple SCF:
                RHF, UHF, ROHF, or DFT counterparts.
                GVB also works (CICOEF may be needed).
                All other calculations must instead use
                RUNTYP=ENERGY to regenerate the density
                matrix.
        = RAMAN computes Raman intensities, see $RAMAN.
        = NACME non-adiabatic coupling matrix element
                between two or more state averaged MCSCF
                wavefunctions.  The calculation has no
                specific input group, but must use only
                SCFTYP=MCSCF with CISTEP=ALDET or ORMAS.
        = NMR   NMR shielding tensors for closed shell
                molecules by the GIAO method.  See $NMR.
        = EDA   Perform energy decomposition analysis.
                Give one of $MOROKM or $LMOEDA inputs.
        = QMEFPEA QM/EFP solvent energy analysis,
                see $QMEFP.
        = TRANSITN Compute radiative transition moment or
                spin-orbit coupling.  See $TRANST.
        = FFIELD applies finite electric fields, most
                commonly to extract polarizabilities.
                See $FFCALC.
        = TDHF  analytic computation of time dependent
                polarizabilities.  See $TDHF.
        = TDHFX extended TDHF package, including nuclear
                polarizability derivatives, and Raman
                and Hyper-Raman spectra.  See $TDHFX.
        = MAKEFP creates an effective fragment potential,
                for SCFTYP=RHF or ROHF only.
                See $MAKEFP, $DAMP, $DAMPGS, $STONE, ...
        = FMO0  performs the free state FMO calculation.
                See $FMO.

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 Note that RUNTYPs which require the nuclear gradient are
        GRADIENT, HESSIAN, OPTIMIZE, SADPOINT,
        GLOBOP, IRC, GRADEXTR, DRC, and RAMAN
```

```
 These are efficient with analytic gradients, which are
 available only for certain CI or MP2 calculations, but no
 CC calculations, as indicated above.  See NUMGRD.
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

NUMGRD             Flag to allow numerical differentiation
                   of the energy.  Each gradient requires
                   the energy be computed twice (forward
                   and backward displacements) along each
                   totally symmetric modes.  It is thus
                   recommended only for systems with just a
                   few symmetry unique atoms in $DATA.
                   The default is .FALSE.

EXETYP = RUN       Actually do the run. (default)
       = CHECK     Wavefunction and energy will not be
                   evaluated.  This lets you speedily
                   check input and memory requirements.
                   See the overview section for details.
                   Note that you must set PARALL=.TRUE.
                   in $SYSTEM to test distributed memory
                   allocations.
       = DEBUG     Massive amounts of output are printed,
                   useful only if you hate trees.
       = routine   Maximum output is generated by the
                   routine named.  Check the source for
                   the routines this applies to.

                 * * * * * * *

ICHARG =           Molecular charge.  (default=0, neutral)

MULT   =           Multiplicity of the electronic state
       = 1         singlet (default)
       = 2,3,...   doublet, triplet, and so on.

   ICHARG and MULT are used directly for RHF, UHF, ROHF.
   For GVB, these are implicit in the $SCF input, while
   for MCSCF or CI, these are implicit in $DRT/$CIDRT or
   $DET/$CIDET input.  You must still give them correctly.

  * * * the next three control molecular geometry * * *

COORD  = choice for molecular geometry in $DATA.
       = UNIQUE    only the symmetry unique atoms will be
```

```
                given, in Cartesian coords (default).
       = HINT   only the symmetry unique atoms will be
                given, in Hilderbrandt style internals.
       = PRINAXIS  Cartesian coordinates will be input,
                and transformed to principal axes.
                Please read the warning just below!!!
       = ZMT    GAUSSIAN style internals will be input.
       = ZMTMPC MOPAC style internals will be input.
       = FRAGONLY  means no part of the system is treated
                by ab initio means, hence $DATA is not
                given. The system is defined by $EFRAG.
```

Note: the choices PRINAXIS, ZMT, ZMTMPC require input of all atoms in the molecule. They also orient the molecule, and then determine which atoms are unique. The reorientation is likely to change the order of the atoms from what you input. When the point group contains a 3-fold or higher rotation axis, the degenerate moments of inertia often cause problems choosing correct symmetry unique axes, in which case you must use COORD=UNIQUE rather than Z-matrices.

Warning: The reorientation into principal axes is done only for atomic coordinates, and is not applied to the axis dependent data in the following groups: $VEC, $HESS, $GRAD, $DIPDR, $VIB, nor Cartesian coords of effective fragments in $EFRAG. COORD=UNIQUE avoids reorientation, and thus is the safest way to read these.

Note: the choices PRINAXIS, ZMT, ZMTMPC require the use of a group named $BASIS to define the basis set. The first two choices might or might not use $BASIS, as you wish.

```
UNITS  = distance units, any angles must be in degrees.
       = ANGS      Angstroms (default)
       = BOHR      Bohr atomic units

NZVAR  = 0  Use Cartesian coordinates (default).
       = M  If COORD=ZMT or ZMTMPC, and $ZMAT is not given:
            the internal coordinates will be those defining
            the molecule in $DATA.  In this case, $DATA may
            not contain any dummy atoms.  M is usually
            3N-6, or 3N-5 for linear.
       = M  For other COORD choices, or if $ZMAT is given:
            the internal coordinates will be those defined
```

```
            in $ZMAT.  This allows more sophisticated
            internal coordinate choices.  M is ordinarily
            3N-6 (3N-5), unless $ZMAT has linear bends.

  NZVAR refers mainly to the coordinates used by OPTIMIZE
  or SADPOINT runs, but may also print the internal's
  values for other run types.  You can use internals to
  define the molecule, but Cartesians during optimizations!

                  * * * * * * *

Pseudopotentials may be of two types:  ECP (effective core
potentials) which generate nodeless valence orbitals, and
MCP (model core potentials) producing valence orbitals with
the correct radial nodal structure.  At present, ECPs have
analytic nuclear gradients and Hessians, while MCPs have
analytic nuclear gradients.

PP     =           pseudopotential selection.
       = NONE      all electron calculation (default).
       = READ      read ECP potentials in the $ECP input.
       = SBKJC     use Stevens, Basch, Krauss, Jasien,
                   Cundari ECP potentials for all heavy
                   atoms (Li-Rn are available).
       = HW        use Hay, Wadt ECP potentials for heavy
                   atoms (Na-Xe are available).
       = MCP       use Huzinaga's Model Core Potentials.
                   The correct MCP potential will be chosen
                   to match the requested MCP valence basis
                   set (see $BASIS).

                  * * * * * * *

LOCAL  =          controls orbital localization.
       = NONE     Skip localization (default).
       = BOYS     Do Foster-Boys-like localization.
       = RUEDNBRG Do Edmiston-Ruedenberg localization.
       = POP      Do Pipek-Mezey population localization.
       = SVD      Do single value decomposition, to project
                  the molecular orbitals onto atoms.  This
                  is available only for SCFTYP=RHF, ROHF,
                  and MCSCF (full space or ORMAS).  The
                  ORIENT keyword in $LOCAL is pertinent.
See the related $LOCAL input.
Localization is not available for SCFTYP=GVB.
```

DFTB only works with LOCAL=POP (and NONE).

* * * * * * *

ISPHER = Spherical Harmonics option
- = -1 Use Cartesian basis functions to construct symmetry-adapted linear combination (SALC) of basis functions. The SALC space is the linear variation space used. (default)
- = 0 Use spherical harmonic functions to create SALC functions, which are then expressed in terms of Cartesian functions. The contaminants are not dropped, hence this option has EXACTLY the same variational space as ISPHER=-1. The only benefit to obtain from this is a population analysis in terms of pure s,p,d,f,g functions.
- = +1 Same as ISPHER=0, but the function space is truncated to eliminate all contaminant Cartesian functions [3S(D), 3P(F), 4S(G), and 3D(G)] before constructing the SALC functions. The computation corresponds to the use of a spherical harmonic basis.

QMTTOL = linear dependence threshhold
Any functions in the SALC variational space whose eigenvalue of the overlap matrix is below this tolerence is considered to be linearly dependent. Such functions are dropped from the variational space. What is dropped is not individual basis functions, but rather some linear combination(s) of the entire basis set that represent the linear dependent part of the function space. The default is a reasonable value for most purposes, 1.0E-6.

When many diffuse functions are used, it is common to see the program drop some combinations. On occasion, in multi-ring molecules, we have raised QMTTOL to 3.0E-6 to obtain SCF convergence, at the cost of some energy.

MAXIT = Maximum number of SCF iteration cycles. This pertains only to RHF, UHF, ROHF, or GVB runs. See also MAXIT in $MCSCF. (default = 30)

```
       * * * interfaces to other programs * * *

MOLPLT = flag that produces an input deck for a molecule
         drawing program distributed with GAMESS.
         (default is .FALSE.)

PLTORB = flag that produces an input deck for an orbital
         plotting program distributed with GAMESS.
         (default is .FALSE.)

AIMPAC = flag to create an input deck for Bader's Atoms
         In Molecules properties code. (default=.FALSE.)
         For information about this program, see the URL
         http://www.chemistry.mcmaster.ca/aimpac

DGRID  = flag to add extra digits in molecular orbitals to
         the log file for use by Kohout's DGrid program:
            http://www2.cpfs.mpg.de/~kohout/dgrid.html
         This is one of the modern alternatives to the old
         AIMPAC codes, in the QTAIM/ELF arena.
         (default .FALSE.)

FRIEND = string to prepare input to other quantum
         programs, choose from
       = HONDO    for HONDO 8.2
       = MELDF    for MELDF
       = GAMESSUK for GAMESS (UK Daresbury version)
       = GAUSSIAN for Gaussian 9x
       = ALL      for all of the above

PLTORB, MOLPLT, and AIMPAC decks are written to file
PUNCH at the end of the job.  Thus all of these correspond
to the final geometry encountered during jobs such as
OPTIMIZE, SAPDOINT, IRC...

In contrast, selecting FRIEND turns the job into a
CHECK run only, no matter how you set EXETYP.  Thus the
geometry is that encountered in $DATA.  The input is
added to the PUNCH file, and may require some (usually
minimal) massaging.

PLTORB and MOLPLT are written even for EXETYP=CHECK.
AIMPAC requires at least RUNTYP=PROP.
```

* * *

NFFLVL used to determine energies and gradients away from equilibrium structures, at the coordinates given in $DATA. The method will use a Taylor expansion of the potential surface around the stationary point. See $EQGEOM, $HLOWT, $GLOWT. This may be used with RUNTYP=ENERGY or GRADIENT.
= 2 uses only Hessian information, which gives a reasonable energy, but not such a good gradient.
= 3 uses Hessian and 3rd nuclear derivatives in the Taylor expansion, producing more accurate values for the energy and for the gradient.

* * * computation control switches * * *

For the most part, the default is the only sensible value, and unless you are sure of what you are doing, these probably should not be touched.

NPRINT = Print/punch control flag
See also EXETYP for debug info.
(options -7 to 5 are primarily debug)
= -7 Extra printing from Boys localization.
= -6 debug for geometry searches
= -5 minimal output
= -4 print 2e-contribution to gradient.
= -3 print 1e-contribution to gradient.
= -2 normal printing, no punch file
= 1 extra printing for basis,symmetry,ZMAT
= 2 extra printing for MO guess routines
= 3 print out property and 1e- integrals
= 4 print out 2e- integrals
= 5 print out SCF data for each cycle. (Fock and density matrices, current MOs
= 6 same as 7, but wider 132 columns output. This option isn't perfect.
= 7 normal printing and punching (default)
= 8 more printout than 7. The extra output is (AO) Mulliken and overlap population analysis, eigenvalues, Lagrangians, ...
= 9 everything in 8 plus Lowdin population analysis, final density matrix.

```
NOSYM  = 0     the symmetry specified in $DATA is used
               as much as possible in integrals, SCF,
               gradients, etc.  (this is the default)
       = 1     the symmetry specified in the $DATA input
               is used to build the molecule, then
               symmetry is not used again.   Some GVB
               or MCSCF runs (those without a totally
               symmetric charge density) require you
               request no symmetry.

ETOLLZ  = threshold to label molecular orbitals by Lz
          values. Small matrices of the Lz operator are
          diagonalized for the sets of MOs whose orbital
          energies are degenerate to within ETOLLZ.  This
          option may be used in molecules with distorted
          linear symmetry for approximate labelling.
          Default: 1.0d-6 for linear, 0 (disable) if not.

INTTYP selects the integral package(s) used, all of which
       produce equally accurate results.  This is therefore
       used only for debugging purposes.
       = BEST  use the fastest integral code available for
               any particular shell quartet (default):
                 s,p,L or s,p,d,L rotated axis code first.
                 ERIC s,p,d,f,g precursor transfer equation
                 code second, up to 5 units total ang. mom.
                 Rys quadrature for general s,p,d,f,g,L,
                 or for uncontracted quartets.
       = ROTAXIS means don't use ERIC at all, e.g. rotated
                 axis codes, or else Rys quadrature.
       = ERIC    means don't use rotated axis codes, e.g.
                 ERIC code, or else Rys quadrature.
       = RYSQUAD means use Rys quadrature for everything.

GRDTYP = BEST    use Schlegel routines for spL gradient
                 blocks, and Rys quadrature for all
                 other gradient integrals.  (default)
       = RYSQUAD use Rys quadrature for all gradient
                 integrals.  This option is only slightly
                 more accurate, but is rather slower.

HSSTYP = BEST    use faster routines.
       = GENERAL use slower code (default).

NORMF  = 0     normalize the basis functions (default)
```

```
       = 1     no normalization

NORMP  = 0     input contraction coefficients refer to
               normalized Gaussian primitives. (default)
       = 1     the opposite.

ITOL   =       primitive cutoff factor (default=20)
       = n     products of primitives whose exponential
               factor is less than 10**(-n) are skipped.

ICUT   = n     integrals less than 10.0**(-n) are not
               saved on disk. (default = 9).  Direct
               SCF will calculate to a cutoff 1.0d-10
               or 5.0d-11 depending on FDIFF=.F. or .T.

ISKPRP = 0     proceed as usual
         1     skip computation of some properties which
               are not well parallelised.  This includes
               bond orders and virial theorem, and can help
               parallel scalability if many CPUs are used.
               Note that NPRINT=-5 disables most property
               computations as well, so ISKPRP=1 has no
               effect in that case.  (default: 0)


            * * * restart options * * *

IREST  =       restart control options
               (for OPTIMIZE run restarts, see $STATPT)
               Note that this option is unreliable!
       = -1    reuse dictionary file from previous run,
               useful with GEOM=DAF and/or GUESS=MOSAVED.
               Otherwise, this option is the same as 0.
       = 0     normal run (default)
       = 1     2e restart (1-e integrals and MOs saved)
       = 2     SCF restart (1-,2-e integrals and MOs saved)
       = 3     1e gradient restart
       = 4     2e gradient restart

GEOM   =       select where to obtain molecular geometry
       = INPUT from $DATA input (default for IREST=0)
       = DAF   read from DICTNRY file (default otherwise)
```

    As noted in the first chapter, binary file restart is not a well tested option!

==========

==========

$SYSTEM group (optional)

This group provides global control information for your computer's operation. This is system related input, and will not seem particularly chemical to you!

MWORDS = the maximum replicated memory which your job can use, on every core. This is given in units of 1,000,000 words (as opposed to 1024*1024 words), where a word is defined as 64 bits. (default=1)

In case finer control over the replicated memory is needed, this value can be given in units of words, with the old keyword MEMORY, instead of MWORDS.

MEMDDI = the grand total memory needed for the distributed data interface (DDI) storage, given in units of 1,000,000 words. See Chapter 5 of this manual for an extended explanation of running with MEMDDI.

note: the memory required on each processor core for a run using p cores is therefore MEMDDI/p + MWORDS.

The parallel runs that currently require MEMDDI are:

```
      SCFTYP=RHF   MPLEVL=2 energy or gradient
      SCFTYP=UHF   MPLEVL=2 energy or gradient
      SCFTYP=ROHF  MPLEVL=2 OSPT=ZAPT energy or gradient
      SCFTYP=MCSCF MPLEVL=2 energy
      SCFTYP=MCSCF using the FULLNR or JACOBI convergers
      SCFTYP=MCSCF analytic hessian
      SCFTYP=any   CITYP=ALDET, ORMAS, GUGA
      SCFTYP=any   energy localization
      SCFTYP=RHF   CCTYP=CCSD or CCSD(T)
```

All other parallel runs should enter MEMDDI=0, for they use only replicated memory.
Some serial runs execute the parallel code (on just 1 CPU), for there is only a parallel code. These serial runs must give MEMDDI as a result:

```
      SCFTYP=ROHF  MPLEVL=2 OSPT=ZAPT gradient/property run
      SCFTYP=MCSCF analytic hessian
```

Two kinds of runs (RI-MP2 and parallel CCSD(T)) use an additional type of memory, for which there is no input

```
keyword.  Please read EXETYP=CHECK output carefully to
learn the total memory/node requirements for these two!

TIMLIM =  time limit, in minutes.  Set to about 95 percent
          of the time limit given to the batch job (if you
          use a queueing system) so that GAMESS can stop
          itself gently.  (default=525600.0 minutes)

PARALL =  a flag to cause the program to execute the
          parallel algorithm, in cases where different
          serial and parallel codes exist, if you happen to
          be running on only one core.
          The default is .FALSE. if you are running on one
          core. The main purpose of this keyword is to
          allow you to do EXETYP=CHECK runs on only one
          core, when your intent is perform the actual
          calculation in parallel.
          PARALL is ignored for runs on more than one core,
          when of course parallel algorithms are executed.

KDIAG  =    diagonalization control switch
       = 0  use a vectorized diagonalization routine
            if one is available on your machine,
            else use EVVRSP. (default)
       = 1  use EVVRSP diagonalization.  This may
            be more accurate than KDIAG=0.
       = 2  use GIVEIS diagonalization
            (not as fast or reliable as EVVRSP)
       = 3  use JACOBI diagonalization
            (this is the slowest method)

COREFL =  a flag to indicate whether or not GAMESS
          should produce a "core" file for debugging
          when subroutine ABRT is called to kill
          a job.  This variable pertains only to
          UNIX operating systems.  (default=.FALSE.)

BALTYP = Parallel load balance scheme:
       = SLB uses  static load balancing.
       = DLB uses dynamic load balancing (default).
         Dynamic load balancing attempts to spread out
         possibly unequal work assignments based on the
         rate at which different nodes complete tasks.
               For historical reasons, it is permissible
               to spell SLB as LOOP, and DLB as NXTVAL.
```

```
MXSEQ2 = 300 (default)
MXSEQ3 = 150 (default)
         Matrix/vector problem size in loops requiring
         either O(N**2) or O(N**3) work, respectively.
         Problems below these sizes are run purely serial,
         to avoid poor communication/computation ratios.

NODEXT = array specifying node extensions in GDDI for each
         file.  Non-zero values force no extension.
         E.g., NODEXT(40)=1 forces file 40 (file numbers
         are unit numbers used in GAMESS, see "rungms" or
         PROG.DOC) to have the name of $JOB.F40 on all
         nodes, rather than $JOB.F40, $JOB.F40.001,
         $JOB.F40.002 etc. This is convenient for FMO
         restart jobs, so that the file name need not be
         changed for each node, when copying the restart
         file. Note that on machines when several CPUs use
         the same directory (e.g., SMP) NODEXT should be
         zero. (default: all zeros)

IOSMP  = Parallelise I/O on SMP machines with multiple hard
         disks.  Two parameters are specified, whose
         meaning should be clear from the example.
              iosmp(1)=2,6
         2 refers to the number of HDDs per SMP box.
         6 is the location of the character in the file
         names that switches HDDs, i.e. if HDDs are mounted
         as /work1 and /work2, then 6 refers to the
         position of the number 1 in /work1. The file
         system should permit disks attached with directory
         names differing by one symbol.
         (default: 0,0, disable the feature)

MODIO  = Global I/O options (bitwise additive)
                (default: 0)
         1 - forbid flushing files
         2 - do not close dictionary file in GDDI
             (only record indices are reset)
         4 - do not print timings on each rank at run end.
         8 - forbid grid data saving in DFT
             (prevent F22 from being opened)
        16 - reduce I/O
        32 - do not open file F15 (in SOSCF) on slaves
             and do not close on all.
```

```
         64 - use in-memory F15 (in SOSCF). This also
              parallelizes one more step in SOSCF.
        128 - always run EVVRSP sequentially. This is useful
              on mixed CPU type clusters.
        256 - reduce timing output.
        512 - use XYZ file to store coordinates.

MEM10   = words used to store dictionary file F10 in memory.
          Selecting this option will skip any I/O for F10.
          Default: 0 (disk-based F10)

=============================================================
```

==========

$BASIS group (optional)

This group allows certain standard basis sets to be easily requested. Basis sets are specified by:

a) GBASIS plus optional supplementations such as NDFUNC,
b) BASNAM to read custom basis sets from your input,
c) EXTFIL to read custom bases from an external file,
d) or omit this group entirely, and give the basis set in the $DATA input, which is completely general.

GBASIS requests various Gaussian basis sets. These include options for effective core and model core potentials.

Rather oddly, GBASIS also can select semi-empirical models, and in that case requests the Slater-type orbitals for the MOPAC-type calculation.

Note: The first two groups of GBASIS keywords below (except G3L and G3LX) define only the basic functions, without any polarization functions and/or diffuse functions. For example, main group elements have the basic functions for their s,p valence orbitals. Polarization and/or diffuse supplements are added separately to these GBASIS values, with keywords NPFUNC, NDFUNC, NFFUNC, DIFFS, DIFFSP, POLAR, SPLIT2, and SPLIT3, which are defined at the end of this input group.

```
GBASIS = STO  - Pople's STO-NG minimal basis set.
                Available H-Xe, for NGAUSS=2,3,4,5,6.
       = N21  - Pople's N-21G split valence basis set.
                Available H-Xe, for NGAUSS=3.
                Available H-Ar, for NGAUSS=6.
       = N31  - Pople's N-31G split valence basis set.
                Available H-Ne,P-Cl for NGAUSS=4.
                Available H-He,C-F for NGAUSS=5.
                Available H-Kr, for NGAUSS=6, note that the
                  bases for K,Ca,Ga-Kr were changed 9/2006.
       = N311 - Pople's "triple split" N-311G basis set.
                Available H-Ne, for NGAUSS=6.
                Selecting N311 implies MC for Na-Ar.
       = G3L  - Pople's G3MP2Large basis set, for H-Kr.
```

```
       = G3LX - Pople's G3MP2LargeXP basis set, for H-Kr.

NGAUSS = the number of Gaussians (N).   This parameter
         pertains to GBASIS=STO, N21, N31, or N311.

GBASIS = MINI - Huzinaga's 3 gaussian minimal basis set.
                Available H-Rn.
       = MIDI - Huzinaga's 21 split valence basis set.
                Available H-Rn.
       = DZV  - "double zeta valence" basis set.
                a synonym for DH for H,Li,Be-Ne,Al-Cl.
                (14s,9p,3d)/[5s,3p,1d] for K-Ca.
                (14s,11p,5d/[6s,4p,1d] for Ga-Kr.
       = DH   - Dunning/Hay "double zeta" basis set.
                (3s)/[2s] for H.
                (9s,4p)/[3s,2p] for Li.
                (9s,5p)/[3s,2p] for Be-Ne.
                (11s,7p)/[6s,4p] for Al-Cl.
       = TZV  - "triple zeta valence" basis set.
                (5s)/[3s] for H.
                (10s,3p)/[4s,3p] for Li.
                (10s,6p)/[5s,3p] for Be-Ne.
                a synonym for MC for Na-Ar.
                (14s,9p)/[8s,4p] for K-Ca.
                (14s,11p,6d)/[10s,8p,3d] for Sc-Zn.
       = MC   - McLean/Chandler "triple split" basis.
                (12s,9p)/[6s,5p] for Na-Ar.
                Selecting MC implies 6-311G for H-Ne.
       = MINIX  The minimal basis set for HF-3C, but no
                energy corrections added.
       = HF-3C  The minimal basis set MINIX and three
                add-on energy corrections (3c). These
                three corrections are D3(BJ), GCP and SRB.
                See $DFT's dispersion corrections.

        * * systematic basis set families * * *

These four families provide a hierachy of basis sets
approaching the complete basis set limits.  These families
include relevant polarization and diffuse augmentations, as
indicated in their names.

GBASIS = CCn  - Dunning-type Correlation Consistent basis
                sets, officially called cc-pVnZ.
                Use n = D,T,Q,5,6 to indicate the level of
```

```
          polarization.
          Available for H-He, Li-Ne, Na-Ar, Ca, Ga-Kr
          and for Sc-Zn for n=T,Q.
= ACCn - As CCn, but augmented with a set of diffuse
          functions, e.g. aug-cc-pVnZ.
          Availability is the same as CCn.
= CCnC - As CCn, but augmented with tight functions
          for recovering core and core-valence
          correlation, e.g. cc-pCVnZ.
          Available H-Ar for n=D,T,Q, also n=5 for H-Ne.
= ACCnC- As CCn, augmented with diffuse as well as
          CCnC's tight functions, e.g. aug-cc-pCVnZ.
          Availability is the same as CCnC.
= CCnWC  the omega form of CCnC, e.g. cc-pwCVnZ, for
          H-Ar, for n=T only.  CCnWC's tight
          functions are considered superior to CCnC's
          for recovery of core/valence correlation.
= ACCnWC augmented form of CCnWC: aug-cc-pwCVnZ.
                 See extended notes below!

= PCseg-n -  Polarization Consistent basis sets.
             n = 0,1,2,3,4 indicates the level of
             polarization. (n=0 is unpolarized, n=1
             is ~DZP, n=2 is ~TZ2P, etc.). These
             provide a hierarchy of basis sets
             suitable for DFT and HF calculations.
             Available for H-Kr.
= APCseg-n - These are the PCseg-n bases, with
             diffuse augmentation.
                 See extended notes below!

                Sapporo valence basis sets:
= SPK-nZP  - Sapporo family of non-relativistic
             bases, n=D,T,Q, available H-Xe
= SPK-AnZP - diffuse augmentation of the above.
= SPKrnZP  - Sapporo family of relativistic bases
             n=D,T,Q, available H-Xe.  These should
             be used only with a relativistic
             transformation of the integrals, such
             as RELWFN=LUT-IOTC.
= SPKrAnZP - diffuse augmentation of the above.
                See extended notes below!

                Sapporo core/valence basis sets:
= SPK-nZC  - Sapporo family of non-relativistic
```

```
                bases, n=D,T,Q, available H-Xe
        = SPK-nZCD - diffuse augmentation of the above.
        = SPKrnZC  - Sapporo family of relativistic bases
                     n=D,T,Q, available H-Rn.
                     To be used only with a relativistic
                     transformation of the integrals, such
                     as RELWFN=LUT-IOTC.
        = SPKrnZCD - diffuse augmentation of the above.
                         See extended notes below!

        = KTZV - Karlsruhe valence triple zeta basis, as
                 developed by Prof.Ahlrichs, see REFS.DOC.
        = KTZVP- Karlsruhe valence triple zeta basis with a
                 set of single polarization (P).
        = KTZVPP-Karlsruhe valence triple zeta basis with a
                 set of double polarization (PP).
                 The Karlsruhe sets are provided for H-Ar.
```

Normally these families are used as spherical harmonics, see ISPHER=1 in $CONTRL. Failure to set ISPHER=1 will result in discrepancies in energy values compared to the literature or other programs, difficulties in converging SCF/DFT, CC, CI, and/or response equation iterations, and longer run times due to retention of unimportant MOs. The calculations will refuse to run without ISPHER being set.

Important note about the PCseg basis set family:

1. These should be used only in spherical harmonic form.
2. The PCn basis sets included in GAMESS versions prior to March 2014 were generally contracted, but were replaced by computationally more efficient segmented contractions, and renamed to PCseg-n. The segemented contractions have the same or slightly better accuracy (especially for n=0) as the original PCn bases, which are no longer available.

Important notes about the CC basis set family:

1. These should be used only in spherical harmonic form.
2. The CC5 and CC6 basis sets (and corresponding augmented versions) contain h-functions, and CC6 also contains i-functions. As of January 2013, GAMESS integral code can correctly use h & i functions, so these three call up the true basis sets. Prior to January 2013, GAMESS' integral codes was restricted to g-functions, so these three

truncated away any h & i functions, to spdfg subsets, and therefore were not the true basis sets.
3. Note that the CC basis sets are generally contracted, which GAMESS can only handle by replicating the primitive basis functions, leading to a less than optimum performance in AO integral evaluation.
4. The implementation of the cc-pVnZ and cc-pCVnZ basis sets for Na-Ar include one additional tight d-function, producing the so-called cc-pV(n+d)Z and cc-pV(n+d)Z sets, which are known to improve results (see J.Chem.Phys. 114, 9244(2001) and Theoret.Chem.Acc. 120, 119(2008)). These tight d versions are invoked by GBASIS=CCn or CCnC (and also their augmented counterparts ACCn or ACC). This means the old (and less accurate) basis sets without the tight d's are not available for Na-Ar.
5. Alkali and alkali earth basis sets (Li,Be,Na,Mg) were changed April 2013 so that regular, diffuse, tight d (for Na/Mg), core/valence, and weighted core/valence sets agree with their official publication: Theor. Chem. Acc. 128, 69(2011).
6. In case you are interested in scalar relativistic effects, the CCT-DK and CCQ-DK sets optimized for use with Douglas/Kroll are available for Sc-Kr. These will be used if you type GBASIS=CCT or CCQ along with RELWFN=RESC, DK, IOTC, or LUT-IOTC, while using NR sets for elements lighter than Sc. DK versions of ACCD or ACCT are available for Sc-Zn (but not for the rest of the row, Ga-Kr).

Notes about the Sapporo basis set family:

1. SPK is the international airport city code for Sapporo.
2. These should be used only in spherical harmonic form.
3. The relativistic core/valence sets are available for all atoms including the 6th row of the periodic table (H-Rn).
4. It is extremely illogical to use any of the all-electron relativistic bases without turning on scalar relativity! So, choose RELWFN=LUT-IOTC (or IOTC, DK, RESC) in $CONTRL.
5. The core/valence basis sets treat (n-1)s,(n-1)p,ns for s-block elements; (n-1)s,(n-1)p,ns,np for p block elements; (n-1)s,(n-1)p,(n-1)d,ns for d block elements, and the 4s-4f,5s-5d,6s for f block (lanthanides). This suggests you should change the default number of core orbitals, such as NACORE in $MP2 or NCORE in $CCINP, to correlate the indicated semi-core orbitals (this is not automatic).

6. The relativistic sets ("r") are identical to the non-relativistic choices ("-") for atoms H-Ar, where scalar relativity has almost no effect on orbital shapes.
7. The relativistic bases were optimized at the 3rd order of the Douglas-Kroll transformation, with a Gaussian nuclei model. It should be fine to use them with any RESC, DK, IOTC, or LUT-IOTC calculation.
8. Because they are stored in an external file supplied with GAMESS, these can only be accessed via GBASIS in this group, not by using them in-line in $DATA.
9. The SPK basis sets were extracted from the data base of Segmented Gaussian Basis Sets, maintained by Takeshi Noro, University of Hokkaido, Sapporo, Japan:
http://setani.sci.hokudai.ac.jp/sapporo/Welcome.do
The mapping between the data base names and the keywords used in GAMESS is (for n=D,T,Q):

data base name	keyword
Sapporo-nZP	SPK-nZP
Sapporo-nZP+diffuse	SPK-AnZP
Sapporo-DK-nZP	SPKrnZP
Sapporo-DK-nZP+diffuse	SPKrAnZP
Sapporo-nZP-2012	SPK-nZC
Sapporo-nZP-2012+diffuse	SPK-nZCD
Sapporo-DK-nZP-2012	SPKrnZC
Sapporo-DK-nZP-2012+diffuse	SPKrnZCD

* * * Effective Core Potential (ECP) bases * * *

GBASIS = SBKJC- Stevens/Basch/Krauss/Jasien/Cundari
valence basis set, for Li-Rn. This choice
implies an unscaled -31G basis for H-He.
= HW - Hay/Wadt valence basis.
This is a -21 split, available Na-Xe,
except for the transition metals.
This implies a 3-21G basis for H-Ne.

* * * Model Core Potential (MCP) bases * * *

Notes: Select PP=MCP in $CONTRL to automatically use the model core potential matching your basis choice below. References for these bases, and other information about

MCPs can be found in the REFS.DOC chapter. Another family covering almost all elements is available in $DATA only.

```
GBASIS = MCP-DZP, MCP-TZP, MCP-QZP -
         a family of double, triple, and quadruple zeta
         quality valence basis sets, which are akin to the
         correlation consistent sets, in that these include
         increasing levels of polarization (and so do not
         require "supplements" like NDFUNC or DIFFSP) and
         must be used as spherical harmonics (see ISPHER).
         Availability:
         MCP-DZP:          56 elements Z=3-88,
                           except V-Zn, Y-Cd, La, Hf-Hg
         MCP-TZP, MCP-QZP: 85 elements Z=3-88, except La
         The basis sets for hydrogen atoms will be the
         corresponding Dunning's cc-pVNZ (N=D,T,Q).

       = MCP-ATZP, MCP-AQZP -
         MCP-TZP and MCP-QZP core potentials whose
         basis sets were augmented with diffuse functions
         Availability: same as for MCP-TZP, MCP-QZP

       = MCPCDZP, MCPCTZP, MCPCQZP -
         based on MCP-DZP, MCP-TZP, MCP-QZP,
         with core-valence functions provided for the
         alkali and alkaline earth atoms Na through Ra.

       = MCPACDZP, MCPACTZP, MCPACQZP -
         based on MCPCDZP, MCPCTZP, MCPCQZP,
         with core-valence functions provided for the
         alkali and alkaline earth atoms Na through Ra, and
         augmented with diffuse functions.
```

The basis sets were extracted from the data base Segmented Gaussian Basis Sets, maintained by Takeshi Noro, Quantum Chemistry Group, Sapporo, Japan:
    http://setani.sci.hokudai.ac.jp/sapporo/Welcome.do
The mapping between the data base names and the names used in GAMESS is

data base name	GAMESS keyword
MCP/NOSeC-V-DZP	MCP-DZP
MCP/NOSeC-V-TZP	MCP-TZP
MCP/NOSeC-V-QZP	MCP-QZP

```
          MCP/NOSeC-V-TZP+diffuse     MCP-ATZP
          MCP/NOSeC-V-QZP+diffuse     MCP-AQZP

          MCP/NOSeC-CV-DZP            MCPCDZP
          MCP/NOSeC-CV-TZP            MCPCTZP
          MCP/NOSeC-CV-QZP            MCPCQZP

          MCP/NOSeC-CV-DZP+diffuse    MCPACDZP
          MCP/NOSeC-CV-TZP+diffuse    MCPACTZP
          MCP/NOSeC-CV-QZP+diffuse    MCPACQZP

GBASIS = IMCP-SR1 and IMCP-SR2 -
         valence basis sets to be used with the improved
         MCPs with scalar relativistic effects.
         These are available for transition metals except
         La, and the main group elements B-Ne, P-Ar, Ge,
         Kr, Sb, Xe, Rn.
         The 1 and 2 refer to addition of first and second
         polarization shells, so again don't use any of the
         "supplements" and do use spherical harmonics.
       = IMCP-NR1 and IMCP-NR2 -
         closely related valence basis sets, but with
         nonrelativistic model core potentials.

GBASIS = ZFK3-DK3, ZFK4-DK3, ZFK5-DK3, or
         ZFK3LDK3, ZFK4LDK3, ZFK5LDK3
These are a family of model core potential basis sets
developed by Zeng/Fedorov/Klobukowski, for the p-block
elements from 2p to 6p.  The potentials were paramaterized
taking into account both DK3 scalar relativistic and DK-SOC
effects.  The fundamental basis functions are from the
Well-Tempered Basis Sets.  The number after ZFK indicates
the augmentation levels, e.g. ZFK3 means the diffuse
functions from aug-cc-pVTZ are added, ZFK4 means from aug-
cc-pVQZ, etc.  The difference between ZFKn-DK3 and ZFKnLDK3
is that the common s and p exponents have been contracted
as a single L-shell for the outermost s and p valence
shells to save time in the "L" case.  The s-block elements
from 1s to 4s have also been put in the library.  For H/He,
all-electron aug-cc-pVnZ basis sets are used.  For Li/Be,
the relativistically contracted atomic natural orbital all-
electron basis sets (ANO-RCC) are used.  For Na/Mg, and
K/Ca, unpublished MCP and basis sets based on ANO-RCC are
available, although the potentials have not been
extensively tested yet.  No d-block elements can be used.
```

```
        * * * semiempirical basis sets * * *

GBASIS = MNDO - selects MNDO model Hamiltonian
       = AM1  - selects AM1 model Hamiltonian
       = PM3  - selects PM3 model Hamiltonian
       = RM1  - selects RM1 model Hamiltonian
       = DFTB - selects tight binding Hamiltonian

Note: The elements for which these exist can be found in
the 'further information' section of this manual.  If you
pick one of these, all other data in this group is ignored.
Semi-empirical runs actually use valence-only Slater type
orbitals (STOs), not Gaussian GTOs, but the keyword remains
GBASIS.

Except for NGAUSS, all other keywords such as NDFUNC, etc.
will be ignored for these.  If you add NGAUSS, STO-NG
expansions of the valence STO functions in terms of
Gaussians will be added to the log file.  Plotting programs
such as MacMolPlt can pick up this approximation to the
STOs used up from the ouput, in order to draw the orbitals.
The default NGAUSS=0 suppresses this output, but values up
to 6 may be given to control the accuracy of the STO-NG
printing.

            --- supplementary functions ---

NDFUNC = number of heavy atom polarization functions to
         be used.  These are usually d functions, except
         for MINI/MIDI.  The term "heavy" means Na on up
         when GBASIS=STO, HW, or N21, and from Li on up
         otherwise.  The value may not exceed 3.  The
         variable POLAR selects the actual exponents to
         be used, see also SPLIT2 and SPLIT3. (default=0)

NFFUNC = number of heavy atom f type polarization
         functions to be used on Li-Cl.  This may only
         be input as 0 or 1.  (default=0)

NPFUNC = number of light atom, p type polarization
         functions to be used on H-He.  This may not
         exceed 3, see also POLAR.  (default=0)
```

```
DIFFSP = flag to add diffuse sp (L) shell to heavy atoms.
         Heavy means Li-F, Na-Cl, Ga-Br, In-I, Tl-At.
         The default is .FALSE.

DIFFS  = flag to add diffuse s shell to hydrogens.
         The default is .FALSE.

Warning: if you use diffuse functions, please read QMTTOL
in the $CONTRL input group for numerical concerns.

POLAR  = exponent of polarization functions
       = COMMON    (default for GBASIS=STO,N21,HW,SBKJC)
       = POPN31    (default for GBASIS=N31)
       = POPN311   (default for GBASIS=N311, MC)
       = DUNNING   (default for GBASIS=DH, DZV)
       = HUZINAGA  (default for GBASIS=MINI, MIDI)
       = HONDO7    (default for GBASIS=TZV)

SPLIT2 = an array of splitting factors used when NDFUNC
         or NPFUNC is 2.  Default=2.0,0.5

SPLIT3 = an array of splitting factors used when NDFUNC
         or NPFUNC is 3.  Default=4.00,1.00,0.25

The splitting factors are from the Pople school, and are
probably too far apart.  See for example the Binning and
Curtiss paper.  For example, the SPLIT2 value will usually
cause an INCREASE over the 1d energy at the HF level for
hydrocarbons.

The actual exponents used for polarization functions, as
well as for diffuse sp or s shells, are described in the
'Further References' section of this manual.  This section
also describes the sp part of the basis set chosen by
GBASIS fully, with all references cited.

Note that GAMESS always punches a full $DATA input group.
Thus, if $BASIS does not quite cover the basis you want,
you can obtain this full $DATA from EXETYP=CHECK, and then
change polarization exponents, add Rydbergs, etc.
```

* * *

This may only be used with COORD=UNIQUE or HINT!

```
BASNAM = an array of names of customized basis set input
         groups.  BASNAM should obey the rule of no more
         than six characters starting with a letter names,
         and must avoid using any GBASIS string.
         However, the individual basis inputs can use any
         of the GBASIS sets by its standard name.
         Basis supplementations such as DIFFS or NDFUNC may
         only be given by explicit numerical values.

This is best explained by an example where a core potential
and valence-only basis set is used on a transition metal,
but not its ligands:

 $contrl scftyp=rohf icharg=+3 mult=4 runtyp=gradient
         pp=read ispher=1 $end
 $system mwords=1 $end
 $guess  guess=huckel $end
 $basis  basnam(1)=metal,  ligO,ligO,ligO,ligO,ligO,ligO,
                   ligH,ligH,ligH,ligH,ligH,ligH,
                   ligH,ligH,ligH,ligH,ligH,ligH $end
 $data
Cr+3(H2O)6 complex...SBKJC & 6-31G(d) geometry
Th

CHROMIUM   24.0    .0000000000  .0   .0000000000
OXYGEN      8.0    .0000000000  .0  2.0398916104
HYDROGEN    1.0    .7757887450  .0  2.6122732372
 $end
!       core potential basis for Chromium
 $metal
sbkjc

 $end
!       normal 6-31G(d) for oxygen ligands
 $ligO
n31 6
d 1 ; 1 0.8 1.0

 $end
!       unpolarized basis for hydrogens
 $ligH
n31 6

 $end
```

```
 $ecp
Cr-ecp SBKJC
O-ecp none
   ...snipped...   there must be 6 O's given here
O-ecp none
H-ecp none
   ...snipped...   there must be 12 H's given here
H-ecp none
 $end
```

* * *

EXTFIL = a flag to read basis sets from an external file, defined by EXTBAS, rather than from $DATA. (default=.false.)

It may be easier to use BASNAM to create custom basis sets! BASNAM has the bonus that your input file contains all information about the calculation, explicitly.

Except for MCP basis sets, no external file is provided with GAMESS, thus you must create your own. The GBASIS keyword must give an 8 or less character string, obviously not using any internally stored names. Every atom must be defined in the external file by a line giving the chemical symbol, and this chosen string. Following this header line, give the basis in free format $DATA style, containing only S, P, D, F, G, and L shells, and terminating each atom by the usual blank line. The external file may have several families of bases in the same file, identified by different GBASIS strings.

==========

==========

$DATA group (required)
$DATAS group (if NESC chosen, for small component basis)
$DATAL group (if NESC chosen, for large component basis)

This group describes the global molecular data such as point group symmetry, nuclear coordinates, and possibly the basis set. It consists of a series of free format card images. See $RELWFN for more information on large and small component basis sets. The input structure of $DATAS and $DATAL is identical to the COORD=UNIQUE $DATA input.

-1- TITLE a single descriptive title card.

-2- GROUP, NAXIS

GROUP is the Schoenflies symbol of the symmetry group, you may choose from
C1, Cs, Ci, Cn, S2n, Cnh, Cnv, Dn, Dnh, Dnd,
T, Th, Td, O, Oh.

NAXIS is the order of the highest rotation axis, and must be given when the name of the group contains an N. For example, "Cnv 2" is C2v. "S2n 3" means S6. Use of NAXIS up to 8 is supported in each axial groups.

For linear molecules, choose either Cnv or Dnh, and enter NAXIS as 4. Enter atoms as Dnh with NAXIS=2. If the electronic state of either is degenerate, check the note about the effect of symmetry in the electronic state in the SCF section of REFS.DOC.

In order to use GAMESS effectively, you must be able to recognize the point group name for your molecule. This presupposes a knowledge of group theory at about the level of Cotton's "Group Theory", Chapter 3.

Armed with only the name of the group, GAMESS is able to exploit the molecular symmetry throughout almost all of the program, and thus save a great deal of computer time. GAMESS does not require that you know very much else about group theory, although a deeper knowledge (character tables, irreducible representations, term symbols, and so on) is useful when dealing with the more sophisticated wavefunctions.

Cards -3- and -4- are quite complicated, and are rarely given. A *SINGLE* blank card may replace both cards -3- and -4-, to select the 'master frame', which is defined on the next page. If you choose to enter a blank line, skip to one of the -5- input sequences.

Note!
If the point group is C1 (no symmetry), skip over cards -3- and -4- (which means no blank card).

-3- X1, Y1, Z1, X2, Y2, Z2

For C1 group, there is no card -3- or -4-.
For CI group, give one point, the center of inversion.
For CS group, any two points in the symmetry plane.
For axial groups, any two points on the principal axis.
For tetrahedral groups, any two points on a two-fold axis.
For octahedral groups, any two points on a four-fold axis.

-4- X3, Y3, Z3, DIRECT

third point, and a directional parameter.
For CS group, one point of the symmetry plane,
noncollinear with points 1 and 2.
For CI group, there is no card -4-.

For other groups, a generator sigma-v plane (if any) is the (x,z) plane of the local frame (CNV point groups).

A generator sigma-h plane (if any) is the (x,y) plane of the local frame (CNH and dihedral groups).

A generator C2 axis (if any) is the x-axis of the local frame (dihedral groups).

The perpendicular to the principal axis passing through the third point defines a direction called D1. If DIRECT='PARALLEL', the x-axis of the local frame coincides with the direction D1. If DIRECT='NORMAL', the x-axis of the local frame is the common perpendicular to D1 and the principal axis, passing through the intersection point of these two lines. Thus D1 coincides in this case with the negative y axis.

The 'master frame' is just a standard orientation for the molecule. By default, the 'master frame' assumes that

1. z is the principal rotation axis (if any),
2. x is a perpendicular two-fold axis (if any),
3. xz is the sigma-v plane (if any), and
4. xy is the sigma-h plane (if any).

Use the lowest number rule that applies to your molecule.

Some examples of these rules:
Ammonia (C3v): the unique H lies in the XZ plane (R1,R3).
Ethane (D3d): the unique H lies in the YZ plane (R1,R2).
Methane (Td): the H lies in the XYZ direction (R2). Since there is more than one 3-fold, R1 does not apply.
HP=O (Cs): the mirror plane is the XY plane (R4).

In general, it is a poor idea to try to reorient the molecule. Certain sections of the program, such as the orbital symmetry assignment, do not know how to deal with cases where the 'master frame' has been changed.

Linear molecules (C4v or D4h) must lie along the z axis, so do not try to reorient linear molecules.

You can use EXETYP=CHECK to quickly find what atoms are generated, and in what order. This is typically necessary in order to use the general $ZMAT coordinates.

* * * *

Depending on your choice for COORD in $CONTROL,

```
    if COORD=UNIQUE, follow card sequence U
    if COORD=HINT,   follow card sequence U
    if COORD=CART,   follow card sequence C
    if COORD=ZMT,    follow card sequence G
    if COORD=ZMTMPC, follow card sequence M

Card sequence U is the only one which allows you to define
a completely general basis here in $DATA.

Recall that UNIT in $CONTRL determines the distance units.

-------------------------------------------------------------

-5U-   Atom input.  Only the symmetry unique atoms are
input, GAMESS will generate the symmetry equivalent atoms
according to the point group selected above.

   if COORD=UNIQUE   NAME, ZNUC, X, Y, Z
   ***************

NAME  = 10 character atomic name, used only for printout.
        Thus you can enter H or Hydrogen, or whatever.
ZNUC  = nuclear charge.  It is the nuclear charge which
        actually defines the atom's identity.
X,Y,Z = Cartesian coordinates.

   if COORD=HINT
   *************

   NAME,ZNUC,CONX,R,ALPHA,BETA,SIGN,POINT1,POINT2,POINT3

NAME = 10 character atomic name (used only for print out).
ZNUC = nuclear charge.
CONX = connection type, choose from
  'LC'   linear conn.              'CCPA' central conn.
  'PCC'  planar central conn.             with polar atom
  'NPCC' non-planar central conn.  'TCT'  terminal conn.
  'PTC'  planar terminal conn.            with torsion
R    = connection distance.
ALPHA= first connection angle
BETA = second connection angle
SIGN = connection sign, '+' or '-'
POINT1, POINT2, POINT3 =
     connection points, a serial number of a previously
     input atom, or one of 4 standard points: 0,I,J,K
```

```
     (origin and unit points on axes of master frame).
     defaults:  POINT1='O', POINT2='I', POINT3='J'

ref- R.L. Hilderbrandt, J.Chem.Phys. 51, 1654 (1969).
You cannot understand HINT input without reading this.

Note that if ZNUC is negative, the internally stored
basis for ABS(ZNUC) is placed on this center, but the
calculation uses ZNUC=0 after this.  This is useful
for basis set superposition error (BSSE) calculations.
-------------------------------------------------------

* * * If you gave $BASIS, continue entering cards -5U-
      until all the unique atoms have been specified.
      When you are done, enter a " $END " card.
* * * If you did not, enter cards -6U-, -7U-, -8U-.

-------------------------------------------------------
-6U-  GBASIS, NGAUSS, (SCALF(i),i=1,4)

GBASIS can have exactly the same meaning as the keyword in
$BASIS.  You may choose from STO, N21, N31, N311, ACCT,
PC4, ...  A few of these require NGAUSS below.

In addition, GBASIS can be S, P (or L), D, F, G, H, or I to
enter an explicit basis set.  L means both an S and P shell
with the same exponent.  See NGAUSS below.

In addition, GBASIS may be defined as MCP, to indicate that
the current atom is represented by a model core potential,
and valence basis set.  An internally stored basis and
potential will be applied (see REFS.DOC for the details).
The MCP basis supplies only the occupied atomic orbitals,
e.g. sp for a main group element, so please supplement with
any desired polarization.  In case the keyword MCP is
followed by the keyword READ, everything will be taken from
the input file, namely the basis functions are read using
the sequence -6U-, -7U-, and -8U-, from lines following the
"MCP READ" line.  In addition, "MCP READ" implies that the
parameters of the model core potentials, together with core
basis functions are in the input stream, in a $MCP input
group.  Other MCP bases are available in the $BASIS input,
but note that to locate the MCP, the atom name must be a
chemical symbol, that is "P" instead of "Phosphorus".
```

```
NGAUSS is the number of Gaussians (N) in the Pople style
basis, or user input general basis.  It has meaning only
for GBASIS=STO, N21, N31, or N311, or explicit GTO types
such as S,P,D,F...

Up to 4 scale factors may be entered.  If omitted, standard
values are used.  They are not documented as every GBASIS
treats these differently.  Read the source code if you need
to know more.  They are seldom given.
-------------------------------------------------------------

* * * If GBASIS is not S,P,D,F,... either add more
      shells by repeating card -6U-, or go on to -8U-.
* * * If GBASIS=S,P,D,F,... enter NGAUSS cards -7U-.

-------------------------------------------------------------
-7U- IG, ZETA, C1, C2

      IG = a counter, IG takes values 1, 2, ..., NGAUSS.
    ZETA = Gaussian exponent of the IG'th primitive.
      C1 = Contraction coefficient for S,P,D,F,G shells,
           and for the s function of L shells.
      C2 = Contraction coefficient for the p in L shells.
-------------------------------------------------------------

* * * For more shells on this atom, go back to card -6U-.
* * * If there are no more shells, go on to card -8U-.

-------------------------------------------------------------
-8U-    A blank card ends the basis set for this atom.
-------------------------------------------------------------

Continue entering atoms with -5U- through -8U- until all
are given, then terminate the group with a " $END " card.

       --- this is the end of card sequence U ---

COORD=CART input:

-------------------------------------------------------------

-5C- Atom input.

Cartesian coordinates for all atoms must be entered.  They
may be arbitrarily rotated or translated, but must possess
```

```
the actual point group symmetry.  GAMESS will reorient the
molecule into the 'master frame', and determine which
atoms are the unique ones.  Thus, the final order of the
atoms may be different from what you enter here.

      NAME, ZNUC, X, Y, Z

NAME  = 10 character atomic name, used only for printout.
        Thus you can enter H or Hydrogen, or whatever.
ZNUC  = nuclear charge.  It is the nuclear charge which
        actually defines the atom's identity.
X,Y,Z = Cartesian coordinates.

-------------------------------------------------------

Continue entering atoms with card -5C- until all are
given, and then terminate the group with a " $END " card.

       --- this is the end of card sequence C ---

COORD=ZMT input:       (GAUSSIAN style internals)

-------------------------------------------------------

-5G-      ATOM

Only the name of the first atom is required.
See -8G- for a description of this information.
-------------------------------------------------------

-6G-      ATOM  i1 BLENGTH

Only a name and a bond distance is required for atom 2.
See -8G- for a description of this information.
-------------------------------------------------------

-7G-      ATOM  i1 BLENGTH  i2 ALPHA

Only a name, distance, and angle are required for atom 3.
See -8G- for a description of this information.
-------------------------------------------------------

-8G-      ATOM  i1 BLENGTH  i2 ALPHA  i3 BETA i4

ATOM    is the chemical symbol of this atom.  It can be
```

```
        followed by numbers, if desired, for example Si3.
        The chemical symbol implies the nuclear charge.
i1      defines the connectivity of the following bond.
BLENGTH is the bond length "this atom-atom i1".
i2      defines the connectivity of the following angle.
ALPHA   is the angle "this atom-atom i1-atom i2".
i3      defines the connectivity of the following angle.
BETA    is either the dihedral angle "this atom-atom i1-
        atom i2-atom i3", or perhaps a second bond
        angle "this atom-atom i1-atom i3".
i4      defines the nature of BETA,
        If BETA is a dihedral angle, i4=0 (default).
        If BETA is a second bond angle, i4=+/-1.
        (sign specifies one of two possible directions).
-------------------------------------------------------------
```

- Repeat -8G- for atoms 4, 5, ...
- The use of ghost atoms is possible, by using X or BQ for the chemical symbol. Ghost atoms preclude the option of an automatic generation of $ZMAT.
- The connectivity i1, i2, i3 may be given as integers, 1, 2, 3, 4, 5,... or as strings which match one of the ATOMs. In this case, numbers must be added to the ATOM strings to ensure uniqueness!
- In -6G- to -8G-, symbolic strings may be given in place of numeric values for BLENGTH, ALPHA, and BETA. The same string may be repeated, which is handy in enforcing symmetry. If the string is preceded by a minus sign, the numeric value which will be used is the opposite, of course. Any mixture of numeric data and symbols may be given. If any strings were given in -6G- to -8G-, you must provide cards -9G- and -10G-, otherwise you may terminate the group now with a " $END " card.

```
-------------------------------------------------------------

-9G-   A blank line terminates the Z-matrix section.

-------------------------------------------------------------

-10G-   STRING VALUE

STRING is a symbolic string used in the Z-matrix.
VALUE  is the numeric value to substitute for that string.
```

Continue entering -10G- until all STRINGs are defined. Note that any blank card encountered while reading -10G- will be ignored. GAMESS regards all STRINGs as variables (constraints are sometimes applied in $STATPT). It is not necessary to place constraints to preserve point group symmetry, as GAMESS will never lower the symmetry from that given at -2-. When you have given all STRINGs a VALUE, terminate the group with a " $END " card.

--- this is the end of card sequence G ---

* * * *

The documentation for sequence G above and sequence M below presumes you are reasonably familiar with the input to GAUSSIAN or MOPAC. It is probably too terse to be understood very well if you are unfamiliar with these. A good tutorial on both styles of Z-matrix input can be found in Tim Clark's book "A Handbook of Computational Chemistry", published by John Wiley & Sons, 1985.

Both Z-matrix input styles must generate a molecule which possesses the symmetry you requested at -2-. If not, your job will be terminated automatically.

COORD=ZMTMPC input: (MOPAC style internals)

-5M- ATOM

Only the name of the first atom is required.
See -8M- for a description of this information.

-6M- ATOM BLENGTH

Only a name and a bond distance is required for atom 2.
See -8M- for a description of this information.

-7M- ATOM BLENGTH j1 ALPHA j2

Only a bond distance from atom 2, and an angle with respect to atom 1 is required for atom 3. If you prefer to hook atom 3 to atom 1, you must give connectivity as in -8M-. See -8M- for a description of this information.

-8M- ATOM BLENGTH j1 ALPHA j2 BETA j3 i1 i2 i3

ATOM, BLENGTH, ALPHA, BETA, i1, i2 and i3 are as described at -8G-. However, BLENGTH, ALPHA, and BETA must be given as numerical values only. In addition, BETA is always a dihedral angle. i1, i2, i3 must be integers only.

The j1, j2 and j3 integers, used in MOPAC to signal optimization of parameters, must be supplied but are ignored here. You may give them as 0, for example.

Continue entering atoms 3, 4, 5, ... with -8M- cards until all are given, and then terminate the group by giving a " $END " card.

--- this is the end of card sequence M ---

==========

This is the end of $DATA!

If you have any doubt about what molecule and basis set you are defining, or what order the atoms will be generated in, simply execute an EXETYP=CHECK job to find out!

==========

$ZMAT group (required if NZVAR is nonzero in $CONTRL)

This group lets you define the internal coordinates in which the gradient geometry search is carried out. These need not be the same as the internal coordinates used in $DATA. The coordinates may be simple Z-matrix types, delocalized coordinates, or natural internal coordinates.

You must input a total of M=3N-6 internal coordinates (M=3N-5 for linear molecules). NZVAR in $CONTRL can be less than M IF AND ONLY IF you are using linear bends. It is also possible to input more than M coordinates if they are used to form exactly M linear combinations for new internals. These may be symmetry coordinates or natural internal coordinates. If NZVAR > M, you must input IJS and SIJ below to form M new coordinates. See DECOMP in $FORCE for the only circumstance in which you may enter a larger NZVAR without giving SIJ and IJS.

**** IZMAT defines simple internal coordinates ****

IZMAT is an array of integers defining each coordinate. The general form for each internal coordinate is
code number,I,J,K,L,M,N

IZMAT =1 followed by two atom numbers. (I-J bond length)
=2 followed by three numbers. (I-J-K bond angle)
=3 followed by four numbers. (dihedral angle)
Torsion angle between planes I-J-K and J-K-L.
=4 followed by four atom numbers. (atom-plane)
Out-of-plane angle from bond I-J to plane J-K-L.
=5 followed by three numbers. (I-J-K linear bend)
Counts as 2 coordinates for the degenerate bend, normally J is the center atom. See $LIBE.
=6 followed by five atom numbers. (dihedral angle)
Dihedral angle between planes I-J-K and K-L-M.
=7 followed by six atom numbers. (ghost torsion)
Let A be the midpoint between atoms I and J, and B be the midpoint between atoms M and N. This coordinate is the dihedral angle A-K-L-B. The atoms I,J and/or M,N may be the same atom number. (If I=J AND M=N, this is a conventional torsion). Examples: N2H4, or, with one common pair, H2POH.

```
Example - a nonlinear triatomic, atom 2 in the middle:
      $ZMAT IZMAT(1)=1,1,2,  2,1,2,3,  1,2,3  $END
This sets up two bonds and the angle between them.
The blanks between each coordinate definition are
not necessary, but improve readability mightily.


     **** the next define delocalized coordinates ****

DLC    is a flag to request delocalized coordinates.
       (default is .FALSE.)

AUTO   is a flag to generate all redundant coordinates,
       automatically.  The DLC space will consist of all
       non-redundant combinations of these which can be
       found.  The list of redundant coordinates will
       consist of bonds, angles, and torsions only.
       (default is .FALSE.)

NONVDW is an array of atom pairs which are to be joined
       by a bond, but might be skipped by the routine
       that automatically includes all distances shorter
       than the sum of van der Waals radii.  Any angles
       and torsions associated with the new bond(s) are
       also automatically included.

Cases where the AUTO generation of DLC coordinates fails to
find the full set of 3N-6 coordinates typically fall 6
short of 3N-6.  These cases are invariably due to the
system being divided into pieces too far apart to have
bonds detected (for example, system A might be H-bonded to
system B, finding 3N-12 coordinates only).  Adding NONVDW
input for that H-bond will tie A and B together, and result
in a correct AUTO generation of all 3N-6 coordinates.
Falling short by an integer multiple of 6 indicates more
than two pieces, requiring several NONVDW pairs.  Falling
short by 3 coordinates indicates one of the separate
systems A or B is likely a single atom, which has no
rotational degrees of freedom, again it should be attached
by NONVDW.

DLC coordinate generation can be fine tuned by IXZMAT,
IRZMAT, IFZMAT whose format is the same as IZMAT:
```

```
IXZMAT is an extra array of simple internal coordinates
       which you want to have added to the list generated
       by AUTO.  Unlike NONVDW, IXZMAT will add only the
       coordinate(s) you specify.

IRZMAT is an array of simple internal coordinates which
       you would like to remove from the AUTO list of
       redundant coordinates.  It is sometimes necessary
       to remove a torsion if other torsions around a bond
       are being frozen, to obtain a nonsingular G matrix.

IFZMAT is an array of simple internal coordinates which
       you would like to freeze.  See also FVALUE below,
       which is --required-- input when IFZMAT is given.
       IFZMAT/FVALUE work with ordinary coordinate input
       using IZMAT, as well as with DLC, but in the former
       case be careful that IFZMAT specifies coordinates
       that were already given in IZMAT.  In addition,
       IFZMAT works only for IZMAT=1,2,3 type coordinates.
       See IFREEZ in $STATPT you wish to freeze regular or
       natural internal coordinates.

FVALUE is an array of values to which the internal
       coordinates should be constrained.  It is not
       necessary to input $DATA such that the initial
       values match these desired final values, but it is
       helpful if the initial values are not too far away.


   **** SIJ,IJS define natural internal coordinates ****

SIJ is a transformation matrix of dimension NZVAR x M,
    used to transform the NZVAR internal coordinates in
    IZMAT into M new internal coordinates.  SIJ is a
    sparse matrix, so only the non-zero elements are
    given, by using the IJS array described below.
    The columns of SIJ will be normalized by GAMESS.
    (Default: SIJ = I, unit matrix)

IJS is an array of pairs of indices, giving the row and
    column index of the entries in SIJ.

example - if the above triatomic is water, using
     IJS(1) = 1,1, 3,1,   1,2, 3,2,   2,3
     SIJ(1) = 1.0, 1.0,   1.0,-1.0,   1.0
```

```
    gives the matrix S=  1.0   1.0   0.0
                         0.0   0.0   1.0
                         1.0  -1.0   0.0

which defines the symmetric stretch, asymmetric stretch,
and bend of water.

references for natural internal coordinates:
  P.Pulay, G.Fogarasi, F.Pang, J.E.Boggs
     J.Am.Chem.Soc. 101, 2550-2560(1979)
  G.Fogarasi, X.Zhou, P.W.Taylor, P.Pulay
     J.Am.Chem.Soc. 114, 8191-8201(1992)
reference for delocalized coordinates:
  J.Baker, A. Kessi, B.Delley
     J.Chem.Phys. 105, 192-212(1996)

=============================================================
```

==========

$LIBE group (required if linear bends are used in $ZMAT)

A degenerate linear bend occurs in two orthogonal planes, which are specified with the help of a point A. The first bend occurs in a plane containing the atoms I,J,K and the user input point A. The second bend is in the plane perpendicular to this, and containing I,J,K. One such point must be given for each pair of bends used.

APTS(1)= x1,y1,z1,x2,y2,z2,... for linear bends 1,2,...

Note that each linear bend serves as two coordinates, so that if you enter 2 linear bends (HCCH, for example), the correct value of NZVAR is M-2, where M=3N-6 or 3N-5, as appropriate.

==========

==========

$SCF group relevant if SCFTYP = RHF, UHF, or ROHF, required if SCFTYP = GVB)

This group of parameters provides additional control over the RHF, UHF, ROHF, or GVB SCF steps. It must be given to define GVB open shell or perfect pairing wavefunctions. See $MCSCF for multireference inputs.

DIRSCF = a flag to activate a direct SCF calculation, which is implemented for all the Hartree-Fock type wavefunctions: RHF, ROHF, UHF, and GVB. This keyword also selects direct MP2 computation. The default of .FALSE. stores integrals on disk storage for a conventional SCF calculation.

FDIFF = a flag to compute only the change in the Fock matrices since the previous iteration, rather than recomputing all two electron contributions. This saves much CPU time in the later iterations. This pertains only to direct SCF, and has a default of .TRUE. This option is implemented only for the RHF, ROHF, UHF cases.

Cases with many diffuse functions in the basis set, or large molecules, may sometimes be "mushy" at the end, rather than converging. Increasing ICUT in $CONTRL by one may help this, or consider turning this parameter off.

---- The next flags affect convergence rates.

DIIS = selects Pulay's DIIS interpolation.
SOSCF = selects second order SCF orbital optimization.
Only one of DIIS or SOSCF may be .TRUE. in any run.
Which is chosen by default depends on the run:
for RHF, GVB, UHF, or ROHF (if Abelian): SOSCF.TRUE.
for any DFT, or for non-Abelian groups: DIIS=.TRUE.

NOCONV = .TRUE. means neither SOSCF nor DIIS will be used, specify NOCONV=.TRUE. DIIS=.FALSE. SOSCF=.FALSE. in the rare case you don't wish to use either one. NOCONV's default is .FALSE., meaning the program will obey your choice of DIIS/SOSCF, or else pick

its default for them.

Once either DIIS or SOSCF are initiated, the following less important accelerators are placed in abeyance:

EXTRAP = selects Pople extrapolation of the Fock matrix.
DAMP = selects Davidson damping of the Fock matrix.
SHIFT = selects level shifting of the Fock matrix.
RSTRCT = selects restriction of orbital interchanges.
DEM = selects direct energy minimization, which is implemented only for RHF. (default=.FALSE.)

defaults for	EXTRAP	DAMP	SHIFT	RSTRCT	DIIS	SOSCF
ab initio:	T	F	F	F	F/T	T/F
semiempirical:	T	F	F	F	F	F

The above parameters are implemented for all SCF wavefunction types, except that DIIS will work for GVB only for those cases with NPAIR=0 or NPAIR=1.

CUHF = flag requesting Constrained UHF, which causes the occupied beta orbitals of a UHF run to lie entirely within the occupied alpha orbital space. This produces results identical to high spin ROHF! Obviously, this keyword pertains only when using SCFTYP=UHF. The default is .FALSE., meaning a spin-contaminated ordinary UHF solution is sought. Applicable to UHF or UDFT energy and gradients, or to UMP2 energy calculations.

---- These parameters fine tune the various convergers.

CONV = SCF density convergence criteria.
Convergence is reached when the density change between two consecutive SCF cycles is less than this in absolute value. One more cycle will be executed after reaching convergence. Less accuracy in CONV gives questionable gradients. The default is 1.0d-05, except runs involving CI, MP2, CC, or TDDFT use 1.0d-06 to obtain more crisply converged virtual orbitals.

```
SOGTOL = second order gradient tolerance.  SOSCF will be
         initiated when the orbital gradient falls below
         this threshold.  (default=0.25 au)

ETHRSH = energy error threshold for initiating DIIS.  The
         DIIS error is the largest element of e=FDS-SDF.
         Increasing ETHRSH forces DIIS on sooner.
         (default = 0.5 Hartree)

MAXDII = Maximum size of the DIIS linear equations, so
         that at most MAXDII-1 Fock matrices are used
         in the interpolation.  (default=10)

SWDIIS = density matrix convergence at which to switch
         from DIIS to SOSCF.  A value of zero means to
         keep using DIIS at all geometries, which is the
         default.  However, it may be useful to have
         DIIS work only at the first geometry, in the
         initial iterations, for example transition
         metal ECP runs which has a less good Huckel
         guess, and then use SOSCF for the final SCF
         iterations at the first geometry, and ever
         afterwards.  A suggested usage might be
         DIIS=.TRUE. ETHRSH=2.0 SWDIIS=0.005.
         This option is not programmed for GVB.

LOCOPT = When set to .TRUE., SCF options are locked
         and do not change during the following:
         SOSCF and DIIS switch (SWDIIS), DFT grid switch,
         RHF -> DFT switch (SWOFF). If .FALSE., any
         of these switches resets some SCF options, such
         as SHIFT or DAMP.  (Default: .FALSE.)

RESET  = In UHF, reset SOSCF or DIIS if energy rises
         (Default: .TRUE. for UHF, .FALSE. otherwise).

DEMCUT = Direct energy minimization will not be done
         once the density matrix change falls below
         this threshold.  (Default=0.5)

DMPCUT = Damping factor lower bound cutoff.  The damping
         damping factor will not be allowed to drop
         below this value. (default=0.0)
note: The damping factor need not be zero to achieve valid
convergence (see Hsu, Davidson, and Pitzer, J.Chem.Phys.,
```

65, 609 (1976), see the section on convergence control),
but it should not be astronomical either.

```
        * * * * * * * * * * * * * * * * * * * * * *
        For more info on the convergence methods,
        see the 'Further Information' section.
        * * * * * * * * * * * * * * * * * * * * * *
```

---- orbital modification options ----

The four options UHFNOS, VVOS, MVOQ, and ACAVO are mutually exclusive. The latter 3 require RUNTYP=ENERGY, and should not be used with any correlation treatment.

UHFNOS = flag controlling generation of the natural orbitals of a UHF function. (default=.FALSE.)

VVOS = flag controlling generation of Valence Virtual Orbitals. See J.Chem.Phys. 120, 2629-2637(2004). The default is .FALSE.

VVOs are a quantitative realization of the concept of the "lowest unoccupied molecular orbital". The implementation allows any elements H-Xe, for RHF, ROHF, and GVB wavefunctions, as well as DFT runs (see also VVOS in $MCSCF). Core potentials may not be used. VVOS should be much better MCSCF starting orbitals than either MVOQ or ACAVO type virtuals.

MVOQ = 0 Skip MVO generation (default)
= n Form modified virtual orbitals, using a cation with n electrons removed. Implemented for RHF, ROHF, and GVB. If necessary to reach a closed shell cation, the program might remove n+1 electrons. Typically, n will be about 6.
= -1 The cation used will have each valence orbital half filled, to produce MVOs with valence-like character in all regions of the molecule. Implemented for RHF and ROHF only.

ACAVO = Flag to request Approximate Correlation-Adapted Virtual Orbitals. Implemented for RHF, ROHF, and GVB (w/o direct SCF). Default is .FALSE.

PACAVO = Parameters used to define the ACAVO generating

operator, which is defined as
a*T + b*Vne + c*Jcore + d*Jval + e*Kcore + f*Kval
The default, PACAVO(1)=0,0,0,0,0,-1, maximizes the exchange interaction with valence MOs (see for example J.L.Whitten, J.Chem.Phys. 56, 5458-5466(1972).
The K-orbitals of D.Feller, E.R.Davidson J.Chem.Phys. 74, 3977-3979(1981) are 0.06*F-K(valence), which is PACAVO(1)= 0.06,0.06,0.12,0.12,-0.06,-1.06.
Of course, canonical virtuals are PACAVO(1)=1,1,2,2,-1,-1.

* * *

UHFCHK = a flag to perform a RHF --> UHF wavefunction stability test (relaxation of RHF orbitals to unequal alpha and beta orbitals). This option is implemented only for RHF, and involves testing only pairs of orbitals at a single time: this is not foolproof! default is .FALSE.

NHOMO = if UHFCHK is selected, the number of orbitals at The top of the occupied orbital space to be checked for instabilities.
Default= -1, meaning check HOMO and HOMO-1.

NLUMO = if UHFCHK is selected, the number of orbitals at the bottom of the virtual space checked. Basis sets with diffuse functions should check many more orbitals, to get past the diffuse MOs.
Default=2, meaning check LUMO, LUMO+1, LUMO+2.

* * *

MOM = flag enabling the Molecular Overlap Method (MOM). Currently works only with SCFTYP=UHF.
MOM computes excitations by selecting orbitals at each iteration to resemble earlier iterations.
See J.Phys.Chem. A 112, 13164-13171(2008).
(default=.FALSE.)
note: MOM typically requires an initial MOREAD set of ground-state MO's, reordered by NORDER=1 in conjunction with the IORDER/JORDER arrays.
The MOM flag is an algorithm very similar to that enabled by the RSTRCT flag. Note: RSTRCT works with all SCF types.

KPROJ determines the flavor of the MOM projections p_j

```
          obtained from the overlap matrix O(i,j).
          KPROJ pertains only if the MOM flag is enabled.
        = 0 p_j = |sum_i O(i,j)|
                  as given in the original MOM article
        = 1 p_j = sum_i O(i,j)  (default)
        = 2 p_j = sum_i O(i,j)*O(i,j),
                  as implemented in Q-Chem

            ----- GVB wavefunction input -----
```

The next parameters define the GVB wavefunction. See also MULT in the $CONTRL input. The GVB wavefunction assumes orbitals are in the order core, open, pairs.

NCO = The number of closed shell orbitals. The default almost certainly should be changed! (default=0).

NSETO = The number of sets of open shells in the function. Maximum of 10. (default=0)

NO = An array giving the degeneracy of each open shell set. Give NSETO values. (default=0,0,0,...).

NPAIR = The number of geminal pairs in the -GVB- function. Maximum of 12. The default corresponds to open shell SCF (default=0).

CICOEF = An array of ordered pairs of CI coefficients for the -GVB- pairs. (default = 0.90,-0.20,0.90,-0.20,...)

For example, a two pair case for water, say, might be CICOEF(1)=0.95,-0.05,0.95,-0.05. If not normalized, as in the default, CICOEF will be. This parameter is useful in restarting a GVB run, with the current CI coefficients.

COUPLE = A switch controlling the input of F, ALPHA, and BETA. (Default=.FALSE.)

Input for F, ALPHA, BETA will be ignored unless you select this variable as .TRUE.

F = An vector of fractional shell occupations.

ALPHA = An array of A coupling coefficients, given in

```
           lower triangular order.

BETA   =   An array of B coupling coefficients, given in
           lower triangular order.
```

Note: The default for F, ALPHA, and BETA depends on the state chosen. Defaults for the most commonly occurring cases are internally stored. See "Further Information" for other cases, including degenerate open shells.

Note: ALPHA and BETA can be given for -ROHF- orbital canonicalization control, see "Further Information".

```
        ----- miscellaneous options -----

NPUNCH =     option for output to the PUNCH file
       =  0  do not punch out the final orbitals
       =  1  punch out the occupied orbitals
       =  2  punch out occupied and virtual orbitals
             The default is NPUNCH = 2.

NPREO  = energy and orbital printing options, applied
         after other output options, for example NPRINT=-5
         for no orbital output overrules NPREO.  NPREO
         affects only printing, see NPUNCH just above.
         Default: 1,9999,2,1 (meaning print all orbitals,
         but no separate list of orbital energies).

         Orbitals from NPREO(1) to NPREO(2) and orbital
         energies from NPREO(3) to NPREO(4) are printed.
         Positive values are explicit orbitals, while
         negative numbers are relative to the HOMO.  Here,
         HOMO means NE/2, ie RHF-like counting, no matter
         what the SCFTYP actually is:
             NPREO(1)=25,35   prints orbitals 25 to 35
             NPREO(1)=-3,-4   prints 8 orbitals: from 3
                              below the HOMO, the HOMO,
                              to 4 above the HOMO.
         NPREO(3) to NPREO(4) define separate print-out of
         the orbital energies, by default this is skipped,
         since the starting value is higher than the end.
         To print only HOMO and "LUMO" LCAO coefficients,
         and all orbital energies, enter:
               NPREO(1)=0,-1,1,9999

        ----- options for virial scaling -----
```

VTSCAL = A flag to request that the virial theorem be satisfied. An analysis of the total energy as an exact sum of orbital kinetic energies is printed. The default is .FALSE.

This option is implemented for RHF, UHF, and ROHF, for RUNTYP=ENERGY, OPTIMIZE, or SADPOINT. Related input is:

SCALF = initial exponent scale factor when VTSCAL is in use, useful when restarting. The default is 1.0.

MAXVT = maximum number of iterations (at a single geometry) to satisfy the energy virial theorem. The default is 20.

VTCONV = convergence criterion for the VT, which is satisfied when 2<T> + <V> + R x dE/dR is less than VTCONV. The default is 1.0D-6 Hartree.

For more information on this option, which is most useful during a geometry search, see M.Lehd and F.Jensen, J.Comput.Chem. 12, 1089-1096(1991).

* * * * * * * * * * * * * * * * * * * *
For more discussion of GVB/ROHF input
see the 'further information' section
* * * * * * * * * * * * * * * * * * * *

==========

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$SCFMI group (optional, relevant if SCFTYP=RHF)

The Self Consistent Field for Molecular Interactions (SCF-MI) method is a modification of the usual Roothaan equations that avoids basis set superposition error (BSSE) in intermolecular interaction calculations, by expanding each monomer's orbitals using only its own basis set. Thus, the resulting orbitals are not orthogonal. The presence of a $SCFMI group in the input triggers the use of this option.

The implementation is limited to ten monomers, treated at the RHF level. The energy, gradient, and therefore semi-numerical hessian are available. The SCF step may be run in direct SCF mode, and parallel calculation is also enabled. The calculation must use Cartesian Gaussian AOs only, not spherical harmonics. The SCF-MI driver differs from normal RHF calculations, so not all converger methods are available. Finally, this option is not compatible with electron correlation treatments (DFT, MP2, CI, or CC).

The first 3 parameters must be given. All atoms of a fragment must appear consecutively in $DATA.

NFRAGS = number of distinct fragments present. Both the supermolecule and its constituent monomers must be well described as closed shells by RHF wavefunctions.

NF = an array containing the number of doubly occupied MOs for each fragment.

MF = an array containing the number of atomic basis functions located on each fragment.

ITER = maximum number of SCF-MI cycles, overriding the usual MAXIT value. (default is 50).

DTOL = SCF-MI density convergence criteria. (default is 1.0d-10)

```
ALPHA     = possible level shift parameter.
            (default is 0.0, meaning shifting is not used)

DIISON    = a flag to active the DIIS convergence.
            (default is .TRUE.)

MXDIIS    = the maximum number of previous effective Fock
and
            overlap matrices to be used in DIIS
(default=10)

DIISTL    = the density change value at which DIIS starts.
            (default=0.01)

A Huckel guess is localized by the Boys procedure onto each
fragment to provide starting orbitals for each:

ITLOC     = maximum number of iteration in the localization
            step (Default is 50)

CNVLOC    = convergence parameter for the localization.
            (default is .01).

IOPT      =   prints additional debug information.
          = 0 standard outout (default)
          = 1 print for each SCF-MI cycle MOs, overlap
              between the MOs, CPU times.
          = 2 print some extra informations in secular
              systems solution.

=============================================================

   "Modification of Roothan Equations to exclude BSSE
       from Molecular Interaction calculations"
    E. Gianinetti, M. Raimondi, E. Tornaghi
    Int. J. Quantum Chem. 60, 157-166 (1996)

   "Implementation of Gradient optimization algorithms
     and Force Constant computations in BSSE-free direct
     and conventional SCF approaches"
    A. Famulari, E. Gianinetti, M. Raimondi, M. Sironi
    Int. J. Quantum Chem. 69, 151-158 (1997)
```

==========

$DFT group (relevant if DFTTYP is chosen)
(relevant if SCFTYP=RHF,UHF,ROHF)

Note that if DFTTYP=NONE, an ab initio calculation will be performed, rather than density functional theory.

This group permits the use of various one electron (usually empirical) operators instead of the true many electron Hamiltonian. Two programs are provided, METHOD= GRID or GRIDFREE. The programs have different functionals available, and so the keyword DFTTYP (which is entered in $CONTRL) and other associated inputs are documented separately below. Every functional that has the same name in both lists is an identical functional, but each METHOD has a few functionals that are missing in the other.

The grid free implementation is based on the use of the resolution of the identity to simplify integrals so that they may be analytically evaluated, without using grid quadratures. The grid free DFT computations in their present form have various numerical errors, primarily in the gradient vectors. Please do not use the grid-free DFT program without reading the discussion in the 'Further References' section regarding the gradient accuracy.

The grid based DFT uses a typical grid quadrature to compute integrals over the rather complicated functionals, using two possible angular grid types.

Achieving a self-consistent field with DFT is rather more difficult than for normal HF, so DIIS is the default converger.

Both DFT programs will run in parallel. See the two lists below for possible functionals in the two programs.

See also the $TDDFT input group for excited states.

METHOD = selects grid based DFT or grid free DFT.
= GRID Grid based DFT (default)
= GRIDFREE Grid free DFT

```
DFTTYP is given in $CONTRL, not here in $DFT!  Possible
values for the grid-based program are listed first,

          ----- options for METHOD=GRID -----

DFTTYP = NONE     means ab initio computation (default)

Many choices are given below, perhaps the most sensible are
               local DFT: SVWN
             pure DFT GGA: BLYP, PW91, B97-D, PBE/PBEsol
          hybrid DFT GGA: B3LYP, X3LYP, PBE0
       pure DFT meta-GGA: revTPSS
     hybrid DFT meta-GGA: TPSSh, M06
but of course, everyone has their own favorite!


               pure exchange functionals:
       = SLATER   Slater exchange
       = BECKE    Becke 1988 exchange
       = GILL     Gill 1996 exchange
       = OPTX     Handy-Cohen exchange
       = PW91X    Perdew-Wang 1991 exchange
       = PBEX     Perdew-Burke-Ernzerhof exchange
These will be used with no correlation functional at all.


               pure correlation functionals:
       = VWN      Vosko-Wilk-Nusair correlation, using
                  their electron gas formula 5 (aka VWN5)
       = VWN3     Vosko-Wilk-Nusair correlation, using
                  their electron gas formula 3
       = VWN1RPA  Vosko-Wilke-Nusair correlation, using
                  their e- gas formula 1, with RPA params.
       = PZ81     Perdew-Zener 1981 correlation
       = P86      Perdew 1986 correlation
       = LYP      Lee-Yang-Parr correlation
       = PW91C    Perdew-Wang 1991 correlation
       = PBEC     Perdew-Burke-Ernzerhof correlation
       = OP       One-parameter Progressive correlation
These will be used with 100% HF exchange, if chosen.


               combinations (partial list):
       = SVWN     SLATER exchange + VWN5 correlation
```

```
                Called LDA/LSDA in physics for RHF/UHF.
        = SVWN1RPA Slater exchange + VWN1RPA correlation
        = BLYP     BECKE exchange + LYP correlation
        = BOP      BECKE exchange + OP correlation
        = BP86     BECKE exchange + P86 correlation
        = GVWN     GILL exchange + VWN5 correlation
        = GPW91    GILL exchange + PW91 correlation
        = PBEVWN   PBE exchange + VWN5 correlation
        = PBEOP    PBE exchange + OP correlation
        = OLYP     OPTX exchange + LYP correlation
        = PW91     means PW91 exchange + PW91 correlation
        = PBE      means PBE exchange + PBE correlation
There's a nearly infinite set of pairings (well, 6*9), so
we show only enough to give you the idea.  In other words,
pairs are formed by abbreviating the exchange functionals
    SLATER=S, BECKE=B, GILL=G, OPTX=O, PW91X=PW91, PBEX=PBE
and matching them with any correlation functional, of which
only two are abbreviated when used in combinations,
    PW91C==>PW91, PBEC==>PBE
The pairings shown above only scratch the surface, but
clearly, many possibilities, such as PW91PBE, are nonsense!


            pure DFT GGA functionals:
        = EDF1     empirical density functional #1, which is
                   a modified BLYP from Adamson/Gill/Pople.
        = PW91     Perdew/Wang 1991
        = PBE      Perdew/Burke/Ernzerhof 1996
        = revPBE   PBE as revised by Zhang/Yang
        = RPBE     PBE as revised by Hammer/Hansen/Norskov
        = PBEsol   PBE as revised by Perdew et al for solids
        = HCTH93   Hamprecht/Cohen/Tozer/Handy's 1998 mod
                   to B97, omitting HF exchange, fitting to
                   93 atoms and molecules
        = HCTH120  later fit to 120 systems
        = HCTH147  later fit to 147 systems
        = HCTH407  later fit to 407 systems (best)
        = SOGGA    PBE revised by Zhao/Truhlar for solids
        = MOHLYP   metal optimized OPTX, half LYP
        = B97-D    Grimme's modified B97, with dispersion
                   correction (this forces DC=.TRUE.)
        = SOGGA11  optimized with broad applicability for
                   chemistry, by Peverati/Zhao/Truhlar
```

```
            hybrid GGA functionals:
       = BHHLYP   HF and BECKE exchange + LYP correlation
       = B3PW91   Becke's 3 parameter exchange hybrid,
                  with PW91 correlation functional
       = B3LYP    this is a hybrid method combining five
                  functionals: Becke + Slater + HF exchange
                  (B3), with LYP + VWN5 correlation.
                  B3LYPV5 is a synonym for B3LYP.
       = B3LYPV1R use VWN1RPA in place of VWN5, matches the
                  e- gas formula chosen by some programs.
       = B3LYPV3  use VWN3 in place of B3LYP's VWN5
       = B3P86    B3-type exchange, P86 correlation, using
                  VWN3 as the LDA part of the correlation.
                  B3P86V3 is a synonym for B3P86.
       = B3P86V1R use VWN1RPA in place of VWN3
       = B3P86V5  use VWN5 in place of VWN3
       = B97      Becke's 1997 hybrid functional
       = B97-1    Hamprecht/Cohen/Tozer/Handy's 1998
                  reparameterization of B97
       = B97-2    Wilson/Bradley/Tozer's 2001 mod to B97
       = B97-3    Keal/Tozer's 2005 mod to B97
       = B97-K    Boese/Martin's 2004 mod for kinetics
       = B98      Schmider/Becke's 1998 mode to B97,
                  using their best "2c" parameters.
       = PBE0     a hybrid made from PBE
       = X3LYP    HF+Slater+Becke88+PW91 exchange,
                  and LYP+VWN1RPA correlation.
       = SOGGA11X a hybrid based on SOGGA11,
                  with 40.15% HF exchange.
Each includes some Hartree-Fock exchange, and also may use
a linear combination of many DFT parts.


          range separated functionals:
These are also known as "long-range corrected functionals".
LC-BVWN, LC-BOP, LC-BLYP, or LC-BPBE are available by
selecting BVWN, BOP, BLYP, or BPBE and also setting the
flag LC=.TRUE. (see LC and also MU below).  Others are
selected by their specific name, without using LC:
       = CAMB3LYP coulomb attenuated B3LYP
       = wB97     omega separated form of B97
       = wB97X    wB97 with short-range HF exchange
       = wB97X-D  dispersion corrected wB97X
M11 is also range-separated, but is listed below with the
other meta-GGAs.
```

```
              "double hybrid" GGA:
       = B2PLYP   mixes BLYP, HF exchange, and MP2!
                  See related inputs CHF and CMP2 below.
          "double hybrid" and "range separated":
       = wB97X-2  intended for use with GBASIS=CCT,CCQ,CC5
       = wB97X-2L intended for use with GBASIS=N311
                  NGAUSS=6 NDFUNC=3 NFFUNC=1 NPFUNC=3
                  DIFFSP=.T. DIFFS=.T.
Note: there are no analytic gradients for "double hybrids".
Note: the B2PLYP family uses the conventional MP2 energy
and may be used for closed shell or spin-unrestricted open
shell cases.  The wB97X-2 family uses the SCS-MP2 energy,
and thus is limited to closed shell cases at present.


              meta-GGA functionals:
These are not hybridized with HF exchange, unless that is
explicitly stated below.
       = VS98     Voorhis/Scuseria, 1998
       = PKZB     Perdew/Kurth/Zupan/Blaha, 1999
       = tHCTH    Boese/Handy's 2002 metaGGA akin to HCTH
       = tHCTHhyb tHCTH's hybrid with 15% HF exchange
       = BMK      Boese/Martin's 2004 parameterization of
                  tHCTHhyb for kinetics
       = TPSS     Tao/Perdew/Staroverov/Scuseria, 2003
       = TPSSh    TPSS hybrid with 10% HF exchange
       = TPSSm    TPSS with modified parameter, 2007
       = revTPSS  revised TPSS, 2009
       = dlDF     a reparameterized M05-2X, reproducing
                  interaction energies which have had all
                  dispersion removed.  This MUST be used
                  with a special -D correction to recover
                  dispersion.  See 'Further References'.
       = M05      Minnesota exchange-correlation, 2005
                  a hybrid with 28% HF exchange.
       = M05-2X   M05, with doubled HF exchange, to 56%
       = M06      Minnesota exchange-correlation, 2006
                  a hybrid with 27% HF exchange.
       = M06-L    M06, with 0% HF exchange (L=local)
       = M06-2X   M06, with doubled HF exchange, to 54%
       = M06-HF   M06 correlation, using 100% HF exchange
       = M08-HX   M08 with 'high HF exchange'
       = M08-SO   M08 with parameters that enforce the
```

```
                correct second order gradient expansion.
       = M11    M11 range-separated hybrid
       = M11-L  M11 local (0% HF exchange) with
                dual-range exchange
```
When the M06 family was created, Truhlar recommended M06 for the general situation, but see his "concluding remarks" in the M06 reference about which functional is best for what kind of test data set. The most recent M11 family is probably a better choice, and two functionals fit all the needs of the older M05/M06/M08 families.

An extensive bibliography for all functionals can be found in the 'Further References' section of this manual.

Note that only a subset of these functionals can be used for TD-DFT energy or gradients. These subsets are listed in the $TDDFT input group.

* * * dispersion corrections * * *

Many exchange-correlation functionals fail to compute intra- and inter-molecular dispersion interactions accurately. Two possible correction schemes are provided below. The first uses empirically chosen C6 and C8 coefficients, while the latter obtains these from the molecular DFT densities. At most, only one of the LRDFLG or DC options below may be chosen.

```
DC     = a flag to turn on Grimme's empirical dispersion
         correction, involving scaled R**(-6) terms.
         N.B.  This empiricism may also be added to plain
         Hartree-Fock, by choosing DFTTYP=NONE with DC=.T.
         Three different versions exist, see IDCVER.
         (default=.FALSE., except if DFTTYP=B97-D, wB97X-D)

IDCVER = 1 means 1st 2004 implementation.
       = 2 means 2nd 2006 implementation DFT-D2,
           default for B97-D, wB97X-D.
       = 3 means 3rd 2010 implementation DFT-D3.
           Default if DC is chosen and IDCVER isn't given.
       = 4 means modified 3rd implementation DFT-D3(BJ).
           (-4 is used for DFT-D3(BJ) for HF-3c).
         Setting IDCVER will force DC=.TRUE.
```

```
GCP     = a flag for the geometric counterpoise scheme
          correction in HF-3c.

SRB     = a flag for short-range basis set incompleteness
          (SRB) correction in HF-3c.

DCCHG   = a flag to use Chai-Head-Gordon damping function
          instead of Grimme's 2006 function. Pertinent only
          for the DFT-D2 method.  Forces DC=.TRUE.
          (default=.FALSE. except for wB97X-D)

DCABC   = a flag to turn on the computation of the E(3) non-
          additive energy term. Pertinent only for DFT-D3,
          it forces DC=.TRUE.  (default=.FALSE.)
```

The following parameters govern Grimme's semiempirical dispersion term. They are basis set and functional dependent, so they exist for only a few DFTTYP. Default values are automatically selected and printed out in the output file for many common density functionals.

The following keywords are for entering non-standard values. For DFT-D2 values, see also:

R.Peverati and K.K.Baldridge
J.Chem.Theory Comput. 4, 2030-2048 (2008).

For DFT-D3 values, and a detailed explanation of each parameter, see:

S. Grimme, J. Antony, S. Ehrlich and H. Krieg,
J.Chem.Phys. 132, 154104/1-19(2010)

and for DFT-D3(BJ):

S. Grimme, S. Ehrlich and L. Goerigk,
J.Comput.Chem. 32, 1456-1465 (2011)

```
DCALP   = alpha parameter in the DFT-D damping function
          (same as alpha6 in Grimme's DFT-D3 notation).
          Note also that alpha8 and alpha10 in DFT-D3 have
          constrained values of:
          alpha8 = alpha6 + 2, alpha10 = alpha8 + 2.
          Default=14.0 for DFT-D3
                 =20.0 for DFT-D2
                 =23.0 for DFT-D1
                 =6.00 for DCCHG=.TRUE.

DCSR    = sR exponential parameter to scale the van der
          Waals radii (same as sR,6 in Grimme's DFT-D3
```

notation). Note also that sR,8 in DFT-D3 have a fixed value of 1.0.
Optimized values are automatically selected for some of the more common functionals, otherwise, the default is 1.00 for DFT-D3, 1.10 for DFT-D2, and 1.22 for DFT-D1.

DCS6 = s6 linear parameter for scaling the C6 term.
Optimized values are automatically selected for some of the more common functionals, otherwise, the default is 1.00.

DCS8 = s8 linear parameter for scaling the C8 term of DFT-D3. Pertinent only for DFT-D3.
Optimized values are automatically selected for some of the more common functionals, otherwise, the default is 1.00.

DCA1 = a1 parameter appearing in the -D3(BJ) dispersion model. Optimized values are automatically selected for a set of known functionals, otherwise the default is 0.50.

DCA2 = a2 parameter appearing in the -D3(BJ) dispersion model. Optimized values are automatically selected for a set of known functionals, otherwise the default is 4.00.

The old keywords DCPAR and DCEXP were replaced by DCS6 and DCSR in 2010. Similarly, DCOLD has morphed into IDCVER.

- - -

The Local Response Dispersion (LRD) correction includes atomic pair-wise -C6/R**6, -C8/R**8, and -C10/R**10 terms, whose coefficients are computed from the molecular system's electron density and its nuclear gradient. The nuclear gradient assumes the dispersion coefficients do not vary with geometry, which causes only a very small error in the gradient. Optionally, 3 and 4 center terms may be added, at the 1/R**6 level; in this case, nuclear gradients may not be computed at all.

Since the three numerical parameters are presently known only for the long-range exchange corrected BOP functional,

```
calculations may specify simply DFTTYP=LCBOPLRD.  The
"LCBOPLRD" functional will automatically select the
following:
     DFTTYP=BOP   LC=.TRUE. MU=0.47
     LRDFLG=.TRUE. LAMBDA=0.232 KAPPA=0.600 RZERO=3.22
leaving only the choice for MLTINT up to you.

References for LRD are
   T.Sato, H.Nakai J.Chem.Phys. 131, 224104/1-12(2009)
   T.Sato, H.Nakai J.Chem.Phys. 133, 194101/1-9(2010)

LRDFLG = flag choosing the Local Response Dispersion (LRD)
         C6, C8, and C10 corrections.  Default=.FALSE.

MLTINT = flag to add the 3 and 4 center 6th order terms,
         the default=.FALSE.  Note that nuclear gradients
         are not available if these multi-center terms
         are requested.

Three numerical parameters may be input.  The defaults
shown are optimized for the BOP functional with the LC
correction for long-range exchange.

LAMBDA = parameter adjusting the density gradient
         correction for the atomic and atomic pair
         polarizabilities.  (default=0.232)
KAPPA  = parameter in the damping function (default=0.600)
RZERO  = parameter in the damping function (default=3.22)

It may be interesting to see a breakdown of the total
dispersion correction, using these keywords:

PRPOL  = print out atomic effective polarizabilities
         (default=.FALSE.)
PRCOEF = N  (default N=0)
         print out dispersion coefficient to N-th order.
PRPAIR = print out atomic pair dispersion energies
         (default=.FALSE.)


              * * * range separation * * *

LC     = flag to turn on the long range correction (LC),
         which smoothly replaces the DFT exchange by the
         HF exchange at long inter-electron distances.
```

(default=.FALSE.)
This option can be used only with the Becke exchange functional (Becke) and a few correlation functionals: DFTTYP=BVWN, BOP, BLYP, BPBE only. For example, B3LYP has a fixed admixture of HF exchange, so it cannot work with the LC option. See H.Iikura, T.Tsuneda, T.Yanai, and K.Hirao, J.Chem.Phys. 115, 3540 (2001).

MU = A parameter for the long range correction scheme. Increasing MU increases the HF exchange used, very small MU produces the DFT limit. (default=0.33)

Other range-separated options exist, invoked by naming the functional, such as DFTTYP=CAMB3LYP (see the DFTTYP keyword for a full list).

* * * B2x-PLYP double hybrid functionals * * *

B2xPLYP Double Hybrid functionals have the general formula:

$$E_{xc} = (1-c_{HF}) * E_{xGGA} + c_{HF} * E_{xHF} + (1-c_{MP2}) * E_{cGGA} + c_{MP2} * E^{(2)}$$

The next keywords allow the choice of cHF and cMP2. Both values must be between 0 and 1 (0-100%).

CHF = amount of HF exchange. (default=0.53)

CMP2 = amount of MP2. (default=0.27)

Some other common double hybrid functionals are available simply by choosing DFTTYP=B2PLYP, and changing the CHF and CMP2 parameters. Popular parametrizations are:

	CHF	CMP2
B2-PLYP (default)	0.53	0.27
B2K-PLYP	0.72	0.42
B2T-PLYP	0.60	0.31
B2GP-PLYP	0.65	0.36

* * * Grid Input * * *

Only one of the three grid types may be chosen for the run. The default (if no selection is made) is the Lebedev grid. In order to duplicate results obtained prior to April 2008, select the polar coordinate grid NRAD=96 NTHE=12 NPHI=24. Energies can be compared if and only if the identical grid type and density is used, analogous to needing to compare with the identical basis set expansions. See REFS.DOC for more information on grids. See similar inputs in $TDDFT.

Lebedev grid:

NRAD = number of radial points in the Euler-MacLaurin quadrature. (default=96)

NLEB = number of angular points in the Lebedev grids. (default=302). Possible values are 86, 110, 146, 170, 194, 302, 350, 434, 590, 770, 974, 1202, 1454, 1730, 2030...

Meta-GGA functionals require a tighter grid to achieve the same accuracy. For this reason a tighter default grid of NRAD=99 and NLEB=590 is chosen by default with all meta-GGA functionals.

The default for NLEB means that nuclear gradients will be accurate to about the default OPTTOL=0.00010 (see $STATPT), 590 approaches OPTTOL=0.00001, and 1202 is "army grade".

The next two specify radial/angular in a single keyword:

SG1 = a flag to select the "standard grid 1", which has 24 radial points, and various pruned Lebedev grids, from 194 down to 6. (default=.FALSE. This grid is very fast, but produces gradients whose accuracy reaches only OPTTOL=0.00050. This grid should be VERY USEFUL for the early steps of a geometry optimization.

JANS = two unpublished grids due to Curtis Janssen, implemented here differently than in MPQC:
= 1 uses 95 radial points for all atoms, and prunes

```
            from a Lebedev grid whose largest size is 434,
            thus using about 15,000 grid points/atom.
        = 2 uses 155 radial points for all atoms, and prunes
            from a Lebedev grid whose largest size is 974,
            thus using about 71,000 grid points/atom.
            This is a very accurate grid, e.g. "army grade".
        The information for pruning exists only for H-Ar,
        so heavier elements will use the large radial/
        Lebedev grid without any pruning.

polar coordinate grid:

NRAD   = number of radial points in the Euler-MacLaurin
         quadrature. (96 is reasonable)

NTHE   = number of angle theta grids in Gauss-Legendre
         quadrature (polar coordinates). (12 is reasonable)

NPHI   = number of angle phi grids in Gauss-Legendre
         quadrature.  NPHI should be double NTHE so points
         are spherically distributed. (24 is reasonable)

The number of angular points will be NTHE*NPHI.  The values
shown give a gradient accuracy near the default OPTTOL of
0.00010, while NTHE=24 NPHI=48 approaches OPTTOL=0.00001,
and "army grade" is NTHE=36 NPHI=72.


                * * * Grid Switching * * *

At the first geometry of the run, pure HF iterations will
be performed, since convergence of DFT is greatly improved
by starting with the HF density matrix.  After DFT engages,
most runs (at all geometries, except for PCM or numerical
Hessians) will use a coarser grid during the early DFT
iterations, before reaching some initial convergence.
After that, the full grid will be used.  Together, these
switchings can save considerable CPU time.

SWOFF =  turn off DFT, to perform pure SCF iterations,
         until the density matrix convergence falls below
         this threshold.  This option is independent of
         SWITCH and can be used with or without it. It is
         reasonable to pick SWOFF > SWITCH > CONV in $SCF.
         SWOFF pertains only to the first geometry that the
```

```
         run computes, and is automatically disabled if you
         choose GUESS=MOREAD to provide initial orbitals.
         The default is 5.0E-3.

SWITCH = when the change in the density matrix between
         iterations falls below this threshhold, switch
         to the desired full grid (default=3.0E-4)
         This keyword is ignored if the SG1 grid is used.

NRAD0  = same as NRAD, but defines initial coarse grid.
         default = smaller of 24 and NRAD/4

NLEB0  = same as NLEB, but defines initial coarse grid.
         default = 110

NTHE0  = same as NTHE, but defines initial coarse grid.
         default = smaller of 8, NTHE/3

NPHI0  = same as NPHI, but defines initial coarse grid.
         default = smaller of 16, NPHI/3


technical parameters:

THRESH = threshold for ignoring small contributions to the
         Fock matrix.  The default is designed to produce
         no significant energy loss, even when the grid is
         as good as "army grade".  If for some reason you
         want to turn all threshhold tests off, of course
         requiring more CPU, enter 1.0e-15.
         default: 1.0e-4/Natoms/NRAD/NTHE/NPHI

GTHRE  = threshold applied to gradients, similar to THRESH.
         < 1 assign this value to all thresholds
         = 1 use the default thresholds (default).
         > 1 divide default thresholds by this value.
         If you wish to increase accuracy, set GTHRE=10.
         The default introduces an error of roughly 1e-7
         (a.u./bohr) in the gradient.
```

The keyword $DFTTYP is given in $CONTRL, and may have these values if the grid-free program is chosen:

```
        ----- options for METHOD=GRIDFREE -----

DFTTYP = NONE     means ab initio computation (default)
                     exchange functionals:
       = XALPHA   X-Alpha exchange (alpha=0.7)
       = SLATER   Slater exchange (alpha=2/3)
       = BECKE    Becke's 1988 exchange
       = DEPRISTO Depristo/Kress exchange
       = CAMA     Handy et al's mods to Becke exchange
       = HALF     50-50 mix of Becke and HF exchange
                     correlation functionals:
       = VWN      Vosko/Wilke/Nusair correlation, formula 5
       = PWLOC    Perdew/Wang local correlation
       = LYP      Lee/Yang/Parr correlation
                     exchange/correlation functionals:
       = BVWN     Becke exchange + VWN5 correlation
       = BLYP     Becke exchange + LYP correlation
       = BPWLOC   Becke exchange + Perdew/Wang correlation
       = B3LYP    hybrid HF/Becke/LYP using VWN formula 5
       = CAMB     CAMA exchange + Cambridge correlation
       = XVWN     Xalpha exchange + VWN5 correlation
       = XPWLOC   Xalpha exchange + Perdew/Wang correlation
       = SVWN     Slater exchange + VWN5 correlation
       = SPWLOC   Slater exchange + PWLOC correlation
       = WIGNER   Wigner exchange + correlation
       = WS       Wigner scaled exchange + correlation
       = WIGEXP   Wigner exponential exchange + correlation

AUXFUN = AUX0  uses no auxiliary basis set for resolution
               of the identity, limiting accuracy.
       = AUX3  uses the 3rd generation of RI basis sets,
               These are available for the elements H to
               Ar, but have been carefully considered for
               H-Ne only.  (DEFAULT)

THREE  = a flag to use a resolution of the identity to
         turn four center overlap integrals into three
         center integrals.  This can be used only if
         no auxiliary basis is employed. (default=.FALSE.)
=============================================================
```

==========

$TDDFT group

(relevant if TDDFT chosen in $CONTRL)

This group generates molecular excitation energies by time-dependent density functional theory computations (or time-dependent Hartree-Fock, also known as the Random Phase Approximation). The functional used for the excited states is necessarily the same one that is used for the reference state, specified by DFTTYP in $CONTRL.

For conventional TD-DFT (TDDFT=EXCITE in $CONTRL), the orbitals are optimized for RHF or UHF type reference states. Analytic nuclear gradients are available for singlet excited states, while the energy of excited states of other multiplicities can be computed. Two-photon absorption cross-sections may be predicted for singlet excited states. Ground state hyperpolarizabilities may be computed with the TDDFT module.

For spin-flip TD-DFT (TDDFT=SPNFLP in $CONTRL), the calculation obtains orbitals for a reference state of either UHF or ROHF type, with MULT in $CONTRL determining the Ms quantum number of the reference. The reference state's Ms is set equal to the S value implied by $CONTRL's MULT=2S+1. The SF-TD-DFT then uses only determinants with Ms=S-1, due to the flip of one alpha spin into a beta spin. This means that target states (which are spin contaminated) will have multiplicities around the range S-1 to S, only. It is quite possible for some of the target states to have a lower energy than the reference!!! Nuclear gradients and properties are available.

See just below for "limitations" below regarding the two different TD-DFT types.

TD-DFT is a single excitation theory. All of the caveats listed in the $CIS input group about states with double excitation character, need for Rydberg basis sets, greatly different topology of excited state surfaces, and so on apply here as well. Please read the introduction to the $CIS input group! If you use very large or very small Gaussian exponents, you may need to increase the number of

radial grid points (the program prints advice in such cases).

TDHF, TDDFT, and CIS are related in the following way:

```
       -- Tamm/Dancoff approximation -->
     |     TDHF                   CIS
DFT  |
     V     TDDFT              TDDFT/TDA
```

Here TDHF means absorption of photons, to produce excited states (TDHF is called RPA in the physics community). This meaning of TDHF should not be confused with the photon scattering processes computed by RUNTYP=TDHF or TDHFX, which generate polarizabilities. Note, in particular, that CITYP=CIS is equivalent to using TDDFT=EXCITE DFTTYP=NONE TAMMD=.TRUE., provided the former is run with no frozen cores. Solvent effects for CIS calculations are therefore available via the TDDFT codes.

Excited state properties are calculated using the TDDFT excited state electronic density only during gradient runs, or by setting TDPRP below.

The TD-DFT codes excite all electrons, that is, there is no frozen core concept. Please see the 4th chapter of this manual for more information on both types of TD-DFT.

"limitations" for TDDFT=EXCITE:

Permissible values for DFTTYP are shown below. These include "NONE" which uses TDHF (i.e. the Random Phase Approximation), noting that extra states may need to be solved for in order to be sure of getting the first few states correctly. If nuclear gradients are needed, you may choose any of the following functionals:

```
NONE
SVWN, SOP, SLYP, OLYP,
BVWN, BOP, BLYP (and their LC=.TRUE. versions)
B3LYP, CAMB3LYP, B3LYPV1R, PBE, PBE0
```

For evaluation of just the excitation energies, you may use many more functionals, notably including the metaGGAs in the last three lines:

```
NONE
SVWN, SVWN1, SPZ81, SP86, SOP, SLYP,
BVWN, BVWN1, BPZ81, BP86, BOP, BLYP, OLYP,
```

B3LYP, CAMB3LYP, B3LYPV1R, B3PW91, X3LYP,
PW91, PBE, PBE0,
VS98, PKZB,
M05, M05-2X, M06, M06-HF, M06-L, M06-2X, M08-HX, M08-SO
TPSS, TPSSm, TPSSh, and revTPSS

The LC flag in $DFT automatically carries over to TDDFT runs. The LC option may be used with the "B" functionals, and (like the similar range-separated CAMB3LYP) is useful in obtaining better descriptions for charge-transfer excitations or Rydberg excitation energies than are the conventional exchange correlation functionals (whether pure or hybrid). The LC flag is also available for excited state gradient computation.

Limits specific to the references for TDDFT=EXCITE are:

For SCFTYP=RHF, excitation energies can be found for singlet or triplet coupled excited states. For singlet excited states only, analytic gradients and properties can be found, for either full TD-DFT or in the Tamm/Dancoff approximation. For RHF references, solvent effects can be included by EFP1 or PCM (or both together), for both TD-DFT excitation energies and their nuclear gradients. DFTB (possibly combined with PCM) may be chosen as well, and analytic gradients for singlet and triplet are available.

For SCFTYP=UHF, excited states with the same spin projection as the ground state are found. MULT in $CONTRL governs the number of alpha and beta electrons, hence Ms=(MULT-1)/2 is the only good quantum number for either the ground or excited states. Since U-TDDFT is a single excitation theory, excited states with <S> values near Ms and near Ms+1 will appear in the calculation. There are no properties other than the excitation energy, nor gradients, nor solvent effects, at present.

"limitations" for TDDFT=SPNFLP:

Spin-flip TDDFT is programmed in the "collinear approximation" which means only the HF exchange term carries a large impact on the excitation energies. Pure DFT functionals may be used, but normally hybrids with large HF exchange fractions are used. The LC option for range-separation hybrids cannot be used, which also removes

CAMB3LYP. Finally, no meta-GGA may be used. Note that spin-flip TD-DFT in the Tamm/Dancoff approximation using DFTTYP=NONE is equivalent to spin-flip CIS.

MULT below is ignored, as the Ms of target states is fixed solely by MULT in $CONTRL. The spin-flip code operates only in the Tamm/Dancoff approximation, so TAMMD below is automatically .TRUE. Nuclear gradients and/or excited state properties are available only in the gas phase. Solvation effects are available for both energy and gradient calculations, for EFP1, C-PCM, or both.

NSTATE = Number of states to be found (excluding the reference state). The default is 1 more state.

IROOT = State used for geometry optimization and property evaluation. (default=1)
TDDFT=EXCITE counts the reference as 0, and this should be the lowest state. Hence IROOT=1 means the 1st excited state, just as you might guess.
TDDFT=SPNFLP labels the reference state as 0, but this might not be the lowest state overall. The meaning of IROOT=1 is the lowest state, omitting the reference state from consideration. Hence IROOT=1 might specify the ground state!

MULT = Multiplicity (1 or 3) of the singly excited states. This keyword applies only when the reference is a closed shell. (default is 1)
This parameter is ignored when TDDFT=SPNFLP.

TDPRP = a flag to request property computation for the state IROOT. Properties can only be obtained when the nuclear gradient is computable, see gradient restrictions noted in the introduction to this group. Properties require significant extra computer time, compared to the excitation energy alone, so the default is .FALSE. Properties are always evaluated during nuclear gradient runs, when they are a free by-product.

```
TPA    = a flag requesting two-photon absorption cross-
         sections.  These are computed for each of the
         NSTATE excited states, after first evaluating
         their excitation energies.  The TPA calculation is
         only available for closed shell references, only
         for singlet excited states (MULT=1), and may not
         be used with the Tamm/Dancoff approximation.
         Solvent effects may be treated by EFP.


TAMMD  is a flag selecting the Tamm/Dancoff approximation
       be used.  This may be used with closed shell
       excitation energies or gradients, or open shell
       excitation energies.  Default = .FALSE.
       This parameter is ignored by TDDFT=SPNFLP, which
       is only coded in the Tamm/Dancoff approximation.


NONEQ  is a flag controlling PCM's solvent behavior:
       .TRUE. splits the dielectric constant into a bulk
       value (EPS in $PCM) and a fast component (EPSINF),
       see Cossi and Barone, 2001.  The idea is that
       NONEQ=.t. is appropriate for vertical excitations,
       and .f. for adiabatic.  (the default is .TRUE.)
       This keyword is ignored by TDDFT=SPNFLP.

      * * * ground state polarizability calculation * * *
          (use TDDFT=HPOL option in $CONTRL)
These two frequency dependent polarizability calculations
may be requested in the same run (more efficient).  These
properties are available only for closed shell references,
require the default MULT=1 value in this input group, and
may not be used with the Tamm/Dancoff approximation.
Solvent effects may be treated by EFP.

ALPHA  = requests the polarizability.       Default=.FALSE.
         If BETA is not chosen, give just one PFREQ.

BETA   = requests the hyperpolarizability.  Default=.FALSE.
         Two values are required for PFREQ.

PFREQ  = an array of one or two input frequencies, omega1
         and omega2, to yield the polarizability
                 alpha(omega1;omega1)  [if BETA=.F.]
                 alpha(omega2;omega2)  [if BETA=.T.]
```

```
              alpha(omega3;omega3)  [if BETA=.T.]
          and/or to yield the hyperpolarizability
              beta(omega3;omega1,omega2).
          The output photon frequency is determined from
          omega3=-(omega1+omega2).  Useful special cases
             second harmonic generation   beta(-2W;W,W),
             electro-optic Pockels effect beta(-W;W,0), and
             optical rectification        beta(0;W,-W)
          are among the possibilities.
          The default is the static polarizability and/or
          static hyperpolarizability: PFREQ(1)=0.0,0.0
          PFREQ is given in atomic units: PFREQ=45.56/lamda,
          for wavelength lambda in nm.


                * * * Grid Selection * * *

The grid type and point density used in $TDDFT may be
chosen independently of the values in $DFT.  Excitation
energies accurate to 0.01 eV may be obtained with grids
that are much sparser than those needed for the ground
state, and this is reflected in the defaults.  Prior to
April 2008, the default grid was NRAD=24 NTHE=8 NPHI=16.

NRAD   = number of radial grid points in Euler-Maclaurin
         quadrature, used in calculations of the second or
         third derivatives of density functionals.
         (default=48)

NLEB   = number of angular points in the Lebedev grid.
         (default=110)

NTHE   = number of theta grid points if a polar coordinate
         grid is used.

NPHI   = number of phi grid points if a polar coordinate
         grid is used.  NPHI should be twice NTHE.

SG1    = flag selecting "standard grid one".
         (default=.FALSE.)

See both $DFT and REFS.DOC for more information on grids.
The "army grade" standard for $TDDFT is NRAD=96 combined
with either NLEB=302 or NTHE=12/NPHI=24.
```

```
      the remaining parameters are technical in nature:

CNVTOL = convergence tolerance in the iterative TD-DFT
         step.  (default=1.0E-7)

MAXVEC = the maximum number of expansion vectors used by
         the solver's iterations, per state (default=50).
         The total size of the expansion space will be
         NSTATE*MAXVEC.

NTRIAL = the number of initial expansion vectors used.
         (default is the larger of 5 and NSTATE).

=============================================================
```

==========

$DFTB group (relevant for GBASIS=DFTB)

Density-functional tight-binding (DFTB) is turned on by selecting GBASIS=DFTB in $BASIS. $DFTB controls optional parameters for a DFTB calculation. DFTB is formulated in a two-center approximation utilizing implicitly a minimal pseudoatomic orbital basis set with corresponding, pretabulated one- and two-center integrals. Because of this, many properties (for instances, multipoles higher than dipoles) and many options are ignored or not available in the current implementations of DFTB. DFTB also uses an independent SCF driver (SCF in DFTB is also called SCC, see below), so most SCF options are not available for DFTB.

Only SCFTYP=RHF and UHF are implemented. SCFTYP=ROHF is available, only when all SPNCST values are zero. DFTB does not explicitly use symmetry (C1 throughout) since integrals are never computed during the calculations. Slater-Koster tables are only defined for spherical functions (5d) so DFTB sets ISPHER=1. Most $GUESS options do not work for DFTB (DFTB does not use initial orbitals in the usual sense). Other than the default (METHOD=HUCKEL, which is ignored), only METHOD=MOREAD works (note that SCC-DFTB can use initial charges on atoms, derived from the orbitals).

RUNTYP=OPTIMIZE, HESSIAN and RAMAN are available for full (non-FMO) DFTB, whereas RUNTYP=OPTIMIZE and OPTFMO are available for FMO-DFTB. Excited state calculations for full DFTB may be performed through the standard (linear-response) time-dependent formalism (only closed shell). PCM can be used for both ground and excited state calculations, and energy and gradient can be evaluated.

In DFTB calculation, the atom type is determined by its name, not its nuclear charge as elsewhere in GAMESS. The nuclear charge (the second column in $DATA) is used only in population analysis, but not in SCF. DFTB uses a notion of "species", which means an atomic type. The species are numbered according to the order in which atoms appear in $DATA. For instances, in water there are two species, O and H. An atomic type of each species needs MAXANG, which for most but not all atoms is set automatically.

```
NDFTB  order of the Taylor expansion of the total energy
       around a reference density in the DFTB model.
       = 1 NCC-DFTB, also called DFTB1.
           NCC stands for non-charge-consistent, i.e., no
           explicity charge-charge interaction term is
           included in the energy calculation.
       = 2 SCC-DFTB, also called DFTB2.
           SCC means a self-charge-consistent approach,
           and SCC implies that SCF iterations are carried
           out that converge monopolar charges towards
           self-consistency.
       = 3 DFTB3, including 3rd order correction using
           Hubbard derivatives (HUBDER).
           In order to reproduce the published DFTB3
           approach, it is necessary to also specify
           DAMPXH=.TRUE. to add other terms.
           Gaus, M. et al. J. Chem. Theory Comput. 2011,
           7, 931-948 is referred to as Gaus2011 below.
           Default: 2.

DAMPXH =  a flag to include the damping function for X-H
          atomic pair in DFTB3. See also DAMPEX, and eq 21
          in Gaus2011.
          The damping function is used when at least one
          atom in a pair is "H". "HYDROGEN" and any other
          name will turn off the damping.
          Default: .FALSE.

DAMPEX =  an exponent used in the damping function for X-H
          atomic pairs.  The default value is 4.2
          (see Table 2 in Gaus2011 for more details).

SRSCC  =  a flag to perform shell-resolved SCC calculation.
          If set to .FALSE., the code uses the Hubbard
          value for an s orbital for p and d orbitals,
          ignoring their Hubbard values defined in Slater-
          Koster tables.
          Using .TRUE. enables the use of proper Hubbard
          values for p and d orbitals, implemented only
          for DFTB1 and DFTB2.
          Default: .FALSE.

ITYPMX    Convergence method of SCC calculations.
```

```
       = -1 Use standard GAMESS convergence methods.
            SOSCF and DIIS are supported, but DEM is not.
       = 0  Broyden's method.
            Interpolation is applied for atomic
            (or shell-resolved when SRSCC=.TRUE.)
            charges, but not Hamiltonian matrix.
       = 1  (reserved)
       = 2  DIIS for charges.
            Default: 0.

ETEMP  = electronic temperature in Kelvin. Non-zero values
         of ETEMP help SCF convergence of nearly-degenerate
         systems by smearing occupation numbers around the
         Fermi-level. Only the Fermi-Dirac distribution
         function is available as a smearing function.  The
         default value is 0 Kelvin, meaning the smearing
         function is not used.
         ETEMP is implemented only for SCFTYP=RHF and when
         FMO is not used.

DISP     dispersion model for DFTB.
       = NONE no Dispersion correction.
       = UFF  UFF-type dispersion correction.
              Parameters for atomic numbers up to 54 are
              available internally or can be supplied in
              DISPPR for any atom.
              Built-in parameters are taken from Rappe
              et al. J. Am. Chem. Soc. 1992, 114, 10024.
       = SK   The Slater-Kirkwood type dispersion
              correction omitting the change polarizability
              depending on the number of bonds.
              No default values of DISPPR are available.
              Some are listed in the manual of the DFTB+
              program.

DISPPR   an array of parameters used for dispersion
         correction, listed in sets for each species.
         For DISP=UFF, DISPPR(1) and DISPPR(2) define the
         non-bonded distance (Angs.) and energy (kcal/mol)
         for the first species, respectively, and so on.
         For DISP=SK, a set for a species has 3 parameters,
         the polarizability (Angstrom^3), cutoff length
         (Angstrom), and atomic charge.
         Default: see DISP.
```

HUBDER an array of Hubbard derivatives for each species (1 per species) used only for DFTB3 calculations. Default values are set only for C, H, N, O, and P using the final row of Table 2 in Gaus2011 (see the paper for other choices).

MAXANG array of maximum angular momentum of each species, which determines the number of basis functions. DFTB uses only valence orbitals and electrons! Most elements have proper default values, but for some atomic types (i.e., species) you need to manually define the values.

QREF array of the number of reference electrons of each species. QREF is usually automatically taken from Slater-Koster parameters, so this option is seldom used.

SPNCST an array of spin constants used in unrestricted (UHF) DFTB calculation. Provide 6 spin constants, W_{ss}, W_{sp}, W_{pp}, W_{sd}, W_{pd}, & W_{dd}, for each species in a continuous array. Constants for some elements can be found in the manual of the DFTB+ program.

MODHSS controls the behavior of the computation of analytic Hessian (bit additive).
1 Do not write integrals on disk.
2 Use a faster algorithm for solving CP-DFTB requiring a lot of memory.
4 Parallelize integral transformation using GDDI.
8 Hessian contributions are calculated one by one.
By default, all of these flags are set to true, unless there is not enough memory or for some other reason.

* * *

The following options are FMO-DFTB specific (Nishimoto, Y. et al. J. Chem. Theory Comput. 2014, 10, 4801-4812.).

FMO-DFTB has many limitations and some FMO options are not supported (for instance, AFO, multilayer FMO etc). Only

```
single layer, restricted closed-shell FMO2-DFTB1, 2, and 3
are implemented at present. SRSCC, ETEMP etc are not
available. The analytic gradient is available for FMO-DFTB,
requiring solving SCZV as in other FMO methods.

MODESD = controls the behavior of ES-DIM (electrostatic
         dimer) approximation (bit additive).
         1 Calculate interfragment repulsive energy for ES
           dimers (almost never used).
         2 Add up all ES-DIM energies. This means that
           individual ES dimer energies are not calculated,
           but only their total lump sum, computed with the
           dynamic load balancing.
         4 Lump ES-DIM routine with static load balancing.
           The bits of 2 or 4 are mutually exclusive.
           Default: 0 (i.e., individual ES dimer energies).

MODGAM = controls the calculation of gamma values
         (interatomic 1/R-like function) in FMO-DFTB2 and
         FMO-DFTB3 (bit additive).
         0 Calculate gamma values on the fly. (default)
         1 Calculate once and prestore gamma values in
           triangular matrix.
         2 Calculate once and prestore gamma values in
           square matrix.
         4 With the bits of 1 or 2, the calculation of
           gamma values is parallelized with GDDI.
           The bits of 1 or 2 are mutually exclusive. These
           options are faster but takes more memory.
           Default: 0


=============================================================
```

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$DFTBSK group (required if GBASIS=DFTB)

This group is required for all DFTB calculations. It defines the file names for Slater-Koster parameters describing pairwise interactions for each pair of species (see $DFTB for the introduction).

The group is free-formatted, and consists of N*N lines, where N is the number of species. Each line has the format:

```
  species-i species-j i-j parameter file name
```

Note that (species-i species-j) is different from (species-j species-i), and both must be given! For example,

```
   C O /home/user/DFTB/mio-0-1/C-O.skf
```

which defines carbon-oxygen parameters to be in that file. Naturally, this file must be readable on the computer where calculations are actually run.

The names of species should be the same as in $DATA (for FMO, in $FMOXYZ). In FMO-DFTB calculations, these names must be atomic symbols (H, He, ...), otherwise names may be used (hydrogen, helium, ...) truncated to 8 symbols. The names may include numbers, as in (H.1).

Slater-Koster parameters are available from

```
          http://www.dftb.org/
```

(for free) and from some other sources. There are many different parameter sets, for instance, the above example uses the "mio-0-1" set. Follow the requirements on proper citations when using these parameters.

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$CIS group required when CITYP=CIS
required when CITYP=SFCIS

The CIS method (singly excited CI) is the simplest way to treat excited states. By Brillouin's Theorem, a single determinant reference such as RHF will have zero matrix elements with singly substituted determinants. The ground state reference therefore has no mixing with the excited states treated with singles only. Reading the references given in Section 4 of this manual will show the CIS method can be thought of as a non-correlated method, rigorously so for the ground state, and effectively so for the various excited states. Some issues making CIS rather less than a black box method are:

a) any states characterized by important doubles are simply missing from the calculation.
b) excited states commonly possess Rydberg (diffuse) character, so the AO basis used must allow this.
c) excited states often have different point group symmetry than the ground state, so the starting geometries for these states must reflect their actual symmetry.
d) excited state surfaces frequently cross, and thus root flipping may very well occur.

The normal CIS implementation allows the use of only RHF references, but can pick up both singlet and triplet excited states. Nuclear gradients are available, as are properties. The CIS run automatically includes computation of the dipole moments of all states, and all pairwise transition dipoles and oscillator strengths.

The spin-flip type of CIS is very similar to spin-flip TD-DFT (the $TDDFT input contains more information about how spin-flip runs select the target state's Ms by $CONTRL's MULT value). The reference state must be UHF or ROHF, with MULT in $CONTRL at least 3. The target states of the CIS have one lower Ms, after one alpha spin in the reference is flipped to beta. Nuclear gradients are possible.

Solvent effects are not available for either CIS or SFCIS.

It is worthwhile to look at the $TDDFT input, which is a very similar calculation. The TD-DFT program offers the possibility of recovering some of the correlation energy, permits some solvent models, and can be used for MEX/CONICL surface intersection searches.

The first six keywords are chemically important, while the remainder are mostly technical.

NACORE = n Omits the first n occupied orbitals from the calculation (frozen core approximation).
For CITYP=CIS, the default for n is the number of chemical core orbitals.
For CITYP=SFCIS, the default, which is also the only possibility, is 0.

NSTATE = Number of states to be found (excluding the reference state). No default is provided.

IROOT = State for which properties and/or gradient will be calculated. Only one state can be chosen. The reference state is referred to as 0, and in the case of CITYP=SFCIS, might have a higher energy than some of the NSTATE target states.

CISPRP = Flag to request the determination of CIS level properties, using the relaxed density. Relevant to RUNTYP=ENERGY jobs, although the default is .FALSE. because additional CPHF calculation will be required. Properties are an automatic by-product of runs involving the CIS or SFCIS nuclear gradient.

HAMTYP = Type of CI Hamiltonian to use, if CITYP=CIS.
= SAPS spin-adapted antisymmetrized product of the desired MULT will be used (default)
= DETS determinant based, so both singlets and triplets will be obtained.

MULT = Multiplicity (1 or 3) of the singly excited SAPS (the reference can only be singlet RHF). Only relevant for SAPS-based CITYP=CIS run, as SFCIS controls the Ms for target states by the value of MULT in $CONTRL.

- - - - - - - - - - - -

DIAGZN = Hamiltonian diagonalization method.
= DAVID use Davidson diagonalization. (default)
= FULL construct the full matrix in memory and diagonalize, thus determining all states (not recommended except for small cases).

DGAPRX = Flag to control whether approximate diagonal elements of the CIS Hamiltonian (based only on the orbital energies) are used in the Davidson algorithm. Note, this only affects the rate of convergence, not the resulting final energies. If set .FALSE., the exact diagonal elements are determined and used. Default=.TRUE.

NGSVEC = Dimension of the Hamiltonian submatrix that is diagonalized to form the initial CI vectors. The default is the greater of NSTATE*2 and 10.

MXVEC = Maximum number of expansion basis vectors in the iterative subspace during Davidson iterations, before the expansion basis is truncated. The default is the larger of 8*NSTATE and NGSVEC.

NDAVIT = Maximum number of Davidson iterations. Default=50.

DAVCVG = Convergence criterion for Davidson eigenvectors. Eigenvector accuracy is proportional to DAVCVG, while the energy accuracy is proportional to its square. The default is 1.0E-05.

CHFSLV = Chooses type of CPHF solver to use.
= CONJG selects an ordinary preconditioned conjugate gradient solver. (default)
= DIIS selects a diis-like iterative solver.

RDCISV = Flag to read CIS vectors from a $CISVEC input group in the input file. Default is .FALSE.

MNMEDG = Flag to force the use of the minimal amount of memory in construction of the CIS Hamiltonian diagonal elements. This is only relevant when DGAPRX=.FALSE., and is meant for debug purposes.

The default is .FALSE.

MNMEOP = Flag to force the use of the minimal amount of memory during the Davidson iterations. This is for debug purposes. The default is .FALSE.

==========

$CISVEC group required if RDCISV in $CIS is chosen

This is formatted data generated by a previous CIS run, to be read back in as starting vectors. Sometimes molecular orbital phase changes make these CI vectors problematic.

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$MP2 group (relevant to SCFTYP=RHF,UHF,ROHF if MPLEVL=2)

Controls 2nd order Moller-Plesset perturbation runs, if requested by MPLEVL in $CONTRL. MP2 is implemented for RHF, high spin ROHF, or UHF wavefunctions, but see also $MRMP for MCSCF. Analytic gradients and the first order correction to the wavefunction (i.e. properties) are available for RHF, ROHF (if OSPT=ZAPT), and UHF. The $MP2 input group is not usually given. See also the DIRSCF keyword in $SCF to select AO integral direct MP2.

The spin-component-scaled MP2 (SCS-MP2) energy of Grimme is printed for SCFTYP=RHF references during energy runs. See also the keyword SCSPT below. Only the CODE=IMS program is able to do analytic gradients for SCS-MP2.

Special serial codes exist for RHF or UHF MP2 energy or gradient, or the ROHF MP2 energy. Parallel codes using distributed memory are available for RHF, ROHF, or UHF MP2 gradients. In fact, the only way that ROHF MP2 gradients can be computed on one node is with the parallel code, using MEMDDI!

MP2 energy values using solution models are computed by using the solvated SCF orbitals in the perturbation step. All of the MP2 nuclear gradient programs contain additional terms required for EFP, PCM, EFP plus PCM, or COSMO solvation models.

NACORE = n Omits the first n occupied orbitals from the calculation. The default for n is the number of chemical core orbitals.

NBCORE = Same as NACORE, for the beta orbitals of UHF. It is almost always the same value as NACORE.

MP2PRP= a flag to turn on property computation for jobs jobs with RUNTYP=ENERGY. This is appreciably more expensive than just evaluating the second order energy correction alone, so the default is to skip properties. Properties are always computed during gradient runs, when they are an almost free byproduct. (default=.FALSE.)

```
OSPT=      selects open shell spin-restricted perturbation.
           This parameter applies only when SCFTYP=ROHF.
           Please see the 'further information' section for
           more information about this choice.
    = ZAPT picks Z-averaged perturbation theory. (default)
    = RMP  picks RMP (aka ROHF-MBPT) perturbation theory.

CODE  =    the program implementation to use, choose from
           SERIAL, DDI, IMS, or RIMP2 according to the
           following chart, depending on SCFTYP and if
           the run involves nuclear gradients,

 RHF     RHF        UHF    UHF       ROHF    ROHF    ROHF
energy gradient   energy gradient   energy gradient energy
                                  OSPT=ZAPT    ZAPT    RMP
SERIAL  SERIAL    SERIAL  SERIAL    SERIAL     -     SERIAL
DDI      DDI       DDI     DDI       DDI     DDI      -
IMS      IMS        -       -         -       -       -
RIMP2     -       RIMP2     -         -       -       -
```

The default for serial runs (p=1) is CODE=IMS for RHF, and CODE=SERIAL for UHF or ROHF (provided PARALL is .FALSE. in $SYSTEM). When p>1 (or PARALL=.TRUE.), the default becomes CODE=DDI. However, if FMO is in use, the default for closed shell parallel runs is CODE=IMS. The "SERIAL" code for OSPT=RMP will run with modest scalability when p>1.

The many different MP2 programs are written for different hardware situations. Here N is the number of atomic basis functions, and O is the number of correlated orbitals in the run:

The original SERIAL programs use N**3 memory, and have larger disk files and generally takes longer than CODE=IMS.

The IMS program uses N*O**2 memory, and places most of its data on local disks (so you must have good disk access), and will run in parallel...ideal for small clusters. Using this program on a node where the disks are of poor quality (SATA-type) and with many cores accessing that single disk may be very I/O bound. Adding more memory can make this program run more efficiently. Network traffic is modest when running in parallel.

The DDI program uses N**4 memory, but this is distributed across all nodes, and there is essentially no I/O...ideal for large parallel machines where the manufacturer has forgotten to include disk drives. MEMDDI must be given in $SYSTEM for these codes, so large problems may require many nodes to aggregate enough MEMDDI. The network traffic is high, so an Infiniband quality network or better preferred. Scalability is very good, for example, this program has been used up to 4,000 cores on Altix/ICE equipment.

All of the programs just mentioned should generate the same numerical results, so select which one best matches your hardware.

The RIMP2 program is an approximation to the true MP2 energy, using the "resolution of the identity" to reduce the amount of data stored (in memory and/or on disk), and also the total amount of computation. See the paper on this program for its reduced CPU and memory requirements. Network traffic is modest. The code has options within the $RIMP2 input to govern the use of replicated memory versus shared memory, as well as the use of disk storage versus distributed memory, so you can tune this to your hardware.

References for the various programs are given in REFS.DOC.

NOSYM = disables the orbital symmetry test completely. This is not recommended, as loss of orbital symmetry is likely to mean a bad calculation. It has the same meaning as the keyword in $CONTRL, but just for the MP2 step. (Default=0)

CUTOFF = transformed integral retention threshold, the default is 1.0d-9 (1.0d-12 in FMO runs).

The following keyword applies only to RHF references:

SCSPT = spin component scaled MP2 energy selection.
= NONE - the energy will be the normal MP2 value. This is the default.
= SCS - the energy used for the potential surface will be the SCS energy value.

Use of SCSPT=SCS causes gradients to be those for the SCS-MP2 potential surface. For CODE=IMS, the nuclear gradient can be evaluated analytically. See NUMGRD in $CONTRL if

for some reason you wish to use the other two closed shell codes for SCS-MP2 gradients.

The following keywords apply to any CODE=SERIAL MP2 run, or to parallel ROHF+MP2 runs using OSPT=RMP:

LMOMP2= a flag to analyze the closed shell MP2 energy in terms of localized orbitals. Any type of localized orbital may be used. This option is implemented only for RHF, and its selection forces use of the METHOD=3 transformation, in serial runs only. The default is .FALSE.

CPHFBS = BASISMO solves the response equations during gradient computations in the MO basis. This is programmed only for RHF references without frozen core orbitals, when it is the default.
= BASISAO solves the response equations using AO integrals, for frozen core MP2 with a RHF reference, or for ROHF or UHF based MP2.

NWORD = controls memory usage. The default uses all available memory. Applies to CODE=SERIAL. (default=0)

METHOD= n selects transformation method, 2 being the segmented transformation, and 3 being a more conventional two phase bin sort implementation. 3 requires more disk, but less memory. The default is to attempt method 2 first, and method 3 second. Applies only to CODE=SERIAL.

AOINTS= defines AO integral storage during conventional integral transformations, during parallel runs.
DUP stores duplicated AO lists on each node, and is the default for parallel computers with slow interprocessor communication, e.g. ethernet.
DIST distributes the AO integral file across all nodes, and is the default for parallel computers with high speed communications. Applies only to parallel OSPT=RMP runs.

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==========

$RIMP2 group (optional, relevant if CODE=RIMP2 in $MP2)

This group controls the resolution of the identity MP2 program, which approximately evaluates the MP2 energy. The RI approximation greatly reduces the computer resources required, while suffering only a small error in the energies. Thus, very large atomic basis sets may be used. The input below controls both utilization of the computer resources, and the accuracy of the calculation. See also $AUXBAS, regarding the auxiliary basis set, whose choice also affects the accuracy of the calculation.

The program is enabled for parallel calculation, and is tuned to today's SMP nodes. It is limited to energy calculations only, without any solvent effects, for RHF or UHF references.

```
IAUXBF = 0 uses Cartesian Gaussians
       = 1 uses spherical harmonics
           for the auxiliary basis set used to expand the
           MP2 energy expression into products of 3-index
           matrices.  The default is inherited from ISPHER.
```

The next two control computer resources, trading memory for disk storage.

```
GOSMP  = flag requesting shared memory use.  The default
         is .TRUE. in multi-core nodes, but .FALSE. in a
         uniprocessor.  This option means only one copy of
         certain large matrices is stored per node.

USEDM  = a flag to store two and three center repulsion
         integrals in distributed memory (.TRUE.), or in
         disk files (.FALSE., which is the default).
         Selection of this flag requires MEMDDI in $SYSTEM.
         The default is .TRUE.
```

The RI approximation reduces CPU time, memory requirements, and total disk storage requirements compared to exact calculation. Experimentation with these two keywords will let you tune the program to your hardware situation. For example, choosing GOSMP=.TRUE. and USEDM=.TRUE. will run without any extra disk files, while setting GOSMP=.TRUE.

and USEDM .FALSE. will minimize memory usage (and network usage) at the expense of doing disk I/O.

Total memory usage per node can be obtained by running EXETYP=CHECK. Note the largest replicated memory printed during the RIMP2's output, dividing by 1000000 to get the correct input for MWORDS (round up a bit). Note the largest shared memory requirement printed, also dividing by 100000, and rounding up a bit. Note the distributed memory requirement, which is already in megawords, and is the correct input for MEMDDI. Then, assuming you use p total compute process on multiple n-way nodes, the memory per node is

GBytes/node= 8(n*MWORDS + shared + n*MEMDDI/p)/1024

Turning off GOSMP reduces the shared memory to 0 but increases MWORDS, which is multiplied by the number of cores per node! Turning off USEDM leads to MEMDDI=0 by using disk storage instead.

If additional memory is available, increasing MWORDS can lead to a reduction in the level of the occupied orbital batch, or "LV". Larger MWORDS permits a smaller LV, which will in turn reduce the required computational time, and the required network traffic or disk I/O. The value of LV used is the last line appearing after "CHECKING SIZE OF OCCUPIED ORBITAL BATCH".

The next four control numerical accuracy, but see $AUXBAS which is even more influential in regards the accuracy!

OTHAUX = flag to orthogonalize the RI basis set by diagonalization of the overlap matrix. If there is reason to suspect linear dependence may exist in the RI basis, select this option to have a more numerically stable result. Larger RI basis sets such as CCT and ACCT, in particular, may benefit from selecting this. (default=.FALSE.)

STOL = threshold at which to remove small overlap matrix eigenvectors, ignored if OTHAUX=.FALSE. This keyword is analogous to QMTTOL in $CONTRL for the true AO basis. (default= 1.0d-6)

IVMTD = selects the procedure for removing redundancies when inverting the two-center, two-e- matrix.

```
       = 0 use Cholesky decomposition (default)
       = 2 use diagonalization

VTOL   = threshold at which to remove redundancies.  This
         is ignored unless IVMTD=2  (default= 1.0d-6)
```

Don't forget to see also the $AUXBAS input group!

An example of this program follows. The molecule is taxol, with 1032 AOs and MOs in the 6-31G(d) basis, correlating 164 valence orbitals. The RI basis set used is SVP, which matches the true basis set in quality. There are 4175 AOs in the RI basis. The job was run on a single 8-way node (n=8, p=1,2,4,8), using MWORDS=50 (leading to LV=6), MEMDDI=580, and the largest shared memory needed is 95 million words. The total node memory is thus
(8 bytes/word)*(8*50 + 95 + 8*580/ 8)/1024 = 8.4 GBytes
easily fitting into a modern 16 GByte node. It reduces to
(8 bytes/word)*(8*50 + 95 + 8*580/16)/1024 = 6.1 GB/node
if two 8-way nodes are used. Scaling is

p	SCF	RI-MP2	job total
1	7391	7919	15366
2	3718	4131	7860
4	1857	2290	4174
8	952	1488	2479
16	486	758	1276 using two 8-way nodes.

numerical results are E(RI-MP2)= -2920.607512
versus the exact E(MP2)= -2920.606231
The 0.0013 error should be measured against the total 2nd order correlation energy, which is -8.7855, while noting the time for the 2nd order E is similar to the SCF time.

==========

==========

$AUXBAS group (required if CODE=RIMP2 in $MP2)

This group specifies the auxiliary basis set used to define the resolution of the identity in the RI-MP2 method. The RI methods are formally exact if the RI basis set is complete, so selecting larger bases improves the results. However, this also increases the computational cost of the run! It is reasonable to use smaller RI basis sets when the AO basis is modest, and increase the RI basis when you use very large AO bases.

```
CABNAM specifies built-in basis sets for the RI:
       = SVP   Ahlrich's SVP basis,   available H-Kr
       = TZVP  Ahlrich's TZVP basis,  available H-Ar
       = TZVPP Ahlrich's TZVPP basis, available H-Ar
       = CCD       cc-pVDZ basis, available H-Ar
       = ACCD  aug-cc-pVDZ basis, available H-Ar
       = CCT       cc-pVTZ basis, available H-Ar
       = ACCT  aug-cc-pVTZ basis, available H-Ar
       = XXXXX externally defined: see EXTCAB.
CABNAM has no default, this is a required input!

Note IAUXBF in $RIMP2 for selecting spherical harmonics
versus Cartesian Gaussians.

EXTCAB = flag to read the basis from an external file.
         (default is .FALSE.)
```

This is analogous to EXTBAS in $BASIS: no external files are provided with GAMESS. The value for CABNAM=XXXX must be 8 or fewer letters: avoid the name of any built in auxiliary basis. Your XXXX bases will be read from a file defined by environment variable EXTCAB, in the execution script. Every atom present in your molecule must be defined in the external file by a line giving its chemical symbol and then XXXX. Following this header, give the basis in free format $DATA style, containing only S, P, D, F, and G shells, terminating each atom by the usual blank line.

==========

==========

$CCINP group (optional, relevant for any CCTYP)

This group controls a coupled-cluster calculation specified by CCTYP in $CONTRL. The reference orbitals may be RHF or high spin ROHF. If this group is not given, as is often the case, all valence electrons are correlated. Several ground state CCTYP choices obey at least a few of the keywords from $EOMINP, so please see that group too. Excited state runs such as CCTYP=EOM-CCSD or CR-EOML read $CCINP to define orbital ranges for the ground state CCSD prior to generating excitations under $EOMINP's control.

A number of CCTYP choices have been superceded by more advanced equations. For example, R-CC and CR-CC were developed prior to their CR-CCL replacement, while CR-EOML supercedes CR-EOM. CR-CCL provides a good approximation to the fully iterated CCSDT method, and so is superior to the familiar CCSD(T). A reasonable menu is:

	RHF	ROHF (high spin)
ground states [properties]:		
	CCSD [CCPRP]	CCSD [n/a]
	CCSD(T)	n/a
	CR-CCL	CR-CCL
excited states [properties]:		
	EOM-CCSD [CCPRPE]	EOM-CCSD
	MULT=1	MULT=1,3,5 or spin-contaminated
	CR-EOML	n/a
ionization processes:		
	EA-EOM3a	n/a
	IP-EOM3a	n/a
	MULT=2,4	

CR-CCL =left-CCSD + CR-CC(2,3) perturbative triples.
CR-EOML=left-EOM-CCSD + CR-CC(2,3) perturbative triples.

Parallel computation is possible for RHF references only, and only for CCTYP=CCSD or CCSD(T). Memory use in parallel runs is exotic: use EXETYP=CHECK with PARALL in $SYSTEM set on prints the per node memory requirements.

See the "Further Information" section of this manual for more details about coupled-cluster runs.

**** The first four pertain to both RHF and ROHF ****

NCORE = gives the number of frozen core orbitals to be omitted from the CC calculation. The default is the number of chemical core orbitals.

NFZV = the number of frozen virtual orbitals to be omitted from the calculation. (default is 0)

MAXCC = defines the maximum number of CCSD (or LCCD, CCD) iterations. This parameter also applies to ROHF's left CC vector solver, but not RHF's left vector. See MAXCCL for RHF. (default=30)

ICONV = defines the convergence criterion for the cluster amplitudes, as 10**(-ICONV). The ROHF reference also uses this for its left eigenstate solver, but see CVGEOM in $EOMINP for RHF references. (default is 7, but it tightens to 8 for FMO-CC.)

**** the next group pertains to RHF reference only ****

CCPRP = a flag to select computation of the CCSD level ground state density matrix (see also CCPRPE in $EOMINP for EOM-CCSD level excited states). The computation takes significant extra time, to obtain left eigenstates, so the default is .FALSE. except for CCTYP=CR-CCL or CR-EOML, where the work required for properties must be done anyway. This keyword is only available in serial runs.

Notes: CCSD is the only level at which properties can be obtained. Therefore this option can only be chosen for CCTYP=CCSD, CR-CCL, EOM-CCSD, CR-EOM, or CR-EOML. A CCSD run requesting CCPRP=.TRUE. will internally change itself to EOM-CCSD to run the left CCSD, but since NSTATE of $EOMINP will still be zero, this remains a ground state calculation. Note that the convergence criterion for left eigenstates is CVGEOM in $EOMINP, which is set to obtain excitation energies, and may need tightening.

There is little reason to select any of these:

MAXCCL = iteration limit on the left eigenstate needed by
CCSD properties, or CR-CCL energies.
This is just a synonym for MAXEOM in $EOMINP.
If you want to alter the left state's convergence
tolerance, use CVGEOM in $EOMINP. The right CCSD
state's convergence is set by MAXCC and ICONV.

NWORD = a limit on memory to be used in the CC steps.
The default is 0, meaning all memory available
will be used.

IREST = defines the restart option. If the value of IREST
is greater or equal 3, program will restart from
the earlier CC run. This requires saving the disk
file CCREST from the previous CC run. Values of
IREST between 0 and 3 should not be used. In
general, the value of IREST is used by the program
to set the iteration counter in the restarted run.
The default is 0, meaning no restart is attempted.

MXDIIS = defines the number of cluster amplitude vectors
from previous iterations to be included in the
DIIS extrapolation during the CCSD (or LCCD, CCD)
iterative process. The default value of MXDIIS is
5 for all but small problems. The DIIS solver can
be disengaged by entering MXDIIS = 0. It is not
necessary to change the default value of MXDIIS,
unless the CC equations do not converge in spite
of increasing the value of MAXCC.

AMPTSH = defines a threshold for eliminating small cluster
amplitudes from the CC calculations. Amplitudes
with absolute values smaller than AMPTSH are set
to zero. The default is to retain all small
amplitudes, meaning fully accurate CC iterations.
Default = 0.0.

**** the next group pertains to ROHF reference only ****
There is little reason to select any of these.

MULT = spin multiplicity to use in the reference
determinant during the CC computation.

```
          The value of MULT given in the $CONTRL input
          determines the spin state for the ROHF orbital
          optimization, and is the default for the CC.
          It would be quite unusual to use a different
          spin in the SCF than in the CC.  The MULT keyword
          in $EOMINP is of greater physical interest.

IOPMET = method for the CR-CC(2,3) triples correction.
       = 0 means try 1 and then try 2 (default)
       = 1, the high memory option
         This option uses the most memory, but the least
         disk storage and the least CPU time.
       = 2, the high disk option
         This option uses least memory, by storing a large
         disk file.  Time is slightly more than IOPMET=1,
         but the disk file is (NO**3 * NU**3)/6 words,
         where NO = correlated orbitals, and NU= virtuals.
       = 3, the high I/O option
         This option requires slightly more memory than 2,
         and slightly more disk than 1, but does much I/O.
         It is also the slowest of the three choices.
Check runs will print memory needed by all three options.

KREST  = 0 fresh start of the CCSD equations (default)
       = 1 restart from AMPROCC file of a previous run

KMICRO = n performs DIIS extrapolation of the open shell
         CCSD, every n iterations (default is 6)
         Enter 0 to avoid using the DIIS converger.

LREST  = 0 fresh start of the left CCSD equations (default)
       = 1 restart from AMPROCC file of a previous run

LMICRO = n performs DIIS extrapolation of the open shell
         left equations, every n iterations (default is 5)
         Enter 0 to avoid using the DIIS converger.
         KMICRO and LMICRO are ignored for trivial
         problem sizes.

=============================================================
```

==========

$EOMINP group

(optional, for CCTYP=EOM-CCSD, CR-EOM, or CR-EOML)
(optional, for CCTYP=EA-EOMx or IP-EOMx)
(optional for CCSD properties, or CCTYP=CR-CCL)

This group controls the calculation of excited states by the equation of motion coupled cluster with single and double excitations, with optional triples corrections. It also pertains to electron attachment and detachment processes, which may result in the system being left in an excited state. EOM-CCSD can be selected for RHF or ROHF reference states, while all other CCTYP listed above can be used only with SCFTYP=RHF.

These EOM-type runs consist of an SCF calculation on the reference state, followed by a ground state CCSD (see the $CCINP input to control the ground state calculation, and the orbital range correlated), followed by an EOM-CCSD, IP-EOMCC, or EA-EOMCC calculations on the target states (see NSTATE below). In some cases, triples corrections based on the method of moments approach may follow.

The input group permits selection of how many states are computed (machine time is linear in the number of states). Since the target state default is simplistic (only one excited state in the totally symmetric representation), it is usually necessary to give this group, to select NSTATE and IROOT sensibly.

Because this input group is used for several CCTYP calculations, not all keywords are used in every case, or the keywords may have slightly different meanings:
a) if the reference type is RHF, and CCTYP is EOM-CCSD, CR-EOM, or CR-EOML, keywords MULT and NACT are ignored.
b) if the reference type is ROHF, and CCTYP is EOM-CCSD, keywords CCPRPE, NACT, MTRIP, MEOM, MCI, MINIT, CVGCI, MAXCI, MICCI are ignored. MULT is sometimes ignored.
c) if the reference type if RHF, and CCTYP is an ionization process (EA/IP), keywords CCPRPE, MTRIP, MEOM, MCI, MINIT, CVGCI, MAXCI, MICCI are ignored.

Additional information on CC and EOM methods can be found in the "Further Information" section of this manual.

```
--- spin and space symmetry, and state selection:

MULT   = Spin multiplicities for the target states.
         The meaning depends on the particular calculation.
         The default for cases using $EOMINP's MULT is -1.
         If any doubly excited states or EA/IP quartets
         are sought, be sure to select MINIT=1 so that
         the initial guess states include these.

  In case the run is IP-EOM or EA-EOM type, the run will
  pass through open shell code, although the reference
  in $CONTRL must be given as RHF and MULT=1.  The IP or EA
  states will be spin adapted.
   MULT = -1 means target both doublet and quartet states
        =  2 means consider only doublet states
        =  4 means consider only quartet states, which can
             be produced at the EOM-CCSD level by a double
             that unpairs two electrons, and attaches (or
             detaches) a third electron.

  In case the run is EOM-CCSD, SCFTYP=ROHF, but $CONTRL
  selects a closed shell reference by MULT=1:
   MULT = -1 means target singlet, triplet, and pentuplets.
        =  1 consider only singlet excited states
        =  3 consider only triplet excited states
        =  5 consider only pentuplet excited states.

  In case the run is EOM-CCSD, SCFTYP=ROHF, and $CONTRL
  selects a genuinely open shell reference, the EOM states
  will not be perfectly spin adapted.  The spin projection
  of Ms from $CONTRL's (MULT-1)/2 is the only good quantum
  number.  The excited states will have S values near to
  Ms, Ms+1, or Ms+2 since single and double excitations are
  treated.  Note that target states with spins LOWER than
  Ms are not generated, even if they exist in nature. The
  output will not print approximate S or <S**2> values,
  but will label spatial symmetry.
   MULT =  input will be ignored

  In case the run is an RHF reference EOM-CCSD (or triples
  correction), the target states are singlets, only.
   MULT =  input will be ignored
```

GROUP the name of the Abelian group to be used, which may be only one of the groups shown in the table below. The default is taken from $DATA, and is reset to C1 if the group is non-Abelian. The purpose is to let the Abelian symmetry be turned off by setting GROUP=C1, if desired. Symmetry is used to help with the initial excited state selection, for controlling the EOMCC calculations, and for labeling the calculated states in the output (not to speed up the calculations).

NSTATE an array of up to 8 integers telling how many excited states of each symmetry type should be computed. The default is

```
   NSTATE(1)=1,0,0,0,0,0,0,0
```

meaning 1 totally symmetric state is to be found. The ground state is always computed, and MUST NOT be included in NSTATE's input, for excited state runs. For EA or IP runs, the NSTATE input MUST include the target ion's ground state, and may include excited states of the ion. See also ISELCT below.

There is no particular reason the first excited state (or ionic ground state) should be totally symmetric, so most runs should give a sensible NSTATE input. Up to 10 states can be found in any irrep. Machine time is linear in the number of states to be found, so be realistic!

NSTATE uses this order for irreducible representations:

irrep	1	2	3	4	5	6	7	8
C1	A							
C2	A	B						
Cs	A'	A''						
Ci	Ag	Au						
C2v	A1	A2	B1	B2				
C2h	Ag	Au	Bg	Bu				
D2	A	B1	B2	B3				
D2h	Ag	Au	B1g	B1u	B2g	B2u	B3g	B3u

As an aside, NSTATE(1)=0,0,0,0,0,0,0,0 for RHF references will calculate the ground state only, generating the type I, II, or possibly III CR-CCSD(T) energies, which aren't otherwise available in a direct ground state calculation.

```
IROOT     selects the state whose energy is to be saved
          for further calculations, such as numerical
          gradients, or whose properties are evaluated,
          see CCPRPE below.
          The first integer lists the irrep number, from
          the same table as NSTATE, and the second lists
          the number of the state.  Thus, IROOT(1)=3,2
          means the second B1 state, if GROUP=C2V.
          (default IROOT(1)=1,0)
```

IROOT's default is moderately sensible for a RHF-based excited state run, corresponding to the ground state (labeled as state 0), as this state must lie in the totally symmetric representation. ROHF-based excitations, or EA/IP runs should select something appropriate!

If degenerate EOM-CCSD states are detected, only one such state will be triples-corrected. The state chosen for possible triples will be the lower irrep number, so make sure IROOT matches this.

```
ISELCT  = an array allowing experts to reduce the number of
          states that are actually solved for.  When given,
          NSTATE determines the number of states generated
          by the initial guess procedures, with ISELECT
          selecting those which carry into the calculation.
          NSTATE(1)=2,2,2,2 with ISELCT(1)=1,3,5,7 prepares
          two guesses in each irrep, but only iterates the
          EOM-CCSD equations for the lowest state in each
          irrep (the guesses are counted serially).
```

The next two keywords address triples corrections. Note that non-iterative triples corrections are not presently available for any SCFTYP=ROHF reference.

```
MTRIP     selects the type of noniterative triples
          corrections to SCFTYP=RHF EOM-CCSD energies.
          MINIT applies only to CCTYP=CR-EOM or CR-EOML:
      1 = compute the CR-EOMCCSD(T) triples corrections
          termed type I and II in the output. This is the
          default, which skips the iterative CISD
          calculations needed to construct the
          CR-EOMCCSD(T) triples corrections of type III.
      2 = after performing an additional CISD calculation,
```

evaluate all types of the CR-EOMCCSD(T) triples corrections, including types I, II, and III. This choice of MTRIP uses approximately 50 % more memory, but less CPU time than MTRIP=4.

3 = evaluate the CR-EOMCCSD(T) corrections of type III only. As with MTRIP=2, this calculation includes the iterative CISD calculation, which is needed to construct the type III triples corrections, in addition to the EOMCCSD and CR-EOMCCSD(T) calculations.

4 = carry out MTRIP=1 calculations, followed by MTRIP=3 calculations, thus evaluating all types of the CR-EOMCCSD(T) corrections (types I, II, and III in the output). As with MTRIP=2, this calculation includes the CISD iterations, which are needed to construct the type III triples corrections, in addition to the EOMCCSD and CR-EOMCCSD(T) calculations.

NACT pertains only to EA-EOM3A or IP-EOM3A runs:

NACT = the number of active MOs used to select the 3p2h or 3h2p excitations in EA-EOMCCSDt (EA-EOM3A) or IP-EOMCCSDt (IP-EOM3A) calculations.
For CCTYP=EA-EOM3A, used to describe the (N+1) e- system, NACT refers to the NACT lowest unoccupied orbitals of the N e- reference system.
For CCTYP=IP-EOM3A, used to describe the (N-1) e- system, NACT refers to the NACT highest occupied orbitals of the N e- reference system.
The default for NACT is 0, which allows no three particle or three hole operators, and thus yields only EA-EOMCC2 or IP-EOMCC2 results.
In other words, you should input a value for NACT!

CCPRPE = a flag to select computation of the EOM-CCSD level excited state density matrices (see also CCPRP in $CCINP for ground states).
The computation takes extra time, to obtain left eigenstates, so the default is .FALSE.

CCPRPE can be used only if SCFTYP=RHF and CCTYP=EOM-CCSD, CR-EOM, or CR-EOML. The property printout includes transition moments and oscillator strengths between all pairs of states, as well as the full range of Gaussian

properties (see $ELMOM, etc), for state IROOT only. CC density matrices are square, not symmetric, which means that CCSD natural orbitals come in left/right pairs. To minimize the amount of output, only left natural orbitals for excited state IROOT will be found in the log file.

--- iterative solver selection:

MEOM selects the solver for the EOMCCSD calculations:
0 = one EOMCCSD root at a time, united iterative space for all calculated roots (default)
1 = one root at a time, separate iterative space for each calculated root
2 = the Hirao-Nakatsuji multi-root solver
3 = one root at a time, separate iterative space for all computed right/left roots. (compare to 1)
4 = one root at a time, united iterative spaces for each right/left root (compare to 0).
For open shell references, or IP/EA runs, there is only one EOM-CCSD solver, so MEOM is ignored.

MEOM=0,1,2 obtain all the right eigenvectors first, and then if properties are being computed, proceed to compute the left eigenvectors. MEOM=3,4 obtain right and left eigenvectors simultaneously, and therefore should only be chosen if you are computing properties (see CCPRP/CCPRPE).

MCI selects the solver for the CISD step, which is irrelevant unless MTRIP is bigger than 1.
1 = one root at a time, separate iterative space for each calculated root (default)
2 = the Hirao-Nakatsuji multi-root solver (slower)

--- initial guess for EOM-CCSD (and possible CISD) solvers:

For both MINIT and MACT below, S and D stand for using all singles or doubles, while s and d mean restricting those excitations, both from and to a smaller number of orbitals. Of course, to define the range of orbitals "active" in the initial guess, inputs NOACT and NUACT (and perhaps MOACT) below must be given. The reason that MINIT=1 is preferred is that low-lying states with non-negligible double excitation character, or significant multi-configurational

```
character are missing in a simple CIS guess, and thus may
not appear in the final converged calculations.

MINIT     selects the initial guess procedure for EOM-CCSD,
          and possibly CISD iterations, in case MTRIP>1.
          MINIT applies to all runs reading $EOMINP.
       1 = Use EOMCCSd to start the EOMCCSD iterations,
          and CISd to start possible CISD iterations.
       2 = Use CIS wave functions to start both EOMCCSD,
          or any possible CISD calculations.
  MINIT's default is 2, but MINIT=1 is HIGHLY RECOMMENDED!

MACT   = fine tuning of MINIT's EOM-CCSD initial guess
         For MINIT=1 MACT=0, use EOMCCSd guess
         For MINIT=1 MACT=1, use EOMCCsd guess
         For MINIT=2 MACT=0, use CIS guess
         For MINIT=2 MACT=1, use CIs guess
         The default for MACT is 0.

MINIT applies to all calculations reading $EOMINP, while
MACT applies only if SCFTYP=ROHF.

   the next three define the initial guess active space:
     There are no default values of NOACT and NUACT,
     so the user MUST provide NOACT and NUACT values
     if they are needed.  NOACT and NUACT are usually
     small (5 or so), but should be chosen to avoid
     splitting any degenerate orbital shells.

NOACT     the number of occupied MOs in the active space
          for little s or little d initial guesses.
NUACT     the number of unoccupied MOs in the active space
          for little s or little d initial guesses.
MOACT     array allows explicit selection of the active
          orbitals used to define the EOMCCSd and CISd
          initial guesses.  If not provided, the MOACT
          array is filled such that the NOACT highest
          occupied and NUACT lowest unoccupied orbitals
          are selected.  If MOACT is given, the number of
          values provided must be NOACT+NUACT.
          MOACT is most useful in the virtual space, where
          the lowest orbitals might be diffuse in nature.
          An example with 15 occupied orbitals, and where
          the user has searched the virtual space looking
          for valence-like orbitals, might be
```

```
                MINIT=1 NOACT=3 NUACT=5
                MOACT(1)=13,14,15, 19,20,24,25,30


--- iteration control:

CVGEOM    convergence criterion on the EOMCCSD excitation
          amplitudes R1 and R2 (default=1.0d-4).
MAXEOM    maximum number of iterations in the EOMCCSD
          calculations (default=50). For MEOM=0 or 1,
          this is the maximum number of iterations per
          each calculated state. For MEOM=2, this is
          the maximum number of iterations for all
          states of the EOMCCSD multi-root procedure.
MICEOM    maximum number of microiterations in the
          EOMCCSD calculations (default=80). Rarely used.
          For MEOM=1 (separate iterative space for each
          root), this is the maximum number of
          microiterations for each calculated state.
          For MEOM=0 or 2 (united iterative space
          for all calculated roots), this is the
          maximum number of microiterations for all
          calculated states. It is much better to
          perform calculations with MICEOM > MAXEOM
          (i.e., in a single iteration cycle). If
          for some reason the EOMCCSD convergence is
          very slow and the iterative space becomes
          very large, it may be worth changing the
          default MICEOM value to MICEOM < MAXEOM
          to reduce the disk usage. This is not
          going to happen too often and normally there
          is no need to change the default MICEOM value.

     The next three apply only to closed shell reference
triples, if the triples method MTRIP is greater than 1:

CVGCI     convergence criterion for the CISD expansion
          coefficients (default=1.0d-4).
MAXCI     maximum number of iterations in the CISD
          calculation (default=50). For MCI=1, this
          is the maximum number of iterations per each
          calculated CISD state. For MCI=2, this is
          the maximum number of iterations for all
          states of the CISD multi-root procedure.
MICCI     maximum number of microiterations in the
```

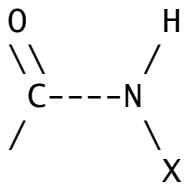
```
          CISD calculation (default=80). Rarely used.
          For MCI=1 (separate iterative space for each
          root), this is the maximum number of
          microiterations for each calculated state.
          For MCI=2 (united iterative space for all
          calculated roots), this is the maximum
          number of microiterations for all calculated
          states. In analogy to MICEOM, it is much
          better to perform the CISD calculations with
          MICCI > MAXCI (i.e., in a single iteration
          cycle).


---- restarts:

JREST  = 0 this is not a restart
       = 1 restart data is read from AMPROCC file
    One use for this is to request additional states, with
    the restart taking any converged roots from disk, and
    doing an initial guess for additional states.
    You must not change MULT when restarting.

=============================================================
```

==========

$MOPAC group (relevant if GBASIS=PM3, AM1, or MNDO)

This group affects only semi-empirical jobs, which are selected in $BASIS by keyword GBASIS.

PEPTID = flag for peptide bond correction.
By default a molecular mechanics-style torsion potential term is added for every peptide bond linkage found. The intent is to correct these torsions to be closer to planar than they would otherwise be in the semi-empirical model. Here, the peptide bond means any



One such torsion is added for O-C-N-H and one for O-C-N-X. This term is parameterized as in MOPAC6. Default=.TRUE.

==========

==========

$GUESS group (optional, relevant for all SCFTYP's)

This group controls the selection of initial molecular orbitals.

```
GUESS = Selects type of initial orbital guess.
      = HUCKEL   Carry out an extended Huckel calculation
                 using a Huzinaga MINI basis set, and
                 project this onto the current basis.
                 This is implemented for atoms up to Rn,
                 and will work for any all electron or
                 core potential basis set.
                 (default for most runs)
      = HCORE    Diagonalize the one electron Hamiltonian
                 to obtain the initial guess orbitals.
                 This method is applicable to any basis
                 set, but does not work as well as the
                 HUCKEL guess.
      = MOREAD   Read in formatted vectors punched by an
                 earlier run.  This requires a $VEC deck,
                 and you MUST pay attention to NORB below.
      = RDMINI   Read in a $VEC deck from a converged SCF
                 calculation using GBASIS=MINI, to project
                 the MINI orbitals onto the current basis.
                 The option improves upon the Huckel guess
                 because it involves SCF orbitals, which
                 are typically easily obtained in the small
                 MINI basis.  This option doesn't work if
                 the current basis uses core potentials.
                 potentials.  The $VEC from the MINI run
                 must contain all virtual orbitals.
      = MOSAVED  (default for restarts)  The initial
                 orbitals are read from the DICTNRY file
                 of the earlier run.
      = SKIP     Bypass initial orbital selection.  The
                 initial orbitals and density matrix are
                 assumed to be in the DICTNRY file.  Mostly
                 used for RUNTYP=HESSIAN when the hessian
                 is being read in from the input.
The next options are less general, being for Fragment
Molecular Orbital runs, or Divide and Conquer runs:
```

```
      = FMO      Read orbitals from the DICTNRY file, from
                 previous FMO run with MODPRP=1.
      = HUCSUB   Perform a Huckel guess in each subsystem
                 of a Divide and Conquer run
      = DMREAD   Read a density matrix from a formatted $DM
                 group, produced by a previous Divide and
                 Conquer run, see NDCPRT in $DANDC.
```

All GUESS types except 'SKIP' permit reordering of the orbitals, carry out an orthonormalization of the orbitals, and generate the correct initial density matrix, for RHF, UHF, ROHF, and GVB, but note that correct computation of the GVB density requires also CICOEF in $SCF. The density matrix cannot be generated from the orbitals alone for MP2, CI, or MCSCF, so property evaluation for these should be RUNTYP=ENERGY rather than RUNTYP=PROP using GUESS=MOREAD.

```
PRTMO = a flag to control printing of the initial guess.
        (default=.FALSE.)

PUNMO = a flag to control punching of the initial guess.
        (default=.FALSE.)

MIX   = rotate the alpha and beta HOMO and LUMO orbitals
        so as to generate inequivalent alpha and beta
        orbital spaces.  This pertains to UHF singlets
        only.  This may require use of NOSYM=1 in $CONTRL
        depending on your situation.  (default=.FALSE.)

NORB  = The number of orbitals to be read in the $VEC
        group.  This applies only to GUESS=MOREAD.
```

For -RHF-, -UHF-, -ROHF-, and -GVB-, NORB defaults to the number of occupied orbitals. NORB must be given for -CI- and -MCSCF-. For -UHF-, if NORB is not given, only the occupied alpha and beta orbitals should be given, back to back. Otherwise, both alpha and beta orbitals must consist of NORB vectors.
NORB may be larger than the number of occupied MOs, if you wish to read in the virtual orbitals. If NORB is less than the number of atomic orbitals, the remaining orbitals are generated as the orthogonal complement to those read.

```
NORDER = Orbital reordering switch.
       = 0  No reordering (default)
       = 1  Reorder according to IORDER and JORDER.
```

```
IORDER = Reordering instructions, giving the new molecular
         orbital order.  This parameter applies to the
         common orbitals (both alpha and beta) except for
         UHF, where IORDER only affects the alpha MOs.
             Examples (let there be 10 occupied orbitals):
               transposition of HOMO and LUMO:
                    IORDER(10)=11,10
               a different transposition:
                    IORDER(10)=15 IORDER(15)=10
               a more general permutation:
                    IORDER(8)=11,8,9,10
               so the new orbital 10 is the original 9th.
         The default is IORDER(i)=i.

JORDER = Reordering instructions.
         Same as IORDER, but for the beta MOs of UHF.

INSORB = the first INSORB orbitals specified in the $VEC
         group will be inserted into the Huckel guess,
         making the guess a hybrid of HUCKEL/MOREAD.  This
         keyword is meaningful only when GUESS=HUCKEL, and
         it is useful mainly for QM/MM runs where some
         orbitals (buffer) are frozen and need to be
         transferred to the initial guess vector set,
         see $MOFRZ.  (default=0)


  * * * the next are 3 ways to clean up orbitals * * *

PURIFY = flag to symmetrize starting orbitals.  This is the
         most soundly based of the possible procedures.
         However it may fail in complicated groups when the
         orbitals are very unsymmetric.  (default=.FALSE.)

TOLZ   = level below which MO coefficients will be set
         to zero.  (default=1.0E-7)

TOLE   = level at which MO coefficients will be equated.
         This is a relative level, coefficients are set
         equal if one agrees in magnitude to TOLE times
         the other.  (default=5.0E-5)

SYMDEN = project the initial density in order to generate
         symmetric orbitals.  This may be useful if the
```

```
        HUCKEL or HCORE guess types give orbitals of
        impure symmetry (?'s present).  The procedure
        will generate a fairly high starting energy, and
        thus its use may not be a good idea for orbitals
        of the quality of MOREAD.  (default=.FALSE.)

=============================================================
```

==========

$VEC group (optional, relevant for all SCFTYP's)
(required if GUESS=MOREAD)

This group consists of formatted vectors, as written onto file PUNCH in a previous run. It is considered good form to retain the titling comment cards punched before the $VEC card, as a reminder to yourself of the origin of the orbitals.

For Morokuma decompositions, the names of this group are $VEC1, $VEC2, ... for each monomer, computed in the identical orientation as the supermolecule. For transition moment or spin-orbit coupling runs, orbitals for states one and possibly two are $VEC1 and $VEC2.

==========

$DM group (relevant in Divide and Conquer runs)

This group consists of a formatted density matrix, read in exactly the format it was written. See GUESS=DM, and NDCPR in $DANDC.

==========

$MOFRZ group (optional, relevant for RHF, ROHF, GVB)

This group controls freezing the molecular orbitals of your choice during the SCF procedure. If you choose this option, select DIIS in $SCF since SOSCF will not converge as well. GUESS=MOREAD is required in $GUESS.

FRZ = flag which triggers MO freezing. (default=.FALSE.)

IFRZ = an array of MOs in the input $VEC set which are to be frozen. There is no default for this.

==========

==========

$STATPT group (for RUNTYP=OPTIMIZE or SADPOINT)

This group controls the search for stationary points. Note that NZVAR in $CONTRL determines if the geometry search is conducted in Cartesian or internal coordinates.

METHOD = optimization algorithm selection. Pick from

NR Straight Newton-Raphson iterate. This will attempt to locate the nearest stationary point, which may be of any order. There is no steplength control. RUNTYP can be either OPTIMIZE or SADPOINT

RFO Rational Function Optimization. This is one of the augmented Hessian techniques where the shift parameter(s) is(are) chosen by a rational function approximation to the PES. For SADPOINT searches it involves two shift parameters. If the calculated stepsize is larger than DXMAX the step is simply scaled down to size.

QA Quadratic Approximation. This is another version of an augmented Hessian technique where the shift parameter is chosen such that the steplength is equal to DXMAX. It is completely equivalent to the TRIM method. (default)

SCHLEGEL The quasi-NR optimizer by Schlegel.

CONOPT, CONstrained OPTimization. An algorithm which can be used for locating TSs. The starting geometry MUST be a minimum! The algorithm tries to push the geometry uphill along a chosen Hessian mode (IFOLOW) by a series of optimizations on hyperspheres of increasingly larger radii. Note that there currently are no restart capabilitites for this method, not even manually.

```
OPTTOL = gradient convergence tolerance, in Hartree/Bohr.
         Convergence of a geometry search requires the
         largest component of the gradient to be less
         than OPTTOL, and the root mean square gradient
         less than 1/3 of OPTTOL.  (default=0.0001)

NSTEP  = maximum number of steps to take.  Restart data
         is punched if NSTEP is exceeded.  The default is
         50 steps for a minimum search, but only 20 for
         a transition state search, which benefit from
         relatively frequent Hessian re-evaluations.


       --- the next four control the step size ---

DXMAX  = initial trust radius of the step, in Bohr.
         For METHOD=RFO, QA, or SCHLEGEL, steps will
         be scaled down to this value, if necessary.
         (default=0.3 for OPTIMIZE and 0.2 for SADPOINT)
         For METHOD=NR, DXMAX is inoperative.
         For METHOD=CONOPT, DXMAX is the step along the
         previous two points to increment the hypersphere
         radius between constrained optimizations.
         (default=0.1)

     the next three apply only to METHOD=RFO or QA:

TRUPD  = a flag to allow the trust radius to change as
         the geometry search proceeds.  (default=.TRUE.)

TRMAX  = maximum permissible value of the trust radius.
         (default=0.5 for OPTIMIZE and 0.3 for SADPOINT)

TRMIN  = minimum permissible value of the trust radius.
         (default=0.05)

      --- the next three control mode following ---

IFOLOW = Mode selection switch, for RUNTYP=SADPOINT.
         For METHOD=RFO or QA, the mode along which the
         energy is maximized, other modes are minimized.
         Usually referred to as "eigenvector following".
         For METHOD=SCHLEGEL, the mode whose eigenvalue
         is (or will be made) negative.  All other
         curvatures will be made positive.
```

For METHOD=CONOPT, the mode along which the geometry is initially perturbed from the minima. (default is 1)
In Cartesian coordinates, this variable doesn't count the six translation and rotation degrees. Note that the "modes" aren't from mass-weighting.

STPT = flag to indicate whether the initial geometry is considered a stationary point. If .true. the initial geometry will be perturbed by a step along the IFOLOW normal mode with stepsize STSTEP. (default=.false.)
The positive direction is taken as the one where the largest component of the Hessian mode is positive. If there are more than one largest component (symmetry), the first is taken as positive.
Note that STPT=.TRUE. has little meaning with HESS=GUESS as there will be many degenerate eigenvalues.

STSTEP = Stepsize for jumping off a stationary point. Using values of 0.05 or more may work better. (default=0.01)

IFREEZ = array of coordinates to freeze. These may be internal or Cartesian coordinates. For example, IFREEZ(1)=1,3 freezes the two bond lengths in the $ZMAT example, which was for a triatomic

```
  $CONTRL NZVAR=3 $END
  $ZMAT IZMAT(1)=1,1,2,  2,1,2,3,  1,2,3  $END
```

while optimizing the angle.

If NZVAR=0, so that this value applies to the Cartesian coordinates instead, the input of IFREEZ(1)=4,8 means to freeze the x coordinate of the 2nd and y coordinate of the 3rd atom.

See also IFZMAT and FVALUE in $ZMAT, and IFCART below, as IFREEZ does not apply to DLC internals.

In a numerical Hessian run, IFREEZ specifies Cartesian displacements to be skipped for a Partial Hessian Analysis. IFREEZ can pertain to EFP particles, but only during RUNTYP=HESSIAN,

where the 6 translational and rotational degrees
of freedom of each EFP come AFTER the QM atom
coordinates. For more information:
J.D.Head, Int.J.Quantum Chem. 65, 827, 1997
H.Li, J.H.Jensen
Theoret. Chem. Acc. 107, 211-219(2002)

IFCART = array of Cartesian coordinates to freeze during
a geometry optimization using delocalized internal
coordinates. This probably works less well than
IFREEZ when it freezes Cartesians. Only one of
IFREEZ or IFCART may be chosen in a single run.

IACTAT = array of "active atoms", which is a complimentary
input to IFREEZ. Any atom *not* included in the
list has its Cartesian coordinates frozen. Thus
IACTAT(1)=3,-5,107,144,202,-211 allows 15 atoms,
namely 3-5, 107, 144, and 202-211 to be optimized,
while all other atoms are frozen. NZVAR in
$CONTRL must be 0 when this option is chosen.

IFREEZ and IACTAT are mutually exclusive. The latter acts
by generating a IFREEZ for all atom coordinates not defined
as "active", so users can input whichever list is shorter.

--- The next two control the hessian matrix quality ---

HESS = selects the initial hessian matrix.
= GUESS chooses an initial guess for the hessian.
(default for RUNTYP=OPTIMIZE)
= READ causes the hessian to be read from a $HESS
group. (default for RUNTYP=SADPOINT)
= RDAB reads only the ab initio part of the
hessian, and approximates the effective
fragment blocks.
= RDALL reads the full hessian, then converts
any fragment blocks to 6x6 T+R shape.
(this option is seldom used).
= CALC compute the hessian, see $FORCE input.

IHREP = the number of steps before the hessian is
recomputed. If given as 0, the hessian will
be computed only at the initial geometry if
you choose HESS=CALC, and never again. If
nonzero, the hessian is recalculated every

```
         IHREP steps, with the update formula used on
         other steps.  (default=0)

HSSEND = a flag to control automatic hessian evaluation
         at the end of a successful geometry search.
         (default=.FALSE.)


   --- the next two control the amount of output ---
    Let 0 mean the initial geometry, L mean the last
    geometry, and all mean every geometry.
    Let INTR mean the internuclear distance matrix.
    Let HESS mean the approximation to the hessian.
    Note that a directly calculated hessian matrix
    will always be punched, NPUN refers only to the
    updated hessians used by the quasi-Newton step.

NPRT   =  1  Print INTR at all, orbitals at all
          0  Print INTR at all, orbitals at 0+L (default)
         -1  Print INTR at all, orbitals never
         -2  Print INTR at 0+L, orbitals never

NPUN   =  3  Punch all orbitals and HESS at all
          2  Punch all orbitals at all
          1  same as 0, plus punch HESS at all
          0  Punch all orbitals at 0+L, otherwise only
             occupied orbitals (default)
         -1  Punch occ orbitals at 0+L only
         -2  Never punch orbitals

---- the next parameters control harmonic constraints ---
Harmonic constraints can be added to the current geometry
by setting ALL the keywords below.  For instance, to
harmonically constrain the distance between atom 3 and 12
to a distance of 2.0 Angstrom and a force constant of 500
kcal/mol, the following example can be used:
   IHMCON(1)=1,3,12  SHMCON(1)=2.0  FHMCON(1)=500.0
The default is all zeros which means do not do this.

IHMCON = array of coordinates to constrain. The input
         is similar to IZMAT in $ZMAT, a code integer,
         and the atoms involved in the coordinate.
         The code integer may only be 1, for stretches.

SHMCON = equilibrium constraint values for the distances
```

```
         specified by IHMCON, given in Angstrom.

FHMCON = array of force constants for the distances
         specified by IHMCON, given in kcal/mol.


 ---- the following parameters are quite specialized ----

PURIFY = a flag to help eliminate the rotational and
         translational degrees of freedom from the
         initial hessian (and possibly initial gradient).
         This is much like the variable of the same name
         in $FORCE, and will be relevant only if internal
         coordinates are in use.  (default=.FALSE.)

PROJCT = a flag to eliminate translation and rotational
         degrees of freedom from Cartesian optimizations.
         The default is .TRUE. since this normally will
         reduce the number of steps, except that this
         variable is set false when POSITION=FIXED is
         used during EFP runs.

ITBMAT = number of micro-iterations used to compute the
         step in Cartesians which corresponds to the
         desired step in internals.  The default is 5.

UPHESS = SKIP     do not update Hessian (not recommended)
         BFGS     default for OPTIMIZE using RFO or QA
         POWELL   default for OPTIMIZE using NR or CONOPT
         POWELL   default for SADPOINT
         MSP      mixed Murtagh-Sargent/Powell update
         SCHLEGEL only choice for METHOD=SCHLEGEL


 ---- NNEG, RMIN, RMAX, RLIM apply only to SCHLEGEL ----

NNEG   = The number of negative eigenvalues the force
         constant matrix should have. If necessary the
         smallest eigenvalues will be reversed. The
         default is 0 for RUNTYP=OPTIMIZE, and 1 for
         RUNTYP=SADPOINT.

RMIN   = Minimum distance threshold. Points whose root
         mean square distance from the current point is
         less than RMIN are discarded. (default=0.0015)
```

```
RMAX   = Maximum distance threshold. Points whose root
         mean square distance from the current point is
         greater than RMAX are discarded. (default=0.1)

RLIM   = Linear dependence threshold. Vectors from the
         current point to the previous points must not
         be colinear.  (default=0.07)
=============================================================

       * * * * * * * * * * * * * * * * * * * * * *
       See the 'further information' section for
       some help with OPTIMIZE and SADPOINT runs
       * * * * * * * * * * * * * * * * * * * * * *
```

==========

$TRUDGE group (required for RUNTYP=TRUDGE)

This group defines the parameters for a non-gradient optimization of exponents or the geometry. The TRUDGE package is a modified version of the same code from Michel Dupuis' HONDO 7.0 system, origially written by H.F.King. Presently the program allows for the optimization of 10 parameters.

Exponent optimization works only for uncontracted primitives, without enforcing any constraints. Two non-symmetry equivalent H atoms would have their p function exponents optimized separately, and so would two symmetry equivalent atoms! A clear case of GIGO.

Geometry optimization works only in HINT internal coordinates (see $CONTRL and $DATA inputs). The total energy of all types of SCF wavefunctions can be optimized, although this would be extremely stupid as gradient methods are far more efficient. The main utility is for open shell MP2 or CI geometry optimizations, which may not be done in any other way with GAMESS. If your run requires NOSYM=1 in $CONTRL, you must be sure to use only C1 symmetry in the $DATA input.

OPTMIZ = a flag to select optimization of either geometry or exponents of primitive gaussian functions.
= BASIS for basis set optimization.
= GEOMETRY for geometry optimization (default). This means minima search only, there is no saddle point capability.

NPAR = number of parameters to be optimized.

IEX = defines the parameters to be optimized.

If OPTMIZ=BASIS, IEX declares the serial number of the Gaussian primitives for which the exponents will be optimized.

If OPTMIZ=GEOMETRY, IEX define the pointers to the HINT internal coordinates which will be optimized.

(Note that not all internal coordinates have to be optimized.) The pointers to the internal coordinates are defined as: (the number of atom on the input list)*10 + (the number of internal coordinate for that atom). For each atom, the HINT internal coordinates are numbered as 1, 2, and 3 for BOND, ALPHA, and BETA, respectively.

P = Defines the initial values of the parameters to be optimized. You can use this to reset values given in $DATA. If omitted, the $DATA values are used. If given here, geometric data must be in Angstroms and degrees.

A complete example is a TCSCF multireference 6-31G geometry optimization for methylene,

```
 $CONTRL SCFTYP=GVB CITYP=GUGA RUNTYP=TRUDGE
         COORD=HINT $END
 $BASIS  GBASIS=N31 NGAUSS=6 $END
 $DATA
Methylene TCSCF+CISD geometry optimization
Cnv 2

C    6.     LC  0.00  0.0  0.00  -  O  K
H    1.    PCC  1.00  53.  0.00  +  O  K  I
 $END
 $SCF    NCO=3 NPAIR=1 $END
 $TRUDGE OPTMIZ=GEOMETRY  NPAR=2
         IEX(1)=21,22   P(1)=1.08 $END
 $CIDRT  GROUP=C2V SOCI=.TRUE. NFZC=1 NDOC=3 NVAL=1
         NEXT=-1 $END
```

using GVB-PP(1), or TCSCF orbitals in the CI. The starting bond length is reset to 1.09, while the initial angle will be 106 (twice 53). Result after 17 steps is R=1.1283056, half-angle=51.83377, with a CI energy of -38.9407538472

Note that you may optimize the geometry for an excited CI state, just specify

```
          $GUGDIA   NSTATE=5  $END
          $GUGDM    IROOT=3   $END
```

to find the equilibrium geometry of the third state (of five total states) of the symmetry implied by your $CIDRT.

==========

==========

$TRURST group (optional, relevant if RUNTYP=TRUDGE)

This group specifies restart parameters for TRUDGE runs and accuracy thresholds.

KSTART indicates the conjugate gradient direction in which the optimization will proceed. (default = -1)
-1 .... indicates that this is a non-restart run.
0 .... corresponds to a restart run.

FNOISE accuracy of function values.
Variation smaller than FNOISE are not considered to be significant (Def. 0.0005)

TOLF accuracy required of the function (Def. 0.001)

TOLR accuracy required of conjugate directions (Def. 0.05)

For geometry optimization, the values which give better results (closer to the ones obtained with gradient methods) are: TOLF=0.0001, TOLR=0.001, FNOISE=0.00001

==========

==========

$FORCE group

(optional, relevant for RUNTYP=HESSIAN,OPTIMIZE,SADPOINT)

This group controls the computation of the hessian matrix (the energy second derivative tensor, also known as the force constant matrix), and an optional harmonic vibrational analysis. This can be a very time consuming calculation. However, given the force constant matrix, the vibrational analysis for an isotopically substituted molecule is very cheap. Related input is HESS= in $STATPT, and the $MASS, $HESS, $GRAD, $DIPDR, $VIB inputs. Calculation of the hessian automatically yields the dipole derivative tensor, giving IR frequencies. Raman intensities are obtained by following with RUNTYP=RAMAN.

METHOD = chooses the computational method:
- = ANALYTIC is a fully analytic calculation. This is implemented for SCFTYP=RHF, UHF, ROHF, GVB (for NPAIR=0 or 1, only), and MCSCF (for CISTEP=ALDET or ORMAS, only). R-DFT and U-DFT are also analytic. This is the default for these cases.
- = SEMINUM does numerical differentiation of analytically computed first derivatives. This is the default for UHF, MCSCF using other CISTEPs, all solvent models, relativistic corrections, and most MP2 or CI runs.
- = FULLNUM numerically differentiates the energy twice, which can be used by all other cases. It requires many energies (a check run will tell how many) and so it is mainly useful for systems with only very few symmetry unique atoms.

The default for METHOD is to pick ANALYTIC over SEMINUM if that is programmed, and SEMINUM otherwise. FULLNUM will never be chosen unless you specifically request it.

RDHESS = a flag to read the hessian from a $HESS input, rather than computing it. This variable pertains only to RUNTYP=HESSIAN. See also HESS= in the

```
          $STATPT input group.  (default is .FALSE.)

PURIFY = controls cleanup
         Given a $ZMAT, the hessian and dipole derivative
         tensor can be "purified" by transforming from
         Cartesians to internals and back to Cartesians.
         This effectively zeros the frequencies of the
         translation and rotation "modes", along with
         their IR intensities.  The purified quantities
         are punched out.  Purification does change the
         Hessian slightly, frequencies at a stationary
         point can change by a wave number or so.  The
         change is bigger at non-stationary points.
         (default=.FALSE. if $ZMAT is given)

PRTIFC = prints the internal coordinate force constants.
         You MUST have provided $ZMAT input to use this.
         (Default=.FALSE.)


  --- the next four apply to numeric differentiation ----

NVIB   =    The number of displacements in each Cartesian
            direction for force field computation.  This
            pertains only to METHOD=SEMINUM, as FULLNUM
            always uses double difference formulae.
       = 1  Move one VIBSIZ unit in each positive
            Cartesian direction.  This requires 3N+1
            evaluations of the wavefunction, energy, and
            gradient, where N is the number of SYMMETRY
            UNIQUE atoms given in $DATA.
       = 2  Move one VIBSIZ unit in the positive direction
            and one VIBSIZ unit in the negative direction.
            This requires 6N+1 evaluations of the
            wavefunction and gradient, and gives a small
            improvement in accuracy.  In particular, the
            frequencies will change from NVIB=1 results by
            no more than 10-100 wavenumbers, and usually
            much less.  However, the normal modes will be
            more nearly symmetry adapted, and the residual
            rotational and translational "frequencies"
            will be much closer to zero. (default)

VIBSIZ =    Displacement size (in Bohrs). This pertains to
            Both SEMINUM and FULLNUM.  Default=0.01
```

```
       Let 0 mean the Vib0 geometry, and
       D mean all the displaced geometries

NPRT   = 1  Print orbitals at 0 and D
       = 0  Print orbitals at 0 only (default)

NPUN   = 2  Punch all orbitals at 0 and D
       = 1  Punch all orbitals at 0 and occupied orbs at D
       = 0  Punch all orbitals at 0 only (default)


  ----- the rest control normal coordinate analysis ----

VIBANL = flag to activate vibrational analysis.
         (the default is .TRUE. for RUNTYP=HESSIAN, and
         otherwise is .FALSE.)

SCLFAC = scale factor for vibrational frequencies, used
         in calculating the zero point vibrational energy.
         Some workers correct for the usual overestimate
         in SCF frequencies by a factor 0.89.  ZPE or other
         methods might employ other factors, see
            J.P.Merrick, D.Moran, L.Radom
            J.Phys.Chem.A  111, 11683-11700 (2007).
         The output always prints unscaled frequencies, so
         this value is used only during the thermochemical
         analysis.  (Default is 1.0)

TEMP   = an array of up to ten temperatures at which the
         thermochemistry should be printed out.  The
         default is a single temperature, 298.15 K.  To
         use absolute zero, input 0.001 degrees.

FREQ   = an array of vibrational frequencies.  If the
         frequencies are given here, the hessian matrix
         is not computed or read.  You enter any imaginary
         frequencies as negative numbers, omit the
         zero frequencies corresponding to translation
         and rotation, and enter all true vibrational
         frequencies.  Thermodynamic properties will be
         printed, nothing else is done by the run.

PRTSCN = flag to print contribution of each vibrational
         mode to the entropy.  (Default is .FALSE.)
```

```
DECOMP = activates internal coordinate analysis.
         Vibrational frequencies will be decomposed into
         "intrinsic frequencies", by the method of
         J.A.Boatz and M.S.Gordon, J.Phys.Chem., 93,
         1819-1826(1989).  If set .TRUE., the $ZMAT input
         may define more than 3N-6 (3N-5) coordinates.
         (default=.FALSE.)

PROJCT = controls the projection of the hessian matrix.
         The projection technique is described by
         W.H.Miller, N.C.Handy, J.E.Adams in J. Chem.
         Phys. 1980, 72, 99-112.  At stationary points,
         the projection simply eliminates rotational and
         translational contaminants.  At points with
         non-zero gradients, the projection also ensures
         that one of the vibrational modes will point
         along the gradient, so that there are a total of
         7 zero frequencies.  The other 3N-7 modes are
         constrained to be orthogonal to the gradient.
         Because the projection has such a large effect on
         the hessian, the hessian is punched both before
         and after projection.  For the same reason, the
         default is .FALSE. to skip the projection, which
         is mainly of interest in dynamical calculations.
```

==========

There is a program ISOEFF for the calculation of kinetic and equilibrium isotope effects from the group of Piotr Paneth at the Technical University of Lodz. This program will accepts data computed by GAMESS (and other programs), and can be requested from paneth@p.lodz.pl

```
=========================================================
```

$CPHF group (relevant for analytic RUNTYP=HESSIAN)

```
    This group controls the solution of the response
equations, also known as coupled Hartree-Fock (CPHF).

POLAR = a flag to request computation of the static
        polarizability, alpha.  Because this property
        needs 3 additional response vectors, beyond those
        needed for the hessian, the default is to skip the
        property.  (default = .FALSE.)

CPHF   = nature of integrals driving the formation of the
         response equation.  The defaults are intelligent,
         so this is meant mostly for experts/debugging.
       = AO    forms response equations from AO integrals,
               which usually takes less memory, and is more
               parallel.  This is the default for RHF, UHF,
               ROHF, R-DFT, or U-DFT.  AO-driven mode is
               not available for any other cases.
       = MO    forms response equations from transformed
               MO integrals.  This is the default for GVB
               or MCSCF.  This is available forRHF or ROHF.
       = AODDI forms response equations from AO integrals,
               using distributed memory (see MEMDDI).  This
               does AO integrals about 2x more than AO,
               but spreads the CPHF memory requirement out
               across multiple nodes.  Coded only for RHF.

SOLVER = linear equation solver choice.  This is primarily
         a debugging option.  For RHF analytic Hessians,
         choose from CONJG (default), DIIS, ONDISK, not all
         of which will work for all CPHF= choices.
         For imaginary frequency dependent polarizability
         responses (MAKEFP jobs), choose GMRES (default),
         biconjugate gradient stabilized BCGST, DODIIS, or
         an explicit solver GAUSS.  Most response equations
         have only one solver programmed, and thus ignore
         this keyword.

NWORD  = controls memory usage for this step.  The default
         uses all available memory.  (default=0)
=========================================================
```

==========

$CPMCHF group

(relevant for analytic RUNTYP=HESSIAN,NACME,CONICAL)

This group controls the solution of the response equations, also called coupled perturbed multiconfiguration Hartree-Fock, for MCSCF wavefunctions. These are needed for analytic hessians (CISTEP=ALDET or ORMAS), or for state-averaged gradients or non-adiabatic coupling matrix element calculations. The full response equations are solved for hessians, while Z-vector equations are used for NACME and SA-gradients.

The default converger is a (linear) conjugate gradient (CG) method, but three others may be chosen. Difficult cases might work upwards from the default CG method by:

```
 $cpmchf $end
 $cpmchf ipdir=50 $end
 $cpmchf gcro=.t.   micit=5  kicit=10 $end
 $cpmchf gcrodr=.t. micit=10 kicit=5  $end
 $cpmchf gcrodr=.t. micit=30 kicit=10 reclin=.false. $end
 $cpmchf gcrodr=.t. micit=20 kicit=10 reclin=.false.
         prcchg=.true. prctol=1.0 $end
 $cpmchf gcro=.t.   micit=50 kicit=100
         prcchg=.true. prctol=1.0 $end
```

where the last one is "the sledgehammer". The options shown in the next to last case very often work, and will be considerably faster than the last set, which should always work. GCRO will typically take many fewer iterations than CG, a measure of its robustness, but will use more machine time due to its microiterations.

--- the next set apply to any CP-MCHF converger ---

MAXIT = maximum iterations. (default=300)

CPTOL = accuracy tolerance for cpmchf equations Ax=b.
(compared to r/||b||, within orbital, CI, and state averaged components) (default=1.0D-07)

PRCCHG = a flag to adjust the linear equation's preconditioning. (Default=.FALSE.)
For ORMAS runs in particular, the standard

```
          preconditioner might lead to ill-conditioning
          with very small elements.  If selected, any
          preconditioner elements below PRCTOL will be
          reset to a value of 1.0

PRCTOL = a tolerance to keep preconditioner elements,
         if PRCCHG is chosen.  Default=1.0D-6

               --- for RUNTYP=NACME ---

NAPICK  = a flag to select running through z-vector setup
          and choose which linear equations to solve.
          .TRUE. leads to z-vector linear equations.
          .FALSE. leads to non-z-vector linear equations.
          The z-vector equations are advantageous when the
          degrees of freedom exceeds the no. of electronic
          states involved in the state-averaging.
          (The defaults are set to enforce this option.)
          The z-vector equations are also advantageous
          when only a few NA couplings out of the total
          total possible couplings are of interest.
          If CISTEP=ORMAS, NAPICK=.TRUE. is forced.
          Selecting NAPICK=.TRUE. requires the choice of
          NA couplings in the NACST array (see below).
          (default=varies... see ROUTINE NACMEX for notes)

NACST   = an array that indicates which NA couplings to
          Calculate, if NAPICK is chosen.  For example, if
          WSTATE in $DET contains at least four states,
          the NACME can be limited to state pairs 1<->2 and
          3<->4 by NACST(1)=3,4, 1,2.  Note that you should
          pick increasing order within any pair of states!
          The program always generates the state-specific
          gradient of every state with a non-zero WSTATE.
          (default=none)


 --- the next three choose the other CPMCHF convergers ---
   If none is selected, conjugate gradient (CG) is used.

GCRODR  = a flag to select Generalized Conjugate Residual
          with inner Orthogonalization with Deflated
          Restarting.  (default=.FALSE.)

GCRO    = a flag to select Generalized Conjugate Residual
```

with inner Orthogonalization. (default=.FALSE.)

CGGCRO = a flag to alternate between GCRO and CG solvers. (default=.FALSE.)

--- next apply only to GCRODR:

RECLIN = a flag to select recycling of Krylov subspaces from the first linear equation. (recycle linear). The first CP-MCHF linear equation is solved and a recyclable subspace is generated. Then, after a projection of approximate solution across the subspace from the first system, the rest of the linear equations are solved. The recycled subspace may or may not give rapid convergence with fewer iterations. See MICIT and KICIT. (default=.TRUE.)

--- next apply only to GCRODR,GCRO,CGGCRO:

MICIT = total size of the Krylov expansion space, namely the number of micro-iterations within an overall iteration. While the MICIT variable has no limit, fifty or more micro-iterations start to become computationally unmanagable for larger systems. The default often must be increased for large systems or for geometries far from equilibrium. In addition, the GCRODR converger has a slightly modified scheme for the micro-iterations. In the first iteration, MICIT micro-iterations are performed in a GMRES(MICIT) iteration. However, for subsequent iterations, (MICIT-KICIT) micro-iterations are performed. (default=5, often increased to 20 or 30)

KICIT = the size of the recyclable Krylov basis saved and modified from iteration to iteration, created from eigenvectors with small eigenvalues. If this space is too small, the run will experience ill-conditioning, but if too large, the search space includes ineffective parts. In case PRCCHG is chosen, make sure the number of vectors reset from small values does not exceed

```
          KICIT, if it does, increase KICIT.
          (default=5, usually small, e.g. 5-10 for GCRODR)

          (MICIT> KICIT for GCRODR)
          (KICIT>=MICIT for GCRO and CGGCRO)


              --- next apply only to (linear) CG:

NACFAC =  number of iterations before softening the current
          convergence tolerance by 1/3, for CG only.  Use
          NACFAC=0 (or MAXIT) to prevent raising the
          from the initial CPTOL.    (default=50)

IPDIR  =  number of iterations before resetting the
          residual from a pseudo-residual to the true
          residual. This reset also resets the search
          directions, since keeping the old 'ill-rounded'
          directions is not very beneficial.
          If a run almost convergences but struggles in
          later iterations, IPDIR=50 is recommended.
          This option appears more useful for NACME
          rather than Hessian runs.
          (default=MAXIT)


              --- next apply only to CGGCRO:

ITERA  = the number of (linear) CG iterations to apply
         before alternation to the GCRO converger.
          (default=5)

ITERB  = the number of GCRO iterations to apply
         before alternation to the (linear) CG converger.
          (default=5)
=========================================================
```

==========

$MASS group (relevant for RUNTYP=HESSIAN, IRC, or DRC)

This group permits isotopic substitution during the computation of mass weighted Cartesian coordinates. Of course, the masses affect the frequencies and normal modes of vibration.

AMASS = An array giving the atomic masses, in amu. The default is to use the mass of the most abundant isotope. Masses through element 104 are stored.

example - $MASS AMASS(3)=2.0140 $END
will make the third atom in the molecule a deuterium.

==========

==========

$HESS group
(relevant for RUNTYP=HESSIAN if RDHESS=.TRUE.)
(relevant for RUNTYP=IRC if FREQ,CMODE not given)
(relevant for RUNTYP=OPTIMIZE,SADPOINT if HESS=READ)

Formatted force constant matrix (FCM), i.e. hessian matrix. This data is punched out by a RUNTYP=HESSIAN job, in the correct format for subsequent runs. The first card in the group must be a title card.

$HESS information is always punched in Cartesians. It will be transformed into internal coordinate space if a geometry search uses internals. It will be mass weighted (according to $MASS) for IRC and frequency runs.

The initial FCM is updated during the course of a geometry optimization or saddle point search, and will be punched if a run exhausts its time limit. This allows restarts where the job leaves off. You may want to read this FCM back into the program for your restart, or you may prefer to regenerate a new initial hessian. In any case, this updated hessian is absolutely not suitable for frequency prediction!

==========

$GRAD group (relevant for RUNTYP=OPTIMIZE or SADPOINT)
(relevant for RUNTYP=HESSIAN when RDHESS=.TRUE.)

Formatted gradient vector at the $DATA geometry. This data is read in the same format it was punched out.

For RUNTYP=HESSIAN, this information is used to determine if you are at a stationary point, and possibly for projection. If omitted, the program pretends the gradient is zero, and otherwise proceeds normally.

For geometry searches, this information (if known) can be read into the program so that the first step can be taken instantly.

==========

==========

$DIPDR group (relevant for RUNTYP=HESSIAN if RDHESS=.T.)

Formatted dipole derivative tensor, punched in a previous RUNTYP=HESSIAN job. If this group is omitted, then a vibrational analysis will be unable to predict the IR intensities, but the run can otherwise proceed.

==========

$ALPDR group (relevant for RUNTYP=RAMAN or HESSIAN)

Formatted alpha polarizability derivative tensor, punched by a previous RUNTYP=RAMAN job. If both $DIPDR and $ALPDR group are found in the input file, the applied electric field computation will be skipped, to immediately evaluate IR and Raman intensities. This restart may be most relevant for isotopic substitution.

If this group is found during RUNTYP=HESSIAN, the Raman intensities will be added to the output. You might want to restart as RUNTYP=HESSIAN instead of RUNTYP=RAMAN in order to have access to PROJCT or the other options available in the $FORCE input group.

==========

==========

$VIB group (relevant for RUNTYP=HESSIAN, METHOD=SEMINUM)

Formatted restart data, consisting of energies, gradients, and dipole moments. This data is read in the same format by which is was written to the RESTART file. Just add a " $END" card, and place this group into the input file to effect a restart. If the final displacement's gradient was written as zero, delete the entire last data set (energy, gradient, and dipole).

In case the numerical hessian was run in groups (see $GDDI), the $VIB entries will be out of order. The unsorted data can be read back in, if and only if the new run is also using processor groups. Note that assembling a complete $VIB could be sent to one core in one group, but use NGROUP=1 to make it look like a "group run".

This group can be used to turn a less accurate single differencing run into a more accurate double differencing run (NVIB in $HESS).

The mere presence of this group triggers the restart.

==========

$VIB2 group (relevant for hessians, METHOD=FULLNUM)
(relevant for gradients, with NUMGRD=.TRUE.)

Formatted restart information, consisting of energy values, as written to the RESTART file. Just add a " $END" line at the bottom, and place this group into the input file to effect a restart. This group has the same name ($VIB2), but different contents, depending on whether you are restarting a numerical gradient or a fully numerical hessian job.

The mere presence of this group triggers the restart.

==========

==========

$VSCF group (optional, relevant to RUNTYP=VSCF)

This group governs the computation of vibrational frequencies including anharmonic effects. Besides the keywords shown below, the input file must contain a $HESS input (and perhaps a $DIPDR input), to start with previously obtained harmonic vibrational information. The VSCF method requires only energies, so any energy type in GAMESS may be used, perhaps with fully numerical harmonic vibrational information. Energies are sampled along the directions of the harmonic normal modes, and usually along pairs of harmonic normal modes, after which the nuclear vibrational wavefunctions are obtained. The dipole on the grid points may be used to give improved IR intensities.

The most accurate calculation computes the potential surface directly, on all grid points, but this involves many energy evaluations. An attractive alternative is the Quartic Force Field approximation of Yagi et al., which computes a fit to the derivatives up to fourth order by computing a specialized set of points, after which this fit is used to generate the full grid of points for the solver.

Since there are a great many independent energy evaluations, no matter which type of surface is computed, the VSCF method allows for computations in subgroups (much like the FMO method). Thus any $GDDI input group will be read and acted upon, if found.

Vibrational wavefunctions are obtained at an SCF-like level, termed VSCF, using product nuclear wavefunctions, along with an MP2-like correction to the vibrational energy, which is termed correlation corrected (cc-VSCF). In addition, vibrational energy levels based on second order degenerate pertubation theory (see VDPT) or a CI analog (see VCI) may be obtained.

Most VSCF applications have been carried out with an electronic structure level of MP2 with triple zeta basis sets. This is thought to give accuracy to 50 wavenumbers for the larger fundamentals. Use of internal coordinates is known to give improved accuracy for lower frequencies, particularly in weakly bound clusters.

Restarts involve the $VIBSCF input (which has different formats for each PETYP), and the READV keyword. Restarts are safest on the same machine, where normal mode phases are reproducible.

References for the VSCF method, the QFF approximation, and the solvers are given in Chapter 4 of this manual, along with a number of sample applications.

* * * * *

The first input variables control the generation of the potential surface on which the nuclear vibrations occur:

PETYP = DIRECT computes the full potential energy surface, according to NCOUP/NGRID. The total number of energy/dipole calculations for NCOUP=2 will be M*NGRID + (M*(M-1)/2)*NGRID*NGRID, where M is the number of normal modes. This is the default.
= QFF the Quartic Force Field approximation to the potential surface is obtained. This is usually only slightly less accurate, but has a greatly reduced computational burden, namely 6*M + 12*M*(M-1)/2 energy/dipoles.

INTCRD = flag setting the coordinate system used for the grids. Any internal coordinates to be used must be defined in $ZMAT, using 3N-6 simple, DLC, or natural internal coordinates. Of course, you must enter NZVAR in $CONTRL as well.
The default is to use Cartesians (default .FALSE.)

INTTYP = 0 default if INTCRD=.FALSE. (ignore this keyword)
= 1 implies that the $ZMAT contains only stretches, bends, and torsions. It also selects an approximate transformation between Cartesian and internal coords.
= 2 the other $ZMAT coordinates may be used, and the coordinate transformation will be iterated to convergence. (default if INTCRD=.TRUE.)

NCOUP = the order of mode couplings included.

= 1 computes 1-D grids along each harmonic mode
= 2 adds additionally, 2-D grids along each pair of normal modes. (default=2)
= 3 adds additionally, 3-D grids for mode triples, for PETYP=DIRECT only.

NGRID = number of grid points to be used in solving for the anharmonic vibrational levels. In the case of PETYP=DIRECT, each of these grid points must be explicitly computed. For PETYP=QFF these grid points are obtained from a fitted quartic force field. Reasonable values are 8 or 16 for DIRECT, with 16 considered significantly more accurate. For PETYP=QFF, the generation of the solver grid is very fast, so use 16 always. (default=16)

AMP = step size for PETYP=DIRECT displacements. The maximum distance along each mode is a function of its frequency,

amplitude(i)=sqrt(2*(AMP+1/2)/freq(i))

so that AMP resembles a vibrational quantum number. The default goes far enough past the classical turning points of the fundamentals to capture the relevant part of the surface. (default = 7.0)

STPSZ = step size for PETYP=QFF displacements. The step along each mode depends on the harmonic frequency, as well as this parameter, whose default is usually satisfactory (default=0.5)

In case the user wants to control each normal mode with a separate parameter, arrays of values may be given, using the keywords AMPX(1)=xx,yy,... or STPSZX(1)=xx,yy,zz...

IMODE = array of modes for which anharmonic effects will be computed. IMODE(1)=10,19 computes anharmonic energies and wavefunctions for modes 10 and 19, only. In the current implementation, pairs of modes cannot be coupled, so NCOUP is forced to 1 if this option is specified. This approximation is intended for larger molecules, where the whole VSCF calculation is prohibitive.

* * * * *

The next set of keywords relates to the solver step which finds the vibrational states. The results always include VSCF and cc-VSCF (SCF and non-degenerate MP2-like solutions). Use of the restart option makes comparing the solvers very fast, compared to the time to generate the electronic potential energy surface's points.

VDPT = option to use 2nd order degenerate perturbation theory, based on the ground and singly excited vibrational levels. Results for virtual CI within the same singly excited space will also be given. Selection of VDPT turns VCI on, as well. (default=.FALSE.)

VCI = option to use the virtual CI solver within a space of the ground and both singly and doubly excited vibrational levels.
Selection of VCI turns VDPT off.
(default=.FALSE.)

The solver always finds the ground vibrational state (v=0) by default, and defaults to finding the fundamentals (v=1 in every mode). It can rapidly find excited levels (such as all v=2) if restarted (see READV) from $VIBSCF, using the following to control the excitation levels:

IEXC = 1 obtain fundamental frequencies (default)
= 2 instead, obtain first overtones
= 3 instead, obtain second overtones

IEXC2 = 0 skip combination bands (default)
= 1 add one additional quanta in other modes
= 2 add two other quanta in one mode at a time.

IEXC	IEXC2	for H2O, which has only three modes:
0	0	only 000 ground state, no transitions
1	0	000, and 100, 010, 001 (fundamentals)
2	0	000, and 200, 020, 002 (1st overtones)
3	0	000, and 300, 030, 003 (2nd overtones)
1	1	000, and 100, 010, 001, 110, 101, 110 (1st overtones and combinations)
1	2	000, and 100, 010, 001, 210, 201, 021
2	1	000, and 200, 020, 002, 120, 102, 012 between them, 1st and 2nd overtones,

and all 2-1-0 combinations.

ICAS1, ICAS2 = starting and ending vibrations whose quanta are included. The default is all modes, ICAS1=1 and ICAS2=3N-6 (or 3N-5).

SFACT = a numerical cutoff for small contributions in the solver. The default is 1d-4: 5d-3 or 1d-3 may affect accuracy of results, 1d-4 is safer, and 1d-5 might not converge.

VCFCT = scaling factor for pair-coupling potential. Sometimes when pair-coupling potential values are larger than the corresponding single mode values, they must be scaled down. It is seldom necessary to select a scaling other than unity. (Default=1.0)

* * * * *

The next two relate to simplified intensity computation. These simplifications are aimed at speeding up MP2 runs, if one does not care so much about intensities, and would like to eliminate the considerable extra time to compute MP2-level dipoles. DMDR must not be used if overtones are being computed.

DMDR = if true, indicates that the harmonic dipole derivative tensor $DIPDR will be read and used, rather than computing dipoles. (default=.FALSE.)

MPDIP = If .TRUE. the run will compute MP2 level dipoles for the IR intensity evaluation.
Entering .FALSE. uses SCF level dipoles instead.
Default=.TRUE. for MP2 runs, except when using the RI-MP2 program, which cannot compute MP2 dipoles, and so chooses .FALSE. here.
It is more accurate to use the DMDR flag instead instead of turning off MPDIP, if an MP2 level $DIPDR is available from the MP2 hessian run.

* * * *

These relate to the initial harmonic mode generation. Normally, a $HESS is provided, from which harmonic

modes are obtained. It is possible to give the harmonic data explicitly with the first two:

RDFRQ = array of harmonic frequencies, starting from the smallest.

CMODE = array of normal mode displacements given in the same order as the frequencies read in RDFRQ. The data should be the x,y,z displacement of the first atom of the first mode, then x,y,z for the second atom, then going on to give each additional mode.

PROJCT = controls the projection of the hessian matrix (same meaning as in $FORCE). Default is .TRUE. which removes small mixings between rotations or translations and the harmonic modes.

* * * *

READV = flag to indicate restart data $VIBSCF should be read in to resume an interrupted calculation, or to obtain overtones in follow-on runs. (default is .FALSE.)

GEONLY = option to generate all points on the potential energy surface needed by the VSCF routine, without energy evaluations. The purpose of this is to prepare a set of geometries at which the energy is needed. A possible use for this is to obtain energies from a different program package, which might have an energy unavailable in GAMESS, but which lacks its own VSCF program. (default=.false.)

==========

$VIBSCF group (optional, relevant to RUNTYP=VSCF)

This is restart data, as written to the disk file RESTART in a complete or partially completed previous run. Append a " $END", and also select READV=.TRUE. to read the data.

$VIBSCF's contents are different for PETYP=DIRECT or QFF.

The format of this group changed in December 2006, so that old groups can no longer be used.
==========

==========

$GAMMA group required if RUNTYP=GAMMA

This group governs evaluation of the 3rd derivative of the energy with respect to nuclear coordinates, by finite differentiation of Hessians (see $FORCE options).

NFCM = n describes the amount of restart data provided.
The default is n=-1, to evaluate everything.
A value of n means that n+1 $FCM groups are to be read from the file (hessian #0 means the equilibrium geometry). Restart data is read from a .gamma file, created by an earlier run.

DELTA = step size, default=0.01 Bohr

PRTALL = flag to print full Hessian and Gamma matrix, the default is .FALSE.

PRTSYM = flag to print unsymmetrical Gamma elements, the default is .FALSE.

PRTBIG = flag to print large Gamma elements, default = .F.

==========

$EQGEOM group required if NFFLVL=2 or 3 in $CONTRL

The coordinates of the stationary point, where the hessian and possibly 3rd derivative information was evaluated, in exactly the format it was printed by RUNTYP=GAMMA.

==========

$HLOWT group required if NFFLVL=2 or 3 in $CONTRL

$GLOWT group required if NFFLVL=3 in $CONTRL

These are the lower triangular parts of the hessian and 3rd derivative matrices, read in the same format as printed by an earlier RUNTYP=GAMMA.

==========

==========

$IRC group (relevant for RUNTYP=IRC)

This group governs the location of the intrinsic reaction coordinate (also called the minimum energy path, MEP), a steepest descent path in mass weighted coordinates, that connects the saddle point to reactants and products. The IRC serves a proof of the mechanism for a reaction, and is a starting point for reaction path dynamics.

The IRC may be found for systems with QM atoms, EFP particles, or the combinations of QM and EFP particles, or QM plus the optional SIMOMM plug-in MM atoms.

Restart data for RUNTYP=IRC is written into the PUNCH file. Information summarizing the reaction path is written to the TRAJECT file, which should be saved, appending these as various restarts are done. The graphics program MacMolPlt can display a movie of the entire mechanism, if you join the entire forward and entire backwards trajectory files, while changing the path distance parameter in the reverse part to a negative value.

----- there are five integration methods chosen by PACE.

PACE = GS2 selects the Gonzalez-Schlegel second order method. This is the default method. Related input is:

- GCUT cutoff for the norm of the mass-weighted gradient tangent (the default is chosen in the range from 0.00005 to 0.00020, depending on the value for STRIDE chosen below.
- RCUT cutoff for Cartesian RMS displacement vector. (the default is chosen in the range 0.0005 to 0.0020 Bohr, depending on the value for STRIDE)
- ACUT maximum angle from end points for linear interpolation (default=5 degrees)
- MXOPT maximum number of constrained optimization steps for each IRC point (default=20)
- IHUPD is the hessian update formula. 1 means Powell, 2 means BFGS (default=2)

```
  GA     is a gradient from the previous IRC point, and is
         used when restarting.
  OPTTOL is a gradient cutoff used to determine if the IRC
         is approaching a minimum.  It has the same meaning
         as the variable in $STATPT.  (default=0.0001)

PACE = LINEAR selects linear gradient following (Euler's
              method).  Related input is:

  STABLZ switches on Ishida/Morokuma/Komornicki reaction
         path stabilization.  The default is .TRUE.
  DELTA  initial step size along the unit bisector, if
         STABLZ is on.  Default=0.025 Bohr.
  ELBOW  is the collinearity threshold above which the
         stabilization is skipped.  If the mass weighted
         gradients at QB and QC are almost collinear, the
         reaction path is deemed to be curving very little,
         and stabilization isn't needed.  The default is
         175.0 degrees.  To always perform stabilization,
         input 180.0.
  READQB,EB,GBNORM,GB are energy and gradient data
         already known at the current IRC point.  If it
         happens that a run with STABLZ on decides to skip
         stabilization because of ELBOW, this data will be
         punched to speed the restart.


PACE = QUAD   selects quadratic gradient following.
              Related input is:

  SAB    distance to previous point on the IRC.
  GA     gradient vector at that historical point.


PACE = AMPC4  selects the fourth order Adams-Moulton
              variable step predictor-corrector.
              Related input is:

  GA0,GA1,GA2 which are gradients at previous points.


PACE = RK4    selects the 4th order Runge-Kutta variable
              step method.  There is no related input.
```

```
----- The next two are used by all PACE choices -----

STRIDE = Determines how far apart points on the reaction
         path will be.  STRIDE is used to calculate the
         step taken, according to the PACE you choose.
         The default is good for the GS2 method, which is
         very robust.  Other methods should request much
         smaller step sizes, such as 0.10 or even 0.05.
         (default = 0.30 sqrt(amu)-Bohr)
NPOINT = The number of IRC points to be located in this
         run. The default is to find only the next point.
         (default = 1)


                    ----- constraint -----
Of course, applying a constraint to the saddle point search
and the reaction path means that you are not locating the
true saddle, nor following the true reaction path.

IFREEZ = array of Cartesian coordinates to freeze.  The
         IRC stepper works in mass-weighted Cartesian
         space, making it impossible to freeze internal
         coordinates.  An input of IFREEZ(1)=4,8 means to
         freeze the x coordinate of the 2nd atom and the
         y coordinate of the 3rd atom, that is, we count
         coordinates x1,y1,z1,x2,y2,z2,x3,y3,z3,...


----- The next two let you choose your output volume -----

    Let F mean the first IRC point found in this run,
    and L mean the final IRC point of this run.
    Let INTR mean the internuclear distance matrix.

NPRT   =  1  Print INTR at all, orbitals at all IRC points
          0  Print INTR at all, orbitals at F+L (default)
         -1  Print INTR at all, orbitals never
         -2  Print INTR at F+L, orbitals never

NPUN   =  1  Punch all orbitals at all IRC points
          0  Punch all orbitals at F+L, only occupied
             orbitals at IRC points between (default)
         -1  Punch all orbitals at F+L only
         -2  Never punch orbitals
```

```
----- The next two tally the reaction path results.  The
      defaults are appropriate for starting from a saddle
      point, restart values are automatically punched out.

NEXTPT = The number of the next point to be computed.
STOTAL = Total distance along the reaction path to next
         IRC point, in mass weighted Cartesian space.



----- The following controls jumping off the saddle point.
      If you give $HESS input, FREQ and CMODE will be
      generated automatically.

SADDLE = A logical variable telling if the coordinates
         given in the $DATA deck are at a saddle point
         (.TRUE.) or some other point lying on the IRC
         (.FALSE.).  If SADDLE is true, either a $HESS
         group or else FREQ and CMODE must be given.
         (default = .FALSE.)  Related input is:

TSENGY = A logical variable controlling whether the energy
         and wavefunction are evaluated at the transition
         state coordinates given in $DATA.  Since you
         already know the energy from the transition state
         search and force field runs, the default is .F.
FORWRD = A logical variable controlling the direction to
         proceed away from a saddle point. The forward
         direction is defined as the direction in which
         the largest magnitude component of the imaginary
         normal mode is positive. (default =.TRUE.)
EVIB   = Desired decrease in energy when following the
         imaginary normal mode away from a saddle point.
         (default=0.0005 Hartree)
FREQ   = The magnitude of the imaginary frequency, given
         in cm**-1.
CMODE  = An array of the components of the normal mode
         whose frequency is imaginary, in Cartesian
         coordinates.  Be careful with the signs!

   You must give FREQ and CMODE if you don't give a $HESS
   group, when SADDLE=.TRUE.  The option of giving these
   two variables instead of a $HESS does not apply to the
```

GS2 method, which must have a hessian input, even for restarts. Note also that EVIB is ignored by GS2 runs.

```
* * * * * * * * * * * * * * * * * * *
For hints about IRC tracking, see
the 'further information' section.
* * * * * * * * * * * * * * * * * * *
```

==========

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$DRC group (relevant for RUNTYP=DRC)

This group governs "direct dynamics", following the dynamical reaction coordinate, which is a classical trajectory based on quantum chemistry potential energy surfaces. These may be either ab initio or semi-empirical, and are computed "on the fly" as the trajectory proceeds.

Because the vibrational period of a normal mode with frequency 500 wavenumbers is 67 fs, a DRC needs to run for many steps in order to sample a representative portion of phase space. Restart data can be found in the job's OUTPUT file, with important results summarized to the TRAJECT file. Almost all DRCs break molecular symmetry, so build your molecule with C1 symmetry in $DATA, or specify NOSYM=1 in $CONTRL. RUNTYP=DRC may not be used with EFP particles.

NSTEP = The number of DRC points to be calculated, not including the initial point. (default = 1000)

DELTAT = is the time step. (default = 0.1 fs)

TOTIME = total duration of the DRC computed in a previous job, in fs. The default is the correct value when initiating a DRC. (default=0.0 fs)

* * *

In general, a DRC can be initiated anywhere, so $DATA might contain coordinates of the equilibrium geometry, or a nearby transition state, or something else. You must also supply an initial kinetic energy, and the direction of the initial velocity, for which there are a number of options:

EKIN = The initial kinetic energy (default = 0.0 kcal/mol)
See also ENM, NVEL, and VIBLVL regarding alternate ways to specify the initial value.

VEL = an array of velocity components, in Bohr/fs. When NVEL is false, this is simply the direction

of the velocity vector. Its magnitude will be automatically adjusted to match the desired initial kinetic energy, and it will be projected so that the translation of the center of mass is removed. Give in the order vx1, vy1, vz1, vx2, vy2, ...

NVEL = a flag to compute the initial kinetic energy from the input VEL using the sum of mass*VEL*VEL/2. This flag is usually selected only for restarts. (default=.FALSE.)

The next three allow the kinetic energy to be partitioned over all normal modes. The coordinates in $DATA are likely to be from a stationary point! You must also supply $HESS input, which is the nuclear force constant matrix at the starting geometry.

VIBLVL = a flag to turn this option on (default=.FALSE.)

VIBENG = an array of energies (in units of multiples of the hv of each mode) to be imparted along each normal mode. The default is to assign the zero point energy only, VIBENG(1)=0.5, 0.5, ..., 0.5 when HESS=MIN, and 0.0, 0.5, ..., 0.5 if HESS=TS. If given as a negative number, the initial direction of the velocity vector is along the reverse direction of the mode. "Reverse" means the phase of the normal mode is chosen such that the largest magnitude component is a negative value. An example might be VIBENG(4)=2.5 to add two quanta to mode 4, along with zero point energy in all modes.

RCENG = reaction coordinate energy, in kcal/mol. This is the initial kinetic energy given to the imaginary frequency normal mode when HESS=TS. If this is given as a negative value, the direction of the velocity vector will be the "reverse direction", meaning the phase of the normal mode will be chosen so its largest component is negative.

* * *

The next two pertain to initiating the DRC along a single normal mode of vibration. No kinetic energy is assigned to the other modes. You must also supply $HESS input for the initial geometry.

NNM = The number of the normal mode to which the initial kinetic energy is given. The absolute value of NNM must be in the range 1, 2, ..., 3N-6. If NNM is a positive/negative value, the initial velocity will lie in the forward/reverse direction of the mode. "Forward" means the largest normal mode component is a positive value. (default=0)

ENM = the initial kinetic energy given to mode NNM, in units of vibrational quanta hv, so the amount depends on mode NNM's vibrational frequency, v. If you prefer to impart an arbitrary initial kinetic energy to mode NNM, specify EKIN instead. (default = 0.0 quanta)

To summarize, there are 5 ways to initiate a trajectory:

1. VEL vector with NVEL=.TRUE. This is difficult to specify at your initial point, and so this option is mainly used when restarting your trajectory. The restart information is always in this format.
2. VEL vector and EKIN with NVEL=.FALSE. This will give a desired amount of kinetic energy in the direction of the velocity vector.
3. VIBLVL and VIBENG and possibly RCENG, to give some initial kinetic energy to all normal modes.
4. NNM and ENM to give quanta to a single normal mode.
5. NNM and EKIN to give arbitrary kinetic energy to a single normal mode.

* * *

The most common use of the next two is to analyze a trajectory with respect to the normal modes of a minimum energy geometry it travels around.

NMANAL = a flag to select mapping of the mass-weighted Cartesian DRC coordinates and velocity (conjugate momentum) in terms of normal modes at a nearby

reference stationary point (which can be either a minimum or transition state). This reference geometry could in fact be the same as the initial point of the DRC, but does not need to be. If you choose this option, you must supply C0, HESS2, and $HESS2 input corresponding to the reference stationary point. (default=.FALSE.)

C0 = an array of the coordinates of the stationary reference point (the coordinates in $DATA might well be some other coordinates). Give in the order x1,y1,z1,x2,y2,... in Angstroms.

* * *

The next options apply to input choices which may read a $HESS at the initial DRC point, namely NNM or VIBLVL, or to those that read a $HESS2 at some reference geometry (NMANAL).

HESS = MIN indicates the hessian supplied for the initial geometry corresponds to a minimum (default).
= TS indicates the hessian is for a saddle point.
HESS2 = MIN (default) or TS, the same meaning, for the reference geometry.

These are used to decide if modes 1-6 (minimum) or modes 2-7 (TS) are to be excluded from the hessian as the translational and rotational contaminants. If the initial and reference geometries are the same, these two hessians will be duplicates of each other.

The next variables can cause termination of a run, if molecular fragments get too far apart or close together.

NFRGPR = Number of atom pairs whose distance will be checked. (default is 0)

IFRGPR = Array of the atom pairs. 2 times NFRGPR values.

FRGCUT = Array for a boundary distance (in Bohr) for atom pairs to end DRC calculations. The run will stop if any distance exceeds the tolerance, or if a value is given as a negative number, if the

```
          distance becomes shorter than the absolute value.
          In case the trajectory starts outside the bounds
          specified, they do not apply until after the
          trajectory reaches a point where the criteria
          are satisfied, and then goes outside again.
          Give NFRGPR values.

                              * * *

     The final variables control the volume of output.
     Let F mean the first DRC point found in this run,
     and L mean the last DRC point of this run.

NPRTSM = summarize the DRC results every NPRTSM steps,
          to the TRAJECT file.  (default = 1)

NPRT   =  1  Print orbitals at all DRC points
          0  Print orbitals at F+L (default)
         -1  Never print orbitals

NPUN   =  2  Punch all orbitals at all DRC points
          1  Punch all orbitals at F+L, and occupied
             orbitals at DRC points between
          0  Punch all orbitals at F+L only (default)
         -1  Never punch orbitals

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$MEX group (relevant if RUNTYP=MEX)

This group governs a search for the lowest energy on the 3N-7 dimensional "seam" of intersection of two different electronic potential energy surfaces. Such Minimum Energy Crossing Points are important for processes such as spin-orbit coupling that involve transfer from one surface to another, and thus are analogous to transition states on a single surface. The present program requires that the two surfaces differ in spin quantum number, or space symmetry, or both. Analytic gradients are used in the search.

In case the two potential surfaces have identical spin and space symmetry, this kind of intersection point is referred to as a Conical Intersection. See $CONICL using RUNTYP=CONICAL instead.

```
SCF1, SCF2   = define the molecular wavefunction types,
               possibly in conjunction with the usual
               MPLEVL and DFTTYP keywords.

MULT1, MULT2 = give the spin multiplicity of the states.

      Permissible combinations of wavefunctions are
           RHF  with ROHF/UHF
           ROHF with ROHF
           UHF  with UHF
      as well as their MP2 and DFT counterparts, and
           GVB  with ROHF/UHF
          MCSCF with MCSCF (CISTEP=ALDET or GUGA only)


NSTEP  = maximum number of search steps (default=50)

STPSZ  = Step size during the search  (default = 0.1D+00)


NRDMOS = Initial orbitals can be read in
       = 0  No initial orbitals (default)
       = 1  Read in orbitals for first state (in $VEC1)
       = 2  Read in orbitals for second state (in $VEC2)
       = 3  Read in orbitals for both ($VEC1 and $VEC2)
```

```
NMOS1  = Number of orbitals for first state's $VEC1.

NMOS2  = Number of orbitals for second state's $VEC2.

NPRT   = Printing orbitals
       = 0  No orbital printed out except at the first
            geometry (default)
       = 1  Orbitals are printed each geometry.  If MCSCF
            is used, CI expansions are also printed.

Finer control of the convergence criterion:

TDE    = energy difference between two states
         (default = 1.0D-05)

TDXMAX = maximum displacement of coordinates
         (default = 2.0D-03)

TDXRMS = root mean square displacement
         (default = 1.5D-03)

TGMAX  = maximum of effective gradient between the two
         states (default = 5.0D-04)

TGRMS  = root mean square effective gradient tolerance
          (default = 3.0D-04)

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Usage notes:

1. Normally $CONTRL will not give SCFTYP or MULT keywords.
SCF1 and SCF2 can be given in any order.  The combinations
permitted ensure roughly equal sophistication in the
treatment of electron correlation.
2. After reading $MEX, SCFTYP and MULT will be set to the
more complex of the two choices, which is considered to be
RHF < ROHF < UHF < GVB < MCSCF.  This permits the $SCF
input defining a GVB wavefunction to be read and tested for
correctness, in a GVB+ROHF run.  Since only one SCFTYP is
stored while reading the input, you might need to provide
some keywords that are normally set by default for the
other (such as ensuring DIIS is selected in $SCF if either
of the states is UHF).
```

3. It is safest by far to prepare and read $VEC1 and $VEC2 groups so that you know what electronic states you start with. It is a good idea to regenerate both states at the end of the MEX search, to be sure that they remain as you began.
4. It is your responsibility to make sure that the states have a different space symmetry, or a different spin symmetry (or both). That is why note 3 is so important.
5. $GRAD1 and/or $GRAD2 groups containing gradients may be given to speed up the first geometry of the MEX search.
6. The search is even trickier than a saddle point search, for it involves the peaks and valleys of BOTH surfaces being generated. Starting geometries may be guessed as lying between the minima of the two surfaces, but the lowest energy on the crossing seam may turn out to be somewhere else. Be prepared to restart!
7. The procedure is a Newton-Raphson search, conducted in Cartesian coordinates, with a Lagrange multiplier imposing the constraint of equal energy upon the two states. The hessian matrices in the search are guessed at, and subjected to BFGS updates. Internal coordinates will be printed (for monitoring purposes) if you define $ZMAT, but the stepper operates in Cartesian coordinates only. No geometry constraints can be applied, apart from the point group in $DATA.

A good paper to read about this kind of search is
A.Farazdel, M.Dupuis J.Comput.Chem. 12, 276-282(1991)

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$CONICL group (relevant if RUNTYP=CONICAL)

This group governs a search for the lowest energy on the 3N-7 dimensional "seam" of intersection of two electronic potential energy surfaces of the same spin and space symmetry. Such Conical Intersections (CI) are important in photochemistry, where they serve as "funnels" for the transfer from an excited state to a lower state. See RUNTYP=MEX and the $MEX input for the simpler case where the two surfaces differ by either space or spin symmetry.

Three search procedures are given, one of which requires the non-adiabatic coupling matrix element (NACME), and two others which do not require NACME information. The conical intersection search is available only for MCSCF (for which NACME are available) or for TD-DFT potential surfaces (where NACME are not available). The TD-DFT must be used in the Tamm/Dancoff approximation (see TAMMD in $TDDFT), but can be either conventional or spin-flip.

The search utilizes some of the options of $STATPT, but note that the Schlegel stepper and HESS=CALC are not permitted. It may be reasonable to try the RFO stepper sometimes. The search can only be run in Cartesian coordinates. Restarts are possible only by updating the coordinates in $DATA.

At present, the only solvation model that is supported is conventional TD-DFT with EFP1.

```
OPTTYP = search procedure choice, see references below!
       = GPWNAC  Gradient Projection with NACME, so this
                 is only available for MCSCF.
       = BPUPD   branching plane updating method (default)
       = PENALTY penalty-constrained optimization method
```

Note that for MCSCF surfaces, if state-averaging is used, the program executes the code needed to produce NACME vectors, to producing the state-averaged gradients. There is essentially no extra time required to produce also the NACME, hence the GPWNAC stepper might as well be used.

```
IXROOT = array of two states whose CI point is sought.
         For example, this might be IXROOT(1)=2,3
         The roots are counted exactly the same as IROOT in
         the $DET or $TDDFT input groups.  For the latter
         case, set IXROOT to 0 if you want the ground state
         to be one of the two surfaces searched on.
         There is no default for IXROOT!

SYMOFF = flag to switch off point group symmetry,
         the default is .TRUE.

DEBUG  = flag to print debugging info, default is .FALSE.

The following are meaningful only for OPTTYP=PENALTY:

TOLSTP = energy difference tolerance
         default=1d-6 Hartree

TOLGRD = gradient convergence tolerance
         default=5d-3 Hartree/Bohr

ALPHA  = parameter ensuring a singularity free penalty,
         default=0.02 Hartree

SIGMA  = Lagrange multiplier for the penalty term.  In
         case the energy gap between the states is not
         acceptable at the CI point, increase the value.
         default = 3.5 (unitless)

An understanding of the search procedures can be gained by
reading the following papers:

  Gradient Projection with NACME:
    M.J.Bearpark, M.A.Robb, H.B.Schlegel
      Chem.Phys.Lett. 223, 269(1994)
  Branching Plane Updating method:
    S.Maeda, K.Ohno, K.Morokuma
      J.Chem.Theor Comput. 6, 1538(2010)
  Penalty constrained update method:
    B.G.Levine, C.Ko, J.Quenneville, T.J.Martinez
      Mol.Phys. 104, 1039(2006)
    B.G.Levine, J.D.Coe, T.J.Martinez
      J.Phys.Chem.B 112, 405(2008)

A comparative study of the first two procedures is
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  T.W.Keal, A.Koslowski, W.Thiel
  Theoret.Chem.Acc. 118, 837(2007)

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$MD group (relevant if RUNTYP=MD)

This group controls the molecular dynamics trajectory for a collection of quantum mechanical atoms and/or Effective Fragment Potential particles.

A typical MD simulation starts with an equilibration phase, running long enough to produce a randomized structure and velocity distribution. Typically equilibration is done with an NVT ensemble, allowing the system to equilibrate to a desired temperature. A production run restarts with the positions and the velocity and quaternion data from the equilibration run, might use either a NVE or NVT ensemble, and collects radial distribution functions and other properties.

Only a few properties are computed from the MD trajectory, apart from correct radial distribution functions. In particular, the pressures, diffusion constants, and heats of vaporization that appear on the printout (presently only for pure EFP runs) are from a preliminary code, which has not yet been verified.

If the system contains only EFP particles, it may be placed in a periodic box, according to the minimum image convention. The optional periodic boundary conditions, along with cut-offs, are given in the $EFRAG input. See also the $EWALD input group for long-range electrostatic treatment if PBC is used.

The first keywords relate to the steps:

MDINT = MD integrator selection.
= FROG (leapfrog). This is less accurate, and lacks the special ensemble stepper option NVTNH.
= VVERLET (velocity Verlet) - default.

DT = MD time step size, in seconds, default=1.0d-15, which is a femtosecond.

NVTNH selects a integrator step appropriate to the desired ensemble. This is only implemented for

velocity Verlet.
= 0 means use NVE Verlet stepping
= 1 means use NVT Verlet stepping
= 2 means use Nose/Hoover chain NVT Verlet stepping
The default is 2 if either NVT option RSTEMP or RSRAND is chosen, but is 0 otherwise.

NSTEPS = number of MD time steps to be found in this run, default=10000.

TTOTAL = total time elapsed in the previous part of a MD trajectory which is being restarted (READ=.TRUE.). The default means this trajectory is a new one, or perhaps the start of a production phase of the MD. (default=0.0 seconds)

* * *

BATHT = bath temperature, in Kelvin (default=300.0)
This value is used during NVT runs, or if the MD is initialized to a Maxwell-Boltzmann velocity distribution.

* * *

Two options exist to create NVT runs, to bring the system to a desired bath temperature. If neither is chosen, the ensemble is NVE:

RSTEMP = flag to rescale the temperature. default=.FALSE.

DTEMP = temperature range for the RSTEMP option. The velocities are rescaled to the bath temperature if T < (BATHT-DTEMP) or T > (BATHT+DTEMP). The default is DTEMP=100.0 degrees.

RSRAND = flag to reset to Maxwell-Boltzmann distribution, using random numbers (same algorithm as MBT and MBR) to choose individual velocity magnitudes and directions. default=.FALSE.

NRAND = number of steps for the RSRAND option. Reassign velocities (translational and rotational) every NRAND time steps. Default=1000.

```
NVTOFF = step number at which to turn off either NVT
         thermostat, and switch to NVE.  At this point, the
         NVTNH parameter will be reset to 0, and the PROD
         flag will be turned on, so that the production
         run will start (gathering and printing the RDF
         information to .log file).  This keyword is also
         useful in NVE runs to postpone the accumulation of
         production information.  The default means no
         switch to NVE (default=0).

JEVERY = report simulation quantities (write info such as
         energies, temps, etc. to .log file) and collect
         RDF info each JEVERY time step.  Default=10

KEVERY = write coordinates (to log and TRAJECT files),
         velocity/quaternion restart info (to the TRAJECT
         file and RDFs (to log file) at each KEVERY step.
         default=100

PROD   = production run, at present this means only that
         information for radial distribution functions is
         collected, and printed.  default=.FALSE.

DELR   = spacing for radial bins in RDF calculations,
         default=0.02 Angstroms.

NPROP  = step number at which to begin collecting data for
         the other properties, such as pressure and
         diffusion constants.  This should be a value
         between 1 and NSTEPS, as it counts off the current
         run's steps.  Default=0.

PBCOUT = print PBC coordinates in the end of simulation
         (i.e. all molecules will be contained in one box)
         Default=.FALSE.

                        * * *

SSBP   = flag to add spherical solvent boundary condition
         using the harmonic restraint potential(V)
              V=0.5*SFORCE*(R-DROFF)**2.
         (Default=.FALSE)

SFORCE = the force constant for SSBP in kcal/mol-A**2
         (default: 0.0).
```

```
CCMS   = flag to add a harmonic potential to constrain
         the center of mass of the QM subsystem. This will
         keep the QM subsystem in QM/MM-MD with spherical
         boundary conditions near the center of sphere.
         (Default=.FALSE)

CFORCE = the force constant for CCMS in kcal/mol-A**2
         (default: 0.0).

DROFF  = is an array of distances such that V=0 if R<DROFF.
         The first and second elements of the array are for
         MM and QM subsystems of QM/MM-MD, respectively.
         (default: 1.0d+10).

USAMP  = flag to apply harmonic constraint potential(V)
              V=0.5*UFORCE*(R-RZERO)**2
         (default: .false.).

UFORCE = the force constant for USAMP in kcal/mol-A**2
         (default: 0.0).

RZERO  = array of reference values for USAMP. Distances and
         angles are in Angstrom and Degree, respectively.
         (default: all 0.0).

IUSTYP   specifies the type of USAMP
               = 0 bond constraint (default value)
               = 1 asymmetric bond constraint
               = 2 angle constraint
               = 3 torsion constraint
               = 4 asymmetric and bond constraint.
                   This is for 2 dimensional umbrella
                   sampling of an atom shift reaction (atom
                   1 is moving from atom 2 to 3), and a
                   bond distance between atom 4 and 5.
                   So it requires 5 elements in IPAIR!
               = 5 asymmetric coordinate + Restraint
                   IPAIR contains three atoms, where atom 1
                   is moving from atom 2 to 3 by asymmetric
                   coordinate.  This restraint forces atom
                   1 to stay between atom 2 and 3.
               = 6 Normal constraining for up to 2 bonds
                   based on flexible constraints. IPAIR
                   must contain 4 values for the two bonds.
```

= 7 Asymmtric coordinate based on flexible constraints. IPAIR should contains all the corresponding atoms.
= 8 The center of mass coordinates of two QM parts. IPAIR should include only the first part of QM atoms.
= 9 The center of mass coordinates with respect to the center of sphere (0,0,0). IPAIR should not be used, since GAMESS will automatically generate the center of mass of your QM part.

IPAIR is an array of atom numbers to which the umbrella sampling potentials are applied. For example, a bond constraint for atom 1 and 2 is IPAIR(1)=1,2. An asymmetric bond constraint requires three atoms, in which the atom 1 migrates from atom 2 to 3. IUSTYP=4 requires 5 atoms: the first three atoms are for asymmetric bond constraint. Default: 0.

* * *

MREMD specifies the type of REMD (Replica Exchange MD). NGROUPS in $GDDI must be greater than 1 in order for this option to be effective. Note that currently REMD works only for NVT.
= 0 no REMD
= 1 one dimension REMD

LEVERY Temperature exchange at LEVERY steps during REMD runs. (default: 1000)
If JEVERY.gt.LEVERY, JEVERY is reset to LEVERY.

* * *

IRATTL an array turning on (1) and off (0) the bond constraints for C-H, N-H, or O-H in that order.

The next three define RATTLE parameters in MD.

RATLEN is the bond length to constrain each bond to (same order as IRATTL). The defaults are:
RATLEN(1)= 1.117 - Yao,Vogeli,Ying&Bax,
J.Am.Chem.Soc.1999,121,4690-4695

```
         RATLEN(2)= 1.037 - Ottiger & Bax,
                       J.Am.Chem.Soc.2008, 130, 16518-16520
         RATLEN(3)= 1.02  - Wikipedia

RATTOL   is the convergence tolerance for the RATTLE
         iterations for each bond type.  The default value
         is 1.0D-6.

IRATIT   is the number of iterations allowed during the
         RATTLE constraint algorithm.
         The default value is 2000.

                              * * *

The following keywords control starting MD conditions.
Normally an MD trajectory is initiated with both MBT and
MBR chosen, while restarts would select only READ.  The
restart data is written to the TRAJECT file.  To restart
requires merging particle coordinates into $DATA and/or
$EFRAG, and placing the new $MD input below your existing
$MD input, thus keeping your choices for the variables
above (both $MD input groups will be read).

MBT    = get translational velocities from a random
         Maxwell-Boltzmann ensemble.  Default=.FALSE.

MBR    = get rotational velocities from a random Maxwell-
         Boltzmann ensemble.  Default=.FALSE.

QRAND  = if .TRUE., generate random quaternions, an option
         that is not normally chosen.
         if .FALSE., use EFP particle coordinates and the
         initial MBT/MBR assigned velocities to set
         correct quaternion data (default is .FALSE.)

READ   = read velocities (translational and rotational) and
         quaternions and their first and second derivatives
         from input file.  Default is .FALSE.  Set the
         other three values MBT/MBR/QRAND off if you choose
         restarting with READ.

For READ=.TRUE., the following restart data is required.
This data may be copied from the TRAJECT file, in exactly
the format it was written out.  The required data depends
on your choice for the integrator, see MDINT above.  In
```

```
addition, you will need to update the particle coordinates
in $DATA and/or $EFRAG, using data from the TRAJECT file.

TVELQM(1)= quantum atom's translational velocities (both).
TVEL(1)= array of EFP translational velocities (both).
RVEL(1)= array of EFP rotational velocities (VVERLET).
RMOM(1)= array of EFP rotational momenta (FROG).
QUAT(1)= array of EFP quaternions (both).
QUAT1D(1)= EFP quaternion first derivatives (VVERLET).
QUAT2D(1)= EFP quaternion second derivatives (VVERLET).

extra reading:
  "Computer Simulation of Liquids"
     M.P.Allen, D.J.Tildesley  Oxford Science, 1987
  "Understanding Molecular Simulation"
     D.Frenkel, B.Smit  Academic Press, 2002

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$RDF group (relevant for RUNTYP=MD)

This group defines the pairs of atoms for which the radial distribution functions are to be computed, at the end of a molecular dynamics trajectory. The input is similar in style to $EFRAG, consisting of separate lines, with the word STOP ending each particular pair.

Line 1. NRDF=<no.RDFs>
gives the number of RDFs which should be computed.

Line 2. <pair title> <FRAG1> <FRAG2> <no.pairs>
gives a string for the printout (a good choice involves both atoms, such as ClCl), the name of the $FRAGNAME containing the first atom of the pair, the name of the $FRAGNAME input group with the second atom of the pair, and how many such pairs exist.

Line 3. <label> <num.atom1> <num.atom2>
gives a label (arbitrary), the position of the atom within the $FRAG1 group, and the 2nd atom's within the $FRAG2. This line must be repeated <no.pairs> times.

Line 4. STOP
the word STOP ends this RDF's pair input.

Lines 2-4 must then be repeated a total of <no.RDFs> times.

An example will make this all clear. If there is only one type of fragment used, such as water (so $EFRAG contains only FRAGNAME=WATER), and assuming that this $WATER group defining the water EFP has atoms in the order O,H,H:

```
$RDF
nrdf=3
OO       water   water    1
  dum   1   1
STOP
OH       water   water    4
  dum   1   2
  dum   1   3
  dum   2   1
  dum   3   1
```

```
STOP
HH       water   water    4
  dum    2   2
  dum    2   3
  dum    3   2
  dum    3   3
STOP
 $end
```

==========

==========

$GLOBOP group (relevant to RUNTYP=GLOBOP)

This controls the Metropolis Monte Carlo search method for finding local and global minima. Systems can include EFP fragments, FMO fragments, or fully ab initio groups or some combination of the three (excluding FMO and ab initio). The present code is backwards compatible with old runtyp=globop inputs.

There are options for a single temperature Monte Carlo search, or a multiple temperature simulated annealing. Local minimization of some or all of the structures selected by the Monte Carlo is an option.

Accepted coordinates and energy can be printed to a trajectory file in the scratch file, using a keyword described below. A perl script named "globop_extract" is provided in the standard GAMESS distribution, which can extract the lowest energies (and matching coordinates) from the TRAJECT data set.

See REFS.DOC for an overview of this RUNTYP.

RNDINI = flag to randomize the particles given in input, usually choosing the particle at random, placing it near the center of the coordinate origin but in such a way that it does not collide with any particles placed earlier. The default is to use coordinates as given in $EFRAG (default .FALSE.)

JSTRND = If RNDiNI and JSTRND are both true, the run ends after the randomization and energy calculation. (default .TRUE.)

RIORD = relevant only if RNDINI is .TRUE.
= RAND selects EFP particles in random order, as well as randomizing their coordinates. (default)
= STANDARD chooses the particles in the same order that they were given in $EFRAG, so only their positions are randomized.

See REFS.DOC for some ideas on how to build clusters with these two inputs.

TEMPI = initial temperature used in the simulation. (default = 20000 K)

TEMPF = final temperature. If TEMPF is not given and NTEMPS is greater than 1, TEMPF will be calculated based on a cooling factor of 0.95.

NTEMPS = number of temperatures used in the simulation. If NTEMPS is not given but TEMPF is given, NTEMP will be calculated based on a cooling factor of 0.95. If neither NTEMP nor TEMPF is given, the job defaults to a single temperature Monte Carlo calculation.

MCTYP = Bitwise label of fragment types being used
1 = ab initio groups
2 = FMO fragments
4 = EFP fragments
6 = FMO and EFP
Older input files or solvation of immobile ab initio molecules should use the default=4

NFRMOV = number of EFP fragments to move on each step. (default=1)

NFMORV = number of FMO fragments or ab initio groups to move on each step. (default=1)

MCMIN = flag to enable geometry optimization to minimize the energy is carried out every NSTMIN steps. (default=.true.)

NGEOPT = number of geometries to be evaluated at each temperature. (default = 100)

NTRAN = number of translational steps in each block. (default=5)

NROT = number of rotational steps in each block. (default=5)

NBLOCK = the number of blocks of steps can be set directly

```
          with this variable, instead of being calculated
          from NGEOPT, NTRAN, and NROT, according to
             NBLOCK=NGEOPT/(NTRAN+NROT)
          If NBLOCK is input, the number of geometries at
          each temperature will be taken as
             NGEOPT=NBLOCK*(NTRAN+NROT)
          Each block has NTRAN translational steps followed
          by NROT rotational steps.

NAIFG  =  number of ab initio groups for odd values of
          MCTYP.  If not the default value, then $GLBFRG
          must be included (default=no. of atoms in $DATA)

AIMOVE =  applicable to MCTYP=4 with ab initio atoms only.
          maximum translation movement of ab initio atoms
          during EFP movement step. (default=0.0)

SCALE  =  2 value array that scales max movement and
          rotation.  first value is translations
          second is rotations (default=1.0,1.0)

ALPHA  =  controls the rate at which information from
          successful steps is folded into the maximum step
          sizes for each of the 6*(number of fragments)
          coordinates.  ALPHA varies between 0 and 1.
          ALPHA=0 means do not change the maximum step
          sizes, and ALPHA=1 throws out the old step sizes
          whenever there is a successful step and uses the
          successful step sizes as the new maxima.  This
          update scheme was used with the Parks method
          where all fragments are moved on every step.  It
          is not normally used with the Metropolis method.
          (default = 0)

BOLTWT =  method for calculating the Boltzmann factor,
          which is used as the probability of accepting a
          step that increases the energy.
        =  STANDARD = use the standard Boltzmann factor,
          exp(-delta(E)/kT)  (default)
        =  AVESTEP = scale the temperature by the average
          step size, as recommended in the Parks reference
          when using values of ALPHA greater than 0.

NSTMIN =  After this number of geometry steps are taken, a
          local (Newton-Raphson) optimization will be
```

carried out. If this variable is set to 1, a local minimization is carried out on every step, reducing the MC space to the set of local minima. Irrelevant if MCMIN is false. (default=10)

OPTN = if set to .TRUE., at the end of the run local minimizations are carried out on the final geometry and on the minimum-energy geometry. (default=.FALSE.)

DACRAT = the desired acceptance ratio, the program tries to achieve this by adjusting the maximum step size. Setting this to 0.0 disables any change to the maximum step size. (default = 0.5)

UPDFAC = the factor used to update the maximum step size in the attempt to achive the desired acceptance ratio (DACRAT). If the acceptance ratio at the previous temperature was below DACRAT, the step size is decreased by multiplying it by UPDFAC. If the acceptance ratio was above DACRAT, the step size is increased by dividing it by DACRAT It should be between 0 and 1. (default = 0.95)

SEPTOL = the separation tolerence between atoms in either the EFP or FMO fragments. If a step moves atoms closer than this tolerence, the step is rejected. (default = 1.5 Angstroms)

XMIN, XMAX, YMIN, YMAX, ZMIN, ZMAX = mimimum and maximum values for the Cartesian coordinates of the fragment. If the first point in a fragment steps outside these boundaries, periodic boundary conditions are used and the fragment re-enters on the opposite side of the box. The defaults of -10 for minima and +10 for maxima should usually be changed.

NPRTGO = controls the amount of output,
= -2 reduces output even more than -1
= -1 reduces output further, needed for MCMIN=.true.
= 0 gives minimal output (default)
= 1 gives the normal GAMESS amount of output
= 2 gives maximum output

```
          For large simulations, even IOUT=0 may produce
          a log file too large to work with easily.
          If geometry optimization is being done at each
          Monte Carlo generated structure, you can use
          the NPRT in $STATPT to further suppress output.

RANDOM =  controls the choice of random number generator.
       =  DEBUG uses a simple random number generator with
          a constant seed. Since the same sequence of
          random numbers is generated during each job, it
          is useful for debugging.
       =  RAND1 uses the simple random number generator
          used in DEBUG, but with a variable seed.
       =  RAND3 uses a more sophisticated random number
          generator described in Numerical Recipes, with a
          variable seed (default).

IFXFRG =  array whose length is the number of fragments.
          It allows one or more fragments to be fixed
          during the simulation.
       =0 allows the fragment to move during the run
       =1 fixes the fragment
          For example, IFXFRG(3)=1 would fix the third
          fragment, the default is IFXFRG(1)=0,0,0,...,0

NPRBND =  number of pairs of atoms to be positionally
          linked.  A non-zero value requires IBNDS to
          be specified in GLBFRG. (default 0)
          NOTE: pair bindings are not conserved during
          a random initialization.  It is strongly
          advised that RNDINI=.t. not be used for
          systems using NPRBND not equal 0

NSMTP  =  number of steps in each secondary Monte Carlo
          that occurs when an FMO or AI group is moved.
          (default 0)

SMTEMP =  Temperature below which the secondary Monte
          Carlo search will be carried out. (default 0)

=============================================================
```

$GLBFRG group (relevant to RUNTYP=GLOBOP)

==========

This group defines the sets of ab initio atoms in $DATA that are treated as groups in Monte Carlo runs. It also defines any groups that are to be frozen, not moved during the Monte Carlo search.

```
AIFRG  = an array assigning atoms to groups. Two styles
         are supported (the choice is made based on
         AIFRG(1): if it is nonzero, choice (a) is taken,
         otherwise AIFRG(1) is ignored and choice (b) is
         taken):
         a) AIFRG(i)=m assigns atom i is to fragment m.
            AIFRG(i) must be given for each atom.
         b) the style is
            a1 a2 ... ak 0
            b1 b2 ... bm 0
            ...
            Elements a1...ak are assigned to fragment 1,
            then b1...bm are assigned to fragment 2,etc.
            An element is one of the following:
                I    or   I -J
            where I means atom I, and a pair I,-J means
            the range of atoms I-J.  There must be no space
            after the "-"!
         Example:
         AIFRG(1)=1,1,1,2,2,1 is equivalent to
         AIFRG(1)=0, 1,-3,6,0, 4,5,0
         Both assign atoms 1,2,3 and 6 to fragment 1,
         and 4,5 to fragment 2.

NAICUT = automatically divides a molecule into fragments by
         assigning NAICUT atoms to each fragment (useful
         for something like water clusters).  This sets
         AIFRG, so it need not be included.  If 0, the
         automatic option is disabled. (default: 0)

IFXFMO = array of FMO fragments or ab initio groups that
         are not moved during the Monte Carlo search.
         if an optimization step (MCMIN or OPTN) is used,
         the fragment/group will likely be moved.
```

```
IBNDS  = Array of atoms to be positionally linked.
         example for two pairs between atoms 1 and 5,
         and 3 and 6.
         IBNDS(1)=1,5,3,6

PRSEP  = Maximum separation allowed for paired atoms.
         The default uses a formula using the average
         atomic radii of each element from Macmolplt, which
         are designed to approximate single bonds.
            PRSEP= (radius_atom1 + radius_atom2)*1.05
         To specify a different max separation, you MUST
         specify a value for each pair of bonded atoms
         given in IBNDS in the same order.  To use the
         default for a given pair, enter 0.
         Example: for 3 pairs with a non-default maximum
         separation for the second pair given in IBNDS use
         PRSEP(1)=0,X,0 where X is the desired separation

INDEP  = Integer flag that toggles whether translations
         of fragments connected by paired atoms are
         propagated to all other connected fragments.
         A value of 1 disables propagation. (Default=0)

=============================================================
```

==========

$GRADEX group (optional, for RUNTYP=GRADEXTR)

This group controls the gradient extremal following algorithm. The GEs leave stationary points parallel to each of the normal modes of the hessian. Sometimes a GE leaving a minimum will find a transition state, and thus provides us with a way of finding that saddle point. GEs have many unusual mathematical properties, and you should be aware that they normally differ a great deal from IRCs.

The search will always be performed in cartesian coordinates, but internal coordinates along the way may be printed by the usual specification of NZVAR and $ZMAT.

METHOD = algorithm selection.
- SR A predictor-corrector method due to Sun and Ruedenberg (default).
- JJH A method due to Jorgensen, Jensen and Helgaker.

NSTEP = maximum number of predictor steps to take. (default=50)

DPRED = the stepsize for the predictor step. (default = 0.10)

STPT = a flag to indicate whether the initial geometry is considered a stationary point. If .TRUE., the geometry will be perturbed by STSTEP along the IFOLOW normal mode. (default = .TRUE.)

STSTEP = the stepsize for jumping away from a stationary point. (default = 0.01)

IFOLOW = Mode selection option. (default is 1)
If STPT=.TRUE., the initial geometry will be perturbed by STSTEP along the IFOLOW normal mode. Note that IFOLOW can be positive or negative, depending on the direction the normal mode should be followed in. The positive direction is defined as the one where the largest component of the Hessian eigenvector is positive.

```
          If STPT=.FALSE. the sign of IFOLOW determines
          which direction the GE is followed in. A positive
          value will follow the GE in the uphill direction.
          The value of IFOLOW should be set to the Hessian
          mode which is parallel to the gradient to avoid
          miscellaneous warning messages.

GOFRST = a flag to indicate whether the algorithm should
          attempt to locate a stationary point.  If .TRUE.,
          a straight NR search is performed once the NR
          step length drops below SNRMAX.  10 NR step are
          othen allowed, a value which cannot be changed.
          (default = .TRUE.)

SNRMAX = upper limit for switching to straight NR search
          for stationary point location.
          (default = 0.10 or DPRED, whichever is smallest)

OPTTOL = gradient convergence tolerance, in Hartree/Bohr.
          Used for optimizing to a stationary point.
          Convergence of a geometry search requires the
          rms gradient to be less than OPTTOL.
          (default=0.0001)

HESS   = selection of the initial hessian matrix,
          when STPT=.TRUE.
        = READ causes the hessian to be read from a $HESS.
        = CALC causes the hessian to be computed. (default)


  ---- the next parameters apply only to METHOD=SR ----

DELCOR = the corrector step should be smaller than this
          value before the next predictor step is taken.
          (default = 0.001)

MYSTEP = maximum number of micro iteration allowed to
          bring the corrector step length below DELCOR.
          (default=20)

SNUMH  = stepsize used in the numerical differentiation
          of the Hessian to produce third derivatives.
          (default = 0.0001)
```

HSDFDB = flag to select determination of third derivatives.
At the current geometry we need the gradient, the Hessian, and the partial third derivative matrix in the gradient direction.

If .TRUE., the gradient is calculated at the current geometry, and two Hessians are calculated at SNUMH distance to each side in the gradient direction. The Hessian at the geometry is formed as the average of the two displaced Hessians.

If .FALSE., both the gradient and Hessian are calculated at the current geometry, and one additional Hessian is calculated at SNUMH in the gradient direction.

The default double-sided differentiation produces a more accurate third derivative matrix, at the cost of an additional wave function and gradient. (default = .TRUE.)

==========

* * * * * * * * * * * * * * * * * * *
See the 'further information' section
for some help with GRADEXTR runs.
* * * * * * * * * * * * * * * * * * *

==========

$SURF group (relevant for RUNTYP=SURFACE)

This group allows you to probe a potential energy surface along a small grid of points. Note that there is no option to vary angles, only distances. The scan can be made for any SCFTYP, or for the MP2 or CI surface. You may specify two rather different calculations to be done at each point on the grid, through the RUNTYPn, SCFTYPn, and electron correlation keywords.

* * * below, 1 and 2 refer to different calculations * * *

RUNTP1,RUNTYP2 = some RUNTYP supported in $CONTRL
First RUNTYP=RUNTP1 and then RUNTYP=RUNTP2 will be performed, for each point on the grid. The second run is omitted if RUNTP2 is set to NONE.
default: RUNTP1=ENERGY RUNTP2=NONE

SCFTP1,SCFTP2 = some SCFTYP supported in $CONTRL
default: SCFTYP in $CONTRL

CITYP1,CITYP2 = some CITYP supported in $CONTRL
default: CITYP in $CONTRL

MPLEV1,MPLEV2 = some MPLEVL supported in $CONTRL
default: MPLEVL in $CONTRL

CCTYP1,CCTYP2 = some CCTYP supported in $CONTRL
default: CCTYP in $CONTRL

DFTYP1,DFTYP2 = some DFTTYP supported in $DFT
default: DFTTYP in $DFT

You may need to help by giving values in $CONTRL that will permit the program to estimate what is coming in the values here. For example, if you want to request hessians here, it may be good to give RUNTYP=HESSIAN in $CONTRL so that in its earliest stages of a job, the program can initialize for 2nd derivatives. There is less checking here than on $CONTRL input, so don't request something impossible such as two correlation methods simultaneously, or analytic hessians for MP2, or other things that are impossible.

```
* * * below, 1 and 2 refer to different coordinates * * *

IVEC1  = an array of two atoms, defining a coordinate from
         the first atom given, to the second.

IGRP1  = an array specifying a group of atoms, which must
         include the second atom given in IVEC1.  The
         entire group will be translated (rigidly) along
         the vector IVEC1, relative to the first atom
         given in IVEC1.

ORIG1  = starting value of the coordinate, which may be
         positive or negative.  Zero corresponds to the
         distance given in $DATA.

DISP1  = step size for the coordinate.  If DISP1 is set
         to zero, then the keyword GRID1 is read.

NDISP1 = number of steps to take for this coordinate.

GRID1  = an array of grid points at which to compute the
         energy.  This option is an alternative to the
         ORIG1, DISP1 input which produces an equidistant
         grid.  To use GRID1, one has to set DISP1=0.0.
         The number of grid points is given in NDISP1, and
         is limited to at most 100 grid points.  The input
         of GRID1(1)=ORIG1,ORIG1+DISP1,ORIG1+DISP1*2,...
         would reproduce an equidistant grid given by ORIG1
         and DISP1.

     ORIG1, DISP1, and GRID1 should be given in Angstrom.
     There are no reasonable defaults for these keywords.

IVEC2, IGRP2, ORIG2, DISP2, NDISP2, GRID2 have the same
meaning as their "1" counterparts, and permit you to make
a two dimensional map along two displacement coordinates.
If the "2" data are not input, the surface map proceeds in
only one dimension.

=============================================================
```

==========

$LOCAL group (relevant if LOCAL=RUEDNBRG or BOYS)
(relevant if LOCAL=POP or SVD)

This group allows input of additional data to control the localization methods. If no input is provided, the valence orbitals will be localized as much as possible, while still leaving the wavefunction invariant. There are many specialized options for Localized Charge Distribution analysis, and for EFP generation.

LOCAL=RUEDENBRG, BOYS, and POP all work by sequences of two by two Jacobi rotations. This needs iteration control, and permits fine tuning of the orbital pairs rotated, leading to keywords such as SYMLOC and MOIN/MOOUT below.

LOCAL=SVD does a direct projection of the RHF, ROHF, or MCSCF orbitals onto the basis set of each atom, taking in turn atoms one by one, with a symmetric orthogonalization between atoms at the end. Consequently, many keywords here pertaining to iteration control and to various orbital restrictions (MOIN, MOOUT, SYMLOC, etc) don't pertain to LOCAL=SVD.

N.B. Since Boys localization needs the dipole integrals, do not turn off dipole moment calculation in $ELMOM.

MAXLOC = maximum number of localization cycles. This applies to BOYS or POP methods only. If the localization fails to converge, a different order of 2x2 pairwise rotations will be tried. (default=250)

CVGLOC = convergence criterion. The default provides LMO coefficients accurate to 6 figures. (default=1.0E-6)

SYMLOC = a flag to restrict localization so that orbitals of different symmetry types are not mixed. This option is not supported in all possible point groups. The purpose of this option is to give a better choice for the starting orbitals for GVB-PP or MCSCF runs, without destroying the orbital's symmetry. This option is compatible with each of

the 3 methods of selecting the orbitals to be included. If chosen in a run requesting VVOS (see $SCF), occupied and virtual orbitals will also not be permitted to mix in a localization of these two separate orbital spaces. (default=.FALSE.)

ORIENT = a flag to request orientation of the localized orbitals for bond-order analysis. After the localization, the orbitals on each atom are rotated only among themselves, in order to direct the orbitals towards neighboring atom's orbitals, to which they are bonded. The density matrix, or bond-order matrix, of these Oriented LMOs is readily interpreted as atomic populations and bond orders. This option can only be used for LOCAL=RUEDNBRG when SCFTYP=MCSCF, or if LOCAL=SVD. (default=.FALSE.)

EXTLOC = options to localize external orbitals, above the valence MBS orbital space (SVD and ATMNOS), and to control internal orbital localization (SPLITxx keywords), in the valence minimal basis space.

= NONE (default)

= SVD Forms the SVD quasi-atomic external orbitals using an SVD with respect to the accurate atomic minimal basis functions. The localization of all internal orbitals means that ORMAS wavefunctions are not left invariant, nor are full spaces which are not full valence type.

= ATMNOS Performs the EXTLOC=SVD option, and then forms the ordered external orbitals using exchange integrals.

= SPLITQA Performs the EXTLOC=SVD and EXTLOC=ATMNOS options, and then, form split-localized orbitals in the internal orbital space, preserving ORMAS subspaces when doing the latter step.

The next two skip localization in the external space, which saves time, for cases where only localization of internal orbitals is needed:

= SPLITQ2 Forms the split-localized orbitals in the internal orbital space, preserving any ORMAS subspaces (wavefunction will be left invariant).

```
       = SPLITQ3 Forms the split-localized orbitals in the
                 internal orbital space, but these split-
                 localized orbitals do not preserve the
                 ORMAS wavefunction.  In other words, the
                 split-localization treats the calculation
                 as if it had a single united active space.

PRTLOC = a flag to control supplemental printout.  The
         extra output is the rotation matrix to the
         localized orbitals, and, for the Boys method,
         the orbital centroids, for the Ruedenberg
         method, the coulomb and exchange matrices,
         for the population method, atomic populations.
         (default=.FALSE.)


 ----- The following keywords select the orbitals which
       are to be included in the localization.  You may
       select from FCORE, NOUTA/NOUTB, or NINA/NINB,
       but may choose only one of these three groups.
       These options do not pertain to LOCAL=SVD:

FCORE  = flag to freeze all the chemical core orbitals
         present.   All the valence orbitals will be
         localized.  You must explicitly turn this
         option off to choose one of the other two
         orbital selection options.  (default=.TRUE.)

                        * * *

NOUTA  = number of alpha orbitals to hold fixed in the
         localization.  (default=0)

MOOUTA = an array of NOUTA elements giving the numbers of
         the orbitals to hold fixed.  For example, the
         input NOUTA=2 MOOUTA(1)=8,13 will freeze only
         orbitals 8 and 13.  You must enter all the
         orbitals you want to freeze, including any cores.
         This variable has nothing to do with cows.

NOUTB =  number of beta orbitals to hold fixed in -UHF-
         localizations.  (default=0)

MOOUTB = same as MOOUTA, except that it applies to the
         beta orbitals, in -UHF- wavefunctions only.
```

* * *

NINA = number of alpha orbitals which are to be included in the localization. (default=0)

MOINA = an array of NINA elements giving the numbers of the orbitals to be included in the localization. Any orbitals not mentioned will be frozen.

NINB = number of -UHF- beta MOs in the localization. (default=0)

MOINB = same as MOINA, except that it applies to the beta orbitals, in -UHF- wavefunctions only.

ORMFUL = this flag is relevant only to CISTEP=ORMAS MCSCF localizations. By default, the localization is restricted such that the multiple active spaces are not mixed, leaving the total wavefunction invariant. It may be used to localize within the full range of active MOs. (Default is .FALSE.)

----- The following keywords are used for the localized charge distribution (LCD), a decomposition scheme for the energy, or multipole moments, or the first polarizability. See also LOCHYP in $FFCALC for the decomposition of hyperpolarizabilities.

EDCOMP = flag to turn on LCD energy decomposition. Note that this method is currently implemented for SCFTYP=RHF and ROHF and LOCAL=RUEDNBRG only. The SCF LCD forces all orbitals to be localized, overriding input on the previous page. See also LMOMP2 in the $MP2 input. (default = .FALSE.)

MOIDON = flag to turn on LMO identification and subsequent LMO reordering, and assign nuclear LCD automatically. (default = .FALSE.)

DIPDCM = flag for LCD molecular dipole decomposition. (default = .FALSE.)

```
QADDCM = flag for LCD molecular quadrupole decomposition.
         (default = .FALSE.)

POLDCM = flag to compute the static alpha polarizability,
         and its decomposition in terms of LCDs.
         LMO dipole polarizabilities are the polarizability
         term in the EFP model.
         The computation is done analytically, for SCFTYP
         of RHF or ROHF, but must be done numerically for
         their DFT counterparts (choose one of POLNUM or
         POLAPP).  No other correlation method makes sense,
         since the point of this keyword is a decomposition
         over localized orbitals.
         LOCAL may be BOYS or RUEDNBRG.
         See also LOCHYP in $FFCALC for a similar breakdown
         of static beta and gamma hyperpolarizabilities.
         Default=.FALSE., except that RUNTYP=MAKEFP turns
         this computation on, automatically.

POLNUM = flag to force numerical rather than analytical
         calculation of the polarizabilities.  This may be
         much faster for larger molecules.  The numerical
         polarizabilities of bonds in or around aromatic
         rings sometimes are unphysical. (default=.FALSE.)
         See D.R.Garmer, W.J.Stevens
             J.Phys.Chem. 93, 8263-8270(1989).
         This keyword cannot be used with POLDYN or POLAPP.

POLAPP = flag to force calculation of the polarizabilities
         using a perturbation theory expression.  This may
         be useful in larger molecules. (default=.FALSE.)
         See R.M. Minikis, V. Kairys, J.H. Jensen
             J.Phys.Chem.A 105, 3829-3837(2001)
         Quality of the results is not as good as POLNUM!
         This keyword cannot be used with POLDYN or POLNUM.

POLANG = flag to choose units of localized polarizability
         output. The default is Angstroms**3, while false
         will give Bohr**3.  (default=.TRUE.)

ZDO    = flag for LCD analysis of a composite wavefunction,
         given in a $VEC input of a van der Waals complex,
         using the zero differential overlap approximation.
         The MOs are not orthonormalized and the inter-
         molecular electron exchange energy is neglected.
```

Also, the molecular overlap matrix is printed
out. This is a very specialized option.
(default = .FALSE.)

----- The following keywords can be used to define the
nuclear part of an LCD. They are usually used to
rectify mistakes in the automatic definition
made when MOIDON=.TRUE. The index defining the
LMO number then refers to the reordered list of LMOs.

NMOIJ = array giving the number of nuclei assigned to a
particular LMO.

IJMO = is an array of pairs of indices (I,J), giving
the row (nucleus I) and column (orbital J)
index of the entries in ZIJ and MOIJ.

MOIJ = arrays of integers K, assigning nucleus K as the
site of the Ith charge of LCD J.

ZIJ = array of floating point numbers assigning a
charge to the Ith charge of LCD J.

IPROT = array of integers K, defining nucleus K as a
proton.

DEPRNT = a flag for additional decomposition printing,
such as pair contributions to various energy
terms, and centroids of the Ruedenberg orbitals.
(default = .FALSE.)

----- The following keywords are used to build large EFPs
from several RUNTYP=MAKEFP runs on smaller molecular
fragments, by excluding common regions of overlap.
For example, an EFP for n-octanol can be build from
two MAKEFP runs, on n-pentane and n-pentanol,

```
           CH3CH2CH2CH2-CH2CH2CH2CH2OH
           CH3CH2CH2CH2[-CH3]
                  [CH3]-CH2CH2CH2CH2OH
```

by excluding operlapping regions shown in brackets
from the two EFPs. See J.Phys.Chem.A 105, 3829-3837,
(2001) for more information.

```
NOPATM = array of atoms that define an area to be excluded
         from a DMA ($STONE) during a RUNTYP=MAKEFP run.
         All atomic centers specified, and the midpoints
         of any bonds to them, are excluded as expansion
         points.  The density due to all LMOs primarily
         centered on these atoms are excluded from the DMA
         (see also KMIDPT).  Furthermore, polarizability
         tensors for these LMOs are excluded.

KPOINT = array of "boundary atoms", those atoms that are
         covalently bonded to the atoms given in NOATM.

KMIDPT = flag to indicate whether the density due to bond
         LMOs (and associated expansion points) between
         the NOPATM atoms and the KPOINT atoms are to be
         included in the DMA.  (default = .TRUE.)

NODENS = an array that specifies the atoms for which the
         associated electronic density will be removed
         before the multipole expansion.  This provides an
         EFP with net integer charge. (P.A.Molina, H.Li,
         J.H.Jensen J.Comput.Chem.  24, 1972-1979(2003).

The following keywords relate to the computation of
imaginary frequency dynamic polarizabilities.  This is
useful in the development of the dispersion energy formula
in the EFP2 model, but may also be computed separately, if
wished.

POLDYN = a flag to compute imaginary frequency dependent
         dynamic polarizabilities (alpha), by analytic
         means.  Available only for uncorrelated RHF.
         (default=.FALSE., but .TRUE. if RUNTYP=MAKEFP)

NDPFRQ = number of imaginary frequencies to compute.
         Default=1 for most runs, but=12 if RUNTYP=MAKEFP.

DPFREQ = an array of imaginary frequencies to be used,
         entered as real numbers (absolute values).  The
         default=0.0 for most runs, which is silly, because
         this just computes the normal static dipole
         polarizability!  For RUNTYP=MAKEFP, the program
         uses 12 internally stored values, which serve as
         the roots for a Gauss-Legendre quadrature to
         extract the C6 dispersion coefficients.  Given in
```

```
         atomic units.

For more information, see
    I.Adamovic, M.S.Gordon  Mol.Phys. 103, 379-387(2005).

================================================================


            * * * * * * * * * * * * * * * * * * *
            For hints about localizations, and
            the LCD energy decomposition, see
            the 'further information' section.
            * * * * * * * * * * * * * * * * * * *

================================================================
```

==========

$TRUNCN group (optional, relevant for RHF)

This group controls the truncation of some of the localized orbitals to just the AOs on a subset of the atoms. This option is particularly useful to generate localized orbitals to be frozen when the effective fragment potential is used to partition a system across a chemical bond. In other words, this group prepares the frozen buffer zone orbitals. This group should be used in conjunction with RUNTYP=ENERGY (or PROP if the orbitals are available) and either LOCAL=RUEDNBRG or BOYS, with MOIDON set in $LOCAL.

DOPROJ = flag to activate MO projection/truncation, the default is to skip this (default=.FALSE.)

AUTOID = forces identification of MOs (analogous to MOIDON in $LOCAL). This keyword is provided in case the localized orbitals are already present in $VEC, in which case this is a faster RUNTYP=PROP with LOCAL=NONE job. Obviously, GUESS=MOREAD. (default=.FALSE.)

PLAIN = flag to control the MO tail truncation. A value of .FALSE. uses corresponding orbital projections, H.F.King, R.E.Stanton, H.Kim, R.E.Wyatt, R.G.Parr J. Chem. Phys. 47, 1936-1941(1967) and generates orthogonal orbitals. A value of .TRUE. just sets the unwanted AOs to zero, so the resulting MOs need to go through the automatic orthogonalization step when MOREAD in the next job. (default=.FALSE.)

IMOPR = an array specifying which MOs to be truncated. In most cases involving normal bonding, the options MOIDON or AUTOID will correctly identify all localized MOs belonging to the atoms in the zone being truncated. However, you can inspect the output, and give a list of all MOs which you want to be truncated in this array, in case you feel the automatic assignment is incorrect.
Any orbital not in the truncation set, whether this is chosen automatically or by IMOPR, is left

completely unaltered.

- - -

There are now two ways to specify what orbitals are to be truncated. The most common usage is for preparation of a buffer zone for QM/MM computations, with an Effective Fragment Potential representing the non-quantum part of the system. This input is NATAB, NATBF, ICAPFR, ICAPBF, in which case the $DATA input must be sorted into three zones. The first group of atoms are meant to be treated in later runs by full quantum mechanics, the second group by frozen localized orbitals as a 'buffer', and the third group is to be substituted later by an effective fragment potential (multipoles, polarizabilities, ...). Note that in the DOPROJ=.TRUE. run, all atoms are still quantum atoms.

NATAB = number of atoms to be in the 'ab initio' zone.

NATBF = number of atoms to be in the 'buffer' zone. The program can obtain the number of atoms in the remaining zone by subtraction, so it need not be input.

In case the MOIDON or AUTOID options lead to confused assignments (unlikely in ordinary bonding situations around the buffer zone), there are two fine tuning values.

ICAPFR = array indicating the identity of "capping atoms" which are on the border between the ab initio and buffer zones (in the ab initio zone).

ICAPBK = array indicating the identity of "capping atoms" which are on the border between the buffer and EFP zones (in the effective fragment zone).

See also IXCORL and IXLONE below.

- - -

In case truncation seems useful for some other purpose, you can specify the atoms in any order within the $DATA group, by the IZAT/ILAT approach. You are supposed to give only one of these two lists, probably whichever is

shorter:

IZAT = an array containing the atoms which are NOT in the buffer zone.

ILAT = an array containing the atoms which are in the buffer zone.

The AO coefficients of the localized orbitals present in the buffer zone which lie on atoms outside the buffer will be truncated.

See also IXCORL and IXLONE below.

- - -

The next two values let you remove additional orbitals within the buffer zone from the truncation process, if that is desirable. These arrays can only include atoms that are already in the buffer zone, whether this was defined by NATBF, or IZAT/ILAT. The default is to include all core and lone pair orbitals, not just bonding orbitals, as the buffer zone orbitals.

IXCORL = an array of atoms whose core and lone pair orbitals are to be considered as not belonging to the buffer zone orbitals.

IXLONE = an array of atoms for which only the lone pair orbitals are to be considered as not belonging to the buffer zone orbitals.

The final option controls output of the truncated orbitals to file PUNCH for use in later runs:

NPUNOP = punch out option for the truncated orbitals
= 1 the MOs are not reordered.
= 2 punch the truncated MOs as the first vectors in the $VEC MO set, with untransformed vectors following immediately after. (default)

==========

==========

$ELMOM group (not required)

This group controls electrostatic moments calculation.

The symmetry properties of multipoles are discussed in
A.Gelessus, W.Thiel, W.Weber
J.Chem.Ed. 72, 505-508(1995)

The quadrupole and octopole tensors on the printout are formed according to the definition of Buckingham. Caution: only the first nonvanishing term in the multipole charge expansion is independent of the coordinate origin chosen, which is normally the center of mass.

IEMOM = 0 - skip this property
1 - calculate monopole and dipole (default)
2 - also calculate quadrupole moments
3 - also calculate octopole moments

WHERE = COMASS - center of mass (default)
NUCLEI - at each nucleus
POINTS - at points given in $POINTS.

OUTPUT = PUNCH, PAPER, or BOTH (default)

* * the following are for atomic multipole moments * *

The Cartesian atomic multipole moments printed are a generalization of Mulliken charges, generated by distributing density factors according to the atomic orbitals used. Only the first point is used as an expansion center, so generally only WHERE=COMASS or providing a single point make sense. For details refer to
W.A.Sokalski, R.A.Poirier
Chem.Phys.Lett. 98, 86-92(1983)
K.M.Langner, P.Kedzierski, W.A.Sokalski,
J.Leszczynski J.Phys.Chem.B 110, 9720-9727(2006)

IAMM = 0 - skip generation of Atomic Multipole Moments
n - generate atomic moments up to rank n
The default is n=0, note that n may not exceed 12.

CUM = Flag to accumulate the atomic moments to their

```
        local atom coordinates, if IAMM was selected.
        When .FALSE., the resulting moments are additive
        and sum up to corresponding molecular moments,
        printed by selecting IEMOM.  Setting this flag to
        .TRUE. recombines the atomic moments to their local
        coordinates system, making them invariant of the
        reference frame.  Default=.FALSE.


IEMINT = 0 - skip printing of integrals (default)
         1 - print dipole integrals
         2 - also print quadrupole integrals
         3 - also print octopole integrals
        -2 - print quadrupole integrals only
        -3 - print octopole integrals only

===============================================================
```

==========

$ELPOT group (not required)

This group controls electrostatic potential calculation.

```
IEPOT = 0 skip this property (default)
        1 calculate electric potential

WHERE  = COMASS   - center of mass
         NUCLEI   - at each nucleus (default)
         POINTS   - at points given in $POINTS
         GRID     - at grid given in $GRID
         PDC      - at points controlled by $PDC.

OUTPUT = PUNCH, PAPER, BOTH (default), or NONE
```

This property is the electrostatic potential V(a) felt by a test positive charge, due to the molecular charge density, of both nuclei and electrons. If there is a nucleus at the evaluation point, that nucleus is ignored, avoiding a singularity. If this property is evaluated at the nuclei, it obeys the equation

$$\sum_{\text{nuclei(a)}} Z(a)\cdot V(a) = 2\cdot V(nn) + V(ne).$$

The electronic portion of this property is called the diamagnetic shielding.

==========

```
=============================================================
```

$ELDENS group (not required)

```
This group controls electron density calculation.

IEDEN  = 0 skip this property (default)
       = 1 compute the electron density.

MORB   = The molecular orbital whose electron density is
         to be computed.  If zero, the total density is
         computed.  (default=0)

WHERE  = COMASS   - center of mass
         NUCLEI   - at each nucleus (default)
         POINTS   - at points given in $POINTS
         GRID     - at grid given in $GRID

OUTPUT = PUNCH, PAPER, or BOTH (default)

IEDINT = 0 - skip printing of integrals (default)
         1 - print the electron density integrals

=============================================================
```

==========

$ELFLDG group (not required)

This group controls electrostatic field and electric field gradient calculation.

```
IEFLD  = 0 - skip this property (default)
         1 - calculate field
         2 - calculate field and gradient

WHERE  = COMASS   - center of mass
         NUCLEI   - at each nucleus (default)
         POINTS   - at points given in $POINTS

OUTPUT = PUNCH, PAPER, or BOTH (default)

IEFINT = 0 - skip printing these integrals (default)
         1 - print electric field integrals
         2 - also print field gradient integrals
        -2 - print field gradient integrals only
```

The Hellman-Feynman force on a nucleus is the nuclear charge multiplied by the electric field at that nucleus. The electric field is the gradient of the electric potential, and the field gradient is the hessian of the electric potential. The components of the electric field gradient tensor are formed in the conventional way, i.e. see D.Neumann and J.W.Moskowitz.

```
* * * * * * * * * * * * * * * * * * * *
For conversion factors, and references
see the 'further information' section.
* * * * * * * * * * * * * * * * * * * *
```

==========

$POINTS group (not required)

This group is used to input points at which properties will be computed. This first card in the group must contain the string ANGS or BOHR, followed by an integer NPOINT, the number of points to be used. The next NPOINT cards are read in free format, containing the X, Y, and Z coordinates of each desired point.

==========

$GRID group (not required)

This group is used to input a grid (plane or cube) on which properties will be calculated. This group should be given if WHERE=GRID in $ELPOT or $ELDENS. This output will be in the PUNCH file whenever OUTPUT=PUNCH or BOTH.

```
MODGRD    = 0 orthonormalize the grid vectors
          = 1 normalize the grid vectors
ORIGIN(i) = coordinates of one corner of the grid/cube.
XVEC(i)   = vector from ORIGIN to an adjacent corner "X" of
            the grid (or cube). The XVEC direction need
            not be parallel to the X-axis of the molecule.
YVEC(i)   = vector to the adjacent corner "Y" of grid/cube.
ZVEC(i)   = vector to the adjacent corner "Z" of the cube,
            given if and only if MODGRD=1.
SIZE      = grid increment in all directions (default 0.25)
UNITS     = units of the above five values, it can be
            either ANGS (the default) or BOHR.
GRDPAD    = grid padding, like GRDPAD in $FMOPRP, but
            applied to non-FMO runs. Default: 0, which
            means padding is not used so one must specify
            ORIGIN.
```

Two dimensional grids may be drawn with the graphics program MEPMAP provided with GAMESS. Several programs will accept the 3-dimensional CUBE format.

Note that MacMolPlt draws 2D and 3D density maps without any need to pre-compute them inside GAMESS by this group.

User *must* input orthogonal XVEC/YVEC/ZVEC directions!

==========

==========

$PDC group (relevant if WHERE=PDC in $ELPOT)

This group determines the points at which to compute the electrostatic potential, for the purpose of fitting atomic charges to this potential. Constraints on the fit which determines these "potential determined charges" can include the conservation of charge, the dipole, and the quadrupole.

```
PTSEL  =        determines the points to be used, choose
       GEODESIC to use a set of points on several fused
                sphere van der Waals surfaces, with points
                selected using an algorithm due to Mark
                Spackman.  The results are similar to those
                from the Kollman/Singh method, but are
                less rotation dependent. (default)
         CONNOLLY to use a set of points on several fused
                sphere van der Waals surfaces, with points
                selected using an algorithm due to Michael
                Connolly.  This is identical to the method
                used by Kollman & Singh (see below)
         CHELPG to use a modified version of the CHELPG
                algorithm, which produces a symmetric
                grid of points for a symmetric molecule.

CONSTR = NONE   - no fit is performed.  The potential at
                  the points is instead output according
                  to OUTPUT in $ELPOT.
         CHARGE - the sum of fitted atomic charges is
                  constrained to reproduce the total
                  molecular charge. (default)
         DIPOLE - fitted charges are constrained to
                  exactly reproduce the total charge
                  and dipole.
         QUPOLE - fitted charges are constrained to
                  exactly reproduce the charge, dipole,
                  and quadrupole.
```

Note: the number of constraints cannot exceed the number of parameters, which is the number of nuclei. Planar molecules afford fewer constraint equations, namedly two dipole constraints and three quadrupole constraints,

```
    instead of three and five, respectively.


* * the next 5 pertain to PTSEL=GEODESIC or CONNOLLY * *

VDWSCL = scale factor for the first shell of VDW spheres.
         The default of 1.4 seems to be an empirical best
         value. Values for VDW radii for most elements up
         to Z=36 are internally stored.

VDWINC = increment for successive shells (default = 0.2).
         The defaults for VDWSCL and VDWINC will result
         in points chosen on layers at 1.4, 1.6, 1.8 etc
         times the VDW radii of the atoms.

LAYER  = number of layers of points chosen on successive
         fused sphere VDW surfaces (default = 4)

Note: RUNTYP=MAKEFP's screening calculation changes the
defaults to VDWSCL=0.5 or 0.8 depending on the type of
Stone analysis, VDWINC=0.1, LAYER=25, and MAXPDC=100,000.

NFREQ  = flag for particular geodesic tesselation of
         points.  Only relevant if PTSEL=GEODESIC.
         Options are:
          (10*h + k)  for   {3,5+}h,k tesselations
         -(10*h + k)  for   {5+,3}h,k tesselations
         Of course both nh and nk must be less than 10,
         so NFREQ must lie within the range -99 to 99.
         The default value is NFREQ=30 (=03)

PTDENS = density of points on the surface of each scaled
         VDW sphere (in points per square au).  Relevant
         if PTSEL=CONNOLLY.  Default=0.28 per au squared,
         which corresponds to 1.0 per square Angstrom, the
         default recommended by Kollman & Singh.

   * * * the next two pertain to PTSEL=CHELPG * * *

RMAX   = maximum distance from any point to the closest
         atom.  (default=3.0 Angstroms)

DELR   = distance between points on the grid.
         (default=0.8 Angstroms)
```

```
MAXPDC = an estimate of the total number of points whose
         electrostatic potential will be included in the
         fit. (default=10000)

CENTER = an array of coordinates at which the moments were
         computed.

DPOLE  = the molecular dipole.

QPOLE  = the molecular quadrupole.

PDUNIT = units for the above values.  ANGS (default) will
         mean that the coordinates are in Angstroms, the
         dipole in Debye, and quadrupole in Buckinghams.
         BOHR implies atomic units for all 3.

  Note: it is easier to compute the moments in the
  current run, by setting IEMOM to at least 2 in
  $ELMOM.  However, you could fit experimental data,
  for example, by reading it in here.

=============================================================

     There is no unique way to define fitted atomic
charges.  Smaller numbers of points at which the electro-
static potential is fit, changes in VDW radii, asymmetric
point location, etc. all affect the results.  A useful
bibliography is

U.C.Singh, P.A.Kollman, J.Comput.Chem. 5, 129-145(1984)
L.E.Chirlain, M.M.Francl, J.Comput.Chem. 8, 894-905(1987)
R.J.Woods, M.Khalil, W.Pell, S.H.Moffatt, V.H.Smith,
   J.Comput.Chem. 11, 297-310(1990)
C.M.Breneman, K.B.Wiberg, J.Comput.Chem. 11, 361-373(1990)
K.M.Merz, J.Comput.Chem. 13, 749(1992)
M.A.Spackman, J.Comput.Chem. 17, 1-18(1996)

Start your reading with the last paper shown.
```

==========

$MGC group (note: requires RUNTYP=GRADIENT)

This group requests the Mean Gradient Charge calculation. You can calculate MGC charges or pointwise gradient charges.

MGCHRG	specifies the MGC calculation. You can specify .TRUE. to activate MGC routine. Default is .FALSE.
NPOINT	specifies pointwise Gradient Charge calculations. If NPOINT.gt.0, then pointwise Gradient Charges will be calculated rather than MGC. Default is 0. If NPOINT.gt.0, user should provide the corresponding positions of unit probe using CP.
CP	specifies the positions of unit probe. So CP is an array of positions.

MGC does not support molecular symmetry, so use NOSYM=1 in $CONTRL to turn symmetry off.

See: C. H. Choi, Chem.Phys.Lett. 524, 107-111 (2012).

==========

==========

$RADIAL group (relevant only to atoms)

This input data governs the computation of radial expectation values <r> and <r**2> for atomic orbitals. The atomic wavefunctions can be any SCFTYP except UHF. The atomic calculation should preserve radial degeneracy in p, d, or f shells, so UHF is not allowed, and furthermore, many atoms will require GVB or MCSCF inputs (see the 'Further References' section about doing atomic SCF). It is OK to use core potentials (MCP or ECP) or to apply scalar relativistic effects, so long as the calculation preserves degeneracy 2l+1 in every occupied shell.

One should keep in mind that there is some arbitrariness in how different SCFTYPs canonicalize orbitals, so that individual orbitals may vary, for exactly the same total wavefunction. For example, ROHF orbitals within the doubly occupied set of orbitals change as a function of the A and B canonicalization inputs (see 'Further References'). Similar comments apply to orbitals from GVB or MCSCF.

It is recommended that you do two runs, first to check if radial degeneracy is maintained (equal eigenvalues for all three p, or all five d orbitals). This preliminary run will help count which orbitals lie in degenerate shells, for MEMSH below. The quality of the numerical radial integration can be assessed from its closeness to 1.0. Radial wavefunctions can be printed, as an option. There are no defaults provided for the first three keywords, which are required inputs, if this group is given.

NSHELL - number of atomic shells to be computed

IDEGSH - an array of NSHELL values, giving the degeneracy of each shell (1, 3, 5, or 7)

MEMSH - an array containing the sum of all IDEGSH values, listing the members of each shell.

RMAX - maximum radius to be considered, in Bohr. The default is most appropriate for valence orbitals, which for bottom row elements may extend to five Angstrons (default=10.0). Inner shell orbitals

```
         may require input of a smaller RMAX, to move some
         of the tick marks closer to the nucleus.

NTICKS - radial increment is RMAX/NTICKS, so the default
         step size is 0.01 Bohr (default NTICKS=1001)

PRTRAD - flag to print each shell's radial wavefunction at
         every radial tick mark (default is .FALSE.)
```

The following example uses a basis that is too small to be converged, printing radial expectation values for manganese as 1s=0.0615, 3p=0.9156, 4s=3.4027, and 3d=1.1095:

```
 $contrl scftyp=rohf mult=6 ispher=1 $end
 $guess  guess=huckel norder=1
         iorder(10)=15,10,11,12,13,14 $end
 $basis  gbasis=n31 ngauss=6 $end
 $scf    rstrct=.true. $end
 $radial nshell=4 idegsh(1)=1,3,1,5
         memsh(1)=1,  7,8,9,  10,  11,12,13,14,15 $end
 $data
Mn atom...(4s)2(3d)5...6-S...spherical harmonics
Dnh 2

Mn 25.0
 $end

=============================================================
```

==========

$MOLGRF group (relevant only if you have MOLGRAPH)

This option provides an interface for viewing orbitals through a commercial package named MOLGRAPH, from Daikin Industries. Note that this option uses three disk files which are not defined in the GAMESS execution scripts we provide, since we don't use MOLGRAPH ourselves. You will need to define files 28, 29, 30, as generic names PRGRID, COGRID, MOGRID, of which the latter is passed to MOLGRAPH.

GRID3D = a flag to generate 3D grid data.
(default is .false.).

TOTAL = a flag to generate a total density grid data.
"Total" means the sum of the orbital densities
given by NPLT array. (default is .false.).

MESH = numbers of grids. You can use different numbers
for three axes. (default is MESH(1)=21,21,21).

BOUND = boundary coordinates of a 3D graphical cell. The
default is that the cell is larger than the
molecular skeleton by 3 bohr in all directions.
E.g., BOUND(1)=xmin,xmax,ymin,ymax,zmin,zmax

NPLOTS = number of orbitals to be used to generate 3D grid
data. (default is NPLOTS=1).

NPLT = orbital IDs. The default is 1 orbital only, the
HOMO or SOMO. If the LOCAL option is given in
$CONTRL, localized orbital IDs should be given.
For example, NPLT(1)=n1,n2,n3,...

CHECK = debug option, printing some of the grid data.

If you are interested in graphics, look at the GAMESS web page for information about other graphics packages with GAMESS, particularly MacMolPlt and Avogadro, both are available for all common desktop operating systems.

==========

==========

$STONE group (optional)

This group defines the expansion points for Stone's distributed multipole analysis (DMA) of the electrostatic potential.

The DMA takes the multipolar expansion of each overlap charge density defined by two Gaussian primitives, and translates it from the center of charge of the overlap density to the nearest expansion point. Some references for the method are

A.J.Stone Chem.Phys.Lett. 83, 233-239 (1981)
A.J.Stone, M.Alderton Mol.Phys. 56, 1047-1064(1985)
A.J.Stone J.Chem.Theory and Comput. 1, 1128-1132(2005)

The existence of $STONE input is what triggers the analysis. The first set of lines must appear as the first line after $STONE (enter a blank line if you make no choice), then enter as many choices as you wish, in any order, from the other sets.

BIGEXP <value>	exponents larger than this are treated by the original Stone expansion, and those smaller by a numerical integration. The default is 0.0, meaning no numerical grid. The other parameters are meaningless if BIGEXP remains zero.
NRAD <nrad>	number of radial grid points (default 100)
NANG <nang>	number of angular grid points, choose one of the Lebedev grid values (default 590)
SMOOTH <nbecke>	degree of Becke smoothing (default=2)
SMRAD <nbckrd>	Radii choice, 0=constant, 1=Bragg-Slater, which is the default.

ATOM i name, where

ATOM is a keyword indicating that a particular

```
                atom is selected as an expansion center.
      i         is the number of the atom
      name      is an optional name for the atom. If not
                entered the name will be set to the name
                used in the $DATA input.

-----------------------------------------------------------

ATOMS           is a keyword selecting all nuclei in the
                molecule as expansion points.  No other
                input on the line is necessary.

-----------------------------------------------------------

BONDS           is a keyword selecting all bond midpoints
                in the molecule as expansion points.  No
                other input on the line is necessary.

-----------------------------------------------------------

BOND i j name, where

      BOND      is a keyword indicating that a bond mid-
                point is selected as an expansion center.
      i,j       are the indices of the atoms defining the
                bond, corresponding to two atoms in $DATA.
      name      an optional name for the bond midpoint.
                If omitted, it is set to 'BOND'.

-----------------------------------------------------------

CMASS           is a keyword selecting the center of mass
                as an expansion point.  No other input on
                the line is necessary.

-----------------------------------------------------------

POINT x y z name, where

      POINT     is a keyword indicating that an arbitrary
                point is selected as an expansion point.
      x,y,z     are the coordinates of the point, in Bohr.
      name      is an optional name for the expansion
                point.  If omitted, it is set to 'POINT'.
```

While making the EFPs for QM/MM run, a single keyword QMMMBUF is necessary. Adding additional keywords may lead to meaningless results. The program will automatically select atoms and bond midpoints which are outside the buffer zone as the multipole expansion points.

QMMMBUF nmo, where

QMMMBUF	is a keyword specifying the number of QM/MM buffer molecular orbitals, which must be the first NMO orbitals in the MO set. These orbitals must be frozen in the buffer zone, so this is useful only if $MOFRZ is given.
NMO	is the number of buffer MO-s (if NMO is omitted, it will be set to the number of frozen MOs in $MOFRZ)

==========

The second and third moments on the printout can be converted to Buckingham's tensors by formula 9 of
A.D.Buckingham, Quart.Rev. 13, 183-214 (1959)
These can in turn be converted to spherical tensors by the formulae in the appendix of
S.L.Price, et al. Mol.Phys. 52, 987-1001 (1984)

==========

$RAMAN group (relevant for all SCFTYPs)

This input controls the computation of Raman intensity by the numerical differentiation produre of Komornicki and others. It is applicable to any wavefunction for which the analytic gradient is available, including some MP2 and CI cases. The calculation involves the computation of 19 nuclear gradients, one without applied electric fields, plus 18 no symmetry runs with electric fields applied in various directions. The numerical second differencing produces intensity values with 2-3 digits of accuracy.

This run must follow an earlier RUNTYP=HESSIAN job, and the $GRAD and $HESS inputs from that first job must be given as input. If the $DIPDR is computed analytically by this Hessian job, it too may be read in, if not, the numerical Raman job will evaluate $DIPDR. Once the data from the 19 applied fields is available, the $ALPDR tensor is evaluated. Then the nuclear derivatives of the dipole moment and alpha polarizability will be combined with the normal coordinate information to produce the IR and Raman intensity of each mode.

To study isotopic substitution speedily, provide $GRAD, $HESS, $DIPDR, and $ALPDR inputs, along with the desired atomic masses in $MASS.

The code does not permit semi-empirical or solvation models to be used.

EFIELD = applied electric field strength. The literature suggests values in the range 0.001 to 0.005. (default = 0.002 a.u.)

==========

==========

$COMP group (relevant for all SCFTYPs)

This input defines the parameters for setting up a composite thermochemical method, to evaluate heats of formation. Some literature methods are available, or you can define your own.

```
RMETHD = hardwired composite methods
         G32CCSD is G3(MP2, CCSD(T))
         G4MP2 is G4(MP2)
         G4MP2-6X is G4(MP2)-6x
         CCCA-S4 is ccCA-S4
         CCCA-CCL is ccCA-CC(2,3)
No further input is required with these standard pathways.

GENERAL SETUP FOR OPTIMIZATIONS, HESSIAN, AND SINGLE POINT
ENERGIES:

IOP    = NUMBER OF OPTIMIZATIONS
IHS    = INDEX OF OPTIMIZATION USED FOR HESSIAN CALCULATION
IENE   = NUMBER OF SINGLE POINT ENERGY CALCULATIONS
         TOTAL # ENERGY CALCULATIONS = IOP + IENE

VARIOUS PARAMETERS FOR COMPOSITE METHOD:

CZPSCL = ZERO POINT ENERGY SCALING FACTOR
CENHLC = HIGHER LEVEL CORRECTION ENERGY
IENREF = REFERENCE ENERGY FOR COMPOSITE ENERGY CALCULATION
CXETH  = ADDED THERMAL ENERGY CORRECTION
CXHTH  = ADDED THERMAL ENTHALPY CORRECTION
CXGTH  = ADDED FREE ENERGY CORRECTION
CCXZPE = ADDED ZERO POINT ENERGY
CNUTRL = NEUTRAL ENERGY FOR HEATS OF FORMATION OF IONS AND
         RADICALS
CHEATS = ACCESSES ATOMIC ENERGIES FOR SPECIFIC COMPOSITE
         METHOD:
         G3MP2 is G3(MP2,CCSD(T)) atom energys
         CCCAS4 is ccCA-S4 atom energies
         CCCACCL is ccCA-CC(2,3) atom energies
CSCALE = PERFORMS SCALAR RELATIVISTIC CORRELATIONS (DK,
         ANESC, RESC)
CXTRAP = CBS EXTRAPOLATION TECHNIQUE
         S4 is a 2-POINT EXTRAPOLATION SCHEME
```

```
CGASES = GAS PHASE ENERGY VALUE FOR HEATS OF SOLVATION
         CALCULATION

ARRAYS FOR PARAMETERS USED FOR EACH COMPOSITE CALCULATION:

CDFTTP() = DFT FUNCTIONALS (DFTTYP VALUES)
ICMPLV() = MOLLER PLESSET ORDER NUMBER
CCCTYP() = COUPLED CLUSTER TYPE
CCITYP() = CONFIGURATION INTERACTION TYPE
CCSCF()  = SCF TYPE (RHF, ROHF, UHF)
      (DEFAULT VALUES IN SUBROUTINE 'CLRALL')

BASIS SET OPTION ARRAYS:

ICISPH() = ISPHER SPHERICAL HARMONICS
CGBASS() = GBASIS INTERNAL BASIS SETS
ICNGSS() = NGAUSS VALUES
ICNDFC() = NDFUNC (D POLARIZATION FUNCTION) VALUES
ICNFFC() = NFFUNC (F POLARIZATION FUNCTION) VALUES
ICNPFC() = NPFUNC (P POLARIZATION FUNCTION) VALUES
CDFFSP() = DIFFSP (SP DIFFUSE FUNCTION) OPTION
CDIFFS() = DIFFS  (S DIFFUSE FUNCTION) OPTION

Additional calculation controls:

CETOT()  = ADDED ENERGY VALUES, ADD VALUE TO SKIP A
           CALCULATION (CETOT(1) SKIPS CALCULATION 1)
ICNACR() = NACORE (# ALPHA CORE ELECTRONS)
ICNBCR() = NBCORE (# BETA CORE ELECTRONS)
ICNCOR() = NCORE(NCCFZC)(# CORE ELECTRONS)
IDOPCM() = PCM CONTROL (0 = OFF, 1 = ON)
ICNDER() = MP2 GRADIENT CONTROL, FOR OPTIMIZATIONS
           (0=OFF, 1=ON)
IEXTRP() = SELECTS CETOT() ENERGIES FOR CBS EXTRAPOLATION
CESCF()  = OBTAINS REFERENCE ENERGY FOR CBS EXTRAPOLATION
CECOR()  = OBTAINS CORRELATION ENERGY FOR CBS EXTRAPOLATION

ENERGY CORRECTION CALCULATION (ICENCA - ICENCB):

ICENCA() = HIGHER LEVEL CALCULATION
ICENCB() = LOWER LEVEL CALCULATION

There are three ways to carry out a G3(MP2,CCSD(T))
calculation, which serve to illustrate the above:
```

```
a) select RUNTYP=G3MP2
b) select RUNTYP=COMP and $COMP's RMETHD=G32CCSD
c) select RUNTYP=COMP and explicitly define it:

$COMP
  iop=2, ihs=1, iene=3, icalc=2, ienref=5,
  cenhlc=-0.009170, czpscl=0.8929, cheats=g3mp2,
  icmplv(2)=2,
  icmplv(4)=2,
  icmplv(5)=2,
  ccctyp(3)=ccsd(t),
  icisph(4)=1,
  cgbass(1)=n31,n31,n31,g3l,n31,
  icngss(1)=6,6,6,0,6,
  icndfc(1)=1,1,1,0,1,
  icnacr(2)=0,
  icnbcr(2)=0,
  icnder(2)=1,
  icenca(1)=3,4,
  icencb(1)=5,5
 $END

In case of failures when the program shifts basis sets, try
running without point group symmetry: NOSYM=1 in $CONTRL.

============================================================
```

==========

$NMR group (optional, relevant if RUNTYP=NMR)

This group governs the analytic computation of the NMR shielding tensor for each nucleus, using the Gauge Invariant Atomic Orbital (GIAO) method, also known as London orbitals. The most useful input values are the first three printing options. The wavefunction must be RHF, the atomic basis set may be spdfg, the EFP model may be used to include solvent effects, and the McMurchie-Davidson integrals used are not fast.

ANGINT = a flag to control the evaluation of the perturbed two-electron integrals by increasing the angular momentum on the unperturbed 2e- integrals. With this selected, only two passes through the 2e- NMR integral code are needed. Otherwise, six slow passes are needed, and option meant only for debugging purposes. (default=.TRUE.)

INMEM A flag to carry all integrals in memory. If selected, the calculation will require several multiples of NAO**4. By default, the calculation will require space on the order of NATOMS*NAO**2, where NAO is the basis set dimension. This is useful for debugging. (default=.FALSE.)

The rest are print flags, in increasing order of the amount of output created, as well as decreasing order of interest. The default for all of these options is .FALSE.

PDIA Print diamagnetic term of the shielding tensor.

PPARA Print paramagnetic term of the shielding tensor.

PEVEC Print eigenvectors of asymmetric shielding tensor.

PITER Print iteration data for the formation of the three first-order density matrices.

PRMAT Print the three first-order perturbed density matrices, the three first-order H matrices for

```
         each nucleus, the unperturbed density matrix, and
         the nine second-order H matrices for each nucleus.

POEINT   Print all one-electron integrals.

PTEINT   Print the perturbed two-electron integrals.

TEDBG    Print VAST amounts of debugging information for
         the McMurchie-Davidson two-electron intgrals.
         Should only be used for the smallest test jobs.

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```

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$MOROKM group (relevant if RUNTYP=EDA)

This performs an analysis of the energy contributions to dimerization (or formation of larger clusters of up to ten monomers), according to the Morokuma-Kitaura and/or Reduced Variational Space schemes. The analysis is limited to closed shell RHF monomers. In other words, the monomers should be distinct molecular species: avoid breaking chemical bonds! For more general energy decompositions, see the $LMOEDA input group. See also PIEDA in the FMO codes.

Solvation models are not supported.

MOROKM = a flag to request Morokuma-Kitaura decomposition. (default is .TRUE.)

RVS = a flag to request "reduced variation space" decomposition. This differs from the Morokuma analysis. One or the other or both may be requested in the same run. (default is .FALSE.)

Generally speaking, RVS handles non-orthogonality of monomers better. When diffuse functions are used, the MOROKM analysis sometimes fails, but RVS will work.

BSSE = a flag to request basis set superposition error be computed. You must ensure that CTPSPL is selected. This option applies only to MOROKM decompositions, as a basis superposition error is automatically generated by the RVS scheme. This is not the full Boys counterpoise correction, as explained in the reference. (default is .FALSE.)

* * *

The inputs here control how the RHF supermolecule, whose coordinates are given in the $DATA input group, is divided into two or more monomers.

IATM = An array giving the number of atoms in each of the monomer. Up to ten monomers may be defined. Your input in $DATA must have all the atoms in

the first monomer defined before the atoms in the second monomer, before the third monomer... The number of atoms belonging to the final monomer can be omitted. There is no sensible default for IATM, so don't omit it from your input.

ICHM = An array giving the charges of the each monomer. The charge of the final monomer may be omitted, as it is fixed by ICH in $CONTRL, which is the total charge of the supermolecule. The default is neutral monomers, ICHM(1)=0,0,0,...

EQUM = an array to indicate all monomers are equivalent by symmetry (in addition to containing identical atoms). If so, which is not often true, then only the unique computations will be done. (default is .FALSE.,.FALSE., ...)

* * *

CTPSPL = a flag to decompose the interaction energy into charge transfer plus polarization terms. This is most appropriate for weakly interacting monomers. (default is .TRUE.)

CTPLX = a flag to combine the CT and POL terms into a single term. If you select this, you might want to turn CTPSPL off to avoid the extra work that that decomposition entails, or you can analyze both ways in the same run. (default is .FALSE.)

RDENG = a flag to enable restarting, by reading the lines containing "FINAL ENERGY" from a previous run. The $EMORO group is single lines read under format A16,F20.10 containing the energies, and a card $END to complete. The 16 chars = anything. (default is .FALSE.)

==========

The present implementation has some quirks:

1. The initial guess of the monomer orbitals is not controlled by $GUESS. The program first looks for a $VEC1, $VEC2, ... group for each monomer. The orbitals must be

obtained for the identical coordinates which that monomer has within the supermolecule. If any $VECn groups are found, they will be MOREAD. If any are missing, the guess for that monomer will be constructed by HCORE. Check your monomer energies carefully! The initial guess orbitals for the supermolecule are formed from a block diagonal matrix containing the monomer orbitals.
2. The use of symmetry is turned off internally.
3. Spherical harmonics (ISPHER=1) may not be used.
4. There is no direct SCF option. File ORDINT will be a full C1 list of integrals. File AOINTS will contain whatever subset of these is needed for each particular decomposition step. So extra disk space is needed compared to RUNTYP=ENERGY.
5. This run type applies only to ab initio RHF treatment of the monomers. To be quite specific: this means that DFT (which involves a grid, not just integrals) will not work, nor will MOPAC's approximated 2e- integrals
6. This kind of calculation will run in parallel.

Quirks 1, 3 and 4 can be eliminated by using PIEDA if only two monomers are present. For more monomers PIEDA results will slightly differ. PIEDA is a special case of FMO, q.v.

References:

C.Coulson in "Hydrogen Bonding", D.Hadzi, H.W.Thompson, Eds., Pergamon Press, NY, 1957, pp 339-360.
C.Coulson Research, 10, 149-159 (1957).
K.Morokuma J.Chem.Phys. 55, 1236-44 (1971).
K.Kitaura, K.Morokuma Int.J.Quantum Chem. 10, 325 (1976).
K.Morokuma, K.Kitaura in "Chemical Applications of Electrostatic Potentials", P.Politzer,D.G.Truhlar, Eds. Plenum Press, NY, 1981, pp 215-242.
The method coded is the newer version described in the 1976 and 1981 papers. In particular, note that the CT term is computed separately for each monomer, as described in the words below eqn. 16 of the 1981 paper, not simultaneously.

Reduced Variational Space:
W.J.Stevens, W.H.Fink, Chem.Phys.Lett. 139, 15-22(1987).

A comparison of the RVS and Morokuma decompositions can be found in the review article: "Wavefunctions and Chemical Bonding" M.S.Gordon, J.H.Jensen in "Encyclopedia of

Computational Chemistry", volume 5, P.V.R.Schleyer, editor,
John Wiley and Sons, Chichester, 1998.

BSSE during Morokuma decomposition:
R.Cammi, R.Bonaccorsi, J.Tomasi
Theoret.Chim.Acta 68, 271-283(1985).

The present implementation:
"Energy decomposition analysis for many-body interactions,
 and application to water complexes"
W.Chen, M.S.Gordon J.Phys.Chem. 100, 14316-14328(1996)

==========

$LMOEDA group (relevant if RUNTYP=EDA)

This group governs the Localized Molecular Orbital Energy Decomposition Analysis, which is capable of more sophisticated treatment of "monomers" than the Morokuma or RVS schemes (see $MOROKM). For example, the wavefunctions of the monomers may be RHF, ROHF, or UHF, the DFT counterparts of each of these, the MP2 counterparts of each of these, or CCSD and CCSD(T) for RHF and ROHF references. Furthermore, division of the system into "monomers" can involve splitting chemical bond pairs, as the MMULT example below shows.

If one or more monomers are open shell, to be treated by ROHF, use SCFTYP=ROHF in $CONTRL. Whenever a monomer has an even number of electrons, so that its MMULT=1 below, SCFTYP=ROHF (or UHF) automatically reduces to RHF on that monomer. Note that open shell monomers sometimes have more than one possible electron occupancy (for example, oxygen atom can fill 3 p orbitals by 4 electrons in various ways), in which case the energy decomposition isn't unique.

CMOEDA = a flag with default .TRUE. to request canonical molecular orbital energy decomposition analysis (CMOEDA), which gives identical intermolecular interaction energy terms as LMOEDA, but different intramolecular electron-electron exchange and electron-electron repulsion energies. The print out is slightly different from LMOEDA. The 2009 paper describes a general molecular orbital (i.e. Hartree-Fock) based EDA method for intermolecular interaction analysis that is independent of the choice of CMO or any types of LMO.

MATOM = an array giving the number of atoms in each monomer. Up to ten monomers may be defined. Your input in $DATA must have all the atoms in the first monomer defined before the atoms in the second monomer, before the third monomer etc. The sum of the MATOM array must be equal to the total number in the supermolecule.

```
MCHARG = an array giving the charge of each monomer.
         Up to ten monomers may be defined. The sum of
         the charges in the monomers must be equal to
         the total charge of the supermolecule.

MMULT  = an array giving the multiplicity of each
         monomer. Up to ten monomers may be defined.
         A positive integer means alpha spin, a negative
         integer means beta spin. For example, if an
         ethane molecule is separated into two neutral
         CH3 groups, MMULT(1)=2,-2 or MMULT(1)=-2,2.

SUPBAS = a flag to request Boys and Bernardi style
         counterpoise method for correcting basis set
         superposition errors.  (default is .TRUE.).
         Usually it works well with Hartree-Fock and
         MP2 and coupled cluster methods, but less well
         with DFT methods due to SCF divergent problems.

The paper describing this method is
    P.Su, H.Li  J.Chem.Phys. 131, 014102/1-15(2009)

Notes:
1. scalar relativistic effects can be handled by ECP or
MCP, but at present, all electron treatment by RELWFN is
not enabled.
2. the initial guess should be HCORE, as there is no option
at present to read monomer orbitals.

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$QMEFP group (relevant for RUNTYP=QMEFPEA)

This run type prints a detailed breakdown of QM/EFP1 and EFP1/EFP1 interaction energies, for combined quantum mechanics/effective fragment potential (QM/EFP) systems. The run first performs a gas phase QM calculation, and then in a second stage, includes the explicit EFP1 solvent molecules. Some methods (any SCFTYP or ground state DFT) permit a a fully self-consistent interaction of the QM and EFP particles. Otherwise, any QM calculation that supports EFP runs and also generates the QM density matrix may be used to obtain the "method 2" interaction energy. Certain non-variational runs must therefore select as .TRUE. the appropriate QM density matrix evaluation: see MPPRP in $MP2, TDPRP in $TDDFT, CCPRP in $CCINP, or CCPRPE in $EOM. Note that calculations for which the QM density is not available cannot be analyzed here, although "method 1" energies can be obtained (by RUNTYP=ENERGY) for other cases, such as the triples corrected CC methods.

Very often, this entire input group is omitted, as the inputs are related to restarts. One very good reason for doing two steps is in case the EFP solvation changes the order of the excited states, so that two different IROOT values must be given to specify the target state.

STEP1 is a flag requesting the gas phase step be run, but note that the EFP particles must be present in the input file's $EFRAG.

STEP2 is a flag requesting the QM+EFP step be run. the default for both is .TRUE. so that the full results are obtained in a single run.

In case STEP1 is .FALSE., three restart data (which may be found in the PUNCH output file) must be given for the second step:

STOTAL total QM energy, without EFP molecules

EMULT expectation value of the QM/EFP electrostatics

```
        for the isolated solute.

EREM    expectation value of the QM/EFP remainder term,
        which is largely exchange repulsion, for the
        isolated solute.


Those QM methods which are not based on fully self-
consistent solutions of the QM/EFP interaction Hamiltonian
(namely TDDFT, CIS, MP2, CCSD, EOM-CCSD) provide results
which include the EFP's perturbation by the correlated
density, and/or a particular excited state's density.  This
approach is termed "Method 2" in the following references:

1. P.Arora, L.V.Slipchenko, S.P.Webb, A.DeFusco, M.S.Gordon
   J.Phys.Chem.A 114, 6742-6750(2010)
2. A.DeFusco, J.Ivanic, M.W.Schmidt, M.S.Gordon
   J.Phys.Chem.A 115, 4574-4582(2011)

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$FFCALC group (relevant for RUNTYP=FFIELD)

This group permits the study of the influence of an applied electric field on the wavefunction. The most common finite field calculation applies a sequence of fields to extract the linear polarizability and the first and second order hyperpolarizabilities (static alpha, beta, and gamma tensors). The method is general, because it relies on finite differencing of the energy values, and so works for all ab initio wavefunctions. If the dipole moments are available (true for SCF or CI functions, and see MPPROP in $MP2), the same tensors are formed by differencing the dipoles, which is more accurate. Some idea of the error in the numerical differentiations can be gleaned by comparing energy based and dipole based quantities.

For analytic computation of static polarizabilities alpha, beta, and gamma (as well as frequency dependent NLO properties), for closed shell cases, see $TDHF and $TDHFX. For analytic computation of the static polarizability alpha, see POLAR in $CPHF.

The standard computation obtains the polarizabilities, by double numerical differentiation. See ONEFLD to apply a single electric field, but for a more general approach to applied static fields, see $EFIELD.

```
OFFDIA = .TRUE. computes the entire polarizability tensors,
                which requires a total of 49 wavefunction
                evaluations (some of gamma is not formed).
       = .FALSE. forms only diagonal components of the
                polarizabilities, using 19 wavefunctions.
                The default is .TRUE.

ESTEP         = step size for the applied electric field
                strength, 0.01 to 0.001 is reasonable.
                (default=0.001 a.u.)
```

The next parameters pertain to applying a field in only one direction:

ONEFLD = flag to apply one field (default=.FALSE.)

SYM = a flag to specify when the field to be applied does not break the molecular symmetry. Since most fields do break the nuclear point group symmetry, the default is .FALSE.

EFIELD = an array of the three x,y,z components of the single applied field.

* * *

LOCHYP = a flag to perform a localized orbital analysis of the alpha, beta, and gamma polarizabilities. See $LOCAL for similar analyses of the energy, multipole moments, or alpha polarizability. References for this keyword are given below.

Finite field calculations require large basis sets, and extraordinary accuracy in the wavefunction. To converge the SCF to many digits is sometimes problematic, but we suggest you use the input to increase integral accuracy and wavefunction convergence, for example

```
$CONTRL ICUT=20 ITOL=30 $END
$SCF    CONV=1d-7 FDIFF=.FALSE. $END
```

Examples of fields that do not break symmetry are a Z-axis field for an axial point group which is not centrosymmetric (i.e. C2v). However, a field in the X or Y direction does break the C2v symmetry. Application of a Z-axis field for benzene breaks D6h symmetry. However, you could enter the group as C6v in $DATA while using D6h coordinates, and regain the prospect of using SYM=.TRUE. If you wanted to go on to apply a second field for benzene in the X direction, you might want to enter Cs in $DATA, which will necessitate the input of two more carbon and hydrogen atom, but recovers use of SYM=.TRUE.

References:

J.E.Gready, G.B.Bacskay, N.S.Hush

```
     Chem.Phys.  22, 141-150(1977)
   H.A.Kurtz, J.J.P.Stewart, K.M.Dieter
     J.Comput.Chem.  11, 82-87(1990).

polarizability analysis:
   S.Suehara, P.Thomas, A.P.Mirgorodsky, T.Merle-Mejean,
   J.C.Champarnaud-Mesjard, T.Aizawa, S.Hishita,
   S.Todoroki, T.Konishi, S.Inoue
     Phys.Rev.B 70, 205121/1-7(2004)
   S.Suehara, T.Konishi, S.Inoue
     Phys.Rev.B 73, 092203/1-4(2006)

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$TDHF group (relevant for SCFTYP=RHF if RUNTYP=TDHF)

This group permits the analytic calculation of various static and/or frequency dependent polarizabilities, with an emphasis on important NLO properties such as second and third harmonic generation. The method is programmed only for closed shell wavefunctions, at the semi-empirical or ab initio level. Ab initio calculations may be direct SCF, or parallel, if desired, except INIG=2.

For a more general numerical approach to the static properties, see $FFCALC. For additional closed shell dynamic polarizabilities and spectra, see $TDHFX. To compute the hyperpolarizability for closed shell DFT, or to use fully general frequency combinations, see TDDFT=HPOL. There is a summary of all possible different types of polarizability computations in the 4th manual chapter.

NFREQ = Number of frequencies to be used. (default=1)

FREQ = An array of energy values in atomic units. For example: if NFREQ=3 then FREQ(1)=0.0,0.1,0.25. By default, only the static polarizabilities are computed. (default is freq(1)=0.0)

The conversion factor from wavenumbers to Hartree is to divide by 219,474.6. To convert a wavelength to Hartree, compute FREQ=45.56/lamda, lambda in nm.

MAXITA = Maximum number of iterations for an alpha computation. (default=100)

MAXITU = Maximum number of iterations in the second order correction calculation. This applies to iterative beta values and all gammas. (default=100)

DIIS = use the DIIS extrapolation using residual induced Fock matrix (default=.TRUE.).

MAXDII = the maximum number of Fock matrices to be used in DIIS extrapolation (default=50).

```
ATOL   = Tolerance for convergence of first-order results.
         (default=1.0d-05)

BTOL   = Tolerance for convergence of second-order results.
         (default=1.0d-05)

RETDHF = a flag to choose starting points for iterative
         calculations from best previous results.
         (default=.true.)


* * * the following NLO properties are available  * * *

    Note: alpha polarizabilities are always calculated.

INIB   = 0 turns off all beta computation (default)
       = 1 calculates only noniterative beta
       = 2 calculate iterative and noniterative beta
           The next flags allow further BETA tuning

BSHG   = Calculate beta for second harmonic generation.

BEOPE  = Calculate beta for electrooptic Pockels effect.

BOR    = Calculate beta for optical rectification.

INIG   = 0 turns off all gamma computation (default)
       = 1 calculates only noniterative gamma
       = 2 calculate iterative and noniterative gamma
           The next flags allow further GAMMA tuning

GTHG   = Calculate gamma for third harmonic generation.

GEFISH = Calculate gamma for electric-field induced
         second harmonic generation.

GIDRI  = Calculate gamma for intensity dependent
         refractive index.

GOKE   = Calculate gamma for optical Kerr effect.
```

These will be computed only if a nonzero energy (FREQ) is requested. The default for each flag is .TRUE., and they may be turned off individually by setting some .FALSE. Note however that the program determines the best way to

calculate them. For example, if you wish to have the SHG results but no gamma results are needed, the SHG beta will be computed in a non-iterative way from alpha(w) and alpha(2w). However if you request the computation of the THG gamma, the second order U(w,w) results are needed and an iterative SHG calculation will be performed whether you request it or not, as it is a required intermediate.

Only the following combinations make sense:

INIB	INIG	giving FREQ(1)=0.0,0.1	e.g. w=0.1
0	0	static alpha,	a(w)
1	0	static alpha,beta	a(w),a(2w)
		noniterative b(OR), b(EOPE), b(SHG)	
2	0	static alpha,beta	a(w),a(2w)
		noniterative b(OR), b(EOPE), b(SHG)	
		iterative b(OR), b(EOPE), b(SHG)	
2	1	static alpha,beta,gamma	a(w),a(2w)
		iterative b(OR), b(EOPE), b(SHG)	
		noniterative g(THG), g(EFISH),	
		g(IDRI), g(OKE)	
2	2	static alpha,beta,gamma	a(w),a(2w)
		iterative b(OR), b(EOPE), b(SHG)	
		noniterative g(THG), g(EFISH),	
		g(IDRI), g(OKE)	
		iterative static gamma, g(OKE),	
		g(THG), g(EFISH),	
		g(IDRI), g(DC-OR)	

This is a quirky program:

1. INIG=2 only runs in serial, and only runs with AO integrals stored on disk.
2. ISPHER=1 may not be chosen.
3. INIB=1 and INIB=2 print the same components for OR, OPE, SHG, but different totals from the whole tensor. It is not clear which is correct.
4. units are not well specified on the output!

References:

for static polarizabilities,
G.J.B.Hurst, M.Dupuis, E.Clementi
J.Chem.Phys. 89, 385-395(1988)

for dynamic polarizabilities,

S.P.Karna, M.Dupuis J.Comput.Chem. 12, 487-504 (1991).
P.Korambath, H.A.Kurtz, in "Nonlinear Optical Materials",
ACS Symposium Series 628, S.P.Karna and A.T.Yeates, Eds.
pp 133-144, Washington DC, 1996.

Review: D.P.Shelton, J.E.Rice, Chem.Rev. 94, 3-29(1994).

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$TDHFX group (relevant for SCF=RHF if RUNTYP=TDHFX)

This group permits the analytical determination of static and/or frequency dependent polarizabilities and hyperpolarizabilities (alpha, beta, and gamma), as well as their first- and second-order geometrical derivatives (of alpha and beta). This permits the prediction of dynamic (nonresonant) Raman and hyper-Raman spectra, yielding both intensities and depolarizations. The method is only available for closed shell systems (RHF).

For other polarizability options, see $FFCALC and $TDHF. For ordinary Raman spectra, see $RAMAN.

You must not use point group symmetry in this kind of calculation (except to enter the molecule's structure), so provide NOSYM=1. Since the derivative level is quite high, it is a good idea to converge the SCF problem crisply, CONV=1.0D-6. These options are not forced by the RUNTYP, so please use explicit input.

The $TDHFX group acts as a script. Each keyword must be on a separate line, terminated by a $END. The available keywords are gathered into 3 sets. Those belonging to the first set must appear before the second set, which must appear before the third set.

Set 1:

Here is a list of keywords that specifies the number of parameters (electric fields and geometrical distortions) that will be taken into account in the computations.

ALLDIRS = compute the responses for all the electric field directions (x,y,z).

DIR idir = compute the responses for one electric field specific direction:
x(idir=1), y(idir=2) and z(idir=3).

USE_C = do the computation in Cartesian coordinates.

USE_Q = do the computation in normal coordinates.

The default is ALLDIRS and USE_C.

Set 2:

The following two keywords must be specified before any computation that requires vibrational frequencies or normal modes of vibration:

FREQ = compute the normal modes and the harmonic vibrational frequencies. Do a HESSIAN job.

FREQ2 = same as FREQ but store the second derivative of the monoelectronic Hamiltonian. Required if you want to determine geometrical second-order derivatives of properties.

Set 3:

The following keywords are related to the generalized iterative method to solve TDHF mixed derivative equations. They can be inserted anywhere in the $TDHFX group and change the behavior of the generalized iterative method for any of the following tasks that might be requested.

DIIS = Use the DIIS method. This is the default method.

NOACCEL = Do not use any accelerating method.

ITERMAX imax = Specify the maximum number of iterations to obtain the converged solution. Default=100.

CONV threshold = the threshold convergence criterion for the U response matrices. Default=1E-5.

Below are the keywords to select a particular computation. The xx_NI version will call a non-iterative procedure.

The laser energy (w) must be given in Hartree. Divide by 219,474.6 to convert a frequency in wavenumbers (cm-1) to a photon energy in Hartree. Wavelength (in nm) is 45.56/w, when w is in Hartree. Static polarizabilities may be obtained from w=0.0.

MU = compute the dipole moment.

```
ALPHA w =
    compute the dynamic polarizability:
          alpha(-w;w).

BETA w1 w2 / BETA_NI w1 w2 =
    compute the dynamic first hyperpolarizability:
          beta(-w1-w2;w1,w2).

GAMMA w1 w2 w3 / GAMMA_NI w1 w2 w3 =
    compute the dynamic second hyperpolarizability:
          gamma(-w1-w2-w3;w1,w2,w3).

POCKELS w / POCKELS_NI w =
     compute electro-optic Pockels effect: beta(-w;w,0).

OR w / OR_NI w =
     optical rectification: beta(0;w,-w).

SHG w / SHG_NI w =
     second harmonic generation: beta(-2w;w,w).

KERR w / KERR_NI w =
     DC Kerr effect: gamma(-w;w,0,0).

ESHG w / ESHG_NI w =
     electric field induced 2nd harm gen: gamma(-2w;w,w,0).

THG w / THG_NI w =
     third harmonic generation: gamma(-3w;w,w,w).

DFWM w / DFWM_NI w =
     degenerate four wave mixing gamma(-w;w,-w,w).

See the review
    D.P.Shelton, J.E.Rice  Chem.Rev. 94, 3-29(1994)
for more information on the quantities just above.  The
next options are nuclear derivatives of some of the above.

DMDX_NI =
     compute the dipole derivative matrix,
     the geometrical first derivative of MU.

DADX w / DADX_NI w =
     compute the polarizability derivative matrix, the
```

```
     geometrical first-order derivative of alpha(-w;w).

DBDX w1 w2 / DBDX_NI w1 w2 =
     compute the geometrical first-order derivative
     of beta(-w1-w2;w1,w2).

D2MDX2_NI =
     compute geometrical second derivatives of MU

D2ADX2_NI w =
     compute geometrical second derivatives of alpha(-w;w).

D2BDX2_NI w1 w2 =
     geometrical second derivatives of beta(-w1-w2;w1,w2).

The next two keywords automatically select paths through
the package generating the required intermediates (both
polarizabilities and their nuclear derivatives) to form
spectra.  The most efficient path through the program will
be selected automatically.

RAMAN w = Summarize the Raman responses in a table, and if
          necessary, compute the geometrical first-order
          derivatives of alpha(-w;w).

HRAMAN w = Summarize the hyper-Raman responses in a table,
           and if necessary, compute the geometrical first-
           order derivatives of beta(-2w;w,w).

The following keywords permit the deletion of disk files
associated with the set of frequencies w1,w2,...

FREE w1
FREE w1 w2
FREE w1 w2 w3

Below is an example of a TDHFX group:

$TDHFX
  ALLDIRS
  USE_Q
  FREQ
  DIIS
  ITERMAX 100
  CONV 0.1E-7
```

```
  HRAMAN 0.02
  FREE 0.02
  FREE 0.02 0.02
  HRAMAN 0.03
$END
```

References:

"Time Dependent Hartree-Fock schemes for analytic evaluation of the Raman intensities"
O.Quinet, B.Champagne J.Chem.Phys. 115, 6293-6299(2001).

"Analytical TDHF second derivatives of dynamic electronic polarizability with respect to nuclear coordinates. Application to the dynamic ZPVA correction."
O.Quinet, B.Champagne, B.Kirtman
J.Comput.Chem. 22, 1920-1932(2001).

"Analytical time-dependent Hartree-Fock schemes for the evaluation of the hyper-Raman intensities"
O.Quinet, B.Champagne J.Chem.Phys. 117, 2481-2488(2002).
errata: JCP 118, 5692(2003)

"Analytical time-dependent Hartree-Fock evaluation of the dynamically zero-point averaged (ZPVA) first hyperpolarizability"
O.Quinet, B.Kirtman, B.Champagne
J.Chem.Phys. 118, 505-513(2003).

Computer quirks:

1. This package uses file numbers 201, 202, ... but some compilers (chiefly g77) may not support unit numbers above 99. The remedy is to use a different computer or compiler.

2. If you experience trouble running this package under AIX, degrade the optimization of subroutine JDDFCK in hss2b.src, by placing this line

```
    @PROCESS OPT(2)
```

immediately before JDDFCK, recompile hss2b, and relink.

==========

==========

$EFRAG group (optional)

The Effective Fragment Potential (EFP) is a potential extracted from rigorous quantum mechanics, permitting the treatment of solvent molecules (or other types of subsystems) with a potential. There are two models, EFP1 and EFP2, with more accurate physics in the latter. For more information, see chapter 4 of this manual.

EFP1 calculations are typically limited to a QM system with water molecules, the latter modeled by RHF-based or DFT-based potentials which are built into the program. The following EFP1/QM calculations are possible:

QM/EFP1		method1	method2	SCF
RHF (and DFT)	gradient			x
UHF (and DFT)	gradient			x
ROHF(and DFT)	gradient			x
MP2(RHF/UHF/ROHF)	gradient	x	x	
CCSD	energy	x	x	
CCSD(T)	energy	x		
CR-CCL	energy	x		
EOM-CCSD	energy	x	x	
CR-EOML	energy	x		
CITYP=CIS (only)	gradient	x	x	
TDDFT(RHF)	gradient	x	x	
GVB	gradient			x
MCSCF	gradient			x

Here, SCF means the QM calculation and the EFP particle's polarizability terms are made fully self-consistent. Otherwise, the QM density felt by the EFP particles is that of the reference (ground) state, termed "method 1". A more accurate and detailed energy calculation is possible when the QM's density is available for a specific correlation treatment and/or a specific excited state. Such "method 2" calculations are available only for RUNTYP=QMEFPEA. The "method 1" calculations can be used for any relevant run type using the energy or analytic nuclear gradients, as indicated. For example, after MP2 geometry optimization, numerical differentiation can produce solvated MP2-level frequencies.

EFP2 calculations should use COORD=FRAGONLY at the present time, as the QM/EFP2 interaction terms are

currently under active development. The programming for EFP2/EFP2 interactions is completed. See RUNTYP=MAKEFP to create EFP2 potentials.

In most cases, the entire EFP1, QM/EFP1, or EFP2 system can be embedded in a PCM continuum (see $PCM).

This group gives the name and position of one or more effective fragment potentials. It consists of a series of free format card images, which may not be combined onto a single line! The position of a fragment is defined by giving any three points within the fragment, relative to the ab initio system defined in $DATA, since the effective fragments have a frozen internal geometry. All other atoms within the fragment are defined by information in the $FRAGNAME input group.

-1- a line containing one or more of these options:

If you choose more options than are able to be fit on a single 80 character line, type an > character to continue onto the next line.

If you do not choose any of these options, input a blank line to accept defaults.

COORD	=CART	selects use of Cartesians coords to define the fragment position at line -3-. (default)
	=INT	selects use of Z-matrix internal coordinates at line -3-.
POLMETHD	=SCF	indicates the induced dipole for each fragment due to the ab initio electric field and other fragment fields is updated only once during each SCF iteration.
	=FRGSCF	requests microiterations during each SCF iteration to make induced dipoles due to ab initio and other fragment fields self consistent among the fragments. (default) Both methods converge to the same

dipolar interaction.

POSITION=OPTIMIZE Allows full optimization within the ab initio part, and optimization of the rotational and translational motions of each fragment. (default)

=FIXED Allows full optimization of the ab initio system, but freezes the position of the fragments. This makes sense only with two or more fragments, as what is frozen is the fragments' relative orientation. FIXED may be used with RUNTYP being OPTIMIZE, SADPOINT, HESSIAN and IRC.

=EFOPT the same as OPTIMIZE, but if the fragment gradient is large, up to 5 geometry steps in which only the fragments move may occur, before the geometry of the ab initio piece is relaxed. This may save time by reusing the two electron integrals for the ab initio system.

NBUFFMO = n First n orbitals in the MO matrix are deemed to belong to the QM/MM buffer and will be excluded from the interaction with the EFP region. This makes sense only if these first MOs are frozen via the $MOFRZ.

The next few inputs apply periodic boundary conditions, which is only possible if the system contains only EFP particles, with no ab initio atoms. The default is to use the minimum image convention, for all terms in the potentials, but see also the $EWALD input group in order to perform the long range electrostatic interactions in a more accurate manner. You may choose no more than one of the possible sets of cutoffs, with the switching function SWR1/SWR2 being the most physically reasonable.

XBOX, YBOX, ZBOX = dimensions of the periodic box, which must be given in Angstroms. If these sizes are omitted, the simulation is an isolated cluster.

```
     SWR1, SWR2        = distance cutoffs for the switching
                         function that gradually drops the
                         interactions from full strength at
                         SWR1 to zero at SWR2.  Choose
                         SWR2 <= min(XBOX/2,YBOX/2,ZBOX/2)
                         and SWR1 <= SWR2 (typically 80%),
                         to cut off interactions within a
                         single box.  In Angstrom

     RCUT                a radial cutoff, implemented as a
                         step function, which should be
                         chosen like SWR2.  In Angstrom

     XCUT, YCUT, ZCUT  = cutoffs (as step functions) beyond
                         which effective fragment potential
                         interactions are not computed,
                         XCUT <= XBOX/2, etc.  Angstroms
```

For a simulation of 64 CCl4 molecules, PBC input might be

```
    xbox=21.77 ybox=21.77 zbox=21.77 swr1=8.0 swr2=10.0
```

Box sizes are typically chosen to give a correct value for the density of the system.

The following turn off selected terms in the potentials, even if data for the term is found in the various $FRAGNAME input groups. These keywords are standalone strings, without a value assigned to them. They allow data from potentials generated by MAKEFP runs to be kept in the $FRAGNAME, for possible future use. The first two are of interest in production runs, while the others are primarily meant for debugging purposes, as the latter terms are normally quite large.

```
     NOCHTR    = switch off charge transfer in EFP2
     NODISP    = switch off dispersion in EFP2
     NOEXREP   = switch off exchange repulsion (EFP1/EFP2)
     NOPOL     = switch off polarization (implies NOPSCR)
     NOPSCR    = switch off polarization screening, only
```

The following parameters are related to screening of some terms in the potentials, when fragments are at close distances. Note that they are relevant only to EFP2 runs. Prior to May 2009, the defaults were

```
      ISCRELEC=0 ISCRPOL=0 ISCRDISP=0
```

```
at which time the defaults were changed to
      ISCRELEC=0 ISCRPOL=1 ISCRDISP=1
If you need to reproduce results or continue an ongoing set
of computations, simply input the old defaults.

   ISCRELEC =   fragment-fragment electrostatic screening,
                a correction for "charge penetration":
                   E(elec) = E(multipoles) + E(chg.pen.)
            = 0 damping by various formulae is controlled
                by SCREEN1, SCREEN2, or SCREEN3 input
                sections in the $FRAGNAME input(s).  If
                none are found, there will be no charge
                penetration screening of electrostatics.
                (default)
            = 1 use an overlap based damping correction
                   E(chg.pen.)= -2(S**2/R)/sqrt(-2ln|S|)
                to the classical multipole energy.  Since
                the overlap integrals used here, as well as
                in ISCRDISP must be evaluated as part of
                the exchange repulsion energy, there is
                essentially no overhead for selecting this.

   ISCRPOL  =   fragment-fragment polarization screening.
            = 0 damping is controlled by POLSCR sections in
                the $FRAGNAME inputs.  If not found, there
                will be no screening.  If POLSCR is found,
                you must also use ISCRELEC=0 and SCREEN3.
            = 1 damping will use a Tang-Toennis style
                Gaussian formula,
                   (1-exp(aR**2)(1+aR**2)
                where the default value of a=0.6.  In order
                to change the 'a' parameter, give
                     POLAB <a's value>
                     STOP
                in the $FRAGNAME input.  A smaller value
                may be useful for ionic EFPs.  (default)

   ISCRDISP =   fragment-fragment dispersion screening
            = 0 Use Tang-Toennies damping, with a fixed
                parameter a=1.5.
            = 1 use an overlap based damping factor,
                   1-S**2(1-2ln|S|+2ln**2|S|)
                instead.  There is no parameterization, so
                there's no other input.  (default)
```

It is possible to choose ISCRELEC, ISCRPOL, and ISCRDISP independently, as they apply to distinct parts of the fragment-fragment effective potential, and apart from POLSCR/SCREEN3, are independently implemented.

FRCPNT this keyword activates decomposing and printing the forces at the desired points in the EFP fragments, in additional to the traditional summing of the forces at the fragments' center-of-masses. This is useful for coarse graining the EFP data. If this option is selected, FORCE POINT section(s) must be given in the $FRAGNAME input(s).

The following keywords are for use with the EFP2-AI (a.k.a. EFP2-QM) dispersion calculation, that is, the calculation of the dispersion energy in a mixed system containing one or more EFP2 fragment(s) and a molecule modeled with a fully ab initio method (e.g. Hartree-Fock).

QMDISP specify whether to perform the calculation of EFP2-AI dispersion
- = 0 do not calculate dispersion, even if both an EFP2 fragment and an ab initio part are present (default)
- = 1 perform the EFP2-AI dispersion calculation

ISCRQMDS specify type of screening to use with EFP2-AI damping
- =-1 turn off damping (for debugging or benchmark comparison purposes)
- = 0 use Tang-Toennies damping, with a fixed parameter a=1.5
- = 1 use a parameter-free, overlap-based damping factor, 1-S**2(1-2ln|S|+2ln**2|S|) (default)

NODSGRD skip calculation of the EFP2-AI dispersion gradient, even if a gradient calculation is specified with RUNTYP=GRADIENT

Note that localized orbitals are necessary for the dispersion energy calculation. Boys localization will be performed by default if QMDISP=1 is specified, with no additional input keywords necessary. An alternate

localization method may be specified using the LOCAL keyword in $CONTRL.

NIDISP7 skip computating the 7th power dispersion.

-2- FRAGNAME=XXX

XXX is the name of the fragment whose coordinates are to be given next, and whose potential may also be in the input stream, as $XXX groups. XXX may not exceed 6 characters. Below, the actual $XXX groups are referred to generically as $FRAGNAME. Specific examples of $FRAGNAME are $C6H6, $BENZEN, $DMSO, ...

All information defining the EFP2-type fragment potential is given in its $FRAGNAME. A few standard EFP2 potentials are provided: see ~/gamess/auxdata/EFP. These are used by placing the desired file(s) into your input.

Two different EFP1-type water potentials are internally stored. FRAGNAME=H2ORHF will select a water potential developed at the RHF/DZP level, while FRAGNAME=H2ODFT will select a potential corresponding to B3LYP/DZP (see $BASIS for the precise meaning of DZP). If you choose either of these internally stored potentials, you need not give any further input to define them.

Since the EFP model consists of distributed multipoles and distributed polarizabilities, it is trivial to map some of the literature's simplified water potentials onto the EFP1 programming. For example, the octupole expansions used in EFP can be truncated to point charges (monopole term). So, FRAGNAME may also be any of the following water models:

SPC, SPCE, TIP5P, TIP5PE, or POL5P

Their EFP/EFP repulsion term is a typical 6-12 Lennard-Jones form. Repulsion between the QM and EFP particles follows the EFP1 style, if any QM atoms are input.

-3- NAME, X, Y, Z (COORD=CART)
NAME, I, DISTANCE, J, BEND, K, TORSION (COORD=INT)

```
NAME     = the name of a fragment point.  The name used
           here must match one of the points in $FRAGNAME.
           For the internally stored H2ORHF and H2ODFT
           potential, the atom names are O1, H2, and H3.

X, Y, Z  = Cartesian coordinates defining the position of
           this fragment point RELATIVE TO THE COORDINATE
           ORIGIN used in $DATA.  The choice of units is
           controlled by UNITS in $CONTRL.

I, DISTANCE, J, BEND, K, TORSION = the usual Z-matrix
           connectivity internal coordinate definition.
           The atoms I, J, K must be atoms in the ab
           initio system from in $DATA, or fragment points
           already defined in the current fragment or
           previously defined fragments.

If COORD=INT, line -3- must be given a total of three times
to define this fragment's position.
If COORD=CART, line -3- must be given three times, which is
sufficient to orient the rigid EFP particle.  However, it
is good form to read in any remaining nuclei in the EFP,
for example all 12 atoms in a benzene EFP, although only
the first three lines determine the entire EFP's position,
whenever you have the data for the extra nuclei.
-------------------------------------------------------

Repeat lines -2- and -3- to enter as many fragments as you
desire, and then end the group with a $END line.

Note that it is quite typical to repeat the same fragment
name at line -2-, to use the same type of fragment system
at many different positions.

=======================================================

        * * * * * * * * * * * * * * * * * * * * *
        For tips on effective fragment potentials
          see the 'further information' section
        * * * * * * * * * * * * * * * * * * * * *
```

==========

$FRAGNAME group

(required for each FRAGNAME given in $EFRAG)

This group gives all pertinent information for a given Effective Fragment Potential (EFP). This information falls into three categories, with the first two shared by the EFP1 and EFP2 models:

electrostatics (distributed multipoles, screening)
polarizability (distributed dipole polarizabilities)

The EFP1 model contains one final term,

fitted exchange repulsion

whereas the EFP2 model contains a collection of terms,

exchange repulsion, dispersion, charge transfer...

An Effective Fragment Potential is input using several different subgroups. Each subgroup is specified by a particular name, and is terminated by the word STOP. You may omit any of the subgroups to omit that term from the EFP. All values are given in atomic units.

```
To input monopoles,              follow input sequence -EM-
To input dipoles,                follow input sequence -ED-
To input quadrupoles,            follow input sequence -EQ-
To input octopoles,              follow input sequence -EO-
To input electrostatic screening,   follow input seq. -ES-
To input polarizable points,     follow input sequence -P-
To input polarizability screening,  follow input seq. -PS-
To input fitted "repulsion",     follow input sequence -R-
To input Pauli exchange,         follow input sequence -PE-
To input dispersion,             follow input sequence -D-
To input charge transfer,        follow input sequence -CT-
```

The data contained in a $FRAGNAME is normally generated by performing a RUNTYP=MAKEFP using a normal $DATA's ab initio computation on the desired solvent molecule. A MAKEFP run will generate all terms for an EFP2 potential, including multipole screening parameters. The screening option is controlled by $DAMP and $DAMPGS input, and by you checking the final fitting parameters for reasonableness.

Note that the ability to fit the "repulsion" term in an EFP1 potential is not included in GAMESS, meaning that EFP1 computations normally use built-in EFP1 water potentials.

```
-------------------------------------------------------

-1-   a single descriptive title card
-------------------------------------------------------

-2-   COORDINATES

COORDINATES signals the start of the subgroup containing
the multipolar expansion terms (charges, dipoles, ...).
Optionally, one can also give the coordinates of the
polarizable points, or centers of exchange repulsion.

-3-   NAME, X, Y, Z, WEIGHT, ZNUC

NAME    is a unique string identifying the point.
X, Y, Z are the Cartesian coordinates of the point, and
        must be in Bohr units.
WEIGHT, ZNUC are the atomic mass and nuclear charge, and
        should be given as zero only for points which are
        not nuclei.

In EFP1 potentials, the true nuclei will appear twice, once
for defining the positive nuclear charge and its screening,
and a second time for defining the electronic distributed
multipoles.

Repeat line -3- for each expansion point, and terminate
the list with a "STOP".
-------------------------------------------------------

Note: the multipole expansion produced by RUNTYP=MAKEFP
comes from Stone's distributed multipole analysis (DMA).
An alternative expansion, from a density based multipole
expansion (DBME) performed on an adaptive grid is placed in
the job's PUNCH file.  This alternative multipole expansion
may be preferable if large basis sets are in use (the DMA
expansion is basis set sensitive).  The DBME values can be
inserted in place of the DMA values, for -EM-, -ED, -EQ-,
and -EO- sections, if you wish.  Experience suggests that
DBME multipoles are about as accurate as those obtained
using DMA.

-EM1-  MONOPOLES

MONOPOLES signals the start of the subgroup containing
```

```
the electronic and nuclear monopoles.

-EM2-  NAME, CHARGE1, CHARGE2

NAME must match one given in the COORDINATES subgroup.
CHARGE1 = electronic monopole at this point.
CHARGE2 = nuclear monopole at this point.  Omit or enter
          zero if this is a bond midpoint or some other
          expansion point that is not a nucleus.

Repeat -EM2- to define all desired charges.
Terminate this subgroup with a "STOP".
-------------------------------------------------------------
-ED1-  DIPOLES

DIPOLES signals the start of the subgroup containing the
dipolar part of the multipolar expansion.

-ED2-  NAME, MUX, MUY, MUZ

NAME must match one given in the COORDINATES subgroup.
MUX, MUY, MUZ are the components of the electronic dipole.

Repeat -ED2- to define all desired dipoles.
Terminate this subgroup with a "STOP".
-------------------------------------------------------------
-EQ1-  QUADRUPOLES

QUADRUPOLES signals the start of the subgroup containing
the quadrupolar part of the multipolar expansion.

-EQ2-  NAME, XX, YY, ZZ, XY, XZ, YZ

NAME must match one given in the COORDINATES subgroup.
XX, YY, ZZ, XY, XZ, and YZ are the components of the
electronic quadrupole moment.

Repeat -EQ2- to define all desired quadrupoles.
Terminate this subgroup with a "STOP".
-------------------------------------------------------------
-EO1-  OCTUPOLES     (note: OCTOPOLES is misspelled)

OCTUPOLES signals the start of the subgroup containing
the octupolar part of the multipolar expansion.
```

```
-EO2-  NAME, XXX, YYY, ZZZ, XXY, XXZ,
             XYY, YYZ, XZZ, YZZ, XYZ

NAME must match one given in the COORDINATES subgroup.
XXX, ...  are the components of the electronic octopole.

Repeat -EO2- to define all desired octopoles.
Terminate this subgroup with a "STOP".
-------------------------------------------------------

-ES1a-  SCREEN

SCREEN signals the start of the subgroup containing
Gaussian screening (A*exp[-B*r**2]) for the distributed
multipoles, which account for charge penetration effects.

SCREEN pertains to ab initio-EFP multipole interactions, in
contrast to the SCREENx groups defined just below for EFP-
EFP interactions.

-ES1b-  NAME, A, B

NAME must match one given in the COORDINATES subgroup.
A, B are the parameters of the Gaussian screening term.

Repeat -ES1b- to define all desired screening points.
Terminate this subgroup with a "STOP".
-------------------------------------------------------

note: SCREENx input (any x) is only obeyed if ISCRELEC=0.
      SCREENx input will be ignored if ISCRELEC=1.

One (and only one) of the following groups should appear to
define the EFP-EFP multipole screening:

-ES2a-  SCREEN1 or SCREEN2 or SCREEN3

SCREEN1 signals the start of the subgroup containing
Gaussian screening (A*exp[-B*r**2]) for the distributed
multipoles, which account for charge-charge penetration
effects.

SCREEN2 signals the start of the subgroup containing
exponential screening (A*exp[-B*r]) for the distributed
```

multipoles, which account for charge-charge penetration effects. This is often the EFP-EFP screening of choice.

SCREEN3 signals the start of the subgroup containing the screening terms (A*exp[-B*r]) for the distributed multipoles, which account for high-order penetration effects (higher terms means charge-charge, as for SCREEN1 or SCREEN2, but also charge-dipole, charge-quadrupole, and dipole-dipole and dipole-quadrupole terms).

-ES2b- NAME, A, B

NAME must match one given in the COORDINATES subgroup.
A, B are the parameters of the exponential screening term.

Repeat -ES2b- to define all desired screening points.
Terminate this subgroup with a "STOP".

-P1- POLARIZABLE POINTS

POLARIZABLE POINTS signals the start of the subgroup containing the distributed dipole polarizability tensors, and their coordinates. This subgroup allows the computation of the polarization energy.

-P2- NAME, X, Y, Z

NAME gives a unique identifier to the location of this polarizability tensor. It might match one of the points already defined in the COORDINATES subgroup, but often does not. Typically the distributed polarizability tensors are located at the centroids of localized MOs.

X, Y, Z are the coordinates of the polarizability point. They should be omitted if NAME did appear in COORDINATES. The units are controlled by UNITS= in $CONTRL.

-P3- XX, YY, ZZ, XY, XZ, YZ, YX, ZX, ZY

XX, ... are components of the distributed polarizability, which is not a symmetric tensor. XY means dMUx/dFy, where MUx is a dipole component, and Fy is a component of an applied field.

```
Repeat -P2- and -P3- to define all desired polarizability
tensors, and terminate this subgroup with a "STOP".
-------------------------------------------------------

-PS1-  POLSCR

This section must not be given if ISCRPOL=1.  If not given,
when ISCRPOL=0, no polarization screening is performed.

POLSCR signals the start of the subgroup containing the
screening (by exp[-B*r]) for the induced dipoles.  It
pertains only to EFP-EFP interactions.  It requires that
you be using SCREEN3 damping of the multipole-multipole
interactions!  It applies to charge/induced dipole,
dipole/induced dipole, quadrupole/induced dipole, and
induced dipole/induced dipole terms.

-PS2-  NAME, B

NAME must match one of the distributed dipole points given
in the POLARIZABLE subgroup.
B is the exponent of the exponential screening term, and a
typical value is about 1.5.

Repeat -PS2- to define all desired screening points.
Terminate this subgroup with a "STOP".
-------------------------------------------------------

FORCE POINT

This section controls coarse graining of the gradient, if
FRCPNT is selected in $EFRAG.  The input consists of the
coordinates of the desired points:
   COM x  y  z
   FP1 x  y  z
   FP2 x  y  x
      ...
   STOP
where x,y,z are the coordinates of center of mass (COM) and
also any desired "force points" FP1, FP2, ...

Terminate this subgroup with a "STOP".
-------------------------------------------------------
```

EFP1 versus EFP2

The EFP1 model consists of a fitted potential, which is a remainder term, after taking care of electrostatics and polarization with the input described above. The fitted term is called a "repulsive potential" because its largest contribution stems from Pauli exchange repulsion. The fit actually contains several other interactions, since it is just a fit to the total interaction potential's remainder after subtracting the elecrostatic and polarization interactions.

The EFP2 model uses analytic representations for exchange repulsion and other terms, and these are documented after the EFP1's "repulsive potential".

-R1- REPULSIVE POTENTIAL

See also the $FRGRPL input group, which defines the fit for the EFP1-EFP1 repulsion term.

REPULSIVE POTENTIAL signals the start of the subgroup containing the fitted exchange repulsion potential, for the interaction between the fragment and the ab initio part of the system. This term also accounts, in part, for other effects, since it is a fit to a remainder. The fitted potential has the form

$$\sum_{i}^{N} C_i * \exp[-D_i * r^{**}2]$$

-R2- NAME, X, Y, Z, N

NAME may match one given in the COORDINATES subgroup, but need not. If NAME does not match one of the known points, you must give its coordinates X, Y, and Z, otherwise omit these three values. N is the total number of terms in the fitted repulsive potential.

-R3- C, D

These two values define the i-th term in the repulsive potential. Repeat line -R3- for all N terms.

Repeat -R2- and -R3- to define all desired repulsive potentials, and terminate this subgroup with a "STOP".

The following terms are part of the developing EFP2 model. This model replaces the "kitchen sink" fitted repulsion in the EFP1 model by analytic formulae. These formulae are to be specific for each kind of physical interaction, and to pertain to any solvent, not just water. The terms which are programmed so far are given below.

-PE1- PROJECTION BASIS SET
-PE2- PROJECTION WAVEFUNCTION n m
-PE3- FOCK MATRIX ELEMENTS
-PE4- LMO CENTROIDS

These four sections contain the data needed to compute the Pauli exchange repulsion, namely

1. the original basis set used to extract the potential.
2. the localized orbitals, expanded in that basis.
3. the Fock matrix, in the localized orbital basis.
4. the coordinates of the center of each localized orb.

The information generated by a MAKEFP that follows these four strings is largely self explanatory. Note, however, that the orbitals (PE2) must have two integers giving the number of occupied orbitals -n- and the size of the basis set -m-. The PE2 and PE3 subsections do not contain STOP lines.

-D1- DYNAMIC POLARIZABLE POINTS

DYNAMIC POLARIZABLE POINTS signals the start of the subgroup containing the distributed imaginary frequency dipole polarizability tensors, and their coordinates. This information permits the computation of dispersion energies.

```
-D2-  NAME, X, Y, Z
```

NAME gives a unique identifier to the location of this polarizability tensor. It might match one of the points already defined in the COORDINATES subgroup, but often does not. Typically the distributed polarizability tensors are located at the centroids of localized MOs.

X, Y, Z are the coordinates of the polarizability point. They should be omitted if NAME did appear in COORDINATES. The units are controlled by UNITS= in $CONTRL.

```
-D3-  XX, YY, ZZ, XY, XZ, YZ, YX, ZX, ZY
```

XX, ... are components of the distributed polarizability, which is not a symmetric tensor. XY means dMUx/dFy, where MUx is a dipole component, and Fy is a component of an applied field.

Repeat -D2- and -D3- to define all desired polarizability tensors, and then repeat for all desired imaginary frequencies. MAKEFP jobs use 12 imaginary frequencies at certain internally stored values, to enable quadrature of these tensors, to form the C6 dispersion coefficient. Thus D2 and D3 input is repeated 12 times. Terminate this subgroup with a "STOP".

```
-QD1- DIPOLE-QUADRUPOLE DYNAMIC POLARIZABLE POINTS
-QD2- data similar to -D2- above
-QD3- data similar to -D3- above
```

These data are used for the 7th power dispersion formula, and are already in the right format from a MAKEFP run. See also NODISP7 above, to skip its use.

```
-CT1- CTVEC n m
-CT2- CTFOK
```

These two sections contain the data needed to compute the charge transfer energy, namely

1. the canonical occupied orbitals, followed by either valence virtuals or canonical virtuals, depending on

CTVVO's setting during the MAKEFP run. These MOs are expanded in the -PE1- basis.
  2. the occupied orbitals' eigenvalues.
The information generated by a MAKEFP that follows these two strings is largely self explanatory. The MO and AO sizes given by -n- and -m- have the same meaning as for the -PE2- group. The CTVEC info does not have a STOP line, but CTFOK does.

The EFP2 model presently can generate the energy for a system with an ab initio molecule and EFP2 solvents, if only Pauli exchange repulsion is used. The AI-EFP gradient for this term is not yet programmed, nor are there AI-EFP codes for dispersion or charge transfer. Thus use of the EFP2 model, for all practical purposes, is limited to EFP-EFP interactions only, via COORD=FRAGONLY.

==========

The $FRAGNAME input group is terminated by a " $END".

==========

$FRGRPL group

This group defines the inter-fragment repulsive potential for EFP1 potentials. It accounts primarily for exchange repulsions, but also includes charge transfer. Note that the functional form used for the fragment-fragment repulsion differs from that used for the ab initio-fragment repulsion, which is defined in the $FRAGNAME input. The form of the potential is

$$\sum_{i}^{N} A_i * \exp[-B_i * r]$$

-1- PAIR=FRAG1 FRAG2

specifies which two fragment repulsions are being defined. $FRAGNAME input for the two names FRAG1 and FRAG2 must have been given.

-2- NAME1 NAME2 A B
or
NAME1 NAME2 'EQ' NAME3 NAME4

NAME1 must be one of the "NAME" points defined in the $FRAG1 group's REPULSION POTENTIAL section. Similarly NAME2 must be a point from the $FRAG2 group. In addition, NAME1 or NAME2 could be the keyword CENTER, indicating the center of mass of the fragment.

A and B are the parameters of the fitted repulsive potential.

The second form of the input allows equal potential fits to be used. The syntax implies that the potential between the points NAME1 and NAME2 should be taken the same as the potential previously given in this group for the pair of points NAME3 and NAME4.

If there are NPT1 points in FRAG1, and NPT2 points in FRAG2, input line -2- should be repeated NPT1*NPT2 times.

```
Terminate the pairs of potentials with a "STOP" card.
Any pairs which you omit will be set to zero interaction.

Typically the number of points on which fitted potentials
might be taken to be all the nuclei in a fragment, plus
the center of mass.
-------------------------------------------------------

Repeat lines -1- and -2- for all pairs of fragments, then
terminate the group with a $END line.

=======================================================
```

==========

$EWALD group (relevant for all-EFP runs with PBC)

This group controls evaluation of the electrostatic energy of EFP calculations by means of the Ewald sum formulae. This gives a more accurate evaluation of these long range interactions than the minimum image convention, which sums only up to a distance of one box, centered on each particle. Ewald sum formulae are not used for the other, shorter range interactions in the EFP model, such as exchange repulsion and polarization, which are always evaluated by the minimum image convention. This group is relevant if and only if a periodic box is defined in the $EFRAG input group.

IFEWLD = a flag to activate Ewald sums for electrostatics
The default is .FALSE.

LEVEL = 1 means Ewald sum charge-charge interactions only, which is the default if IFEWLD is turned on.
= 2 charge-charge, charge-dipole, dipole-dipole
= 3 charge-charge, charge-dipole, dipole-dipole, and charge-quadrupole terms should be Ewald summed.

TNFOIL = a flag to select tin foil boundary conditions, which uses a metallic continuum past the cutoffs, instead of a vacuum. The default is .TRUE.

BETA = parameter for the direct summation, in 1/Bohr. It should be 1.7/cutoff. Cutoffs are specified in $EFRAG, with the periodic box sizes, use a cutoff in units Angstrom in this formula, as the value 1.7 includes the conversion factor. The default=0.2

KMAX = number of reciprocal vectors in each direction. This should be kmax >= 3.2L/cutoff, where the radial cutoff, and box side L are both given in your $EFRAG. The default=10

==========

==========

$MAKEFP group (relevant if RUNTYP=MAKEFP)

This group controls generation of the effective fragment potential (EFP2 style) from the wavefunction of a single monomer. EFP generation is allowed for SCFTYP=RHF and ROHF. Multipole moments for electrostatics are always generated, and the default for the keywords below is to generate all additional terms.

FRAG = a string of up to 8 letters to identify this EFP.
For example, WATER or BENZENE or CH3OH or ...
(default=FRAGNAME, which you can hand edit later)

SCREEN = a flag to generate screening information for the multipole electrostatics, and maybe polarizability screening. See $DAMP and $DAMPGS.
(default=.TRUE. for RHF, so far ROHF is not coded)

POL = a flag to generate dipole polarizabilities.
(default=.TRUE.)
See POLNUM in $LOCAL for an alternative way to generate the polarizabilities, which may be faster for large molecules.

EXREP = a flag to generate exchange repulsion parameters.
(default=.TRUE.)

CHTR = a flag to generate charge transfer parameters.
(default=.TRUE. for RHF, so far ROHF is not coded)

CTVVO = a flag to specify what type of charge transfer data is generated. (default=.TRUE.)
.FALSE. means all canonical virtuals are used.
.TRUE. means Valence Virtual Orbitals will be created, by forcing VVOS in $SCF is forced on. The VVOs are many fewer in number, so the charge transfer calculation is greatly accelerated.

DISP = a flag to generate information for dispersion.
(default=.TRUE. for RHF, so far ROHF is not coded)

```
DISP7   = a flag to generate data for the 1/r^7 dispersion
          term (default=.TRUE.).  This creates the EFP term
          'DIPOLE-QUADRUPOLE DYNAMIC POLARIZABLE POINTS'


   See also similar inputs NOPOL, NOEXREP, NOCHTR, NODISP
in the $EFRAG input group, to ignore these terms if they
are generated.

=============================================================
```

==========

$PRTEFP group (optional)

This group provides control for generating integer charge EFP fragments for constructing large EFPs. See P.A.Molina, H.Li, J.H.Jensen J.Comput.Chem. 24, 1971-1979 (2003)

This group is mainly used in RUNTYP=MAKEFP runs. However, in MOPAC RUNTYP=ENERGY runs, the presence of a $PRTEFP group causes AM1 or PM3 charges to be printed and punched out in a suitable format for EFP calculations.

NOPRT = an array specifying the atoms for which EFP multipole and polarizability points will not be printed/punched out.
Example: For a molecule with the connectivity A1-A2-A3-A4-A5, NOPRT(1)=4,5 means that multipoles centered on atoms 4 and 5, and bond midpoints BO34 and BO45 are not part of the EFP.

MIDPRT = an array specifying atoms whose bond midpoints neglected by using NOPRT should be printed out.
Example: MIDPRT(1)=3 forces the printout of bond midpoint BO34.

The neglect of monopoles leads to EFPs with overall non-integer charge. The next keyword defines "collection points" to which the removed monopoles are added. Thus, the net charge of the EFP=ICHARG. The presence of this "fictitious" charge is compensated for by adding an opposing dipole to the collection point.

NUMFFD = an array that defines (1) a collection point, (2) the number of atoms contributing to monopoles to this point, and (3) the numbers of the atoms. More than one collection point can be defined. An opposing dipole is calculated as -0.5Q*r (Q = sum of neglected monopoles, r = distance between collection point and nearest neglected monopole) and placed at the collection point.

Example: NUMFFD(1)=3,2,4,5. The sum of monopoles

```
         at A4, A5, BO34 and BO45 (Q) is added to the A3
         monopole.  A dipole, -0.5Q*r, is placed on A3,
         where r is the distance between A3 and BO34.
         If MIDPRT(1)=3, Q does not include the BO34
         monopole, r is the distance between BO34 and A4,
         and the resulting dipole is centered on BO34.

================================================================
```

==========

$DAMP group (optional, relevant if RUNTYP=MAKEFP)

This group provides control over the screening of the charge term in the distributed multipole expansion used by the EFP model for electrostatic interactions, to account for charge penetration. See

M.A.Freitag, M.S.Gordon, J.H.Jensen, W.A.Stevens
J.Chem.Phys. 112, 7300-7306(2000)
L.V.Slipchenko, M.S.Gordon
J.Comput.Chem. 28, 276-291(2007)

The screening exponents are optimized by fitting a damped multipolar electrostatic potential to the actual quantum mechanical potential of the wavefunction, computed on concentric layers of united spheres (namely, "GEODESIC" layers for WHERE=PDC in $ELPOT). See $STONE's generation of the unscreened classical multipoles, $PDC's generation of the true quantum potentia, and $DAMPGS.

Different multipole damping functions can be generated. The first contains a single exponential form,

```
(1 - beta*exp(-alpha*r))
```

and the second function is a single Gaussian form,

```
(1 - beta*exp(-alpha*r**2))
```

The exponent 'alpha' values are optimized (normally with beta=one), with starting values defined in $DAMPGS. The exponential fit is used for fragment-fragment charge penetration screening, while the Gaussian fit is used in ab initio-fragment screening. See equations 28 and 4 in the reference. These two screen only the charge-charge interactions.

It is also possible to generate a "higher order exponential" screening term, meaning that in addition to the charge-charge energy, also affects charge-dipole, charge-quadrupole, and dipole-dipole energy terms.

Words of advice:

1. Higher order screening is usually similar in accuracy to just charge-charge screening, except in molecules without dipole moment, such as ethylene or benzene.

2. If the bond midpoints have smaller charges, it may be more physically reasonable to screen only the atomic monopoles, see ISCCHG.
3. Use of the numerical Stone distributed multipole analysis may not be fully converged with respect to the level of highest used multipole moment (octapole) and corresponding energy terms (quadrupole-quadrupole), which makes screening much more problematic.
4. Accuracy of screening with the damping function of a single exponential form depends on a region of fitting the quantum mechanical electrostatic potential, i.e., a radius of first sphere with grid points (parameter VDWSCL in $PDC). A general trend is that for molecules with stronger electrostatic interaction, and, consequently, shorter intermolecular separations, e.g., methanol and water, smaller values of VDWSCL are preferable, whereas for weaker interacting molecules, e.g., dichloromethane and acetone, bigger VDWSCL values are more acceptable. Our recommended VDWSCL values are 0.4-0.5 for methanol, 0.5-0.8 for water, and 0.7-0.9 for weaker bonded molecules. Note that VDWSCL values of 1.0 and higher often result in not converged or badly converged damping parameters, and are not recommended. The default VDWSCL value is 0.7.
5. If the non-linear parameters alpha increase to 10, that term is effectively removed from the screening. This happens sometimes with buried atoms, and fairly often with bond mid-points.
6. Double check the numerical results carefully.

ISCCHG = 0 use both atoms and bond midpoints as screening centers (the default)
1 use only atoms as screening centers

IFTTYP = selects the type of multipole screening fit:
0 means generate a Gaussian fit, for use as SCREEN input in $FRAGNAME.
2 means generate an exponential charge-charge fit, for use as SCREEN2 input in $FRAGNAME.
3 means generate an exponential higher order fit, for use as SCREEN3 input in $FRAGNAME.

If you wish to use Gaussian screening for EFP-EFP, simply copy the SCREEN output into a SCREEN1 section.

```
IFTFIX = 0 means the coefficients in the fit (beta) are
           free parameters
         1 means the coefficients are held to unity.
           In case the linear coefficients become large,
           and particularly if they are negative, a fit
           with unit coefficients is more reasonable.
```

The default is to do both fits in one run, IFTTYP(1)=2,0, using unit coefficients, IFTFIX(1)=1,1.

The remaining parameters are seldom given:

```
NMAIN  = the number of centers to receive a smaller alpha
         initial value, 2.0, which defaults to the number
         of atoms.  The remaining centers, usually the
         bond midpoints, receive a larger starting value,
         4.0.  $DAMPGS gives more control of the values.
MAXIT  = maximum iterations in the fit, default=30.
THRSH  = printing threshold for large deviations.  The
         default is 100.0 kcal/mol.
```

==========

==========

$DAMPGS group (relevant if $DAMP was given)

This is a free-format, line by line input group that sets the initial values damping functions used to screen the multipole expansion. A check run may be helpful in listing the names of the expansion points that are chosen by MAKEFP jobs. Very often the input group contains only type -1- lines, and only in its second form.

```
-1-       <exp.pt.> <nterms>
    or    <exp.pt.>=<prev.exp.pt.>
```

This line gives the name of the expansion point, and how many terms are in the damping function (always 1 at present). The second form of this line lets you equate the current point to some previous point's values in $DAMPGS, skipping line -2-.

```
-2-   <coef> <exponent>
```

The linear coefficient (usually 1.0) and exponent of this term in the damping function. Repeat -2- <nterms> times. If not given, the starting exponent for atoms is 2.0, and for bond midpoints, 4.0.

An example, for water, enforcing equivalent points, is:

```
 $dampgs
O1 1
  1.0  2.0
H2 1
  1.0  2.0
H3=H2
BO21 1
  1.0  4.0
BO31=BO21
 $end
```

or much more simply, since the left is default exponents,

```
 $dampgs
H3=H2
BO31=BO21
 $end
```

The "BO" is short for bond midpoint.

==========

==========

$PCM group (optional)

This group controls solvent effect computations using the Polarizable Continuum Model. If this group is found in the input file, a PCM computation is performed. The default calculation, chosen by selecting only the SOLVNT keyword, is to compute the electrostatic free energy. Appropriate numerical constants are provided for a wide range of solvents. Typical input might be as simple as

```
 $PCM SOLVNT=H2O $END
```

There is in fact little need to give other PCM input data, except perhaps atomic radii in $PCMCAV if your molecule contains an unusual atom.

Additional keywords (ICOMP, ICAV, IDISP, or IREP/IDP) allow for more sophisticated computations, namely cavitation, repulsion, and dispersion free energies. The methodology for these is general, but numerical constants are provided only for water.

Alternatively, the PCM codes for electrostatics can be combined with U. Minnesota codes to implement the SMD solvation model. SMD combines the electrostatics with an alternative cavitation, dispersion, and solute structure reorganization (CDS) correction. Since SMD also changes the atomic radii, the electrostatics interaction is changed. See keyword SMD below (and the 4th chapter of this manual).

Calculations are possible on either a solute embedded in a PCM continuum, or a system combining a solute & EFP explicit solvent molecules, embedded in a PCM continuum. The energy and/or nuclear gradients are programmed for RHF, ROHF, UHF, GVB, and MCSCF wavefunctions, and for DFT or MP2 level calculations using RHF, ROHF, and UHF. Closed shell TD-DFT excited states have analytic gradients, as well. Polarizabilities in solution may be found by RUNTYP=TDHF. Parallel computation is enabled, with scaling similar to the scaling of the corresponding gas phase calculation. PCM is not programmed for CI or Coupled Cluster. PCM is enabled for use during semiempirical MOPAC runs.

See the Fragment Molecular Orbital section of the References chapter for information on using PCM within the FMO model.

There is additional information on PCM in the References chapter of this manual. This includes information on which keyword combinations were default values in the past.

IEF switch to choose the type of PCM model used.
The default is -10, iterative C-PCM.
= 0 isotropic dielectrics using the original formulation of PCM for dielectrics (D-PCM)
= 1 anisotropic dielectric using the Integral Equation Formalism (IEF) of PCM, see $IEFPCM
= 2 ionic solutions using IEF-PCM, see $IEFPCM
= 3 isotropic dielectrics using IEF-PCM with matrix inversion solver, see $IEFPCM
= -3 isotropic dielectric IEF-PCM with iterative solver, see $PCMITR.
= 10 conductor-like PCM (C-PCM) with matrix inversion. Charge scaling is (Eps-1.0)/Eps
=-10 C-PCM, with iterative solver. See $PCMITR.
= 9,11,13 IEF-PCM for certain non-standard environment. (See $REORG input for details)
= 14 also models isotropic dielectric like IEF=3 but uses a slightly different implementation of IEF equations (See $REORG input for further details)

C-PCM is normally a better choice than IEF-PCM. The iterative solvers chosen by IEF=-3 or -10 usually reproduce the energy of the explicit solvers IEF=3 or 10 to within 1.0d-8 Hartrees, and will be much faster and use less memory for large molecules. D-PCM should be considered obsolete, and choices 1 and 2 are seldom made.

* * *

SOLVNT = keyword naming the solvent, whose choices depend on use of non-SMD or SMD models. For the former, the eight numerical constants defining the solvent are internally stored for:

WATER (or H2O)	
CH3OH	C2H5OH
CLFORM (or CHCl3)	CTCL (or CCl4)

```
            METHYCL (or CH2Cl2)      12DCLET (or C2H4Cl2)
            BENZENE (or C6H6)        TOLUENE (or C6H5CH3)
            CLBENZ (or C6H5Cl)       NITMET (or CH3NO2)
            NEPTANE (or C7H16)       CYCHEX (or C6H12)
            ANILINE (or C6H5NH2)     ACETONE (or CH3COCH3)
            THF                      DMSO (or DMETSOX)
         SMD has many additional solvents, see below.
```

The default solvent name is "INPUT" which means you must give the numerical values defining some other solvent, as described below.

* * * non-SMD calculations * * *

The next set of parameters controls the computation: parameterization of the solvents, ICOMP which has an impact on the PCM electrostatics, and other keywords related to cavitation, dispersion, and repulsion corrections: ICAV, IDISP, IREP/IDP.

ICOMP = Compensation procedure for induced charges.
Gradient runs require ICOMP be 0 or 2 only.
= 0 None. (default)
= 1 Yes, each charge is corrected in proportion to the area of the tessera to which it belongs.
= 2 Yes, using the same factor for all tesserae.
= 3 Yes, with explicit consideration of the portion of solute electronic charge outside the cavity, by the method of Mennucci and Tomasi. See $NEWCAV.

Technical issues are: IEF=0 should normally choose ICOMP=2. Options IEF=1 or 2 are incompatible with gradients and must choose ICOMP=0, and presently contain bugs (do not choose these!). IEF=3 may not choose ICOMP=3, but if diffuse basis functions are in use, it may benefit from ICOMP=2.

ICAV = calculate the cavitation energy, by the method of Pierotti and Claverie. The cavitation energy is computed at the end of the run (e.g. at the final geometry) as an additive constant to the energy.
= 0 skip the computation (default)

```
       = 1 perform the computation.

  If ICAV=1, the following parameter is relevant:

TABS   = the temperature, in Kelvin. (default=298.0)
```

There are two procedures for the calculation of the repulsion and dispersion contributions to the free energy. Parameterizations were obtained for RHF cases, so the implementation permits their use only for RHF.

IDISP is older, and is incompatible with IREP and/or IDP. Nuclear gradients are available for IDISP (select either ICLAV or ILJ in $DISREP). The older GEPOL-GB tessellation does some gradient terms numerically, which results in a less accurate gradient.

```
IDISP  = Calculation of both dispersion and repulsion
         free energy through the empirical method of
         Floris and Tomasi.
       = 0 skip the computation (default)
       = 1 perform the computation.  See $DISREP.
```

The next two options add repulsive and dispersive terms to the solute hamiltonian, in a more ab initio manner, by the method of Amovilli and Mennucci. These may be used only in single point energy calculations (see IDISP if you wish to use gradients).

```
IREP   = Calculation of repulsion free energy
       = 0 skip the computation (default)
       = 1 perform the computation.  See $NEWCAV.

IDP    = Calculation of dispersion free energy
       = 0 skip the computation (default)
       = 1 perform the computation.  See $DISBS.

  If IDP=1, then three additional parameters must be
  defined.  The two solvent values correspond to water,
  and therefore these must be input for other solvents.

WA     = solute average transition energy.  This is
         computed from the orbital energies for RHF,
```

```
          but must be input for MCSCF runs.
          (default=1.10)
WB      = ionization potential of solvent, in Hartrees.
          (default=0.451)
ETA2    = square of the zero frequency refractive index
          of the solvent.  (default=1.75)

--- the next 8 values define the solvent, if SOLVNT=INPUT:

RSOLV  = the solvent radius, in units Angstrom
EPS    = the dielectric constant
EPSINF = the dielectric constant at infinite frequency.
          This value must be given only for RUNTYP=TDHF,
          if the external field frequency is in the optical
          range and the solvent is polar; in this case the
          solvent response is described by the electronic
          part of its polarization.  Hence the value of the
          dielectric constant to be used is that evaluated
          at infinite frequency, not the static one (EPS).
          This value also must be given for TD-DFT/PCM,
          when NONEQ is selected in $TDDFT.
          For nonpolar solvents, the difference between
          the two is almost negligible.
TCE    = the thermal expansion coefficient, in units 1/K
VMOL   = the molar volume, in units ml/mol
STEN   = the surface tension, in units dyne/cm
DSTEN  = the thermal coefficient of log(STEN)
CMF    = the cavity microscopic coefficient

Values for TCE, VMOL, STEN, DSTEN, CMF need to be given
only for the case ICAV=1.  Input of any or all of these
values will override an internally stored value, if you
have chosen a solvent by its name.

              * * * SMD calculations * * *

The Solvation Model Density (SMD) uses the solute's quantum
mechanical density (the D in the model's name) for IEF-PCM
or C-PCM's electrostatics.  It adds "CDS" corrections for
cavitation, dispersion, and solvent structure, all of which
have nuclear gradient contributions coded.  The SMD model's
parameters were developed using IEF-PCM and GEPOL cavity
construction, but SMD may also be used with the more robust
C-PCM model and FIXPVA cavity tessellation.
```

```
SMD    = a flag to select "Solvation Model Density".
         default=.FALSE.  If chosen, naming the solvent
         by SOLVNT=xxx picks numerical values for the
         six SOLX keywords just below, which may then be
         omitted.  The SMD model knows 178 solvents, see
         chapter 4 of this manual for a listing.

SOLA   = Abraham's hydrogen bond acidity
SOLB   = Abraham's hydrogen bond basicity
SOLC   = aromaticity: fraction of non-H solvent atoms
         which are aromatic Carbon atoms
SOLG   = macroscopic surface tension at the air/solvent
         interface, in units of cal/mole/angstrom**2
SOLH   = halogenicity: fraction of non-H solvent atoms
         which are F, Cl, or Br
SOLN   = index of refraction at optical frequencies at
         298K, n-sub-20-super-D.

In addition to the parameters just above, SMD provides its
own set of radii for each atom's sphere, so $PCMCAV input
must not be given.  Of course, if you choose SMD=.TRUE.,
with its built in CDS correction, you must select
ICOMP=ICAV=IDISP=IREP=IDP=0!  See also SMVLE in $SVP.

                          * * *

--- interface to Fragment Molecular Orbital method:

IFMO     specifies "n" for the n-body FMO expansion of the
         total electron density to be used in PCM.
         Default=0 should be used for any non-FMO run.
         Non-zero IFMO can be used only within the regular
         FMO framework (q.v. for further FMO limitations):
         IFMO should be less or equal than NBODY in $FMO,
         Not all PCM options can be used with FMO!
         The following are explicitly permitted:
            IEF=-3,-10; ICOMP=0,1,2; MTHALL=2,4;
            IDISP=0,1; IDP=0; IREP=0,1.
            Gradient runs require ICOMP=0.
         IFMO may take the values of -1,0,1,2,3.
         For FMO, IFMO=-1 chooses PCM<1>,
                  IFMO= 1 chooses PCM[1],
                  IFMO= 2, NPCMIT=2 chooses PCM[1(2)],
                  IFMO= 2, NPCMIT>2 chooses PCM[2],
                  IFMO= 3, NPCMIT=2 chooses PCM[1(3)],
```

```
                IFMO= 3, NPCMIT>2 chooses PCM[3].
        The fully analytic gradient requires IFMO=-1 or 1.

--- the next set of keywords defines the molecular cavity,
used for electrostatic (surface charge) calculations.  See
also $PCMCAV, $TESCAV, and $NEWCAV for other cavities.

NESFP  =   option for spheres forming the cavity:
       = 0 centers spheres on each nucleus in the quantum
           solute, and every atom in EFP.  (default)
       = N use N initial sphere, whose centers XE, YE, ZE
           and radii RIN must be specified in $PCMCAV.

   The cavity generation algorithm may use additional
spheres to smooth out sharp grooves, etc. If you are
interested in smoother cavities, see the SVPE and SS(V)PE
methods, which use a cavity based on isodensity surfaces.
The following parameters control how many extra spheres are
generated:

OMEGA and FRO = GEPOL parameters for the creation of the
         'added spheres' defining the solvent accessible
         surface. When an excessive number of spheres is
         created, which may cause problems of convergence,
         the value of OMEGA and/or FRO must be increased.
         For example, OMEGA from 40 to 50 ... up to 90,
                      FRO from 0.2 ... up to 0.7.
         (defaults are OMEGA=40.0, FRO=0.7)

RET    = minimum radius (in A) of the added spheres.
         Increasing RET decreases the number of added
         spheres.  A value of 100.0 (default) inhibits the
         addition of any spheres, while 0.2 fills in many.
         The use of added spheres is strongly discouraged.

MODPAR = cavity generation's parallelization option:
         0 parallelize tessellation, 1= do not parallelize.
         The present parallel code is inefficient, so
         MODPAR=0 is recommended.  (default=0)
         Don't confuse this with running PCM in parallel!

MXSP   = the maximum number of spheres.
         Default: MXATM parameter in GAMESS.

MXTS   = the maximum number of tesserae.
```

```
          Default: Nsph*NTSALL*2/3, where Nsph is the number
          of spheres (usually equal to the number of atoms).
          If less than 20 spheres are present, default is
          Nsph*NTSALL. For GEPOL-RT, NTSALL=960 is used in
          setting the default value.

          Note on MXSP and MXTS: PCM usually constructs
          more than one cavity (for example, a different one
          for the cavitation energy).  MXSP and MXTS must be
          large enough to handle every possible cavity.


--- arcane parameters:

IPRINT = 0 normal printing (default)
       = 1 turns on debugging printout

IFIELD = At the end of a run, calculate the electric
         potential and electric field generated by the
         apparent surface charges.
       = 0 skip the computation (default)
       = 1 on nuclei
       = 2 on a planar grid

  If IFIELD=2, the following data must be input:

AXYZ,BXYZ,CXYZ = each defines three components of the
                 vertices of the plane where the reaction
                 field is to be computed (in Angstroms)
      A ===> higher left corner of the grid
      B ===> lower left corner of the grid
      C ===> higher right corner of the grid
NAB = vertical subdivision (A--B edge) of the grid
NAC = horizontal subdivision (A--C edge) of the grid.

=============================================================
```

==========

$PCMCAV group (optional)

This group controls generation of the cavity holding the solute during Polarizable Continuum Model runs. The cavity is a union of spheres, according to NESFP given in $PCM. The data in this group supplements cavity data given in $PCM. It is unlikely that users will input anything here, except perhaps a few RIN values. The data given here must be in Angstrom units.

XE,YE,ZE = arrays giving the coordinates of the spheres.
    if NESFP=0, the atomic positions will be used.
    if NESFP>0, you must supply NESFP values here.

RADII = three tables of values (Angstroms!) are available:
        VANDW selects van der Waals radii (default)
              This table has radii for atoms
              H,He, B,C,N,O,F,Ne,   Na,Al,Si,P,S,Cl,Ar,
                     K,As,Se,Br,Kr, Rb,Sb,Te,I, Cs,Bi
              internally tabulated, otherwise give RIN.
      = VDWEFP, similar to VANDW, except that radii not
              tabulated by VANDW are assigned as 1.60A.
              This option is most useful for protein-EFP
              calculations.
      = SUAHF, the simplified united atomic radii will be
              be used for the array RIN, namely
        H:0.01   C:1.77   N:1.68   O:1.59   P:2.10   S:2.10
        For the other elements with Z<16, 1.50 is used.
        For the elements with Z>16, 2.30 will be applied.

RIN = an array giving the sphere radii. Radii given here
      will overwrite the values selected by RADII's tables.
      RIN values are multiplied by ALPHA, see just below.
      if NESFP=0, the program will look up the internally
                  data according to the RADII keyword.
      if NESFP>0, give NESFP values.

Example: Suppose the 4th atom in your molecule is Fe, but
         all other atoms have van der Waals radii. You
         decide a good guess for Fe is twice the covalent
         radius: $PCMCAV RIN(4)=2.33 $END. Due to ALPHA,
         traditionally 1.2, the Fe radius will be 2.796.

The source for the van der Waals radii is "The Elements", 2nd Ed., John Emsley, Clarendon Press, Oxford, 1991, except for C,N,O where the Pisa group's experience with the best radii for PCM treatment of singly bonded C,N,O atoms is taken. The radii for a few transition metals are given by A.Bondi, J.Phys.Chem. 68, 441-451(1964).

ALPHA = an array of scaling factors, for the definition of the solvent accessible surface. If only the first value is given, all radii are scaled by the same factor. (default is ALPHA(1)=1.2)

EPSHET = an array of dielectric constants, for each atom in the heterogeneous CPCM. The default is to use the same dielectric for every atom, namely the value of EPS in $PCM. (only if IEF=10 or -10). The default EPSHET(1)=X,X,X,X where EPS=X means homogeneous CPCM.

==========

==========

$TESCAV group (optional)

This group controls the tessellation procedure for the cavity surfaces in PCM computations. The default values for this group will normally be satisfactory. Use of the FIXPVA mechanism for dividing the surface of the atomic spheres into tesserae should allow for convergent PCM geometry optimizations. To converge to small OPTTOL values may require the use of internal coordinates, since the tessellation amounts to a finite grid (so the PCM energy is not strictly rotationally invariant).

Cartesian geometry optimizations may require a high density of tesserae on the cavity surface:
NTSALL=240 (or 960)
This may require raising the maximum number of tesserae, see MXTS in $PCM. It is reasonable to just try internal coordinates first, as this should be sufficient w/o increasing the tesserae density. See also IFAST=1 in $PCMGRD.

--- The first two arrays control the density of tesserae and the method to generate the tesserae.

INITS = array defines the initial number of tesserae for each sphere. Only 60, 240 and 960 are allowed, but the value can be different for each sphere. (Default is INITS(1)=60,60,60,...) See NTSALL.

METHOD = array defining the tessellation method for each sphere. The value can be different for each sphere. The default is 4 for all spheres, e.g. METHOD(1)=4,4,4,... See also MTHALL.
= 1 GEPOL-GB, "Gauss-Bonet" tessellation.
= 2 GEPOL-AS, "area scaling" tessellation.
= 3 GEPOL-RT, "regular tessellation".
= 4 FIXPVA, "Fixed points with variable area".
FIXPVA gives smooth potential surfaces during geometry optimizations, works with $PCM options ICAV and IDISP (but not with IDP or IRP), and is the preferred tessellation method.

--- The next three parameters are presets for filling the

```
    arrays INITS and METHOD with identical values.

NTSALL =  60, 240 or 960 (default = 60)
          All values in the array INITS are set to NTSALL

MTHALL =  1, 2, 3, or 4 (default = 4)
          All values in the array METHOD are set to MTHALL

MTHAUT =  0 or 1 (default = 0)
          If RUNTYP=OPTIMIZE and frozen atoms are defined
          by IFCART, MTHAUT=1 will select METHOD=1 for
          frozen atoms. See also AUTFRE and NTSFRZ.

note: Explicitly defining INITS and METHOD from the input
      deck will overrule the presets from NTSALL, MTHALL
      and/or MTHAUT.

--- The following two parameters control GEPOL-RT

AREATL =  The area criterion (A*A) for GEPOL-RT.
          Tesserae with areas < AREATL at the boundary of
          intersecting spheres will be neglected.
          Default=0.010 A*A. Smaller AREATL cause larger
          number of tesserae.  AREATL < 0.00010 is not
          recommended.

BONDRY =  Controls (by scaling) the distance within which
          tesserae are considered "close" to the boundary.
          Such tesserae will be recursively divided into
          smaller ones until their areas are < AREATL.
          The default (= 1.0) means the distance is the
          square root of the tessera area.
          A large BONDRY value like 1000.0 will lead to
          fine tessellation for the entire surface with
          all tessera areas < AREATL.

--- The next two parameters are only relevant if MTHAUT=1

AUTFRE =  Distance (A) for frozen atoms to be treated as
          moving atoms when MTHAUT=1. Default=2.0 A.

NTSFRZ =  60, 240 OR 960, initial tessera number for
          frozen atoms. Default=60

=======================================================
```

==========

$REORG group (optional)

This group controls the calculation of solvent reorganization energy within the framework of IEF-PCM. Presence of the $PCM group is a requirement for this group to work. Specialized keywords in the $PCM group that work with $REORG group are given below.

```
--------------
$PCM *** Only IEF=9,11,13,14 options are compatible ***
--------------
IEF=9 (models an environment with electrode and solvent
       where the electrode is treated as a perfect
       conductor => dielectric constant = infinity)
   =11 (models an environment with electrode + self-
        assembled monolayer (SAM) + solvent)
   =13 (models an environment with electrode + double
        layer (DL) + ionic solution)
   =14 (models homogeneous solvent)
```

Note that extra keywords in the $REORG group are required for the above keywords to work in the $PCM group. Also note that IEF=14 option in $PCM along with an appropriate choice of keywords in $REORG group may not reproduce the solution phase free energies obtained with the IEF=3 keyword in $PCM group because they use slightly different implementations of IEF-PCM equation (See JCP 2002, 117, 7266).

```
--------------
$REORG
--------------
LAMDA = 1 (calculates solvent reorganization energies
           with the total solvent polarization of the
           product; not recommended)
      = 2 (employs inertial polarization of the product)
```

The solvent reorganization energies for electron transfer and proton-coupled electron transfer reactions are calculated in a modular fashion. First, the equilibrium solvent response is separated into the inertial and non-inertial components and the corresponding surface charges are written to the punch file (*.dat). This process needs to be performed for both the oxidized and reduced states =>

separate inputfiles for oxidized and reduced states at the same solute geometry. The surface charges of these 2 states are then copied to a separate inputfile to calculate the non-equilibrium solvent free energies. To calculate the non-equilibrium solvent free energy for the oxidized state, one needs to copy the surface charges corresponding to the oxidized state first followed by the surface charges corresponding to the reduced state. Similarly, for the calculation of the non-equilibrium solvent free energy for the reduced state the surface charges corresponding to the oxidized state should follow the surface charges corresponding to the reduced state.

An equilibrium calculation is implied by the presence of IPCHG = 1

whereas a non-equilibrium calculation requires the following
2 keywords instead:

IRCHG = 1
RLMIT = BO (Born-Oppenheimer limit)
= SC (Self-consistent limit)

In the BO limit, the non-inertial charges are read from the inputfile (reactant state) and kept fixed during calculation whereas in the SC limit, the non-inertial charges are computed on-the-fly. In both cases, the inertial charges are read from the inputfile (product state).

A special type of calculation can be performed by taking the inertial surface charges to be the average of the reactant and product states. This calculation is triggered by RLMIT = SCTS option.

****** Model Specific Keywords ******

|electrode + solvent: IEF=9 in $PCM|

DISIHP = distance of Inner Helmholtz Plane (IHP) from the electrode in angstroms; The default value is RSOLV (radius of a solvent molecule).
RADCAT = the radius of the solvated electrolyte ion in angstroms; The default is 5.0 angstroms.

```
          Note that the center of mass (COM)
          of the molecule is placed at a distance "d"
          (= 2*DISIHP + RADCAT) from the electrode-solvent
          interface; this distance also defines the
          location of the Outer Helmholtz Plane (OHP); In
          principle, one can manipulate the distance of COM
          of the molecule from the electrode-solvent
          interface by changing the value of RADCAT.
          For example, setting RADCAT = 0.0 will place the
          COM at the outermost boundary of the 1st solvation
          shell; alternatively, setting RADCAT = -RSOLV
          will place the COM of the molecule at IHP. The
          latter choice of keyword may, however, result in
          an unphysical situation where a portion of
          the solute molecule may penetrate the electrode.
          To circumvent this situation, the distance between
          the COM of the molecule and the electrode-solvent
          interface is then reset to "d1" (= largest value
          of the z-coordinates of the surface tesserae plus
          10^(-5))


        |electrode + SAM + solvent: IEF=11 in $PCM|

ESAM   = dielectric constant of SAM; The default is 3.0
WSAM   = width of SAM in angstroms; The default is 15.0
DISTMS = distance of COM of the molecule from the SAM-
solvent
          interface in angstroms; The default is 5.0


      |electrode + DL + ionic solution: IEF=13 in $PCM|

DISIHP = distance of IHP from the electrode in angstroms;
          The default value is RSOLV
RADCAT = the radius of the solvated electrolyte ion
          in angstroms. The default is 5.0 angstroms
DISM   = ionic strength in Molar units (moles/Lt). The
          default is 0.0
EPSOHP = dielectric constant of the solvent between the 1st
          solvent sheath closest to the electrode and the
          OHP.  The default is EPS/2.0
EPSIOP = electronic dielectric constant of the solvent
          between the 1st solvent sheath closest to the
          electrode and the OHP. The default is EPSINF
```

```
EPSIHP = dielectric constant of the solvent between the
         electrode and 2*DISIHP. The default is EPSINF.
EPSIIP = electronic dielectric constant of the solvent
         between the electrode and the 1st solvent sheath
         closest to the electrode. The default is EPSINF
DLDIST = measure of the distance of the COM of the molecule
         from the DL-ionic solution interface in angstroms.
         The default is 0.0, which puts the COM of the
         molecule at a distance "d1" (=largest value of the
         z-coordinates of the surface tesserae + 10^(-5))
         from the DL-ionic solution interface.


            RECOMMENDED KEYWORDS FOR OTHER $ GROUPS
          (for less computation time/faster convergence)

--------------
$CONTRL
--------------
COORD=UNIQUE
UNITS=ANGS
RUNTYP=ENERGY
*** RUNTYP=OPTIMIZE is incompatible ***

--------------
$SCF
--------------
DIRSCF=.T.
DIIS=.T.
DAMP=.T.
*** For transition metal complexes ETHRSH = 2.0 is strongly
    recommended ***

--------------
$TESCAV
--------------
MTHALL=4 (strongly recommended)
NTSALL=60

--------------
$PCMCAV
--------------
RADII=VANDW (or SUAHF)

For transition metal complexes (strongly recommended)
```

```
--------------
$DFT
--------------
JANS=1


          *********** Example ***************
A typical set of keywords for the equilibrium calculation
of the oxidized state during the reduction of quinone in
DMF solvent with IEF=13 model is given by:
          ************************************
 $CONTRL
 COORD=UNIQUE UNITS=ANGS
 ISPHER=-1 MAXIT=200
 ICHARG=0 MULT=1 RUNTYP=ENERGY EXETYP=RUN
 SCFTYP=RHF DFTTYP=B3LYPV3 NPRINT=9
 $END
 $SYSTEM MWORDS=1000 $END
 $SCF DIIS=.T. DAMP=.T. DIRSCF=.T. $END
 $BASIS GBASIS=N31 NGAUSS=6 NDFUNC=1 NPFUNC=1 $END
 $PCM IEF=13 SOLVNT=DMSO EPS=37.219 EPSINF=2.046 $END
 $TESCAV MTHALL=4 NTSALL=60 $END
 $PCMCAV RADII=VANDW $END
 $REORG
 LAMDA=2 IPCHG=1
 RADCAT=4.0
 DISM=0.1 EPSOHP=18.6095
 $END
 $DATA
solvent dmf, double layer + ionic solution
 C1
C    6.0    -0.62400  -0.02800  -0.34790
C    6.0     0.71910  -0.02690  -0.34810
C    6.0     1.49200   1.24330  -0.34830
C    6.0     0.71700   2.51230  -0.34810
C    6.0    -0.62610   2.51120  -0.34790
H    1.0    -1.21110  -0.94200  -0.34770
H    1.0     1.30760  -0.94000  -0.34830
H    1.0     1.30410   3.42630  -0.34830
H    1.0    -1.21460   3.42430  -0.34770
C    6.0    -1.39900   1.24100  -0.34770
O    8.0    -2.62410   1.24000  -0.34740
O    8.0     2.71710   1.24440  -0.34860
$END
          ************************************
```

```
-------------------------------------------------------------
-
The two most important solvent parameters required to
calculate solvent reorganization energies are 1) EPS
(static dielectric constant of the solvent) and 2) EPSINF
(optical dielectric constant). In the above example, DMF is
not present in the standard GAMESS solvent database and so,
the radius a DMF molecule is approximated with the radius
of a DMSO molecule whereas the static and optical
dielectric constants (EPS and EPSINF) are provided
explicitly in the inputfile via keywords.

** Note also that a similar set of keywords as above can be
employed to compute just the solution phase free energy in
certain non-standard environments (IEF=9,11,13) **
-------------------------------------------------------------
-
The inputfile for the corresponding reduced state is
obtained by setting ICHARG=-1; MULT=2; SCFTYP=UHF.

Inputfile for the calculation of the corresponding non-
equilibrium free energy of the oxidized state is obtained
by replacing IPCHG=1 with IRCHG=1 and adding RLMIT=SC (or
BO) to the $REORG group. In addition, the user has to copy
the surface charges of the oxidized and reduced states from
the corresponding .dat files and place the surface charges
at the end of the inputfile. Note that the order in which
the surface charges are placed in the input file matters.

A python script is provided with the GAMESS code that runs
the equilibrium calculations, generates the inputfiles for
the non-equilibrium calculations, runs them and finally
prints out the solvent reorganization energies.

*** The above group of keywords may also be employed to
    generate potential energy scans in the presence of
    the solvent if the user wants to keep the inertial
    solvent polarization fixed during the scan. In this
    case, the solute cavity is also assumed to be unchanged
    during the scan. ***

=============================================================
```

==========

$NEWCAV group (optional)

This group controls generation of the "escaped charge" cavity, used when ICOMP=3 or IREP=1 in $PCM. This cavity is used only to calculate the fraction of the solute electronic charge escapes from the original cavity.

IPTYPE = choice for tessalation of the cavity's spheres.
= 1 uses a tetrahedron
= 2 uses a pentakisdodecahedron (default)

ITSNUM = m, the number of tessera to use on each sphere.
if IPTYPE=1, input m=30*(n**2), with n=1,2,3 or 4
if IPTYPE=2, input m=60*(n**2), with n=1,2,3 or 4
(default is 60)

*** the next three parameters pertain to IREP=1 ***

RHOW = density, relative to liquid water (default = 1.0)

PM = molecular weight (default = 18.0)

NEVAL = number of valence electrons on solute (default=8)

The defaults for RHOW, PM, and NEVAL correspond to water, and therefore must be correctly input for other solvents.

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$PCMGRD group (optional)

```
    This group controls the PCM gradient computations.  It
is of a technical nature, and is seldom given.

IPCDER = selects different methods for PCM gradients
         1  use Ux(q) approximation (C-PCM and IEF-PCM),
            or use charge-derivative method (D-PCM).
            This is the default for D-PCM.
         2  Variable-Tessera-Number Approximation.
            Implemented only for C-PCM and IEF-PCM, and
            the default for GEPOL-AS tesselation.
         3  The same as 2, but for FIXPVE tessellation.
The program will pick the correct default for IPCDER!

note: If ICAV = 1 or IDISP = 1 in $PCM, the derivatives
      of the cavitation energy or dispersion-repulsion,
      respectively, will automatically be calculated.
      You must be using the following input:
        $PCM ICAV=1 IDISP=1 $END
        $DISREP ICLAV=1 $END

IFAST  = Controls the PCM calculations for RUNTYP=OPTIMIZE.
         0  update PCM charges at each SCF cycle at every
            geometry (default)
         1  update PCM charges at each SCF cycle for the
            initial geometry.
            For the subsequent geometries, calculate PCM
            charges at the first SCF cycle and use the PCM
            charges for the following SCF cycles; after
            the density change falls below DENTOL, update
            the PCM charges one time (to save CPU time).
```

==========

==========

$IEFPCM group (optional)

This group defines data for the integral equation formalism version of PCM solvation. It includes special options for ionic or anisotropic solutions.

The next two sets are relevant only for anisotropic solvents, namely IEF=1:

EPS1, EPS2, EPS3 =
diagonal values of the dielectric permittivity tensor with respect to the laboratory frame. The default is EPS in $PCM

EUPHI, EUTHE, EUPSI =
Eulerian angles which give the rotation of the solvent orientation with respect to the lab frame. The term lab frame means $DATA orientation. The default for each is zero degrees.

The next two are relevant to ionic solvents, namely IEF=2:

EPSI = the ionic solutions's dielectric, the default is EPS from $PCM.

DISM = the ionic strength, in Molar units (mol/dm**3) The default is 0.0

==========

==========

$PCMITR group (optional, for IEF=-3 or -10 in $PCM)

This group provides control over the iterative isotropic IEF-PCM calculation. See

C.S.Pomelli, J.Tomasi, V.Barone
Theoret.Chem.Acc. 105, 446-451(2001)
H.Li, C.S.Pomelli, J.H.Jensen
Theoret.Chem.Acc. 109, 71-84(2003)

MXDIIS = Maximum size of the DIIS linear equations, the value impacts the amount of memory used by PCM. Memory=2*MXDIIS*NTS, where NTS is the number of tesserae. MXDIIS=0 means no DIIS, instead the point Jacobi iterative method will be used. (Default=50)

MXITR1 = Maximum number of iters in phase 1. (Default=50)

MXITR2 = Maximum number of iters in phase 2. (Default=50)

note: if MXDIIS is larger than both MXITR1 and MXITR2 MXDIIS will be reset to be the larger of these two.

THRES = Convergence threshold for the PCM Apparent Surface Charges (ASC). (Default=1.0D-08)

THRSLS = Loose threshold used in the early SCF cycles when the density change is above DENSLS. If THRSLS < THRESH, this option is turned off. Default is 5.0D-04.

DENSLS = If the density change is above DENSLS the loose threshold THRSLS applies. (Default = 0.01 au)

IDIRCT = 1, Directly compute the electronic potential at each tessera and the ASC potential at the electronic coordinates, with no disk storage. (Default)
0, Compute and save above data to hard disk.

Keywords for region wise multipole expansion of ASCs in approximating interaction among tesserae:

(C.S.Pomelli, J.Tomasi THEOCHEM 537, 97-105(2001))

IMUL = Region wise multipole expansion order in the approximate interaction among tesserae.
= 0, Neglected (Only for test purposes)
= 1, Monopole
= 2, Monopole+Dipole
= 3, Monopole+Dipole+Quadrupole (Default)

RCUT1 = Cutoff radius (Angstrom) for mid-range interactions among tesserae. Default=15.0 A
If RCUT1 is larger than your molecule, the option is effectively turned off.

RCUT2 = Cutoff radius (Angstrom) for long range interactions among tesserae. Default=30.0 A

The remaining keywords apply only to PCM calculations with a QM/EFP solute (see Li et al.)

Keywords for region wise multipole expansion of ASCs in approximating interaction between ASCs and QM region:

IMGASC = 1, Use region wise multipole expansion of ASCs to compute the ASC potential at QM region.
0, no use of the multipole expansion method. (default)

RASC = Cutoff radius (Angstrom) for used of the IMGASC multipole expansion (Default=20.0 A)

Keywords for multipole expansion of the QM region in approximating the QM region potential:

IMGABI = 0, multipole expansion of the QM region is turned off (default).
1, turn multipole expansion of the QM region on.

RABI = Cutoff radius (Angstrom) for used of the IMGABI multipole expansion (Default=4.0 A)

Keywords for the coupling of PCM and EFP polarizability tensors:

IEFPOL = 1, PCM ASCs induce EFP dipoles.(default)

```
          0, PCM ASCs do not induce EFP dipoles.

REFPOL =  When IEFPOL=1, if the distance (Angstrom) between
          a polarizability point and a tessera is less than
          REFPOL, they are considered too close and the
          field from the tessera will not induce dipole for
          the polarizability point. Default=0.0 A means
          always induce the dipole.

=============================================================
```

==========

$DISBS group (optional)

This group defines auxiliary basis functions used to evaluate the dispersion free energy by the method of Amovilli and Mennucci. These functions are used only for the dispersion calculation, and thus have nothing to do with the normal basis given in $BASIS or $DATA. If the input group is omitted, only the normal basis is used for the IDP=1 dispersion energy.

NADD = the number of added shells

XYZE = an array giving the x,y,z coordinates (in bohr) of the center, and exponent of the added shell, for each of the NADD shells.

NKTYPE = an array giving the angular momenta of the shells

An example placing 2s,2p,2d,1f on one particular atom,

```
 $DISBS  NADD=7 NKTYP(1)= 0 0 1 1 2 2 3
         XYZE(1)=2.9281086   0.0  .0001726   0.2
                 2.9281086   0.0  .0001726   0.05
                 2.9281086   0.0  .0001726   0.2
                 2.9281086   0.0  .0001726   0.05
                 2.9281086   0.0  .0001726   0.75
                 2.9281086   0.0  .0001726   0.2
                 2.9281086   0.0  .0001726   0.2  $END
```

==========

==========

$DISREP group (optional)

This group controls evaluation of the dispersion and repulsion energies by the empirical method of Floris and Tomasi. The group must be given when IDISP=1 in $PCM, whenever the solvent is not water. Only one of the two options ICLAV or ILJ should be selected. Due to its lack of parameters, almost no one chooses ILJ.

```
ICLAV = selects Claverie's disp-rep formalism.
      = 0 skip computation.
      = 1 Compute the solute-solvent disp-rep interaction
          as a sum over atom-atom interactions through a
          Buckingham-type formula (R^-6 for dispersion,
          exp for repulsion).  (default)
          Ref: Pertsin-Kitaigorodsky "The atom-atom
               potential method", page 146.

ILJ   = selects a Lennard-Jones formalism.
      = 0 skip computation. (default)
      = 1 solute atom's-solvent molecule interaction is
          modeled by Lennard-Jones type potentials, R^-6
          for dispersion, R^-12 for repulsion).

---- the following data must given for ICLAV=1:

RHO   = solvent numeral density
N     = number of atom types in the solvent molecule
NT    = an array of the number of atoms of each type in a
        solvent molecule
RDIFF = distances between the first atoms of each type
        and the cavity
DKT   = array of parameters of the dis-rep potential for
        the solvent
RWT   = array of atomic radii for the solvent

The defaults are appropriate for water,
   RHO=3.348D-02
   N=2
   NT(1)=2,1
   RDIFF(1)=1.20,1.50
   DKT(1)=1.0,1.36
   RWT(1)=1.2,1.5
```

```
DKA   = array of parameters of the dis-rep potential for
        the solute.  Defaults are provided for some common
        elements:
        H: 1.00   Be: 1.00   B: 1.00   C: 1.00
        N: 1.10    O: 1.36   P: 2.10   S: 1.40

RWA   = array of atomic radii for the solute to compute
        dis-rep.  Defaults are provided for some common
        elements:
        H: 1.20   Be: 1.72   B: 1.72   C: 1.72
        N: 1.60    O: 1.50   P: 1.85   S: 1.80

Other elements have DKA and RWA values of 0.0 and so must
be  given in the input deck, or the dispersion/repulsion
energy will be 0.  For EFP/PCM calculations, only QM atoms
need DKA and RWA values to calculate the DIS-REP energy.

---- the following data must given for ILJ=1:

RHO   = solvent numeral density
EPSI  = an array of energy constants referred to each atom
        of the solute molecule.
SIGMA = an array of typical distances, relative to each
        solute atom
=============================================================
```

==========

$SVP group (optional)

The presence of this group in the input turns on use of the Surface and Simulation of Volume Polarization for Electrostatics (SS(V)PE) solvation model, or the more exact Surface and Volume Polarization for electrostatics (SVPE) model. These treat the solvent as a dielectric continuum, and are available with either an isodensity or spherical cavity around the solute. The solute may be described only by RHF, UHF, ROHF, GVB, or MCSCF wavefunctions. The energy is reported as a free energy, which includes the factor of 1/2 that accounts for the work of solvent polarization assuming linear response. Gradients are not yet available.

In addition, the CMIRS (Composite Method for Implicit Representation of Solvent) model may be invoked to combine SS(V)PE with the DEFESR (Dispersion, Exchange, and Field-Extremum Short-Range) model to achieve a more complete treatment of solvation. The field-extremum contribution is designed to describe hydrogen bonding effects.

The current version 1.0 of CMIRS has parameters for water solvent with isodensity cavities having contours of 0.0005, 0.001, or 0.002 au for use with the B3LYP/6-31+G*, B3LYP/G3large, HF/6-31+G*, or HF/G3large electronic structure methods. In addition, parameters are also available for cyclohexane and benzene solvents with isodensity cavities having contours of 0.0005, 0.001, or 0.002 au for use with the B3LYP/6-31+G* method.

Typical use of these methods will involve a prior step to do an equivalent calculation on the given solute in the gas phase. This provides a set of orbitals that can be used as a good initial guess for the subsequent run including solvent. It also provides the gas phase energy (input as keyword EGAS) that can be subtracted from the energy in solvent to obtain the free energy of solvation.

Many runs will be fine with all parameters set at their default values. The most important parameters a user may want to consider changing are:

NVLPL = treatment of volume polarization

```
          0 - SS(V)PE method, which simulates volume
              polarization by effectively folding in an
              additional surface polarization (default)
          N - SVPE method, which explicitly treats volume
              polarization with N extra layers

DIELST = static dielectric constant of solvent
          (default = 78.39, appropriate for water)

IVERT  = 0 do an equilibrium calculation (default)
         1 do a nonequilibrium calculation to get the final
           state of a vertical excitation - this requires
           that IRDRF=1 to read the $SVPIRF input group
           that was punched with IPNRF=1 in a run on the
           initial state - note that a meaningful result is
           obtained only if the initial and final states
           both come from the same wavefunction/basis set/
           geometry/solvation model.

DIELOP = optical dielectric constant of solvent -
         this only relevant if IVERT=1
         (default 1.776, appropriate for water)

EGAS   = gas phase energy (optional): if given, the program
         will output the free energy of solvation and the
         change in solute internal energy due to solvation.
         Note that a meaningful result is obtained only if
         EGAS comes from the same wavefunction/basis set/
         geometry as is used in the solvation calculation

ISHAPE = sets the shape of the cavity surface
         0 - electronic isodensity surface (default)
         1 - spherical surface

RHOISO = value of the electronic isodensity contour used to
          specify the cavity surface, in electrons/bohr**3
          (relevant if ISHAPE=0; default=0.001)

RADSPH = sphere radius used to specify the cavity surface.
         A positive value means it is given in Bohr,
         negative means Angstroms. (relevant if ISHAPE=1;
         default is half the distance between the
         outermost atoms plus 1.4 Angstroms)

INTCAV = selects the surface integration method
```

0 - single center Lebedev integration (default)
1 - single center spherical polar integration,
not recommended; Lebedev is far more efficient

NPTLEB = number of Lebedev-type points used for single center surface integration. The default value has been found adequate to obtain the energy to within 0.1 kcal/mol for solutes the size of monosubstituted benzenes. (relevant if INTCAV=0) Valid choices are 6, 14, 26, 38, 50, 86, 110, 146, 170, 194, 302, 350, 434, 590, 770, 974, 1202, 1454, 1730, 2030, 2354, 2702, 3074, 3470, 3890, 4334, 4802, 5294, or 5810. (default=1202)

NPTTHE, NPTPHI = number of (theta,phi) points used for single center surface integration. These should be multiples of 2 and 4, respectively, to provide symmetry sufficient for all Abelian point groups. (relevant if INTCAV=1; defaults = 8,16; these defaults are probably too small for all but the tiniest and simplest of solutes.)

TOLCHG = a convergence criterion on the program variable named CHGDIF, which is the maximum change in any surface charge from its value in the previous iteration (default=1.0D-6). This is checked in each SCF iteration, although the actual value is not printed until final convergence is reached.

The single-center surface integration approach may fail for certain highly nonspherical molecular surfaces. The program will automatically check for this and bomb out with a warning message if need be. The single-center approach succeeds only for what is called a star surface, meaning that an observer sitting at the center has an unobstructed view of the entire surface. Said another way, for a star surface any ray emanating out from the center will pass through the surface only once. Some cases of failure may be fixed by simply moving to a new center with the ITRNGR parameter described below. But some surfaces are inherently nonstar surfaces and cannot be treated with this program until more sophisticated surface integration approaches are implemented.

ITRNGR = translation of cavity surface integration grid

```
          0 - no translation (i.e., center the grid at the
              origin of the atomic coordinates)
          1 - translate to center of nuclear mass
          2 - translate to center of nucl. charge (default)
          3 - translate to midpoint of outermost atoms
          4 - translate to midpoint of outermost
              non-Hydrogen atoms
          5 - translate to user-specified coordinates,
              in Bohr
          6 - translate to user-specified coordinates,
              in Angstroms

TRANX, TRANY, TRANZ = x,y,z coordinates of translated
          cavity center, relevant if ITRNGR=5 or 6.
          (default = 0,0,0)

IROTGR = rotation of cavity surface integration grid
          0 - no rotation
          1 - rotate initial xyz axes of integration grid to
              coincide with principal moments of nuclear
              inertia (relevant if ITRNGR=1)
          2 - rotate initial xyz axes of integration grid to
              coincide with principal moments of nuclear
              charge (relevant if ITRNGR=2; default)
          3 - rotate initial xyz axes of integration grid
              through user-specified Euler angles as defined
              by Wilson, Decius, Cross

ROTTHE, ROTPHI, ROTCHI = Euler angles (theta, phi, chi) in
               degrees for rotation of the cavity surface
               integration grid, relevant if IROTGR=3.
               (default=0,0,0)

IOPPRD = choice of the system operator form. The default
          symmetric form is usually the most efficient, but
          when the number of surface points N is big it can
          require very large memory (to hold two N by N
          matrices). The nonsymmetric form requires solution
          of two consecutive system equations, and so is
          usually slower, but as trade-off requires less
          memory (to hold just one N by N matrix). The two
          forms will lead to slightly different numerical
          results, although tests documented in the third
          reference given in Further Information show that
          the differences are generally less than the
```

```
          inherent discretization error itself and so are
          not meaningful.
          0 - symmetric form (default)
          1 - nonsymmetric form
```

* * *

The CMIRS (Composite Method for Implicit Representation of Solvent) model is a combination of SS(V)PE with the DEFESR (Dispersion, Exchange, and Field-Extremum Short-Range) model. It borrows use of a grid from the DFT code, and therefore is currently implemented only for the $DFT METHOD=GRID choice in $CONTRL: note that HF calculations can be done with DFTTYP=HFX in $CONTRL. If default parameters are desired (which correspond to water solvent, an isodensity cavity with contour 0.001 au, and the B3LYP/6-31+G* electronic structure method), then only the IDEF flag needs to be set.

```
IDEF     = flag to activate DEFESR calculations
           0 - DEFESR energies are not computed (default)
           1 - DEFESR energies are also computed

RHOSOLV  = average electron density of solvent for use in
           the dispersion model (default=0.05 au for water)

DISDMP   = dispersion damping factor (default 7.0 bohr).
           This value has been found to be nearly optimal
           for all solvent/cavity/methods tested.

DISLIN   = dispersion linear parameter
           (default=0.0109369 au).
           It is sensitive to the solvent/cavity/method.

EXCLIN   = exchange linear parameter
           (default=0.0460402 au).
           It is sensitive to the solvent/cavity/method.

NGSLGR   = order of Gauss-Laguerre numerical integration
           used for the exchange term (default=6).
           Possible values are 1 to 25.

FNNL,FPNL = field-negative and field-positive nonlinear
           parameters (default=3.6 and 3.6).  These values
```

have been found to be nearly optimal for all solvent/cavity/methods tested.

FNLIN,FPLIN = field-negative and field-positive linear parameters (defaults=-945.810 and -17.8279 au). They are sensitive to the solvent/cavity/method. For solvents like cyclohexane and benzene that have negligible hydrogen-bonding capability they can be set to 0.

SMVLE = flag to turn on an alternative (to DEFESR) semi-empirical correction for local electrostatic effects based on the electric field's normals to the surface cavity. This also adds cavitation/dispersion/solvent structure (CDS) effects drawn from the SMD model, see SMD in $PCM. (Default=.FALSE.)

* * *

The remaining parameters below are rather specialized and rarely of concern. They should be changed from their default values only for good reason by a knowledgeable user.

TOLCAV = convergence criterion on maximum deviation of calculated vs. requested RHOISO (relevant if ISHAPE=0; default=1.0D-10)

ITRCAV = maximum number of iterations to allow before giving up in search for isodensity surface. (relevant if ISHAPE=0; default=99)

NDRCAV = highest analytic density derivative to use in the search for isodensity surface.
0 - none, use finite differences (default)
1 - use analytic first derivatives

LINEQ = selects the solver for the linear equations that determine the effective point charges on the cavity surface.
0 - use LU decomposition in memory if space permits, else switch to LINEQ=2
1 - use conjugate gradient iterations in memory if space permits, else use LINEQ=2 (default)

```
          2 - use conjugate gradient iterations with the
              system matrix stored externally on disk.

CVGLIN = convergence criterion for solving linear equations
         by the conjugate gradient iterative method
         (relevant if LINEQ=1 or 2; default = 1.0D-7)

CSDIAG = a factor to multiply diagonal elements to improve
         the surface potential matrix, S.
         (default = 1.104, optimal for Lebedev integration)

IRDRF  = a flag to read in a set of point charges as an
         initial guess to the reaction field.
         0 - no initial guess reaction field (default)
         1 - read point charges from $SVPIRF input group.
             It is up to the user to be sure that the
             number of charges read is appropriate.

IPNRF  = a flag to punch the final reaction field.
         0 - no punch (default)
         1 - punch in format of $SVPIRF input group

=============================================================
```

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$SVPIRF group (optional; relevant for SVP runs)

Formatted card images of reaction field point charges, as punched by setting IPNRF=1 in a previous SVP run. These can be used by setting IRDRF=1 in a subsequent SVP run to provide an initial guess to the reaction field.

These charges from the initial state are required if IVERT=1 in $SVP to do a vertical excitation calculation on the final state.

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$COSGMS group (optional)

The presence of this group in the input turns on the use of the conductor-like screening model (COSMO) with molecular shaped cavity for closed and open shell HF, DFT, and MP2. Open shells may be high spin-restricted or any sort of spin-unrestricted case. The energy and/or the gradient can be computed for each of these.

The implementation of the COSMO cavity has a limit of about 150-200 atoms. Like other limits in GAMESS, this can be raised according to directions in the Programmer's Reference.

EPSI = the dielectric constant, 80 is often used for H2O
This parameter must be given, except for the perfect conductor approximation (see PRFCND).

PRFCND = perfect conductor approximation, sets EPSI equal to infinity. Relevant only if EPSI is not given. (default=.FALSE.)

COSRAD = the multiplicative factor for the van der Waals radii used for cavity construction. (default=1.2)

NSPA = the number of surface points on each atomic sphere that form the cavity. (default=92)

DISEX = parameter for the refinement of crevices (default=10.0D+00)

OUTCHG select the method for the correction of the outlying charge error (OCE).
= DMULTI sets the multipole expansion method.
= DBLCAV sets the double cavity method (default).

COSWRT = flag to generate the .cosmo output file, used as input to the COSMO-RS program, from the company COSMOlogic. A replacement output source file is needed (full version of cosprt.src). Users need to sign a special license agreement to enable this option, see http://ocikbws.uzh.ch/gamess
COSWRT forces PRFCND=.T. and requires GBASIS=KTZVP

```
          and DFTTYP=BP86, because COSMO-RS is parametrized
          for use only with this specific setup.
          (default=.FALSE.)

DCOSMO = flag to use the DCOSMO-RS method.  This requires
          reading in a supplementary .pot file, obtained
          by processing COSWRT's .cosmo output with the
          COSMO-RS software.  (default is .FALSE.)

COSBUG = flag to turn on debugging printout.

     Additional information on the COSMO model can be
     found in the References chapter of this manual.

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```

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$SCRF group (optional)

The presence of this group in the input turns on the use of the Kirkwood-Onsager spherical cavity model for the study of solvent effects. The method is implemented for RHF, UHF, ROHF, GVB and MCSCF wavefunctions and gradients, and so can be used with any RUNTYP involving the gradient. The method is not implemented for MP2, CI, any of the semiempirical models, or for analytic hessians.

DIELEC = the dielectric constant, 80 is often used for H2O

RADIUS = the spherical cavity radius, in Angstroms

G = the proportionality constant relating the solute molecule's dipole to the strength of the reaction field. Since G can be calculated from DIELEC and RADIUS, do not give G if they were given.

==========

Additional information on the SCRF model can be found in the Further Information chapter.

==========

$ECP group (required if PP=READ in $CONTRL)

This group lets you read in effective core potentials, for some or all of the atoms in the molecule. You can use built in potentials for some of the atoms if you like. This is a free format (positional) input group. Since the input is a little tricky, it is good to look at the two examples at the end of this group.

*** Give a card set -1-, -2-, and -3- for each atom ***

-card 1- PNAME, PTYPE, IZCORE, LMAX+1

PNAME is a 8 character descriptive tag for this potential.

If PNAME is repeated later, for the same type of element, the previously defined potential is copied to this atom. No other information should be given on this card, and cards -2- and -3- must be skipped.

Do not use this "copy" option when there is no core potential, instead type "NONE" over and over again.

PTYPE = GEN a general potential should be read.
= SBKJC look up the Stevens/Basch/Krauss/Jasien/ Cundari potential for this type of atom.
= HW look up the Hay/Wadt built in potential for this type of atom.
= NONE treat all electrons on this atom.

IZCORE is the number of core electrons to be removed. Obviously IZCORE must be an even number, or in other words, all core orbitals being removed must be completely occupied.

LMAX+1 is the one higher than the maximum angular momentum occupied in the core orbitals being removed:
to remove s,p,d,f core orbitals (LMAX=0,1,2,3)
we use p,d,f,g core potentials (LMAX+1=1,2,3,4).
LMAX+1 is not permitted to exceed 4.

*** Give IZCORE and LMAX only if PTYPE is GEN ***

*** For the first occurrence of PNAME, if PTYPE is GEN, ***
*** then give cards -2- and -3-. Otherwise go to -1-. ***

```
*** Card sets -2- and -3- are repeated LMAX+1 times     ***

    The potential U(LMAX+1) is given first, followed by
    difference potentials U(L)-U(LMAX+1), for L=0,LMAX.
    Note that is a minus sign, not a hyphen!
    The LMAX potential, and the differences of potentials
    are expanded by Gaussians, on these two cards.

-card 2-    NGPOT

NGPOT is the number of Gaussians in this part of the
      fit to the local effective potential.

-card 3-    CLP,NLP,ZLP   (repeat this card NGPOT times)

CLP is the coefficient of this Gaussian in the potential.
NLP is the power of r for this Gaussian, 0 <= NLP <= 2.
ZLP is the exponent of this Gaussian.

Note that PTYPE lets you to type in one or more atoms
explicitly, while using built in data for other atoms.

By far the easiest way to use the SBKJC potential for all
atoms in the formic acid molecule is to request PP=SBKJC in
$CONTRL.  But here we show two alternatives.  Note that
both examples copy one oxygen potential to the other, and
both explicitly declare there is no potential on every
hydrogen.

Assume that the atoms in $DATA are generated in the order
C, H, O, O, H.

The first way is to look up the program's internally stored
SBKJC potentials one atom at a time:

 $ECP
C-ECP SBKJC
H-ECP NONE
O-ECP SBKJC
O-ECP
H-ECP NONE
 $END

The second oxygen duplicates the first, no core electrons
are removed on hydrogen.  The order of the atoms must
```

follow that generated by $DATA. All atoms must be given here in $ECP, not just the symmetry unique atoms.

The second example reads all SBKJC potentials explicitly:

```
 $ECP
C-ECP GEN 2 1
1      ----- CARBON U(P) -----
 -0.89371  1  8.56468
2      ----- CARBON U(S)-U(P) -----
  1.92926  0  2.81497
 14.88199  2  8.11296
H-ECP NONE
O-ECP GEN 2 1
1      ----- OXYGEN U(P) -----
 -0.92550  1 16.11718
2      ----- OXYGEN U(S)-U(P) -----
  1.96069  0  5.05348
 29.13442  2 15.95333
O-ECP
H-ECP NONE
 $END
```

Again, the 2nd oxygen copies from the first. It is handy to use the rest of card -2- as a descriptive comment.

As a final example, for antimony we have LMAX+1=3 (the core 3d is removed, so LMAX=2). One must first enter U(f), followed by U(s)-U(f), U(p)-U(f), U(d)-U(f).

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$MCP group (required if MCP READ was given on card -6U-)

This group lets you read in model core potentials, for some or all of the atoms in the molecule. This is a fixed format input group. For the review of the MCP method, see M.Klobukowski, S.Huzinaga, and Y.Sakai, pp. 49-74 in J. Leszczynski, "Computational Chemistry", vol. 3 (1999) .

*** Give input -1-, -2-, ..., -9- for each MCP atom ***

-card 1- ANAT

ANAT is a 8 character name for the MCP atom. It must match the name given for that atom in the $DATA input group.

-card 2- NOAN, (NO(IS),NG(IS), IS=1,4) FORMAT(9I3)
IS = 1, 2, 3, 4 for s, p, d, and f symmetry, resp.

NOAN is the number of terms in the MCP
NO(IS) is the number of core orbitals in symmetry IS
NG(IS) is the number of basis functions used to expand the core orbitals in symmetry IS

-card 3- ZEFF, MCPFMT FORMAT(F10.2, A8)

ZEFF is the number of valence electrons, e.g. 7.0 for Fluorine
MCPFMT is the format for reading floating-point numbers in the MCP data

-card 4- (ACOEF(L), L=1,NOAN) FORMAT(MCPFMT)

ACOEF(L) is the L-th coefficient in the expansion of the model core potential; more than one line may be provided
ACOEF(L) is the defined as A(l) in Eq. (38) of the MCP review paper.

-card 5- (AEXPN(L), L=1,NOAN) FORMAT(MCPFMT)

AEXPN(L) is the L-th exponent in the expansion of the model core potential; more than one line may be provided

```
               AEXPN(L) is the defined as alpha(l) in Eq.
               (38) of the MCP review paper.

-card 6-    (NINT(L), L=1,NOAN)                FORMAT(10I3)

      NINT(L)  is the power of R in the expansion of the
               model core potential; NINT(L) is defined
               as n(l) in Eq. (38) of the MCP review paper.

 *** For each symmetry IS present in the core orbitals ***
 *** read the card set -7-, -8-, and -9-               ***

-card 7-    (BPAR(K), K=1,NO(IS))           FORMAT(MCPFMT)
      BPAR(K)  is the constant in the core projector
               operator, B(k) in Eq. (41) of the review.

-card 8-    (EX(I), I=1,NG(IS))             FORMAT(MCPFMT)
      EX(I)    is the exponent of the I-th Gaussian
               function used to expand the core orbitals

 *** Repeat -9- for each core orbital in symmetry IS ***

-card 9-    (C(I), I=1,NG(IS))              FORMAT(MCPFMT)
      C(I)     expansion coefficients of the core orbital

 The following example input file is for H2CO, and by
the way, provides another example of COORD=HINT.

!
 $CONTRL  RUNTYP=ENERGY  COORD=HINT  PP=MCP $END
 $DATA
Formaldehyde H2CO
CNV      2

C   6.0     LC   0.00          0.0     0.0  - O K
 MCP READ               <<<< this is an MCP atom
  L       3             <<<< (311/311/1) basis
  1  18.517235         -0.16370140          0.22673090E-01
  2  2.5787547         -0.26304451          0.19109693
  3 0.58994362          0.58040872          0.50918856
  L       1
  1 0.17330638           1.0000000           1.0000000
  L       1
  1 0.60957120E-01       1.0000000           1.0000000
  D 1;  1  0.600  1.0
```

```
O  8.0   LC   1.2031          0.0     0.0  - O K
 MCP READ                <<<< this is an MCP atom
  L       3              <<<< (311/311/1) basis
  1  44.242510          -0.13535836          0.17372951E-01
  2  6.2272700          -0.30476423          0.16466813
  3  1.4361751           0.43955753          0.46721611
  L       1
  1 0.40211473           1.0000000           1.0000000
  L       1
  1 0.12688798           1.0000000           1.0000000
  D 1;  1  1.154  1.0

 H  1.0   PCC  1.1012   121.875  0.0  + O K I
  TZV                   <<<< not an MCP atom, TZV+pol basis
 P 1;  1  1.100  1.0

 $END

 $MCP                           <<<< start of the MCP data
                                <<<< empty lines allowed
MCP for  C  NR (2S/2P)    S(2)P(2)  <<<< comment
                                <<<< empty lines allowed
  C                                   <<<< MCP for the atom C
  2  1 14                             <<<< NOAN, NO(1), NG(1)
      4.00(4D15.8)                    <<<< ZEFF, MCPFMT
  .41856306      .99599513E-01        <<<< ACOEF
  16.910482      7.4125554            <<<< AEXPN
  0  0                                <<<< NINT
  22.676882                           <<<< B(1s)
  26848.283      8199.1206      2798.3668      1048.2982
  423.36984      181.26843      81.068295      37.403931
  17.629539      8.4254263      4.0611964      1.9672294
  .95541420      .46459041
  .10743274D-03  .21285491D-03  .99343100D-03 .28327774D-02
  .83154481D-02  .21694082D-01  .52916004D-01 .11618593D+00
  .21812785D+00  .32180986D+00  .29375407D+00 .10974353D+00
  .70844050D-02  .17825971D-02

MCP for  O  NR (2S/2P)            S(2)P(4)

  O                                    <<<< MCP for the atom O
  2  1 16
      6.00(4D15.8)
  .31002267      .27178756E-01
```

```
  25.973731      13.843290
  0  0
  41.361784
  57480.749      17270.167      5766.9282      2107.0076
  829.06758      346.04791      151.12147      68.233250
  31.542773      14.815300      7.0298236      3.3561489
  1.6077662      .77153240      .37052330      .17799002
  .85822477D-04  .18173691D-03  .84803428D-03 .25439914D-02
  .76877460D-02  .20823429D-01  .52424753D-01 .11864010D+00
  .22782741D+00  .33492260D+00  .28833079D+00 .93046197D-01
  .55937988D-02  .16121923D-02  .10915544D-04 .21431633D-03

 $END
```

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$RELWFN group (optional)

This group is relevant if RELWFN in $CONTRL choses any of the relativistic transformations for elimination of the small components of relativistic wavefunctions, to produce corrected single component wavefunctions. These scalar relativistic corrections may be included during any self-consistent method, and any correlation treatment may be used. Wavefunctions incorporating scalar relativity may also be used by the spin-orbit coupling perturbation program (see RUNTYP=TRANSITN, and NESOC just below).

The RELWFN keywords are intended for use in all-electron calculations only. Scalar relativistic effects may also be treated by the use of ECP-type or MCP-type core potentials, in which case see the PP keyword in $CONTRL.

One family of ESC methods began with the relativistic elimination of small components (RESC), continued through second and third order Douglas/Kroll (DK), reaching an infinite order two component scheme (IOTC) equivalent to converging the DK series. The pinnacle of this line is the local unitary transformation approximation to full IOTC (LUT-IOTC). RELWFN=LUT-IOTC is the most numerically accurate and fastest running method available, so the use of LUT-IOTC is recommended.

Within this ESC progression, only one electron kinetic energy, nuclear attraction, and overlap integrals (and associated one electron gradient terms) are modified. Note that scalar 2e- relativistic corrections exist in nature, as well as the Dirac-Coulomb equation, but are not treated by RESC, DK, IOTC, or LUT-IOTC. One electron effects are larger by far, being about 1,147 Hartree for a gold atom, compared to 27 Hartrees for Au's two electron correction.

The Normalized Elimination of Small Components (NESC) treats corrections to two electron integrals by means of a relativistically averaged basis set. This is in addition to the one electron modifications mentioned above. All of the relativistic methods in GAMESS neglect two-electron corrections coming from pVp integrals.

Analytic gradients are available for any RELWFN choice, provided the basic quantum chemistry method itself has gradient programming. NESC, RESC, and LUT-IOTC have fully analytical gradients. For DK and IOTC, the relativistic gradient contributions are evaluated numerically by a double difference formula, so that one might think of their gradients as "semi-analytic". Relativistic force constant matrices are evaluated by semi-numerical differencing of relativistic gradients. The accuracy of the LUT-IOTC gradients is similar to non-relativistic runs, and should be suitable for frequency evaluation.

For NESC, RESC, any order DK, or IOTC (but not LUT-IOTC), the 1e- part of the Breit-Pauli operator's integrals are corrected only to first order (DK1): this is keyword NESOC=1 below. It has been observed by many people that even the first order correction is small, and thus should be sufficient.

Scalar relativity produces great changes in radial sizes of atomic orbitals, so care must be paid to the basis set. Certainly at the bottom of the periodic table, one must use basis sets which have been contracted using some kind of relativistic treatment (literature basis sets often use 2nd order DK when contracting, and these are fine to use with RELWFN=LUT-IOTC. The best choices available, at present, are the Sapporo core/valence type relativistic bases (see SPKrnDZ, n=D,T,Q in $BASIS), available H-Rn. Alternatives include the University of Tokyo's DK3 basis sets for H-Lr obtained at U. of Tokyo which exist in the form of general contractions. The web site

http://www.riken.jp/qcl/publications/dk3bs/periodic_table.html

gives the supplemental data from

T.Tsuchiya, M.Abe, T.Nakajima, K.Hirao
J.Chem.Phys. 115,4463-4472(2001)

which may be processed into $DATA input with the helper program dk3.f found in source code distributions of GAMESS. Using uncontracted WTBS basis sets may be reasonable for very small molecules. Finally, one might check the PNNL web site looking for other relativistic basis sets.

For NESC, you must provide three basis sets, for the large and small components and an averaged one, which are given in $DATAL, $DATAS, $DATA, respectively. The only

possible choice for these basis sets is due to Dyall, and these are available from
http://www.emsl.pnl.gov:2080/forms/basisform.html Their names are similar to cc-pVnZ(pt/sf/lc), pt=point or fi=finite nucleus, sf for spin-free and the final field is lc=large component ($DATAL), sc=small component ($DATAS), and wf is a typo for Foldy-Wouthuysen 2e- basis ($DATA). In GAMESS you can only use point nucleus approximation, so do not select any of the 'finite nucleus size' type. The need to input three basis sets means that you cannot use $BASIS input, and you must use COORD=UNIQUE style input in the various $DATA's. The three $DATA input groups must contain identical information except for the primitive expansion coefficients, as the three basis sets must have the same exponents. In case the options below to treat only some atoms relativistically is chosen, all non-relativistic atoms must have identical basis input in all three groups.

During geometry optimizations, in rare cases, the number of nearly linearly independent functions in the Resolution of the Identity (RI) used to evaluate the most difficult integrals may change at some new geometry. If so, the job will quit with an error message, and the user must restart it again manually.

* * * the next parameter applies only to RELWFN=DK:

NORDER gives the order of the DK transformation to be applied to the one-electron potential:
= 1 corresponds to the free particle
= 2 is the most commonly implemented DK method. It has all relativistic corrections to second order. (default)
= 3 represents 3rd order DK transformation. It does not include all 3rd order relativity corrections, in the sense of collecting all terms in the same order of c (speed of light), due to using only a 2nd order form of the Coulomb potential (1/rij). However, DK3 gives the closest approximation to the Dirac-Coulomb equation of all methods here.

* * * the next parameter applies to spin-orbit coupling:

```
NESOC  requests the Douglas-Kroll 1st order relativistic
       corrections for the 1e- SOC integrals.  It has been
       observed that the 1st order correction is often
       sufficient.
       NESOC is relevant only if OPERAT=HSO1, HSO2P, or
       HSO2, for RUNTYP=TRANSITN.
     = 0 no corrections (default for no relativity)
         This is the only choice possible for LUT-IOTC.
     = 1 apply DK1 correction to one-electron spin-orbit
         integrals.  This is the default if any of RESC,
         NESC, DK, or IOTC scalar relativity was chosen).

       * * * the next few parameters are used by * * *
               LUT-IOTC, IOTC, DK, and RESC:

MODEQR are options for quasi-relativistic calculations.
       The default is 1.  Most runs will select 1, or else
       9 if additional accuracy is needed in generating the
       RI basis due to a large span in Gaussian exponents.
       These are additive (bitwise) options, meaning you
       would enter 11 to request options 1+2+8:

       = 0 use the input contracted atomic basis set for
           the Resolution of the Identity (RI) used to
           simplify the pVp relativistic integrals, in
           order to evaluate them in closed form.
           The accuracy of the RI will be severely
           compromised, so this option is not recommended.
       = 1 use the Gaussian primitives constituting the
           input contracted atomic basis set to define the
           RI.  This produces a considerable increase in
           accuracy of the integrals compared to "0".
       = 2 The uncontracted GTO basis set will be used in
           spherical harmonic form, which helps eliminate
           linear dependence cleanly from the RI steps.
           However, this option is not available for
           nuclear gradients, so it is not used by default.
           You might choose to this for extra accuracy,
           when doing final single point energy runs.
           ISPHER=1 to choose spherical harmonics for the
           contracted basis used elsewhere in the run may
           always be used, and should be selected if "2"
           is chosen.
       = 4 avoid redundant exponents when splitting L
           shells into s and p, when generating the
```

internally uncontracted basis set. This is necessary if you are using s or p primitives with the same exponents as in some L shell. This is unlikely to occur, but if so, the L shell must be entered before the s or p. Option 4 requires option 1.

= 8 use 128 bit precision in the RIs. Select this option if your exponent range is larger than 64 bits can handle - it is a little difficult to relate Gaussian exponents to overlap matrix precision, but if the range of exponents reaches ten, one should think about using 128 bit math. This is a concern mainly for 6th row elements, where it may easily be probed by comparing the the energy and gradient for MODEQR=1 to 9.

Notes:

1. 128 bit math can be very slow, depending on your CPU and/or compiler's support for it. Only relativistic 1e- integrals use 128 bits.
2. LUT-IOTC's local nature makes "8" much more economical than for the other ESC schemes.
3. If your FORTRAN library does not support the REAL*16 data type (128 bits), the code compiles itself in 64 bit mode, and will halt if you ask for 128 bits.

QMTTOL same as in $CONTRL, but used for the preparation of the RI space (see MODEQR suboption "1"). LUT-IOTC's RI applies to atomic domains, separately, whereas RESC, DK, and IOTC use this parameter for the entire molecule's uncontracted basis set, where linear dependence is an even greater concern.
Usually values considerably smaller than the QMTTOL of $CONTRL, which applies to the contracted working basis may be used, improving accuracy.
The default is 1d-10.

QRTOL accuracy parameter for relativistic gradients.

RESC or LUT-IOTC: tolerance for equating nearly degenerate eigenvalues of the kinetic energy and overlaps, when evaluating the gradient.
Values that are too large (>1e-6) cause numerical errors in the gradient, approximately on the same order as QRTOL.

Values that are too small can cause large gradient errors due to divsion by small numbers not screened away by QRTOL.
(LUT-IOTC default = smaller of 1d-10 or QMTTOL)
(RESC default = smaller of 1d-08 or QMTTOL)

DK or IOTC: Coordinate offset in bohr used for the numerical differentiation of the relativistic contributions to the gradient (analogous to VIBSIZ in $HESS). Only totally symmetric coordinate directions are explored (analogous to NUMGRD in $CONTRL). All other gradient terms are still computed analytically, but the effect of this single numerical step is to make DK or IOTC gradients be somewhat less accurate than most analytic gradients. See also NVIB.
Default for DK or IOTC: 0.01 Bohr

NVIB The number of offsets per coordinate (similar to NVIB in $FORCE). NVIB can be 1 or 2 (or -1 or -2). This parameter applies only to DK or IOTC gradients, as RESC and LUT-IOTC are fully analytic.
Positive values correspond to the projected mode, in which translations, rotations, and any modes which are not totally symmetric are projected out.
Negative values correspond to using Cartesian coordinates.
In most cases projected modes are superior; however they can cause slight distortions away from the true symmetry -IF- you specify lower symmetry than the molecule actually possesses. (default=2)

* * * the next parameter applies only to LUT-IOTC:

TAU The distance cutoff to consider "local" for the local unitary transformation approximation. The value should include any bonded atom pairs, but is chosen to eliminate most next nearest neighbor atom pairs. Increasing TAU causes LUT-IOTC to converge to the full IOTC result (apart from some technical differences in the RI treatment of integrals).
The default is 3.5 Angstroms.

* * * the next few parameters apply mainly to NESC:

NRATOM the number of different elements to be treated nonrelativistically. For example, in Pb(CH3)2, to treat only lead relativistically, enter NRATOM=2. The elements to be treated nonrelativistically are defined by CHARGE. (default=0)
For NESC, this parameter affects the choice of the basis sets, you should use identical large, small, and averaged basis set for such atoms.
For DK or RESC, MODEQR=1 won't uncontract to the primitives of such atoms.

CHARGE is an array containing nuclear charges of the atoms to be treated nonrelativistically.
For example, CHARGE(1)=6.0,1.0, to drop all C/H atoms in Pb(CH3)2.

*** for those who wish to live in other universes ***

CLIGHT gives the speed of light (atomic units), introduced as a parameter in order to reproduce exactly results published with a slightly different choice.
Default: 137.0359895

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$EFIELD group (not required)

This group permits the study of the influence of an external electric field on the molecule. The method is general, and so works for all wavefunctions, and for both energies and nuclear gradients.

EVEC = an array of the three x,y,z components of the applied electric field, in a.u., where 1 Hartree/e*bohr = 5.1422082(15)D+11 V/m A typical size for the EVEC components is therefore about 0.001 a.u.

SYM = a flag to specify when the field breaks the the molecular symmetry. Since most fields break symmetry, the default is .FALSE.

==========

Restrictions: analytic hessians are not available, but numerical hessians are. Because an external field causes a molecule with a dipole to experience a torque, geometry optimizations must be done in Cartesian coordinates only. Internal coordinates eliminate the rotational degrees of freedom, which are no longer free.

A nuclear hessian calculation will have two rotational modes with non-zero "frequency", caused by the torque. A gas phase molecule will rotate so that the dipole moment is anti-parallel to the applied field. To carry out this rotation during geometry optimization will take many steps, and you can help save much time by inputting a field opposite the molecular dipole. There is also a stationary point at higher energy with the dipole parallel to the field, which will have two imaginary frequencies in the hessian. These will appear as the first two modes in a hessian run, but will not have the i for imaginary included on the printout since they are rotational modes.

sign conventions:
Dipole vectors are considered to point from the negative end of the molecule to the positive end. Thus HCl at the MP2/aug-cc-pVDZ level's geometry of R=1.2831714 has a positive dipole, if we place Cl at the origin and H along

the positive z-axis. The sign convention on applied fields is such that a +1 charge particle feels a force in the positive direction under a positive field, namely, as if there was a negative plate at large +Z and a positive plate at large -Z. Hence positive fields enhance HCl's dipole:

```
      EVEC(z)      E(MP2)       mu(MP2)
      -0.001  -460.2567905970  1.112875
      -0.0001 -460.2571917846  1.153172
       0.0    -460.2572372416  1.157646
      +0.0001 -460.2572828745  1.162119
      +0.001  -460.2577014871  1.202350
```

and the higher energy for each negative EVEC means HCl would prefer to turn around in the field.

Thus, one use for this group is calculation of the electric dipole by finite difference, for wavefunctions that cannot yield molecular properties due to not having a relaxed density matrix. Perform two RUNTYP=ENERGY jobs per component, with fields 0.001 and -0.001 a.u. The central difference formula for each component of the dipole is

```
   mu = 2.541766*(E(+0.001)-E(-0.001)/0.002, in Debye.
```

The differentiation using data from HCl gives 1.157635.

For an application to molecular ionization in intense fields generated by lasers, see

H.Kono, S.Koseki, M.Shiota, Y.Fujimura
J.Phys.Chem.A 105, 5627-5636(2001)

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$INTGRL group (optional)

This group controls AO integral formats. Probably the only values that should ever be selected are QFMM or NINTIC, as the program picks sensible values otherwise.

QFMM = a flag to use the quantum fast multipole method for linear scaling Fock matrix builds. This is available for RHF, UHF, and ROHF wavefunctions, and for DFT, but not with any other correlation treatment. You must select DIRSCF=.TRUE. in $SCF if you use this option. The RHF and closed shell DFT gradients also uses QFMM techniques. The Optimal Parameter FMM code will run at a comparable speed to a ordinary run doing all integrals for molecules about 15 Angstroms in size, and should run faster for 20 Angstroms or more. See also the $FMM input. (default=.FALSE.)

SCHWRZ = a flag to activate use of the Schwarz inequality to predetermine small integrals. There is no loss of accuracy when choosing this option, and there are appreciable time savings for bigger molecules. Default=.TRUE. for over 5 atoms, or for direct SCF, and is .FALSE. otherwise.

NINTMX = Maximum no. of integrals in a record block. (default=15000 for J or P file, =10000 for PK)

NINTIC = Controls storage of integrals in memory, with any remaining integrals will be stored on disk. Caution: memory set aside for this parameter is unavailable to the quantum chemistry methods. Positive NINTIC indicate the number of integrals, negative the amount of memory used for integrals and labels (in words). At present NINTIC works robustly for RHF, ROHF, or UHF, is thought to work for GVB or MCSCF and mostly works for sequential MP2 as well. Direct SCF does not use this option! (default=0).

```
   Various antiquated or antediluvian parameters follow:

 NOPK   = 0 PK integral option on, which is permissible
            for RHF, UHF, ROHF, GVB energy/gradient runs.
        = 1 PK option off (default for all jobs).
            Must be off for anything with a transformation.

 NORDER = 0 (default)
        = 1 Sort integrals into canonical order.  There
            is little point in selecting this option, as
            no part of GAMESS requires ordered integrals.
            See also NSQUAR through NOMEM.

 NSQUAR = 0 Sorted integrals will be in triangular
            canonical order (default)
        = 1 instead sort to square canonical order.
 NDAR   = Number of direct access logical records to be
          used for the integral sort (default=2000)
 LDAR   = Length of direct access records (site dependent)
 NBOXMX =  200   Maximum number of bins.
 NWORD  =    0   Memory to be used (default=all of it).
 NOMEM  =    0   If non-zero, force external sort.

   The following parameters control integral restarts.
      IST=JST=KST=LST=1   NREC=1    INTLOC=1
Values shown are defaults, and mean not restarting.
=============================================================
```

==========

$FMM group (relevant if QFMM selected in $INTGRL)

This group controls the quantum fast multipole method evaluation of Fock matrices. The defaults are reasonable, so there is little need to give this input.

ITGERR = Target error in final energy, to 10**-(ITGERR) Hartree. The accuracy is usually better than the setting of ITGERR, in fact QFMM runs should suffer no loss of accuracy or be more accurate than a conventional integral run (default=7).

QOPS = a flag to use the Quantum Optimum Parameter Searching technique, which finds an optimum FMM parameter set. (Default=.TRUE.)

If QOPS=.FALSE., the ITGERR value is not used. In this case the user should specify the following parameters:

NP = the highest multipole order for FMM (Default=15).

NS = the highest subdivision level (Default=2).

IWS = the minimum well-separateness (Default=2).

IDPGD = point charge approximation error (10**(-IDPGD)) of the Gaussian products (Default=9).

IEPS = very fast multipole method (vFMM) error, (10**(-IEPS)) (Default=9)

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$TRANS group

(optional for -CI- or -MCSCF-)
(relevant to analytic hessians)
(relevant to energy localization)

This group controls the integral tranformation. MP2 integral transformations are controlled instead by the $MP2 input group. There is little reason to give any but the first variable.

DIRTRF = a flag to recompute AO integrals rather than storing them on disk. The default is .FALSE. for MCSCF and CI runs. If your job reads $SCF, and you select DIRSCF=.TRUE. in that group, a direct transformation will be done, no matter how DIRTRF is set.

Note that the transformation may do many passes over the AO integrals for large basis sets, and thus the direct recomputation of AO integrals can be very time consuming.

CUTTRF = Threshold for keeping transformed two electron integrals. (default= 1.0d-9, except FMO=1.0d-12)

IPURFY = orbital purification, like PURIFY in $GUESS.
= 0 skip orbital purification before transform.
= 1 perform purification once per geometry, for example, in the first iteration of MCSCF only.
= 2 purify during every MCSCF iteration.
The default is 0. Use of 2 causes example 9 to take one more iteration to converge, due to the small upsetting of the orbitals between each iteration by this purification. This option is useful if PURIFY in $GUESS at the initial geometry is insufficient purification.

NOSYM = disables the orbital symmetry test completely. This is not recommended, as loss of orbital symmetry is likely to mean a calculation is turning into garbage. It has the same meaning as the keyword in $CONTRL, but pertains to just the integral transform. (Default is 0)

```
The remaining keywords refer almost entirely to the serial
integral transformation codes, not the distributed memory
routines:

 MPTRAN = method to use for the integral transformation.
          the default is try 0, then 1, then 2.
          0 means use the incore method
          1 means use the segmented method.
          2 means use the alternate method, which uses
            less memory than 2, but much more disk.

 NWORD  = Number of words of fast memory to allow.  Zero
          uses all available memory. (default=0)

 AOINTS = AO integral storage during parallel runs.
          It pertains only to CPHF=MO analytic Hessians.
          DUP stores duplicated AO lists on each node.
          DIST distributes the AO integral file across
          all nodes.

 ===========================================================
```

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$FMO group (optional, activates FMO option)

The presence of this group activates the Fragment Molecular Orbital option, which divides large molecules (think proteins or clusters) into smaller regions for faster computation. The small pieces are termed 'monomers' no matter how many atoms they contain. Calculations within monomers, then 'dimer' pairs, and optionally 'trimer' sets act so as to approximate the wavefunction of the full system. The quantum model may be SCF, DFT, DFTB, MP2, CC, MCSCF, TDDFT, or CI.

Sample inputs, and auxiliary programs, and other information may be found in the GAMESS source distribution in the directory ~/gamess/tools/fmo.

NBODY = n-body FMO expansion:
- 0 only run initial monomer guess (maybe remotely useful to create the restart file, or as an alternative to EXETYP=CHECK).
- 1 run up to monomer SCF
- 2 run up to dimers (FMO2, the default)
- 3 run up to trimers (FMO3)

IEFMO = switch to turn on EFMO (effective fragment potential based Fragment Molecular Orbital)
- 0 = use FMO (default)
- 1 = use EFMO

MODEFM array of five values controlling EFMO, each allows a bit-wise combination of several options. Default is MODEFM(1)=0,0,0,0,0

The first element is control over electrostatics
- 0 no screening of electrostatics
- 1 exponential screening of electrostatics by fixed value to fit the classical potential to the QM-potential, set SCREEN(1)=-1 in $FMO. (experimental)
- 2 Add octupole energy into electrostatic energy
- 4 use Hui Li's density based multipole expansion
- 8 ignore torque contributions to the gradient

```
          16 generate electrostatics on bond midpoints too
       The second element controls polarizabilities.
           0 Tang-Toenis type screening
           1 do not include any polarization at all
           4 add percentage discrimination based on
             distance to atoms
           8 ignore torque contributions to the gradient
          16 use full polarization tensors
          32 move polarizability tensors to nearest atom
             before induction
          64 do not evaluate electrostatic field, induced
             dipoles or gradient contributions from
             neighbouring fragments.  This assumes
             fragments are made in a sequential fashion.
         128 use Ruedenberg localization for localization
             of orbitals
       The third element affects dispersion
           0 no dispersion interactions
           1 include dispersion
       The fourth element affects charge transfer
           0 no charge transfer interactions
           1 include charge transfer
       The fifth element affects exchange repulsion
           0 no exchange interactions
           1 include exchange repulsion


MODFD  = switch to freeze the electronic state of some
         fragments. FMO/FD and FMO/FDD require
         RUNTYP=OPTIMIZE and two layers in FMO.
         0 = regular FMO
         1 = FMO/FD (frozen domain)
         3 = FMO/FDD (frozen domain and dimers)

NDUALB = switch to use dual basis approach with
         auxilliary polarization, AP, (i.e., a different
         basis set is used to estimate the polarization).
         The two basis sets in FMO/AP are entered in
         the multibasis fashion (not in the multilayer),
         i.e., as H.1 and H.2 in $DATA, not as H-1 and H-2.
         The dual basis set has some restrictions.
         Gradient (but not Hessian) is available.
         0 = usual FMO
         1 = dual basis FMO/AP
```

```
       I. The following parameters define layers.

NLAYER = the number of layers (default: 1)

MPLEVL = an array specifying n in MPn PT for each layer,
         n=0 or 2. (default: all 0s).
         Note that MCQDPT is not available and therefore
         one may not choose this for MCSCF.

DFTTYP = an array specifying the DFT functional type for
         each layer. (default: DFTTYP in $DFT).
         See $DFT for possible functionals. All functionals
         except dual hybrids may be used.
         Only grid-based DFT is supported.

SCFTYP = an array specifying SCF type for each layer.
         At present the only valid choices are RHF, ROHF,
         UHF, and MCSCF.
         (default: SCFTYP in $CONTRL for all layers).

CCTYP  = an array specifying CC type for each layer, which
         may be only the following choices from $CONTRL:
             LCCD, CCD, CCSD, CCSD(T), CCSD(T), CCSD(TQ),
             CR-CCL, or non-size extensive R-CC or CR-CC.
         Since FMO's CC methods involve adding corrections
         from pairs of monomers together, it is better to
         choose a size extensive method.

TDTYP  = an array specifying TDDFT type for each layer,
         of the same kind as TDDFT in $CONTRL.
         Default: TDDFT in $CONTRL for all layers.

CITYP  = an array specifying CI type for each layer, see
         CITYP in $CONTRL.  At present, only CIS may be
         used (FMO1-CIS energy only, i.e., nbody=1).
         Default: CITYP from $CONTRL, for all layers.

       II. Parameters defining FMO fragments:

NFRAG  = the number of FMO fragments (default: 1)

LAYER  = an array defining the layer for each fragment.
         Default: all fragments in layer 1, i.e.,
         LAYER(1)=1,1,1,...,1
```

```
FRGNAM = an array of names for each fragment (each 1-8
         character long) (default: FRG00001,FRG00002...).

INDAT  = an array assigning atoms to fragments. Two styles
         are supported (the choice is made based on
         INDAT(1): if it is nonzero, choice (a) is taken,
         otherwise INDAT(1) is ignored and choice (b) is
         taken):
         a) INDAT(i)=m assigns atom i is to fragment m.
            INDAT(i) must be given for each atom.
         b) the style is
            a1 a2 ... ak 0
            b1 b2 ... bm 0
            ...
            Elements a1...ak are assigned to fragment 1,
            then b1...bm are assigned to fragment 2,etc.
            An element is one of the following:
                I    or   I -J
            where I means atom I, and a pair I,-J means
            the range of atoms I-J.  There must be no space
            after the "-"!
         Example:
         indat(1)=1,1,1,2,2,1 is equivalent to
         indat(1)=0, 1,-3,6,0, 4,5,0
         Both assign atoms 1,2,3 and 6 to fragment 1,
         and 4,5 to fragment 2.

ICHARG = an array of charges on the fragments
         (default: all 0 charges)

MULT   = an array of multiplicities for each fragment.
         For MCSCF only the unique MCSCF fragment may be
         something other than a singlet.
         For ROHF and UHF multiple open-shell fragments
         are allowed, which may have any multiplicity;
         for dimers the high spin coupling will be used.
         (default: all 1's)

SCFFRG = an array giving the SCF type for each fragment.
         For MCSCF, only one fragment may be MCSCF and
         the rest should be RHF. For ROHF, UHF and U-DFT
         multiple open-shell fragments are allowed, but
         for ground state runs only.
         The values in SCFTYP overwrite SCFFRG, that is, if
```

you want to do a 2-layer calculation, the first layer being RHF and the other MCSCF, then you would use SCFTYP(1)=RHF,MCSCF and SCFFRG(N)=MCSCF, where you should replace N by your MCSCF fragment number. Then the first layer will be all RHF and the other will have one MCSCF fragment. In special cases, some SCFFRG values may be set to NONE, in which case SCF is not performed. This is useful in conjunction with ATCHRG.
(default: SCFTYP in $CONTRL).

MOLFRG = an array listing fragments for selective FMO, where not all dimers (and/or trimers) are computed. Setting MOLFRG imposes various restrictions, such as RUNTYP=ENERGY only. See MODMOL. For subsystem analysis (MODMOL=8), MOLFRG(i) defines which subsystem fragment i belongs to. Default: all 0.

MODMUL Use the multipole expansion to compute electrostatic interactions exactly, bit additive.
1 Compute individual contributions for each ES dimer.
2 Compute the sums for all ES dimer contributions and add them to the energy and gradient.
8 Compute one-electron ESP gradients (implemented for RESPPC<=0 only).
Only one of bits 1 or 2 may be turned on.
Default: 0

IACTFG = array specifying fragments in the active domain in FMO/FD(D). Ranges can be specified as in INDAT, so INDAT(1)=1,2,-5,8 means fragments 1,2,3,4,5,8. All IACTFG fragments should be in the 2nd layer, and the interfragment distance between fragments in IACTFG and the 1st layer's fragments should not be zero (i.e., no detached bonds between them). Default: all zeroes.

NOPFRG = printing and other additive options, specified for each fragment,
1 set the equivalent of $CONTRL NPRINT=7 (printing option). Useful if you want to print orbitals only for a few selected monomers.
2 set MVOQ to +6 to obtain better virtual orbitals

```
         (ENERGY runs only, useful mostly to prepare good
         initial orbitals for MCSCF).
       4 generate cube file for the specified fragment,
         the grid being chosen automatically.
         (default: all 0s)
      64 use frozen atomic charges (defined in ATCHRG)
         instead of the variational ones to compute
         converged fragment densities, to describe the
         electrostastic field from a fragment acting upon
         other fragments.
     128 apply options 1 and 4 above only at the final SCF
         iteration (correlation or GRADIENT only).

NACUT  = automatically divides a molecule into fragments by
         assigning NACUT atoms to each fragment (useful for
         something like water clusters).  This sets FRGNAM
         and INDAT, so they need not be given.  If 0, the
         automatic option is disabled. (default: 0)

IEXCIT = options for FMO based TDHF, TDDFT, or CI
         calculations:

IEXCIT(1): ordinal number for the excited state fragment.
           There is no default for IEXCIT(1), you should
           always set it.
IEXCIT(2): chooses the many-body level excitation n, e.g.
           for FMOn-TDDFT.
           n=1 means only the fragment given in IEXCIT(1)
           will be excited.
           n=2 adds dimer corrections (from fragment
           pairs involving IEXCIT(1)).
           IEXCIT(2) must not exceed NBODY.  Default: 1.
IEXCIT(3): (relevant for FMO2-TDDFT only)
           = 0 economic mode: only TDDFT dimer calculations
               are performed (skipping all other dimers).
           = 1 all dimer calculations are performed to
               obtain not just the excitation but also the
               total excited state energy.
           Default: 0.
IEXCIT(4): excited state matching method in FMO2-TDDFT used
           to determine which excitations in dimers
           correspond to those in the TDDFT fragment given
           in IEXCIT(1).  Default=2.
           = 0 trivial or identity matching (assume the
               same order of the excited states in monomers
```

and dimers.
= 1 match the dominant orbital pair (aka DRF) coefficient.
= 2 match the whole excitation vector.
Methods 1 and 2 try to match monomer dimer orbitals first, and then use DRF coefficients. In difficult cases (i.e., if the orbitals in a dimer are very delocalised), methods 1 and 2 may not be able to find the right transition, so some visual checking is recommended.

ATCHRG = array of atomic charges, to be used with NOPFRG, set for some fragments to 64 (i.e., to freeze some of fragment electrostatic potentials during SCC).
Nota bene: the order of atoms in ATCHRG is not the same as in FMOXYZ. In ATCHRG, you should specify atomic charges for all atoms in fragment 1, then for fragment 2 etc, as a single array. For covalently connected fragments there are formally divided atoms (some redundant), and ATCHRG should then list charges for them as well, all in the exact order of atoms in which fragments are defined in FMO. The number of entries in ATCHRG is NATFMO+NBDFG, where NATFMO is the number of atoms in $FMOXYZ and NBDFG is the number of bonds defined in $FMOBND.

NATCHA = option applicable to molecular clusters made exclusively of the same molecules. Only NATCHA atoms are then specified in ATCHRG, and the rest are copied from the first set.

RAFO = array of three thresholds defining model systems in FMO/AFO. All of them are multiplicative factors applied to distances. Two atoms are considered covalently bonded if they are separated by the predefined distance determined by their van der Waals radii. Larger RAFO values make further separated atoms to be considered as bonded.

All atoms within RAFO(1) distance from BDA or BAA are included into the model system in AFO ($FMOBND lists BDAs and BAAs in this order as -BDA BAA). Atoms within RAFO(2) from the set defined by RAFO(1) are replaced by hydrogens. AO coefficients expanding localized orbitals to be frozen are saved for use in FMO for atoms within RAFO(3) from BDA

```
or BAA. A nonzero RAFO(1) turns on FMO/AFO, else FMO/HOP is
used. Default: 0,0,0.

MODMOL  = additive options for dimers and trimers in the
          selective FMO based on MOLFRG.
        1 limits correlated calculations to a) dimers/
          trimers including one fragments in MOLFRG, and
          b) monomers appearing in such dimers/trimers.
          In other words, this is a cross option, to study
          interactions between MOLFRG and the rest.
        2 modifies the choice of dimers/trimers to those
          in which all fragments are listed in MOLFRG
          (i.e., option 2 requires also 1, resulting in 3).
          In other words, this is an intra option, to study
          interactions within MOLFRG.
        4 do not store NFRAG**3 arrays in FMO3, to be used
          with MODMOL=2, to reduce memory in very special
          cases. No property summary will be provided, just
          whatever is printed in SCF for each trimer.
        8 do subsystem analysis. See MOLFRG.
                Default: 0 (do not use MOLFRG)

NFRND   = additive options controlling interface and
          compatibility of GAMESS' FMO with other programs.
        2 output basis set for each n-mer.  Such an FMO
          output can be split with tools/fmo/misc/frgout,
          and thus obtained fragment output files can be
          read into various GUIs (e.g., MacMolPlt), for
          example to plot MOs of individual n-mers (but not
          of the whole system), e.g., to help understand an
          excited state calculation.
        4 punch normal modes in RUNTYP=FMOHESS for
          GUIs (e.g., MacMolPlt) to visualize vibrations.
          This also prints a frequency table in the output.
        8 write out coordinates

       III. Parameters defining FMO approximations

MODESP = options for ESP calculations.
       0 the original distance definition (uniform),
       1 an improved distance definition (many-body
         consistent, applied to unconnected n-mers),
       2 an improved distance definition (many-body
         consistent, applied to all n-mers).
         (default: 0 (FMO2) or 1 (FMO3))
```

```
MODGRD =  0 subtract the external potential from the
            Lagrangian (default).
          1 do not do that.
          2 add ESP derivatives (MODESP should be 0)
          8 add Mulliken charge derivatives to MODGRD=2
         16 do not add HOP derivatives (required for AFO)
         32 add CPHF-related terms (known as SCZV) needed
            for the fully analytic gradient, which may
            be combined with EFP or PCM<1>.
            This option requires MODESP=0 and for MP2
            also RESPPC=0.
            Note that 2+8 terms should be added, too,
            so MODGRD=42 (=2+8+32) gives the fully analytic
            gradient.
       There are three main usages (some further limitations
       are not listed below, e.g., for combinations with PCM
       or EFP):
          MODGRD=0  gives the least accurate gradient,
                    available for almost any FMO method
                    (except CIS and when ab initio gradient
                    in GAMESS is not available, e.g., CC).
          MODGRD=10 is medium accurate, unavailable for CI,
                    CC, ROHF and MCSCF.
          MODGRD=42 is analytic, only for RHF, UHF, ROHF,
                    RDFT, UDFT, and RMP2.  RMP2 requires
                    RESPCC=0.
       Note that RUNTYP=FMOHESS should use MODGRD=2, and
       such runs cannot calculate analytic gradient.

       Default: 10 (=2+8, for FMO2) or 0 (for FMO3).

RESPAP = cutoff for Mulliken atomic population approx,
         namely, usage of only diagonal terms in ESPs.
         It is applied if the distance between two monomers
         is less than RESPAP, the distance is relative to
         van der Waals radii; e.g. two atoms A and B
         separated by R are defined to have the distance
         equal to R/(RA+RB), where RA and RB are van
         der Waals radii of A and B).  RESPAP has no units,
         as may be deduced from the formula.
         RESPAP=0.0 disables this approximation.
         (default: 0.0)

RESPPC = cutoff for Mulliken atomic point charge
```

approximation, namely replacing 2e integral contributions in ESPs by effective 1e terms). See RESPAP. (default: 2.0 (FMO2) or 2.5 (FMO3))

RESDIM = cutoff for approximating the SCF energy by electrostatic interaction (1e terms), see RESPAP. This parameter must be nonzero for ab initio electron correlation methods. RESDIM=0 disables this approximation. (default: 2.0 (FMO2) or RITRIM(1)+RITRIM(3) for FMO3 energy, 0 for FMO3 gradient)

RCORSD = cutoff that is compared to the distance between two monomers and all dynamic electron correlation during the dimer run is turned off if the distance is larger than this cutoff. RCORSD must be less than or equal to RESDIM and it affects only MP2, CC, CI, and TDDFT.
(default: 2.0 (FMO2), RITRIM(1)+RITRIM(4) for FMO3 energy, 0 for FMO3 gradient)

RITRIM = an array of 4 thresholds determining neglect of 3-body terms (FMO3 only). The first three are for uncorrelated trimers and the exact definition can be found in the source code. The fourth one neglects correlated trimers with the separation larger than the threshold value. RITRIM(4) should not exceed RITRIM(3).
(default: 1.25,-1.0,2.0,2.0, which corresponds to the medium accuracy with medium basis sets, see REFS.DOC).

SCREEN = an array of two elements, alpha and beta, giving the exponent and the multiplicative factor defining the damping function
1-beta*exp(-alpha*R**2).
This damping function is used to screen the potential due to point charges of bond detached atoms and it can only be applied for RESPPC=-1, i.e., when ESP is approximated by point charges. Default: 0,0 (no screening). Other sensible values are 1,1.

ORSHFT = orbital shift, the universal constant that multiplies all projection operators. The value of

```
          1e+8 was sometimes erroneously quoted instead of
          the actual value of 1e+6 in some FMO publications.
          (default: 1e+6).

MAXKND = the maximum number of hybrid orbital sets (one set
          is given for each basis set located at the atoms
          where bonds are detached).  See also $FMOHYB.
          (default: 10)

MAXCAO = the maximum number of hybrid orbitals in an LMO
          set.  (default: 5)

MAXBND = the maximum number of detached bonds.
          (default: NFG*2+1)
=============================================================
```

==========

$FMOPRP group (optional for FMO runs)

Options setting up SCF convergers, parallelization and properties are given here.

I. Parameters for SCF convergers and initial guess

MAXIT = the maximum number of monomer SCF iterations.
(default 30)

CONV = monomer SCF energy convergence criterion.
It is considered necessary to set CONV in $SCF to a value less or equal to the CONV in $FMO.
Usually 1e-7 works well, but for poorly converging monomer SCF (frequently seen with DFT) one order, smaller value for CONV in $SCF is recommended, (1e-7 in $FMO and 1e-8 in $SCF) (default: 1e-7).

NGUESS = controls initial guess (cumulative options, add all options desired) (default=2):
1 run free monomer SCF
2 if set, dimer density/orbitals are constructed from the "sum" of monomer quantities, otherwise Huckel guess will be used for dimers, and the same applies to trimers.
4 insert HMO projection operator in Huckel guess
8 apply dimer HO projection to dimer initial guess
16 do RHF for each dimer and trimer, then run DFT.
128 do not use orbitals from the previous geometry during geometry optimization. This is mostly useful for multilayer optimizations, when this choice must always be set if basis sets differ.
256 if SCF does not converge, try the alternative converger (flip between SOSCF and DIIS). If 2048 is not added, the alternative converger will start up with the final orbitals of the unconverged SCF.
512 reorder initial orbitals manually using $GUESS options (IORDER), applies to MCSCF layers only.
2048 a modifier of 256 - when both 256 and 2048 are set, the alternative converger will use the same initial set of initial orbitals as the

unconverged SCF.

IJVEC = Index array enabling reading $VEC inputs defining initial orbitals for individual n-mer runs. This consists of quintuplets: ifg1,jfg1,kfg1,ilay1,norb1, ifg2,jfg2, ... The first pair indexes $VEC1 with ifg1,jfg1,kfg1 for layer ilay1 expecting norb1 MOs. The second quintuplet handles $VEC2 etc. ifg,0,0,ilay1,norb1 is used for monomer IFG, ifg,jfg,0,ilay1,norb1 is used for dimer IFG,JFG. ifg equal to 0 in a quintuplet ends the list. $VEC groups must be used consequently from $VEC1. (default: all 0s; at most 100 can be given)

MODORB = controls whether orbitals and energies are exchanged between fragments (additive options).
1 exchange orbitals if set, otherwise densities
2 exchange energies
DFT, ROHF, UHF and MCSCF, SCZV and PIEDA require MODORB=3. MODORB=3 is in general more robust, because it provides a better initial guess. (Default: 0 for RHF, 3 for DFT/ROHF/UHF/MCSCF.)

MCONV = an array specifying SCF convergers for each FMO step. Individually (MCONV(2) is for monomers, MCONV(4) for dimers, MCONV(9) for trimers). Each array element is set to A1+A2+A3, where A1 determines SCF and A2 MCSCF convergers, and A3 is the direct/conventional bit common for all SCF methods. MCONV is an additive option:

A1(SCF):		A2(MCSCF):		A3(direct)	
1	EXTRAP	1024	FOCAS	256	FDIFF
2	DAMPH	2048	SOSCF	512	DIRSCF
4	VSHIFT	4096	DROPC		
8	RSTRCT	8192	CANONC		
16	DIIS	16384	FCORE		
32	DEM	32768	FORS		
64	SOSCF	65536	n/a		
128	LOCOPT	131072	EKT		
		262144	LINSER		
		524288	JACOBI		
		1048576	QUD		

There are some limitations on joint usage for each that can be understood from $SCF or $MCSCF.

If set to -1, the defaults given in $SCF or $MCSCF are used. See MCONFG. (default: all -1's).

MCONFG = an array specifying SCF convergers for each fragment during the monomer SCF runs. The value -1 means use the default (defined by MCONV).
The priority in which convergers are chosen is:
MCONFG (highest), if not defined MCONV,
if not defined, $SCF (lowest).
This option is useful in case of poor convergence caused by charge fluctuations and SCF converger problems in particular, SOSCF instability for poor initial guess. Default: all -1.

ESPSCA = scale factors for up to nine initial monomer SCF iterations. ESPs will be multiplied by these factors, to soften the effect of environment and help convergence. At most nine factors can be defined. (default: all 1.0's)

CNVDMP = damping of SCF convergence, that is, loosen convergence during the initial monomer SCF iterations to gain speed. CONV in $SCF and ITOL and ICUT in $CONTRL are modified.
CONV is set roughly to min(DE/CNVDMP,1e-4), where DE is the convergence in energy at the given monomer SCF iteration. It is guaranteed that CONV,ITOL and ICUT at the end will be set to the values given in $SCF. Damping is disabled if CNVDMP is 0. Reasonable values are 10-100.
Care should be taken for restart jobs: since restart jobs do not know how well FMO converged, restart jobs start out at the same rough values as nonrestart jobs, if CNVDMP is used. Therefore for restart jobs either set CNVDMP appropriately for the restart (i.e., normally 10-100 times larger than for the original run) or turn this option off, otherwise regressive convergence can incur additional iterations (default: 0).

COROFF = parameter turning off DFT in initial monomer SCF, similar to SWOFF. COROFF is used during monomer SCF, and it turns off DFT until monomer energies converge to this threshold. If COROFF is nonzero, SWOFF is ignored during monomer SCF, but is used

for dimers and trimer iterations. Setting COROFF=1e-3 and SWOFF=0 usually produces good DFT convergence. COROFF may be thought as a macro-analogue of SWOFF. If monomer SCF converges poorly (>25 iterations), it is also recommended to raise CONV in $SCF to 1e-8 (if CONV in $FMO is 1e-7). Default:1.0E-3 (0.0 skips this option).

NPCMIT = the maximum number of FMO/PCM[m] iterations, applicable to m>1 only (for m=1, $FMOPRP MAXIT is used). NPCMIT=2 can be thought as having special meaning: it is used to define FMO/PCM[l(m)] runs by forcing the FMO/PCM loop run only twice, which corresponds to determining PCM charges during the first iteration (and the m-body level) and then using them during the second iteration (l-body). For FMO/PCM[l(m)] only l=1 is implemented and "m" is given in $PCM IFMO. Default: 30.

CNVPCM = convergence threshold for FMO/PCM[m] iterations, applicable to m>1 only (for m=1, $FMOPRP CONV is used). CNVPCM is applied to the total FMO energy Default: 1.0D-07 Hartree.

PCMOFF = parameter turning PCM off in initial monomer SCF iterations, analogous to COROFF. PCM is turned off, until convergence reaches PCMOFF. PCMOFF=0 disables this feature. Default: 0.0

NCVSCF = an array of 2 elements to alter SCF convergers. After NCVSCF(1) monomer SCF iterations the SCF converger will switch between SOSCF <-> FULLNR. This option is useful in converging difficult cases in the following way:

```
 $SCF diis=.t. soscf=.f. $end
 $FMOPRP NCVSCF(1)=2 mconv(4)=65 $end
```

This results in the initial 2 monomer SCF iterations being done with DIIS, then a switch to SOSCF occurs. mconv(4)=65 switches to SOSCF for dimers.
Note that NCVSCF(1) will only overwrite MCONV, but not MCONFG. The SCF converger in MCONV(2) will be enforced after NCVSCF(2) monomer SCF iterations, overwriting MCONFG as well. This is useful for the most obnoxiously converging cases. See other

FMO documentation.
Default: 9999,9999 (which means do not use).

NAODIR = a parameter to decide whether to enforce DIRSCF. Useful for incore integral runs in parallel. NAODIR is the number of AO orbitals that is expected to produce 100,000,000 non-zero integrals. Using this and assuming NAO**3.5 dependence, the program will then guess how many integrals will each n-mer have and whether they will fit into the available memory. If they are determined not to fit, DIRSCF will be set true. This option overwrites MCONV but not MCONFG. If set to 0, then the default in-core integral strategy is used. (default=0)

VDWRAD = array of van der Waals radii in Angstrom, one for each atom in the periodic table. Reasonable values are set only for a few light atoms and otherwise a value of 2.5 is used. VDWRAD values are used only to compute distance between fragments and thus somewhat affect all distance-based approximations.

II. Parameters defining parallel execution

MODPAR = parallel options (additive options)
(default: 13, which is 1+4+8)
1 turns on/off heavy job first strategy (reduces waiting on remaining jobs at barrier points) (see also 8)
4 broadcast all fragments done by a group at once rather than fragment by fragment.
8 alters the behavior of fragment initialixation: if set, fragments are always done in the reverse order (nfg, nfg-1, ...1) because distance calculation costs decrease in the same order and they usually prevail over making Huckel orbitals or running free monomer SCF. Note that during SCC (monomer SCF) iterations the order in which monomers are done is determined by MODPAR=1.
16 if set, hybrid orbital projectors will not be parallelized (may be useful on slow networks)
32 reserved
64 Broadcast F40 for FMO restarts. F40 should only

```
          be precopied to the grand master scratch
          directory and it should NOT exist on all slaves.
        256 Replace I/O to fragment density file by
          parallel broadcasts from group masters
        512 Use DDI memory to store fragment densities
          during the monomer step, using supervector
          (smallest memory).
       1024 Use DDI memory to store fragment densities
          during the monomer step, using supervector
          (smallest communications).
          Only one option out of 512 and 1024 may be used.


NGRFMO = an array that sets the number of GDDI compute
         groups during various stages of the calculation.
         The first ten elements are used for layer 1, the
         next 10 for layer 2, etc.
            ngrfmo(1) monomer SCF
            ngrfmo(2) dimers
            ngrfmo(3) trimers
            ngrfmo(4) correlated monomers
            ngrfmo(5) separated dimers
            ngrfmo(6) SCF monomers in FMO-MCSCF (MCSCF
               monomer will be done with ngrfmo(1) groups)
            ngrfmo(7) SCF dimers in FMO-MCSCF (MCSCF dimer
               be done with ngrfmo(2) groups)
            ngrfmo(8-10) reserved
         If any of them is zero, the corresponding stage
         runs with the previously defined number of groups.
         If NGRFMO option is used, it is recommended to set
         NGROUP in $GDDI to the total number of nodes.
         (default: 0,0,0,0).

MANNOD = manually define node division into groups.
         Contrary to MANNOD in $GDDI and here it is defined
         for each FMO stage (see NGRFMO) in each layer.
         If MANNOD values are set at all, it is required
         that they be given corresponding to the first
         nonzero NGRFMO value. The MANNOD values should be
         given for each nonzero NGRFMO.
         E.g. ngrfmo(1)=6,3,0,0,0, 0,0,0,0,0,  4,3
              mannod(1)=4,2,2,2,2,2, 5,5,4, 4,4,3,3, 6,6,2
         where 6 groups are defined for monomers in layer
         1, then 3 for dimers in layer 1, and 4 and 3
         groups for monomers and dimers in layer 2.
```

(default: all -1 which means do not use).

Note that nodes with very large counts may be too large for good scaling with certain kinds of FMO runs. Any such fat nodes can be divided into "logical nodes" by using the kickoff option :cpus= for TCP/IP, or DDI_LOGICAL_NODE_SIZE for MPI runs. See the DDI instructions.

LOADBF = an array for semi-dynamic load balancing, specifying the basis set sizes. If it is exceeded, static load balancing is used. LOADBF has the same structure as NGRFMO.
(Default: all 0's (disabling this feature).

LOADGR = an array for semi-dynamic load balancing, specifying the group sizes to be used with LOADBF. LOADGR has the same structure as NGRFMO.
LOADGR is normally used with MANNOD, because it is only useful with uneven group sizes. The main purpose is to handle cases when only a few very large fragments are mixed with many small ones.
An example: LOADBF(1)=200,400 LOADGR(1)=1,4 NGRFMO(1)=3,5 MANNOD(1)=11,1,1, 3,3,3,3,1
Monomers whose size exceeds 200 basis functions are executed on 1 group consisting of 11 nodes with static load balancing. Other monomers are computed on 2 groups consisting of 1 node with dynamic load balancing. Dimers whose size exceeds 400 basis functions are executed on 4 groups consisting of 3 nodes with static load balancing. Other monomers are computed on 1 group consisting of 1 node with dynamic load balancing.
Note that after finishing static work load, large groups will join the dynamic load balancing pool.
(Default: all 0's (disabling this feature).

III. Orbital conversion

File F40 that contains orbital density can be manipulated in some way to change the information stored in it without running any FMO calculations. Such conversion requires irest=2 and the basis sets in the input should define the old (before conversion) format. The results will be stored in F30. You should then rename it to F40 and use in a consequent run (with irest>=2).

Two basic conversion types are supported: A) changing RHF into MCSCF and B) changing basis sets for RHF. RHF and MCSCF use different stucture of the restart file (F40) and therefore conversion is necessary.

For type A the following orbital reordering manipulation before storing the results can be done, for example
```
 $guess guess=modaf norder=1 iorder(28)=34,28
```

Type B is typically used for preparing good initial orbitals for hard to converge cases. E.g., you can use something like 6-21G to converge the orbitals and then convert F40 to be used with 6-311G*. At present there is a limitation that only density based (MODORB=0) files may be converged, i.e. you cannot do it for DFT and MCSCF.

MAXAOC = The new (i.e., after conversion) maximum number of AOs per fragment. If you don't know what it should be you can run a CHECK job with the new basis set and find the number in "Max AOs per frg:". If this number is equal to the old value, then type A is chosen.

IBFCON = the array giving pairs of the old and new numbers of AOs for each atom in $DATA (type B only).

MAPCON = maps determining how to copy old orbitals into new (type B only). See the example.

Example: $DATA contains only H and O (in this order), F40 was computed with 6-31G and you want to convert to 6-31G**. One water per fragment.
```
         MAXAOC=25   25=5*2+15=new basis size for 6-31G**
         IBFCON(1)=2,5, 9,15
           2 and 5 for H (6-31 and 6-31G**), 9 and 15 for O
         MAPCON(1)=1,2,0,0,0,
                   1,2,3,4,5,6,7,8,9,0,0,0,0,0,0
```
Here we copy the two s functions of each H, and add p polarization p to each H (3 0's), and similarly we copy nine s,p functions for O, and add d polarization (6 0's)

In order to construct MAPCON, you should know in what order Gaussian primitives are stored. The easiest way to learn

```
this is to run a simple calculation and check the output
(SHELL information).

       IV. Printing, properties, restart, and dimensions.

NPRINT = controls print-out (bit additive)
         bits 1-2
           0 normal output
           1 reduced output (recommended for single points)
           2 small output (recommended for MD)
           3 minimal output (for large scale production MD)
         4 print interfragment distances.  Note: any of
           RESPAP, RESPPC, or RESDIM must be non-zero or
           otherwise nothing will be printed. If you only
           want the distances but no approximations, set
           the thresholds to huge values, e.g. resdim=1000.
         8 print Mulliken charges.
           Note: RESPPC must be set (non-zero), see above.
        16 special test run to check for errors in $FMOBND.
        32 increase the print-out/punch-out level a) on the
           last SCC iteration for monomers and b) for all
           dimers/trimers. It can be employed to plot
           fragment MOs while using $CONTRL NPRINT=-5 to
           reduce monomer output.
        64 print atomic coordinates for each fragment.
       128 skip printing ES dimer energies during their
           calculation (but a summary will list them).
           Note that choosing 128+2 will reduce the
           NFG^2 memory requirement for DFTB in half.

PRTDST = array of four print-out thresholds:
         1. print all pairs of fragments separated by less
         than PRTDST(1).
         2. print a warning if two fragments are closer
         than PRTDST(2), intended mostly to monitor
         suspicious geometries during optimization.
         3. print a warning if two fragments are closer
         than PRTDST(3) and have no detached bond between
         them, intended to check input.
         PRTDST(3) values should slightly exceed the
         longest detached bond in the system.
         4. PRTDST(4) has a completely different meaning.
         In the summary of pair interactions, only those
         values will be printed, which are larger than
         PRTDST(4), in the units of kcal/mol.
```

```
          Using zero for PRTDST(1) and PRTDST(2) turns them
          off.  Similarly, use PRTDST(3)=-1 to turn it off.
          PRTDST has no units, as it applies to unitless FMO
          distances (e.g., 0.5 means half the sum of van der
          Waals radii for the closest pair of atoms).
          (default: 0.0, 0.5, 0.6, 0.0)

IREST  = restart level (to use it, you must copy .F40.000
          to the scratch disk of either the first node only
          (if MODPAR=64) or all nodes (otherwise).
          Multilayer FMO can be restarted if either all
          layers use the same basis set or if you save
          the .F40.000 file for layer 1 and use it for the
          same layer.
          0 no restart
          2 restart monomer SCF (SCC).
          4 restart dimers. Requires monomer energies be
            given in $FMOENM. Some or no dimer energies
            may also be given in $FMOEND, in which case
            those dimers with energies will not be run.
            Usually the only property that can be obtained
            with IREST=4 is the energy. The only exception
            is: a) 1024 was added to IREST when monomer SCF
            was run and b) property restart files (*.F38*)
            from each node were saved and copied to the
            scratch directory for the IREST=1028 job. If
            these two conditions are met, gradient and ES
            moments can be restarted with IREST=1028.
       1024 write property restart files during monomer SCF
            and/or use them to restart gradient and/or ES
            moments. No other property may be restarted.
Note that monomer restarts (irest=2) do not need adding
1024, as the properties are recomputed.  1024 should only
be used for IREST=4 (or for IREST=0 to save restart data).

MODPRP = some extra FMO properties (bit additive)
          Default: 0.
         1 total electron density (AO-basis matrix, written
           to F10: useful to create initial orbitals for ab
           initio).
         2 reserved.
         4 electron density on a grid.
         8 if set, the grid output is a "sparse cube
           file", otherwise a "Gaussian cube file".
        16 automatically generate grid for modprp = 4 or 8.
```

```
      32 molecular electrostatic potential on a grid.
     128 spin density on a grid
         Only one bit out of 4 and 8 may be set.
         Default: 0.

NGRID  = three integers, giving the number of 3D grid
         points for monomers with NOPFRG=4 in x,y and z
         directions (default 0,0,0).

GRDPAD = Grid padding. Contributions to density on grid
         will be restricted to the box surrounding an n-mer
         with each atom represented by a sphere of GRDPAD
         vdW radii. In general the finer effects one is
         interested in, the larger GRDPAD should be. For
         example, if one plots not density, but density
         differences and a very small cutoff is used, then
         a larger value of GRDPAD (2.5 or 3.0) may be
         preferred.
         Default: 2.0.

IMECT  = The partitioning method for the interfragment
         charge transfer (computed from Mulliken charges).
         IMECT pertains only to those dimers between which
         a bond is detached.
         IMECT=0,1,2,3,4 are supported (see source code).
         (default: 4)

         V. Interaction analysis (PIEDA)

IPIEDA = 0 skip the analysis (default)
         1 perform brief PL-state analysis (FMO pair
           interactions)
         2 perform full PL-state analysis with the PL0-
           state data.
         PCM may be used with IPIEDA=0 or 1.

NOBDA  = gives the number of detached bonds.  This
         parameter should be set to a nonzero value only in
         runs that produce BDA pair energies.  (default: 0)

ROBDA  = array of the detached bond lengths, whose number
         is NOBDA.  ROBDA must be given if EOBDA is used.

EOBDA  = the array of BDA pair energies, whose number is
         NOBDA*4.
```

```
EFMO0  = the array of the free state fragment energies,
         first NFRAG correlated, then NFRAG uncorrelated
         values.

EPL0DS = monomer polarization energies, first NFRAG values
         of PL0d, then NFRAG values of PL0s, then NFRAG
         values of PL0DI.

EINT0  = the total components for the PL0 state:
         ES0, EX0, CT+mix0, DI0.
```

None of the PIEDA input values (except IPIEDA) are to be manually prepared, all should come from the punch file of preceeding calculations.

The brief order of IPIEDA=2 execution is:
1. run FMO0.
2. compute BDA energies (if detached bonds are present), using sample files in tools/fmo/pieda. To do this, one needs only R0BDA for a given system. R0BDA is punched by any FMO run at the very beginning, so NBODY=0 type of run might be used to generate it.
3. The results of (1) are EFMO0; the results of (2) are E0BDA; use them to run PL0, whose results will be EPL0DS and EINT0.
4. Run PL with the results of (1),(2) and (3).

The alternative is to run IPIEDA=1, which requires none of the above data, but it will use E0BDA is available.

==========

==========

$FMOXYZ group (given for FMO runs)

This group provides an analog of $DATA for $FMO, except that no explicit basis set is given here. For DFTB and FMO/MM runs see notes at the end of this subsection - these runs have some specific requirements. $FMOXYZ contains any number of lines of the following type:

```
A.N Q X Y Z
```

A is the dummy name of an atom.
N is an optional basis set number (if omitted, it will be set to 1). N is intended for mixed basis set runs, for example, if you want to put diffuse functions on carboxyl groups.
Q is the atomic charge.
Z is the integer atomic charge.
X, Y and Z are Cartesian coordinates. These obey UNITS given in $CONTRL.

There is no default, this group must always be given for FMO runs. Alternatively, you may use the chemical symbol instead of Q. Note that "A" is ignored in all cases, but must be given.

Here is how $DATA is used in FMO:
Each atom given in $DATA defines the basis set for that atom type, entirely omitting Cartesian coordinates (which are in $FMOXYZ). There are two ways to input basis sets in FMO.

I. easy!

This works only if you want to use the same built-in basis set for all atoms. It is possible to use EXTFIL as usual for externally defined basis sets.

1. Define $BASIS as usual
2. Put each atom type in $DATA, e.g. for (H2O)2,

```
 $DATA
H2O
C1 ! FMO does not support symmetry, so always use C1
```

```
H 1
O 8
 $end
```

II. advanced.

This allows you to mix basis sets, have multiple layers or a non-standard without involving EXTFIL.

1. Do not define $BASIS.
2. Put each atom type in $DATA, followed by basis set, either explicit or built in.

The names of atoms in $DATA have the following format, where brackets indicate optional parameters:
S[.N][-L]
N and L may be omitted (taking the default value of 1),
S is the atom name (discarded upon reading),
N is the basis set ordinal number,
L is the layer.
S[.N][-L] may not exceed 8 characters.

Example: 2-layer water dimer. In the first layer, you want to use STO-3G for the first molecule and your own basis set for the second. In the second layer, you want to use 6-31G and 6-31G* for the 1st and 2nd molecules, respectively.

```
$DATA
water dimer (H2O)2
C1
H-1 1   ! explanation: layer 1, basis 1 (STO-3G) for Hydr.
sto 3

O-1 8   ! explanation: layer 1, basis 1 (STO-3G) for Oxygen
sto 3

H.2-1 1 ! layer 1, basis 2 (manual) for hydrogen
s 1 ; 1 2.0 1

O.2-1 8 ! explanation: layer 1, basis 2 (manual) for Oxygen
s 2
1 100.0 0.8
2  10.0 0.6
l 1
1 5.0 1 1
```

```
H-2 1   ! explanation: layer 2, basis 1 (6-31G) for Hydr.
n31 6

O-2 8   ! explanation: layer 2, basis 1 (6-31G) for Oxygen
n31 6

H.2-2 1 ! layer 2, basis 2 (6-31G* = 6-31G) for Hydrogen
n31 6

O.2-2 8 ! explanation: layer 2, basis 2 (6-31G*) for Oxygen
n31 6
d 1 ; 1 0.8 1

 $end
```

Your $FMOXYZ matching this $DATA will then look as follows:

```
 $FMOXYZ
O 8 x y z
H 1 x y z
H 1 x y z
O.2 8 x y z
H.2 1 x y z
H.2 1 x y z
 $END
```

Note that if you define mixed basis sets for the atoms where bond detachment occurs (do not do this for basis sets with diffuse functions), then you should provide all required sets in $FMOHYB as well, and define $FMOBND properly.

For DFTB, atom names used in $FMOXYZ should match the usage in other places, such as $DFTBSK.

For FMO-based IMOMM (FMO/MM) atomic coordinates are given in $TINXYZ rather than in $FMOXYZ! There are no FMO-specific options to turn on FMO/MM (use the same style as for regular SIMOMM, complemented by FMO groups).

==========

==========

$AFOMOD group (relevant for FMO/AFO)

This group allows user to define model systems for some detached bonds, especially useful if the automatic algorithm fails to build them. The group can have several models given consequently. An example for one model is:

```
 $AFOMOD
1 4
   13   6.0     2.60639409    -1.41944144     0.87137460
    9   8.0     0.86256622    -1.53249713     0.69963114
   19   1.0     3.89530684    -3.08353483     0.30432753
    8   1.0     0.40393212     0.22566831    -0.24641973
 $END
```

Here, 1 is the bond in $FMOBND (numbered consequently) to which the model is applied. 4 is the number of atoms in the model.

In the data set, the first number (above, 13 etc) is the atomic number in $FMOXYZ, followed by atomic charge and Cartesian coordinates. New atoms such as hydrogen atoms added as caps should be assigned formal numbers of some heavy atoms present in the system, with the charge of 1.0 in $AFOMOD. These atoms will be identified as caps if the charges in $FMOMOD and $FMOXYZ differ. For example, if you add a new hydrogen cap and atom 12 in your system is carbon,

```
   12   1.0     0.40393212     0.22566831    -0.24641973
```

will define a hydrogen cap. Non-hydrogen caps can be done likewise, just be sure that charges differ.

==========

==========

$OPTFMO group (relevant if RUNTYP=OPTFMO)

This group controls the search for stationary points using optimizers developed for the Fragment Molecular Orbital (FMO) method. There is no restriction on the number of atoms in the molecule, whereas optimising FMO with standard optimizers (RUNTYP=OPTIMIZE) has a restriction to 2000 atoms (unless you rebuild your GAMESS appropriately). OPTFMO runs may be restarted by providing the updated coordinates in $FMOXYZ and, optionally, optimization restart data (punched out for each step) in $OPTRST (the data differs for each method).

```
METHOD = optimization method
         STEEP  steepest descent
         CG     conjugate gradient
         BFGSL  approximate BFGS numeric updates of the
                inverse Hessian, that do not require
                explicitly storing that matrix.
         HSSUPD numeric updates of the inverse Hessian
         Default: HSSUPD.

HESS   = initial inverse Hessian for METHOD=HSSUPD
         GUESS diagonal guess of 3
         READ  read from F38 (advanced option)
         Default: GUESS.

UPDATE = inverse Hessian update scheme for METHOD=HSSUPD
         BFGS Broyden-Fletcher-Goldfarb-Shanno
         DFP  Davidon-Fletcher-Powell
         Default: BFGS.

OPTTOL = gradient convergence tolerance, in Hartree/Bohr.
         Convergence of a geometry search requires the
         largest component of the gradient to be less
         than OPTTOL, and the root mean square gradient
         less than 1/3 of OPTTOL.  (default=0.0001)

NSTEP  = maximum number of steps to take.  Restart data
         are punched at each step. (default=200)

IFREEZ = array of coords to freeze during optimization.
```

```
          The usage is the same as for the similar option in
          $STATPT.

IACTAT = array of active (not frozen) atoms in geometry
          optimizations, see $STATPT for its description.

STEP   = initial step factor. This multiplies the gradient
          to prevent large steps. The values of 0.1-0.2 are
          considered useful in the vicinity of minimum, and
          0.5-1.0 is probably OK at the start. (default: 1)

STPMIN = the minimum permitted value of dynamically chosen
          STEP size (see STPFAC). (default: 0)

STPMAX = the maximum permitted value of dynamically chosen
          STEP size (see STPFAC). (default: 1)

STPFAC = Dynamic adjustment of STEP. If the energy goes
          down considerably, the new STEP is set to the old
          STEP multiplied by 1/STPFAC, if the energy goes up
          significantly, STEP is set to STEP*STPFAC, both
          constrained by STPMIN and STPMAX.  The default is
          1, which means do not use dynamic adjustment. The
          value 0.9 may be useful if dynamically adjusted
          steps are desired.

=============================================================
```

==========

$FMOHYB group (optional, for FMO runs)
(this group was previously known as $FMOLMO)

Hybrid orbitals are used to describe bond detachment when dividing a molecule into fragments. These are the familiar sp3 orbitals for C, plus the 1s core orbital. One set is given for each basis set used. The number of basis functions L1 (see below) should match your basis set(s). This group is not required if no detached bonds are present, for example in water clusters, where the FMO boundaries do not detach bonds. FMO/AFO also does not use $FMOHYB and this group may be omitted.

Format:
```
NAM1 L1 M1
I1,1  J1,1  C1,1  C2,1  C3,1 ...  CL1,1
...
I1,M1 J1,M1 C1,M1 C2,M1 C3,M1 ... CL1,M1
NAM2 L2 M2
I2,1  J2,1  C1,1  C2,1  C3,1 ...  CL1,1
...
I2,M2 J2,M2 C1,M2 C2,M2 C3,M2 ... CL2,M2
```
where NAM are set names (up to 8 characters long), L1 is the basis set size, M1 is the number of hybrid orbitals in this set.

Ci,j are LCAO coefficients (i is AO, j is MO) so it is the transposed matrix of what is usually considered. Ii,j and Ji,j are bond assignment numbers, defining to which side the corresponding projection operator is added. Usually one of each pair of I and J is 1, and the other 0.
(default: nothing, that is, no detached bonds).

Orbitals to be put into $FMOHYB are provided for many common basis sets (see gamess/tools/fmo/HMO).

==========

==========

$FMOBND group (optional, for FMO runs)

The atom indices involved in the bond detachment are given, in pairs for each bond. Bonds are always detached between fragments, layers in multilayer FMO are defined fragment-wise, i.e., whole fragments are assigned to layers.

```
-I1 J1 NAM1,1 NAM1,2 ... NAM1,n ICH1 IMUL1
-I2 J2 NAM2,1 NAM2,2 ... NAM2,n ICH2 IMUL2...
```

I and J are positive integers giving absolute atom indices. NAMs are hybrid orbital set names, defined in $FMOHYB.

Each line is allowed to have different set of NAMs, which can happen if different type of bonds are detached, for example, one line describing C-C bond and another C-N. Every bond given is detached in such a way that the I-atom will get nothing of it, effectively remove one electron (1/2 of a single covalent bond) from its fragment. The J-atom will get all of the bond and thus adds one electron to its fragment (e.g., formally heterolytic assignment, although in practice all electrons remain through the Coulomb field). The number 'n' above is the number of layers.

ICH and IMUL are ignored in FMO/HOP. For FMO/AFO, they define the charge and multiplicity of the model system constructed for the given bond (both 0 by default). IMUL follows the same rules and in $CONTRL. In FMO/AFO any name should be used in place of NAM as NONE, if ICH or MUL should be specified, otherwise only -I and J may be given (i.e., omitting NAM, ICH and MUL).
(default: nothing, that is, no detached bonds).

Example, for a two-layer run with STO-3G and 6-31G* in the first and second layers, respectively.

```
 $FMOBND
-10 15 STO-3G 6-31G*
-20 27 STO-3G 6-31G*
 $END
```

==========

```
=========================================================

$FMOEFP group                        (optional, for FMO runs)


This group is used to specify some parameters for FMO/EFP
including interaction energy analysis (IEA) of solute-
solvent interactions.

NLEVEL = chooses the physical model of FMO/EFP,
       = 0: do not use EFP even if they are defined in
            the input file.
       = 1: subsystem-specific FMO/EFP (T. Nagata et al.,
            J.Chem.Phys. 134, 034110, 2011)
       = 2: monomer-concerted FMO/EFP (T. Nagata et al.,
            J. Phys. Chem. A, 116, 9088-9099, 2012).
Default: 1 if any EFP is present, and 0 otherwise.

NLEVEL=2 is an approximation to NLEVEL=1.  Subsystem-
specific means that the EFP polarization is evaluated for
each monomer and dimer separately.  Monomer-concerted means
that the polarization is evaluated once for the total
electrostatic field of all FMO (and EFP) fragments (i.e.,
monomers).  The monomer-concerted treatment is somewhat
like FMO/PCM[1], where EFP is treated analogously to PCM in
the way of doing it once for the total field.  Then the
induced dipoles on EFP are fixed and used to evalute the
polarization energy of FMO dimers.

IEACAL = controls IEA runs
       =  0: do not do IEA (default)
       = -1: original version (JPC-A 116,9088(2012))
       =  1: run IEA (newer version)
       IEACAL=-1 and 1 differ only for IEA with IEABDY=2,
       in the dimer polarization terms (factor of 2).

ITRLVL = extract polarization contributions in IEA
       = 0: do usual SCC iterations (default)
       = 1: extract ES0 contributions using free state
            densities
       = 2: calculate ES using densities of the solute
            (PL?) state

IEABDY = do IEA up to n-mers, for example, IEABDY=2 means
```

```
         do IEA up to dimers in FMO.  (default=2)

NPRIEA = bit-additive print-out options for IEA
       = 0: no additional print-out (default)
       = 1: print contribution of all EFPs to each FMO
       = 2: print contribution of all EFPs to each FMO atom
       = 4: print individual FMO fragments/EFP fragments
       = 8: print contributions for EFP points/FMO atoms

IPFMO = an array of the size of the number of FMO
        fragments, giving a list of FMO fragments
        for which IEA is done.
        Default: 1, 2, 3, ... (all FMO fragments)

IPEFP = an array of the size of the number of EFP
        fragments, giving a list of EFP fragments
        for which IEA is done.
        Default: 1, 2, 3, ... (all EFP fragments)

=============================================================
```

==========

$FMOENM group (optional, for FMO runs)

This group defines monomer energies for restart jobs. The group should be taken from a previous run.

The format is IFG and ILAY, followed by 4 monomer energies, of which only the first two are used (noncorrelated and correlated).

IFG is the fragment number and ILAY is the layer number. This group is required for FMO restarts IREST=4.

==========

$FMOEND group (optional, for FMO runs)

Dimer energies for restart jobs. The group should be taken from a previous run.

The format is IFG, JFG and ILAY, followed by 2 dimer energies, (E'IJ and Tr(deltaDIJ*VIJ)). IFG and JFG describe the dimer and ILAY is the layer number.

This group is optional for FMO restarts IREST=4 and is otherwise ignored. Note that for parallel restarts, $FMOEND inputs from all nodes should be collected and merged into one group.

==========

$OPTRST group (optional, for RUNTYP=OPTFMO)

Restart data for FMO geometry optimizations. The data inside vary for each optimization method, and are supposed to be taken from a previous run (from the punch file).

==========

==========

$GDDI group (parallel runs only)

This group controls the partitioning of a large set of processors into sub-groups of processors, each of which might compute separate quantum chemistry tasks. If there is more than one processor in a group, the task assigned to that group will run in parallel within that processor group. Note that the implementation of groups in DDI requires that the group boundaries be on SMP nodes, not individual processor cores.

For example, the FMO method can farm out its different monomer or dimer computations to different processor subgroups. This is advantageous, as the monomers are fairly small, and therefore do not scale to very many processors. However, the monomer, dimer, and maybe trimer calculations are very numerous, and can be farmed out on a large parallel system.

At present, only a few procedures in GAMESS can utilize processor groups, namely
a) the FMO method which breaks large calculations into many small ones,
b) VSCF, which has to evaluate the energy at many geometries,
c) numerical derivatives which do the same calculation at many geometries (for gradients, see NUMGRD in $CONTRL, for hessians, see HESS=SEMINUM/FULLNUM in $FORCE),
d) replica-exchange MD (see REMD in $MD).

NGROUP = the number of groups in GDDI. Default is 0 which means standard DDI (all processes in one group).

PAROUT = flag to create punch and log files for all nodes. If set to .false, these files are only opened on group masters.

BALTYP = load balancing at the group level, otherwise similar to the one in $SYSTEM. BALTYP in $SYSTEM is used for intragroup load balancing and the one in $GDDI for intergroup. It applies only to FMO

```
          runs.  (default is DLB)

MANNOD = manual node division into groups.  Subgroups must
         split up on node boundaries (a node contains one
         or more cores).  Provide an array of node counts,
         whose sum must equal the number of nodes fired up
         when GAMESS is launched.
         Note the distinction between nodes and cores, also
         called processers, If you are using six quad-core
         nodes, you might enter
             NGROUP=3 MANNOD(1)=2,2,2
         so that eight CPUs go into each subgroup.
         If MANNOD is not given (the most common case), the
         NGROUP groups are chosen to have equal numbers of
         nodes in them.  For example, a 8 node run that
         asks for NGROUP=3 will set up 3,3,2 nodes/group.

Note that nodes with very large core counts may be too
large for good scaling with certain kinds of subgroup runs.
Any such 'fat' nodes can be divided into "logical nodes" by
using the kickoff option :cpus= for TCP/IP-based runs, or
the environmental variable DDI_LOGICAL_NODE_SIZE for MPI-
based runs.  See the DDI instructions.

Note on memory usage in GDDI:  Distributed memory MEMDDI is
allocated globally, MEMDDI/p words per computing process,
where p is the total number of processors.  This means an
individual subgroup has access to MANNOD(i)*ncores*MEMDDI/p
words of distributed memory.  Thus, if you use groups of
various sizes, each group will have different amounts of
distributed memory (which can be desirable if you have
fragments of various sizes in FMO).

=============================================================
```

==========

$ELG group (polymer elongation calculation)

This group of parameters provides control of elongation calculations, which steadily increase the size of aperiodic polymers, by adding attacking monomers to the end of an existing chain. The existing chain consists of two parts: an A region, with a frozen electron density, farthest from the new monomer, and a B region at whose end the monomer attacks. The wavefunction of the B region and the new monomer are optimized quantum mechanically. Disk files containing integrals and/or wavefunction information must be saved from one elongation run to the next.

A large number of examples are provided with the source code distribution, see ~/gamess/tools/elg for this, perhaps starting with the (gly)5, (gly)6, (gly)7 examples. See the literature cited below for more help.

```
NELONG = a flag to activate an elongation calculation,
          0 means normal GAMESS run (default)
          1 same as 0 but without reorientation of geometry
          2 means elongation starting cluster calculation,
            this initiates a chain's A and B regions.
          3 implies the monomer elongation of the chain.

NATM   = NUMBER OF ATOMS IN A-REGION
         Coordinates of the A-region atoms must be listed
         at the beginning of the input geometry in $DATA

NASPIN = multiplicity of the A-region

NTMLB  = NUMBER OF TERMINAL ATOMS IN B-REGION

NCT    = CONTROLLER FOR AO-CUT
         0 means no AO-cut
         1 means AO-cut activated

IPRI   = PRINT LEVEL
         0 minimum printing (default)
         3 debugging printing

LDOS   = LOCAL DENSITY OF STATES CALCULATION
```

```
          0 means no LDOS calculation
          1 means LDOS calculation

I2EA    = READ-IN 2E-INTEGRALS FOR A-REGION
          0 means A-region 2e-integrals are recalculated
          1 means A-region 2e-integrals are read from a
            previous calculation

ATOB    = Flag to shift one unpaired electron to the A- or
          the B-region, for covalently bonded A and B.
          .TRUE. means shift one electron to B-region
          .FALSE. means shift one electron to A-region

For more information on this method, see

A.Imamura, Y.Aoki, K.Maekawa
      J.Chem.Phys. 95, 5419-5431(1991)
Y.Aoki, A.Imamura  J.Chem.Phys. 97, 8432-8440(1992)
Y.Aoki, S.Suhai, A.Imamura
      Int.J.Quantum Chem. 52, 267-280(1994)
Y.Aoki, S.Suhai, A.Imamura
      J.Chem.Phys. 101, 10808-10823(1994)

and particularly the new implementation described in

"Application of the elongation method to nonlinear optical
properties: finite field approach for calculating static
electric (hyper)polarizabilities"
  F.L.Gu, Y.Aoki, A.Imamura, D.M.Bishop, B.Kirtman
  Mol.Phys. 101, 1487-1494(2003)
"A new localization scheme for the elongation method"
  F.L.Gu, Y.Aoiki, J.Korchowiec, A.Imamura, B.Kirtman
  J.Chem.Phys. 121, 10385-10391(2004)
"Elongation method with cutoff technique for linear SCF
scaling"
  J.Korchowiec, F.L.Gu, A.Imamura, B.Kirtman, Y.Aoki
  Int.J.Quantum Chem. 102, 785-794(2005)
"Elongation method at Restricted Open-Shell Hartree-Fock
level of theory"
  J.Korchowiec, F.L.Gu, Y.Aoki
  Int.J.Quantum Chem.  105, 875-882(2005)

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```

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$DANDC group (optional, relevant if SCFTYP=RHF or UHF)

This group controls the divide-and-conquer (DC) SCF calculations, in which the total 1-electron density matrix is obtained as sum of subsystem density matrices. In this calculation, the total system is partitioned into several disjoint subsystems (central regions). A subsystem density matrix is expanded by bases in the central region and its neighboring environmental region (buffer).

The present implementation allows energy and analytic nuclear gradients, for HF, DFT, and semi-empirical runs, for SCFTYP=RHF or UHF only. The discrete EFP and various continuum solvation models are available. DC correlation energies are also available for either MP2 and CC, see $DCCORR, without nuclear gradients. Dynamic and static polarizabilities (but no hyperpolarizabilities) based on DC-HF are available by specifying RUNTYP=TDHF (not TDHFX).

The initial guess is given by a density matrix, not orbitals. The only available options are GUESS=HUCKEL, HCORE, HUCSUB, DMREAD, and MOREAD (the latter means orbitals for the entire system).

For a review paper on Divide-and-Conquer in GAMESS:
M.Kobayashi, H.Nakai
in Linear-Scaling Techniques in Computational Chemistry and Physics: Methods and Applications (Springer), Chap. 5 (2011)
For more information on the DC-SCF method, see
W.Yang, T.-S.Lee
J.Chem.Phys. 103, 5674-5678(1995)
T.Akama, M.Kobayashi, H.Nakai
J.Comput.Chem. 28, 2003-2012(2007)
T.Akama, A.Fujii, M.Kobayashi, H.Nakai
Mol.Phys. 105, 2799-2804(2007)
T.Akama, M.Kobayashi, H.Nakai
Int.J.Quant.Chem. 109, 2706-2713(2009)
M.Kobayashi, T.Yoshikawa, H.Nakai
Chem.Phys.Lett. 500, 172-177(2010) [open-shell]
M.Kobayashi, T.Kunisada, T.Akama, D.Sakura, H.Nakai
J.Chem.Phys. 134, 034105/1-11(2011) [gradient]

```
    For more information on DC-MP2 and DC-CC, see
        M.Kobayashi, Y.Imamura, H.Nakai
          J.Chem.Phys. 127, 074103/1-7(2007)
        M.Kobayashi, H.Nakai
          J.Chem.Phys. 129, 044103/1-9(2008)
        M.Kobayashi, H.Nakai
          J.Chem.Phys. 131, 114108/1-9(2009)
        M.Kobayashi, H.Nakai
          Int.J.Quant.Chem. 109, 2227-2237(2009)
    For more information on DC-TDHF polarizability, see
        T.Touma, M.Kobayashi, H.Nakai
          Chem.Phys.Lett. 485, 247-252(2010)
```

Of course, the trick to methods that divide up a large problem into small ones is to control the errors that result. A simple way to set up a DC-MP2 calculation is with atomic partitions:

```
 $contrl scftyp=rhf mplevl=2 runtyp=energy $end
 $system mwords=25 $end
 $scf    dirscf=.true. $end
 $dandc  dcflg=.true. subtyp=atom bufrad=8.0 $end
 $dccorr dodccr=.true. rbufcr=5.0 $end
 $guess  guess=hucsub $end  (if DC-SCF is used)
```

This leads to as many subsystems as there are atoms, with the buffer region around the central atom being defined by a radius. This input recognizes that exchange effects in Hartree-Fock are longer range than correlation, and thus uses dual level radii. It may be reasonable to simply do a conventional and thus fully accurate SCF computation by DCFLG=.FALSE., obtaining only the MP2 correlation energy by the divide and conquer method. Faster run times may result from other partitionings, such as manually dividing a protein into subsystems containing a single amino acid.

```
DCFLG =        flag to activate DC-SCF calculation.
               (default=.FALSE.)

  Note:  If you want to treat only the correlated MP2/CC
         procedure in the DC manner, after a standard HF
         calculation, this option may be set to .FALSE.

SUBTYP =        chooses a method to construct disjoint
                subsystems (central region).
       = ATOM   individual atom is 1 subsystem.
```

```
                (default if NSUBS=0 or not given)
        = MANUAL manually selects using NSUBS and LBSUBS
                keywords. (default if NSUBS>=1)
        = CARD   reads from card. $SUBSCF is used for SCF
                and $SUBCOR for MP2/CC calculation.
        = AUTO   constructs subsystems automatically by
                dividing total system by cubic grid.
                Grid size can be set by SUBLNG.
        = AUTBND considers bond strength after AUTO.

NSUBS  = number of subsystems when SUBTYP=MANUAL.

LBSUBS = an array assigning atoms to subsystems.
         The style is the same as INDAT keyword in $FMO.
         Two styles are supported (the choice is made based
         on LBSUBS(1): if it is nonzero, choice (a) is
         taken, otherwise LBSUBS(1) is ignored and choice
         (b) is taken):
         a) LBSUBS(i)=m assigns atom i is to subsystem m.
            LBSUBS(i) must be given for each atom.
         b) the style is
            a1 a2 ... ak 0
            b1 b2 ... bm 0
            ...
            Elements a1...ak are assigned to subsystem 1,
            then b1...bm are assigned to subsystem 2,etc.
            An element is one of the following:
                I    or   I -J
            where I means atom I, and a pair I,-J means
            the range of atoms I-J.  There must be no space
            after the "-"!
         Example:
         LBSUBS(1)=1,1,1,2,2,1 is equivalent to
         LBSUBS(1)=0, 1,-3,6,0, 4,5,0
         Both assign atoms 1,2,3 and 6 to subsystem 1,
         and 4,5 to subsystem 2.

SUBLNG = grid length of cube used in SUBTYP=AUTO or AUTBND.
         This value should be in the unit given by UNITS
         keyword in $CONTRL.  (default=2.0 Angstroms).

BUFTYP = chooses a method to construct buffer region.
       = RADIUS selects atoms included in spheres centered
                at atoms in the central region (default).
                The radius is given by BUFRAD keyword for
```

```
                DC-SCF and by the RBUFCR keyword in $DCCORR
                for DC-MP2/CC.
        = RADSUB selects subsystems containing one or more
                atom(s) which is included in spheres
                centered at atoms in the central region.
                This selection can avoid cutting bonds
                within each subsystem.
        = CARD   reads from $SUBSCF or $SUBCOR card.
                Only available when SUBTYP=CARD.

BUFRAD = buffer radius in DC-SCF calculation. This value
         should be in the units given by UNITS keyword in
         $CONTRL (default=5.0 Angstroms).

FRBETA = inverse temperature parameter of Fermi function
         used in DC-SCF procedure in a.u. (default=200.0)
         Reducing this value may improve SCF convergence
         but may obtain worse total energy.

MXITDC = maximum number of iteration cycles for determining
         Fermi level (default=100). Usually, you need not
         care about this keyword.

FTOL   =   Fermi function cutoff factor (default=15.0).
       = p The value of Fermi function less than 10**(-p)
           is considered as 0. The value greater than
           [1 - 10**(-p)] is considered as 1.

NDCPRT =    DC print-out option which is the sum of
            followings (default=0).
       = +1 not used (reserved).
       = +2 prints density matrix ($DM section) on punch.
       = +4 prints energy corresponding to each subsystem.
            Gives correct energy only in HF calculation.
       = +8 prints orbitals in each subsystem.

IORBD  =   selects molecular orbital in total system whose
           electron density is to be computed.
           Print format is given in $ELDENS.
       = -1, -2, ...  correspond to HOMO, HOMO-1, ...
       = 1, 2, ...    correspond to LUMO, LUMO+1, ...
       = 0            no calculation (default).

In the DC-SCF procedure, the available SCF acceleration
techniques are DIIS, DAMP, EXTRAP as well as DC-DIIS and
```

VFON which are specific to the DC-SCF. In DC-SCF calculation, only DIIS is used by default. DC-DIIS (DIIDCF=.TRUE.) is not normally needed for convergence.

The following keywords control (DC-)DIIS convergence:

```
DIITYP =        selects the error vector used in the
                standard DIIS extrapolation
       = FDS    Pulay's modified DIIS (e=FDS-SDF). Although
                this type of error vector behaves well in
                standard SCF, it may not for DC-SCF.
       = DELTAF Pulay's original DIIS (e[i]=F[i]-F[i-1]),
                or so-called Anderson mixing (default).

DIIQTR = .TRUE.  uses orthogonal basis (in entire system)
                 for DIIS extrapolation.  Normally, this
                 does not make sense in DC-SCF run.
         .FALSE. uses atomic basis function for DIIS
                 extrapolation (default).


EXTDII = energy error threshold in absolute value for
         exiting DIIS (default=0.0).

PEXDII = percentage threshold of energy error change for
         exiting DIIS (default=1.0). PEXDII is
         preferential to EXTDII.

DIIDCF = a flag to activate DC-DIIS interpolation
         (default=.FALSE.).

ETHRDC = energy error threshold for initiating DC-DIIS.
         Increasing ETHRDC forces DC-DIIS on sooner
         (default = 1.D-4 if DIIDCF=.TRUE.).
```

The following keywords control the convergence acceleration based on the varying fractional occupation number (VFON). The final electronic temperature is given by FRBETA.

```
FONTYP =        selects the variation pattern of electronic
                temperature (beta) in SCF iteration
       = DIIER  logarithmic variation with respect to DIIS
                error.
       = NONE   no variation (default).
```

```
BETINI = initial beta value in a.u.
         (default = FRBETA/4 for FONTYP=DIIER).

FONSTA = threshold to start variation of beta
         (default=1.0 for FONTYP=DIIER).

FONEND = threshold to stop variation of beta
         (default=1.D-4 for FONTYP=DIIER).

When FONTYP=DIIER, the beta value used in the iteration
(of which the DIIS error is DIISer) is the following:
     beta = BETINI [for DIISER>FONSTA]
          = FRBETA [for DIISER<=FONEND]
          = FRBETA + C_FON * Log(DIISer/FONEND) [otherwise]
where (C_FON = (BETINI-FRBETA) / Log(FONSTA/FONEND)


Option for the type of nuclear gradient:

NDCGRD =   selects the DC-SCF gradient implementation
        = 0 use a formula proposed by Yang and Lee in 1995
        = 1 use a formula proposed by Kobayashi et al. in
          2011 (default)


Next are options for printing density of states (DOS).

DOSITV = Interval between plot points in Hartree. The
         default is zero,meaning no DOS print-out. If
         you print out DOS, DOSITV=0.05 may be sufficient.

DOSRGL = Left end of the plot range in Hartree.
         (default=-2.0)

DOSRGR = Right end of the plot range in Hartree.
         (default=+2.0)

BDOS   = Inverse temperature parameter (beta) for
         distributing states. This value should not be
         given because it is set to be equivalent to FRBETA
         in $DANDC by default.

=============================================================
```

==========

$DCCORR group (optional)

relevant for MPLEVL=2
relevant for CCTYP=LCCD, CCD, CCSD, CCSD(T), R-CC

This group controls the linear-scaling DC-based MP2 or CC calculations. In this method, subsystem correlation energy is evaluated in each subsystem by means of subsystem MOs. Total correlation energy is obtained by summing up subsystem contributions.

The present implementation allows only RHF reference. DC-MP2 calculations can be run in parallel (using CODE=DDI, IMS, or SERIAL in $MP2), but DC-CC is limited to serial execution. DC-MP2 with CODE=IMS is only compatible with DIRSCF=.TRUE. Coupled cluster code is only available for CCTYP=LCCD, CCD, CCSD, CCSD(T), or R-CC. No solvation models are available. This group must be given if the "double-hybrid" DFT is used (e.g., DFTTYP=B2PLYP).

Note: Although $DANDC input is usually used together to select subsystem and buffer information, DC-SCF calculation is not indispensable to perform DC correlation calculation. You can perform DC correlation calculation without DC-SCF by setting DCFLG=.FALSE. in $DANDC and DODCCR=.TRUE.

For more information (and references), see $DANDC.

DODCCR = a flag to activate DC-MP2/CC calculation. This is forced to be .TRUE. if DCFLG=.TRUE. in $DANDC. This keyword enables to perform DC-MP2/CC calculation after standard (non-DC) RHF.

RBUFCR = buffer radius used in DC-MP2/CC calculation. This value should be in the unit given by UNITS option in $CONTRL. By default, RBUFCR is set to be equal to BUFRAD in $DANDC.
This keyword is mainly used to perform so-called dual-buffer DC-MP2/CC calculations, see the paper on the DC-CC method for more details.

RMKORB = a flag to remake orbitals in each subsystems. This

```
          is forced to be .TRUE. if RBUFCR is different from
          BUFRAD in $DANDC or standard HF calculation was
          performed. Apart from these cases, RMKORB=.FALSE.
          by default. This keyword is meant for debug
          purposes.

HFFRM   = a flag to use the Fermi level determined in the
          preceding HF calculations even when RMKORB=.TRUE.
          (default=.FALSE.)
          The Fermi level is used to classify the subsystem
          orbitals into occupied and virtual ones. Usually,
          this option does not change the results except
          for the use of diffuse basis functions.

WOCC    = a parameter determining proportion of occupied
          contribution.  This should be between 0 and 1.
          The proportion of virtual contribution becomes
          [1 - WOCC]. (default=1.0)
          This is forced to be 1.0 in DC-CC calculation,
          except when WOCC=0.0, which only calculates
          virtual contribution.
          We recommend 1.0 to obtain accurate results.

ONLYOC =          a flag to disable MP2 calculation for
                  virtual contributions. This is forced to
                  be .FALSE. if WOCC is not 1.0, and to be
                  .TRUE. in DC-CC calculation.
        = .TRUE.  Performs DC-MP2 calculation only for
                  occupied contributions. This option will
                  accelerate the CPU time. (default)
        = .FALSE. Performs DC-MP2 calculation for occupied
                  and virtual contributions.

ITPART =    specifies the partitioning for (T) correction.
            This is only relevant to CCTYP=CCSD(T) or R-CC.
        = XY (two-digit integer)
            uses [X,Y] type partitioning defined in the
            following article: J.Chem.Phys.131,114108(2009)
            (default=00)

ISTCOR =   restart option for DC-MP2/CC.
        = 0 does DC-MP2/CC calculation from the beginning
            (default).
        = n reads subsystem correlation energies
            corresponding to subsystem 1-(n-1) from input
```

```
            and perform DC-MP2/CC calculation from n-th
            subsystem.  $MP2RES and $CCRES inputs are
            required for DC-MP2 and DC-CC calculations,
            respectively.

FZCORE =    a flag to freeze core electrons in DC-MP2 or
            DC-CC calculation. Other frozen orbital options
            options such as NACORE in $MP2 and NCORE in
            $CCINP do not pertain to DC-MP2/CC calculations.
            The default is .TRUE. to freeze cores.

================================================================
```

==========

$SUBSCF group (relevant during Divide and Conquer)
$SUBCOR group

These groups specify the central and buffer regions when SUBTYP=CARD or BUFTYP=CARD in $DANDC. $SUBSCF is used for DC SCF and $SUBCOR is for DC-MP2/CC. If BUFTYP is not CARD, only central region is specified by these groups. They consist of free format integer numbers of which the style is like this:

```
 $SUBSCF
! SUBSYSTEM     1
  1  3 -5  0
  2  6 -8  0 0
! SUBSYSTEM     2
  2  6 -9 11  0
  1  3  4  10  12 -14 0 0
! SUBSYSTEM     3
  ...
 $END
```

Lines starting with ! are comments neglected when reading.

First, atoms in the central region of subsystem 1 is specified according to the (b) style of LBSUBS in $DANDC. A single 0 separates the central and buffer region of the same subsystem. Then, specify atoms in the buffer region of subsystem 1. A double 0 separates subsystems. These are iterated until all subsystems are specified.

In the above case, the subsystems are the followings:

```
Subsystem 1 central: 1,3,4,5
            buffer : 2,6,7,8
Subsystem 2 central: 2,6,7,8,9,11
            buffer : 1,3,4,10,12,13,14
```

==========

==========

$MP2RES group (restart data for DC-MP2 runs)
$CCRES group (restart data for DC-CC runs)

Restart data (consisting of subsystem correlation energies) for Divide and Conquer correlation calculations. The appropriately named input group is required if ISTCOR is selected in $DCCORR. The format of these two groups is slightly different for DC-MP2 or DC-CC, but the data should be given in exactly the same format that it was written to file RESTART, adding only a $END line.

Examples:

```
 $MP2RES
    1  -0.133110332082E+00   0.000E+00  -0.133110332082E+00
    2  -0.130740147906E+00   0.000E+00  -0.130740147906E+00
    3  -0.130483660838E+00   0.000E+00  -0.130483660838E+00
 $END

 $CCRES
2
    1  -0.135031928183E+00  -0.132440119981E+00
    2  -0.132589691149E+00  -0.131009546477E+00
    3  -0.132673391144E+00  -0.130832334600E+00
    4  -0.133163592168E+00  -0.131377855474E+00
 $END
```

The integer in the first line indicates the CC method.

==========

==========

$CIMINP group (required when CIMTYP is not NONE)

This group controls a CIM calculation of the type specified by CIMTYP in $CONTRL. The $CIMINP input variables can be divided into a few categories:

*** The variable required by all CIM runs ***

SUBMTD = assigns the default method for each CIM subsystem. In single-level CIM calculations, SUBMTD applies to all CIM subsystems and no further information about quantum-chemistry methods used in subsystem calculations is needed. In order to run a multi-level CIM calculation (CIMTYP=SECIM or GSECIM only), information about subsystems treated with methods other than SUBMTD must be provided in $CIMATM (CIMTYP=SECIM) or $CIMFRG (CIMTYP=GSECIM). The allowed values of SUBMTD are:

= NONE or HF means no post-HF calculation will be performed. In this case, information about methods used in subsystem calculations must be provided in $CIMATM (CIMTYP=SECIM) or $CIMFRG (CIMTYP=GSECIM) and at least one atom in $CIMATM or at least one group of atoms in $CIMFRG must be treated by the allowed post-HF approach.
= MP2 means an MP2 subsystem calculation (SCFTYP=RHF only).
= CCD means a CCD subsystem calculation (SCFTYP=RHF only).
= CCSD means a CCSD subsystem calculation.
= CCSD(T) means a CCSD(T) subsystem calculation (SCFTYP=RHF only).
= CR-CCL means a CR-CC(2,3) subsystem calculation.

Note: There is no default for SUBMTD; the user must specify one of the above values.

The remaining $CIMINP input variables are optional.

*** the details of CIM subsystem design ***

ZETA = threshold for assigning environment orbitals to central occupied LMOs in the SECIM/GSECIM algorithm (CIMTYP=SECIM or GSECIM only). Default=0.003.

ZETA1 = threshold for assigning primary environment orbitals to central occupied LMOs in the DECIM algorithm (CIMTYP=DECIM only). Default=0.01.

ZETA2 = threshold for assigning secondary environment orbitals to irreducible central domains in the DECIM algorithm (CIMTYP=DECIM only). Default=0.05.

ATMMLK = the Mulliken population cutoff for assigning central LMO(s) to each non-hydrogen atom and its adjacent hydrogen atom(s) (the SECIM case) or to the user-specified set of two or more non-hydrogen atoms and hydrogen atoms bounded to those atoms provided in $CIMFRG (the GSECIM case) in initial steps of the SECIM/GSECIM algorithm. The same parameter is also used to assign AO domains to occupied LMOs of extended subsystems within the SECIM/GSECIM methodology (CIMTYP=SECIM or GSECIM only). Default=0.15.

BUFDST = cutoff distance (in Angstrom) for buffer atoms included in extended subsystems. Default=4.0.

MRGSUB = determine whether or not to incorporate smaller subsystems into larger ones if the former are completely embedded in the latter.

= 0 do not incorporate smaller subsystems into larger ones, i.e., retain all subsystems resulting from the initial steps of the CIM algorithms without eliminating redundancies.

= 1 incorporate smaller subsystems into larger ones if the methods used for smaller subsystems and larger ones that contain them are identical or if the method used for a given smaller subsystem is a lower-level approach compared to the method used for the larger subsystem that contains it. Otherwise, i.e., if the method

used for a given smaller subsystem is a higher-level approach compared to the method used for the larger subsystem, retain the smaller subsystem and the method used for it without embedding it into the larger one. The ordering of theory levels from low to high level is MP2<CCD<CCSD<CCSD(T)<CR-CC(2,3). This is the default choice for MRGSUB.

= 2 always incorporate smaller subsystems into larger ones and, if the method used for a given smaller subsystem is different than the method used for the larger subsystem that contains it, apply the higher-level approach to the larger subsystem after embedding the smaller one in it.

ETA = the threshold for selecting the final sets of unoccupied orbitals associated with CIM subsystems from the larger sets of unoccupied orbitals associated with the corresponding extended subsystems. A given unoccupied orbital 'a' is kept in the calculations if the norm of the difference between 'a' and the projected form of 'a' obtained by projecting it on the AO space of the corresponding CIM subsystem is less than ETA. The larger the ETA value the larger the number of unoccupied orbitals associated with extended subsystems is retained. Default=0.2.

FCORE = a flag to exclude the chemical core orbitals in the correlated CIM calculations. Default = .TRUE.

MOFIX = determines whether or not to read information about the orbital composition of CIM subsystems from the external ${JOB}.dmn file (environment variable CIMSYS).

= 0 do not read information from the ${JOB}.dmn file if it exists prior to calculation. The ${JOB}.dmn file with the orbital composition of CIM subsystems is produced by the present run.

= 1 read information about the occupied LMOs of each subsystem from the previously generated CIMSYS file to perform the CIM calculation with partially fixed domains. The unoccupied LMOs

```
           of each subsystem are generated by the present
           run. The CIMSYS file from the previous CIM run
           must be saved on the disk as the ${JOB}.dmn
           file.
       = 2 read info about the occupied and unoccupied
           LMOs of each subsystem from the previously
           generated CIMSYS file to perform the fixed
           domain CIM calculation. The CIMSYS file from the
           previous CIM run must be saved on the disk as
           the ${JOB}.dmn file.

   *** The variables controlling subsystem calculations ***

CCONV  = the convergence criterion for the cluster
         amplitudes in CCD or CCSD subsystem iterations.
         Default=1.0E-6.

ENRGML = the way to determine the correlation energy
         contribution due to the individual occupied LMO
         'i' if 'i' is central in two or more subsystems
         that are treated at different theory levels when
         running multi-level SECIM or GSECIM calculations.

       = AVERAGE   use the average energy, i.e., average
                   the correlation energy contributions due
                   to LMO 'i' that correspond to all
                   subsystems where 'i' is central
                   (default).
       = HIGHER    use the correlation energy contribution
                   that corresponds to the subsystem in
                   which 'i' is central and which is
                   treated by the highest-level approach.
                   The ordering of theory levels from low
                   to high level is
                   MP2 < CCD < CCSD < CCSD(T) < CR-CC(2,3).


        *** for highly specialized users ***

     The parameters below are rather specialized and rarely
of concern. They should be changed from their default
values only for good reason by a knowledgeable user.

SUBTYP = type of orbitals used in subsystem calculations.
       = QCMO      use the quasi-canonical molecular
```

```
                orbitals (default).
        = LMO   use the localized molecular orbitals
                (SUBMTD=CCSD, NONE, or HF only). IF
                SUBMTD=NONE or HF, the only method that
                can be accepted in $CIMFRG or $CIMATM is
                CCSD.

SUBRHF = a flag to choose the RHF-based and not ROHF-based
         algorithm for the closed-shell subsystems even if
         the total system is an open shell. The program
         aborts when one or more open-shell subsystems are
         treated with MP2, CCD, or CCSD(T). Default=.TRUE.

MOSORT = a flag to reorder the occupied LMOs after
         localization according to labels of atoms, so
         that one avoids the potential ambiquities in the
         order in which smaller subsystems are absorbed
         by the larger ones that may occasionally emerge
         in DECIM calculations. Default=.TRUE.

ORTHO  = a flag enforcing strict orthogonality among the
         occupied and unoccupied LMOs in the extended and
         final CIM subsystems after projecting these LMOs
         on the subsystem AO spaces. Default = .FALSE.

   *** Advanced run options for choosing between sequential
       and parallel CIM calculations, and information about
       restarts and parallel OpenMP and MPI runs ***

Keyword MTDCIM that can be used to decide if individual
subsystem calculations, after the initial RHF or ROHF,
orbital localization, and subsystem generation steps, are
performed sequentially or in parallel. This keyword can be
used to restart CIM runs if any subsystem calculation
fails. The following values of MTDCIM are allowed:

MTDCIM = 0  a sequential CIM calculation will be performed
            (default). If the calculation does not complete
            due to the failure of one of the subsystem
            calculations, the program will abort, but the
            user will be able to restart it using one of
            the two restart methods described below.
       = 1  gracefully stop the calculation after the
            Hartree-Fock calculation, orbital localization,
            and CIM subsystem construction are completed.
```

The $JOB.cim file, which contains the
information about all subsystems needed to
to complete the CIM run, and multiple
input files $JOB.Sys-N.inp, where N is the
subsystem number, for individual subsystem
calculations with GAMESS, are generated,
but not run. This option is particularly useful
for parallel calculations.

= 2 resume the calculation once all $JOB.Sys-N.cim
subsystem files are generated by running GAMESS
calculations for all subsystems (for example,
in parallel). This option is particularly
useful for parallel calculations, but it can
also be used to restart the CIM sequential run.

==========

* *
For information on Cluster-in-Molecules,
see the 'further information' section
* *

==========

$CIMATM group

(optional for CIMTYP=SECIM in $CONTRL;
relevant to multi-level SECIM calculations)

In free format, provide an array of the comma or dash separated integers labeling the atoms, followed, in each row of the array, by the name of the method to be applied to the group of atoms listed in that row. A method must be supplied for each group of atoms in $CIMATM. The hydrogen atoms do not have to be specified, since each hydrogen atom is assigned to the nearest non-hydrogen atom, although there may be cases where listing hydrogens is useful if there is ambiguity in assigning hydrogens to non-hydrogen atoms. No atom can be listed more than once. Atoms that are not represented in $CIMATM are treated with the method defined by SUBMTD in $CIMINP. For example,

```
 $CIMATM
 1-4,11,12 CR-CCL
 9,10 CCSD
 $END
```

implies that atoms 1-4, 11, and 12 (and adjacent hydrogens, if any) will be treated by CR-CC(2,3) and atoms 9 and 10 (and adjacent hydrogens, if any) by CCSD. The remaining atoms will be treated by the method defined by SUBMTD in $CIMINP.

==========

$CIMFRG group

(required when CIMTYP=GSECIM in $CONTRL;
relevant to single- and multi-level GSECIM calculations)

In free-format, provide an array of the comma or dash separated integers labeling the atoms. Integers in each row, which must be listed in parentheses, represent the user-specified group of atoms that are used to identify central occupied LMOs in the initial steps of the GSECIM subsystem design. When generating subsystems, the atoms specified in a given row will always be kept together. Optionally, one can provide the name of the method to be

applied to the group of atoms listed in a given row. The hydrogen atoms do not have to be included, since each hydrogen atom is assigned to the nearest non-hydrogen atom, although there may be cases where listing hydrogens is useful if there is ambiguity in assigning hydrogens to non-hydrogen atoms. The subsystems involving atoms that are not represented in $CIMFRG will be determined using the standard SECIM algorithm and treated with the method defined by SUBMTD in $CIMINP. For example,

```
 $CIMFRG
 1 (3-4,6) CR-CCL
 2 (1-2,11) CCSD
 3 (14,34,50)
 4 (16,18,54)
 5 (21-22,26,30)
 6 (37-38,42,46)
 $END
```

implies that atoms 3, 4, and 6 (and adjacent hydrogens, if any) will be used to identify central LMOs that define the 1st subsystem in the initial steps of the GSECIM algorithm, which will be treated by CR-CC(2,3). Similarly, atoms 1, 2, and 11 (and adjacent hydrogens, if any) will be used to identify central LMOs that define the 2nd subsystem in the initial steps of the GSECIM algorithm, which will be treated by CCSD, whereas atoms 14, 34, and 50 (and adjacent hydrogens, if any) will be used to identify central LMOs that define the 3rd subsystem in the initial steps of the GSECIM algorithm which will be treated by the method defined by SUBMTD in $CIMINP, etc. The remaining atoms will be treated by the standard SECIM algorithm and the method defined by SUBMTD in $CIMINP.

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$QUANPO group (optional, relevant if QuanPol is used)

QuanPol (quantum chemistry polarizable force field program) can perform MM, QM/MM or QM/MM/Continuum solvent MD simulation, geometry optimization, saddle point search and Hessian vibration frequency calculation, using HF, DFT, GVB, MCSCF, MP2 or TDDFT wavefunctions.

"QuanPol: A full spectrum and seamless QM/MM program", Journal of Computational Chemistry, 2013, 34, 2816-2833.

Either $FFDATA (explicit input of coordinates and force field parameters) or $FFPDB (Protein Data Bank coordinates and built-in force fields) needs to be present, to define the MM atoms. Quantum atoms, if any, are given in $DATA as usual. If no quantum atom is used, use COORD=FRAGONLY in $CONTRL. For free energy perturbation calculations, $FFDATA and $FFDATB are required to define the reference and target MM states, and $QUANPO keywords MATOMA and MATOMB are required to define the reference and target QM states.

Force field data sets are located by the environment variable QUANPOL. Some parameter and topology files from the CHARMM, AMBER and MMFF94 programs are included in QUANPOL and can be read by QuanPol.

When some of the $QUANPO inputs become lengthy, use multiple lines and '>' at the end of each line to glue them together.

**** set up MM force field ****

```
MXFFAT = maximum number of MM atoms.
MXBOND = maximum number of MM bonds.
MXANGL = maximum number of MM bond angles.
MXDIHR = maximum number of MM dihedral rotation angles.
MXDIHB = maximum number of MM dihedral bending angles.
         (i.e. improper torsion in CHARMM).
MXWAGG = maximum number of MM wagging angles.
MXCMAP = maximum number of CHARMM correction map cases.
```

```
All of the amove are for memory allocation purposes.
Defaults are automatically determined and are almost always
good.

NFFTYP = select the force field type (no default)
       =           0   user defined force field
       = 20000-29999   CHARMM
       = 30000-39999   AMBER (including GAFF)
       = 40000-49999   OPLSAA
       = 50000-59999   MMFF94

User defined force field can be input from $FFDATA, and/or
by using IADDWAT and supplying water potential in the
path/gamess/auxdata/QUANPOL/WATERIONS.DAT file. For
NFFTYP=0 the default WT14CH and WT14LJ are both 1.0. For
any molecule, it is a good idea to use LOUT=1 and NFFTYP=0
to generate a template $FFDATA, and then
modify it.

CHARMM force field can be established for amino acids,
nucleic acids and simple ions by using the top/par files
from CHARMM developers.  It is not made available for
general molecules.  WT14CH=1.0, WT14LJ=1.0 (but uses a
second set of LJ potential).  Note CHARMM typically
requires the use of ISHIFT=4, ISWITCH=1, SWRA=10, SWRB=12.
These must be input in $QUANPO.
* To use CHARMM36, give the following in $QUANPO:
NFFTYP=20000 NFFFILE=2
TOPFILE='path/gamess/auxdata/QUANPOL/top_all36_prot.rtf'
PARFILE='path/gamess/auxdata/QUANPOL/par_all36_prot.prm'
* To use CHARMM27, give the following in $QUANPO:
NFFTYP=20000 NFFFILE=2
TOPFILE='path/top_all27_prot_na.rtf'
PARFILE='path/par_all27_prot_na.prm'

AMBER force field can be established for amino acids,
nucleic acids and simple ions by using the top/par files
from AMBER developers.  It is not made available for
general molecules.  However, QuanPol LOUT=1 is able to
read AMBER GAFF files in the mol2 format (generated by
AmberTools), and read the AMBER gaff.dat parameter file
to establish the force field.  WT14CH=1/1.2, WT14LJ=0.5
(if a second set of LJ potential is used, WT14LJ is set
to be 1.0).  AMBER typically requires the use of
```

```
ISHIFT=0, ISWITCH=0, together with SWRB=12 or a larger
value.  These must be input in $QUANPO.
* To use AMBER12 polarizable protein force field:
NFFTYP=30000 NFFFILE=3 IDOPOL=100
TOPAMIA='path/all_amino12pol*.in'
TOPNTER='path/all_aminont12pol*.in'
TOPCTER='path/all_aminoct12pol*.in'
PARFIL2='path/frcmod.ff12pol*'
PARFILE='path/gamess/auxdata/QUANPOL/parm99.dat'
* To use AMBER12 nonpolarizable protein force field:
NFFTYP=30000 NFFFILE=3 IDOPOL=0
TOPAMIA='path/gamess/auxdata/QUANPOL/amino12.in'
TOPNTER='path/gamess/auxdata/QUANPOL/aminont12.in'
TOPCTER='path/gamess/auxdata/QUANPOL/aminoct12.in'
PARFILE='path/gamess/auxdata/QUANPOL/parm10.dat'
PARFIL2='path/gamess/auxdata/QUANPOL/frcmod.ff12SB'
* To use AMBER10 nonpolarizable protein/na force field:
NFFTYP=30000 NFFFILE=3 IDOPOL=0
TOPAMIA='path/gamess/auxdata/QUANPOL/amino10.in'
TOPNTER='path/gamess/auxdata/QUANPOL/aminont10.in'
TOPCTER='path/gamess/auxdata/QUANPOL/aminoct10.in'
TOPNUCA='path/gamess/auxdata/QUANPOL/nucleic10.in'
PARFILE='path/gamess/auxdata/QUANPOL/parm10.dat'
* To use AMBER02 polarizable protein/na force field:
NFFTYP=30000 NFFFILE=3 IDOPOL=100
TOPAMIA='path/gamess/auxdata/QUANPOL/all_amino02.in'
TOPNTER='path/gamess/auxdata/QUANPOL/all_aminont02.in'
TOPCTER='path/gamess/auxdata/QUANPOL/all_aminoct02.in'
TOPNUCA='path/gamess/auxdata/QUANPOL/all_nuc02.in'
PARFILE='path/gamess/auxdata/QUANPOL/parm99.dat'
PARFIL2='path/gamess/auxdata/QUANPOL/frcmod.ff02pol.r1'
* To use AMBER94 nonpolarizable protein/na force field:
NFFTYP=30000 NFFFILE=3 IDOPOL=0
TOPAMIA='path/gamess/auxdata/QUANPOL/all_amino94.in'
TOPNTER='path/gamess/auxdata/QUANPOL/all_aminont94.in'
TOPCTER='path/gamess/auxdata/QUANPOL/all_aminoct94.in'
TOPNUCA='path/gamess/auxdata/QUANPOL/all_nuc94.in'
PARFILE='path/gamess/auxdata/QUANPOL/parm94.dat'
* To use AMBER94 nonpolarizable protein/na force field:
NFFTYP=30000 NFFFILE=2 IDOPOL=0
TOPFILE=
'path/gamess/auxdata/QUANPOL/top_amber_cornell.inp'
PARFILE=
'path/gamess/auxdata/QUANPOL/par_amber_cornell.inp'
```

OPLSAA force field can be established for amino acids
and simple ions by using the top/par files from the
CHARMM package. It is not made available for general
molecules. WT14CH=0.5, WT14LJ=0.5 (if a second set of
LJ potential is used, WT14LJ is set to be 1.0). QuanPol
does not have the original OPLS switching functions for
charge-charge potential. The original OPLS uses a
switching function in 10.5-11.0 A (but in some cases
12.5-13.0 and 14.5-15.0 A) for both charge-charge and
LJ potentials.
* To use OPLSAA-96 nonpolarizable protein force field:
NFFTYP=40000 NFFFILE=2
TOPFILE='path/gamess/auxdata/QUANPOL/top_opls_aa.inp'
PARFILE='path/gamess/auxdata/QUANPOL/par_opls_aa.inp'

MMFF94 is implemented in QuanPol for general organic
molecules and some metal ions as described in the
original MMFF94 papers, and tested with the validation
suit (http://server.ccl.net/cca/data/MMFF94/) of 761
tests. All 761 tests can pass, with the largest positive
difference of +0.011 kcal/mol, the largest negative
difference of -0.007 kcal/mol, and a root mean square
difference of 0.002 kcal/mol. Therefore, this is a
complete implementation of MMFF94. It also works for
proteins and DNA/RNA molecules. When using LOUT=1 and
NFFTYP=50000 to generate MMFF94 force field for a
molecule in $FFDATA or $FFPDB, the parameter file
'MMFF-I_AppendixB.ascii' must be used. This file can be
downloaded from a JCC ftp server:
'ftp.wiley.com/public/journals/jcc/suppmat/17/490/'.
The keyword MMFF94Q is required for some cases.
The charge-charge interaction has a buffer distance of
0.05 A in MMFF94. However, in QuanPol implementation
when ISHIFT>0, or IEWALD>0, or ISOFTCR>0 is used, this
buffer distance is not used (i.e. set to be zero).
There are a dielectric constant D and an index n in the
MMFF94 formula. Only D=1.0 and n=1 are implemented in
QuanPol. WT14CH=0.75, WT14LJ=1.0 (MMFF94 uses a 14-7
potential). It is not clear what shifting function,
switching function and cutoff distances should be used
in MMFF94 bulk MD simulations.
* To use MMFF94 nonpolarizable force field:
LOUT=1 NFFTYP=50000
PARFILE='path/MMFF-I_AppendixB.ascii'

```
MMFF94s is a variant of MMFF94.  To use MMFF94s, one
needs to download two parameter files from:
ftp://ftp.wiley.com/public/journals/jcc/suppmat/20/720
These two files are named 'Table1.txt' and 'Table2.txt'.
One should replace the corresponding sections in
'MMFF-I_AppendixB.ascii' with 'Table1.txt' and
'Table2.txt', and save it as a new file such as
'MMFF94s.par'.  QuanPol can reproduce MMFF94s results
available in the validation suit of 265 tests
(http://server.ccl.net/cca/data/MMFF94s/index.shtml).
* To use MMFF94s nonpolarizable force field:
LOUT=1  NFFTYP=50000
PARFILE='path/MMFF94s.par'

LOUT   = create a $FFDATA group containing force field
         parameters for a molecule.  Require inputting
         a $FFDATA group containing only COORDINATES.
       = 0   no action (default)
       = 1   create the $FFDATA group for a molecule
             using force fields defined by NFFTYP.
       For NFFTYP=0:
         Can use JRATTLE to define coordination bonds that
         are usually not considered as covalent bonds.
         The equilibrium bond lengths and angles are
         set to be those in the input geometry.  Trivial
         force constants and potential parameters are
         assigned to covalent and noncovalent terms.
         Users are supposed to know and edit the output
         $FFDATA to assign formal charges to ions and
         ionized groups.  This option is most useful for
         preparing a simplified force field for the QM
         molecule to be used in QuanPol QM/MM calculation.
       For NFFTYP=30000:
         Need
PARFILE='path/gamess/auxdata/QUANPOL/gaff.dat'
              TOPFILE='path/xxx.mol2'
         The xxx.mol2 file is generated by AmberTools.
       For NFFTYP=50000:
         Need PARFILE='path/MMFF-I_AppendixB.ascii'.
         Formal charges on some atoms/ions must be
         specified via keyword MMFF94Q.

MMFF94Q= n, I1, Q1, I2, Q2, ... In, Qn
       = specify the formal charge for up to 50 atoms
         when LOUT=1 and NFFTYP=50000 are selected.
```

```
          Note the default formal charge is zero, and
          does not need user specification.  QuanPol
          is able to determine almost all formal charges
          for H, C, N, O, F, Si, P, S, Cl, Br, I atoms
          and simple ions.  Therefore, MMFF94Q
          is required only for multivalent metal
          ions (e.g. Fe, Cu) and some special molecules.
          MMFF94 atom types depend on formal charges.
          n   = number of atoms (default=0)
          In  = atom sequential number in $FFDATA
          Qn  = formal charge (e.g. -0.50, +2.0, +3.0)
          For example, MMFF94Q=1 30 +3.0 is to assign
          the 30th atom with +3.0 e charge.

   **** set up QM/MM ****
```

QuanPol automatically performs QM/MM calculation when $FFDATA (or $FFPDB) and $DATA are both detected in the input deck and the numbers of QM atoms and MM atoms are both greater than zero. Any MM atom that has virtually the same Cartesian coordinates of a QM atom will be identified and labeled, and vice versa. QM atoms will be enforced to have the coordinates and masses of their matching MM atoms.

If there is no covalent bond between the QM and MM regions, QM atoms will only feel the noncovalent interaction potentials, such as charge, induced dipole and LJ (or QMMMREP potential if LJQMMM=0), of the MM atoms. There will be no covalent interactions between QM and MM atoms. In general, there are no covalent and noncovalent interactions between QM atoms, with one exception for IFEPTOP=1 with MATOMA > MATOMB. In this case, the bond, angle, dihedral rotation/bending, and wagging terms involving any QM dummy atoms (i.e. those appear in QM state A but not in QM state B) are retained and scaled by WSIMUL. When WSIMUL=1.0, the pure state B has a full strength of these MM covalent terms to ensure that the QM dummy atoms stay in their positions. Using WSIMUL is good because (1-WSIMUL)*QM + WSIMUL*MM is just right.

If there are covalent bonds between QM atoms and MM atoms all covalent force field interactions will remain in full strengths if they involve at least one MM atom. If the

QM atoms are capping QM H atoms, the bond, angle and dihedral rotation (only these three) terms involving the QM H atoms and other QM atoms (but no MM atoms) will be retained and scaled by RETAIN, which is defaulted as 0.5. This is to compensate for the weakening of the covalent terms due to the elongation of the capping H atom bond length. If the QM atoms are not capping QM H atoms with elongated bond lengths, it is not necessary to compensate for the covalent terms, and RETAIN should be 0. All covalent terms involving only QM atoms are excluded, but may be retained for IFEPTOP=1 with MATOMA > MATOMB (see the above paragraph).

To prepare an input file for QM/MM with covalent bonds:

a. Prepare a good input for pure MM calculation.
b. Copy some MM atoms from $FFDATA to $DATA to be QM atoms. It is not necessary to delete these atoms from $FFDATA. $DATA can have atoms not in $FFDATA.
c. If necessary, change one or several of the QM atoms in $DATA to be capping H atoms. The simplest way is to only change the nuclear charge to 1.0 because GAMESS recognizes atoms using their nuclear charges rather than their names. The atom names can also be changed to enhance readibility. For example, for an alpha carbon in a protein, the following can be seen in $DATA:

```
    CX      1.0      X       Y       Z
```

   The Cartesian coordinates X, Y, Z cannot be changed.

QuanPol will automatically match QM and MM atoms and

a. Zero off all covalent force field terms that involve only QM atoms. Scale the covalent force field terms (only bond, angle and dihedral rotation) that involve QM and capping QM H atoms by RETAIN, which is typically 0.5.
b. Zero off force field charges and polarizabilities for all QM atoms.
c. Zero off force field LJ potentials for all QM atoms if LJQMMM=0 is used. Retain LJ terms for QM atoms if LJQMMM=1 is used, but exclude any LJ terms between QM atoms.
d. Zero off QMMMREP terms for all QM atoms, and also for MM atoms that form covalent bonds to QM atoms.
e. Apply special QMREP to capping QM H atoms.

```
RETAIN = retaining factor (0.0 - 1.0, default=0.5) for
         force field covalent terms that involve only QM
         atoms, one of which is a capping H atom with
         a repulsion potential.  The purpose is to
         strengthen the weakened QM covalent terms
         involving the capping H atom.

QMREP  = NQMREP, IATOM1, NTERM1, C11, Z11, C12, Z12 ...,
                 IATOM2, NTERM2, C21, Z21, C22, Z22 ...
       = specify effective Gaussian repulsion potentials
         at capping QM atoms (typically H atoms in
         place of C and N atoms of a peptide) to produce
         the desired longer bond lengths.
           NQMREP = number of QM atoms with Gaussian
                    potentials.  Up to 200 atoms.
           IATOMn = QM atom sequential number in $DATA.
                    When MATOMB > 0, IATOMn is only for
                    state A.
           NTERMn = number of Gaussians at IATOMn, Up to 4
           C11,.. = strength part of the Gaussian, e/bohr
           Z11,.. = radial part of the Gaussian, 1/bohr**2
                    Must enter NTERMn pairs of C and Z for
                    atom IATOMn.
         For example, to define 1 Gaussian for QM atom 1
         and 3 Gaussians for QM atom 7, give
           QMREP=2,1,1,3.0,3.0,7,3,8.0,6.0,3.0,3.0,0.3,1.0
         For H atom forming C-H bond, a single Gaussian
         with C=3.0 e/bohr and Z=3.0 bohr**(-2) is a good
         option because it can create an equilibrium bond
         length of ~1.50 angstrom for a C-C bond in
         proteins.
                       ** QMREP default **
         QuanPol always automatically applies a single
         Gaussian potentials (C=3.0, Z=3.0) to all QM
         capping H atoms.  Explicit input of QMREP can
         override the QuanPol default values.  If no
         QMREP is wanted for a capping H atom, simply
         input C=0.0 and Z=0.0 for the capping H atom.

LJQMMM = specify how the QM-MM repulsion and dispersion
         are handled in a QM/MM system.
       = 0   use QMMMREP (Gaussian potentials on MM)
       = 1   use MM Lennard-Jones terms (default)

RDAMP  = specify the effective distance (A) in the damping
```

```
          function for polarizability.  Default=3.0 A.
          QuanPol scales MM polarizability using a Gaussian
          function of interatomic distances R (in bohr):
              S(R) = EXP[-0.0863*(R-RDAMP)**2]
          This method works only for QM/MM.  R are QM-MM
          distances.  A MM polarizability point is scaled
          by all QM atoms within RDAMP to the MM point.

INTCHG = specify how noninteger charge is treated in
          QM/MM.  When covalent bonds are cut, the MM
          region is often left with a noninteger charge.
        = 0   no action (not recommended).
        = 1   add missing charge to the MM atoms that form
              covalent bonds to QM atoms.
              For multiple such MM atoms, the missing
              charge is evenly distributed. (default)

   **** set up optimization and MD simulation ****

Use $CONTRL RUNTYP=OPTIMIZE, HESSIAN and MD to run
QuanPol geometry optimization (including saddle point
or transition state search), vibration frequency
calculation and MD simulation.  For optimization jobs,
most of the $STATPT options can be used, but not all.
$STATPT PROJCT=.T. makes little sense to QM/MM jobs so
it is always false.  The Hessian from pure MM
calculation can be used with MMHESS=1 and IHESS=1 to
guide QM/MM geometry search (RUNTYP=OPTIMIZE).

For Hessian jobs, the $FORCE options are not used.  For
pure MM systems, all MM atoms (if less than 2000 and
LACTMM=0) or active site MM atoms (when LACTMM > 0) are
included in Hessian calculation.  For QM/MM systems,
only QM atoms are used to construct the force constant
matrix, but MM effects are included.  When LACTQM > 0
is used, only the active site QM atoms are displaced to
calculate force constants, nonactive site QM atoms are
not displaced (time saving!) and some trivial negative
force constants are used to produce imaginary vibration
frequencies of 1.000*i cm-1.  To get isotope effects,
an already computed $HESS group can be supplied in the
input file, together with a modified atomic mass in
the PARAMETER section of $FFDATA ($MASS will not work).
Of course, Hessian jobs do not work with RATTLE at all.
QuanPol QM/MM Hessian jobs are restartable by using
```

```
the saved $VIB group in the new input.

DT     = MD time step size.  Default=1.0D-15 second is
         usually good, especially when RATTLE is used.
         QuanPol sets a maximum value of 0.2 bohr/DT
         (i.e., 10583.5 m/s for DT=1 fs) for each
         velocity component when ITSTAT is applied.
         Such a limit can prevent chaotic behavior,
         which may occur frequently for large systems.

NSTEP  = number of MD or OPTIMIZE steps (default=1000).
         This NSTEP overrides the $STATPT NSTEP.

MMHESS = specify if the supplied $HESS group for QM/MM
         geometry optimization is generated from pure
         MM Hessian calculation.  If yes, the force
         constant matrix will be re-ordered to match
         the atom sequence in the QM/MM job, in which
         the Hessian always has QM atoms placed ahead
         of MM atoms. Default = 0.
       = 0   no, the $HESS does not need re-ordering.
             This means that the $HESS is from a
             previous QM/MM calculation.
       = 1   yes, the $HESS needs re-ordering to match
             QM/MM atoms.  This means that the $HESS
             is from a pure MM Hessian calculation.

LACTMM = n, K1, R1, ..., Kn, Rn  (case 1, when n =< 10)
       = define sphere radii in angstrom for n MM atoms
         in $FFDATA.  All MM and QM atoms included in
         these spheres are defined as active site atoms.
         At most 2000 QM and MM atoms can be active site
         atoms so R should be typically < 16.5 A.
         Default n=0 means that all MM atoms are active
         site atoms but note that LACTQM may also invoke
         some active site MM atoms.  Apparently, atomic
         position changes will affect the number of
         active site atoms.  To be consistent, use the
         automatically generated LACTMM for restart jobs.
         For example, LACTMM=2 100 16.5 106 15.0 is to
         define all QM and MM atoms within 16.5 A to
         the 100th MM atom and those within 15.0 A to
         the 106th MM atom as active site atoms.
         To explicitly define n (n=<10) MM atoms as
         active site atoms, one can give a series of
```

small radii such as 0.1 A after each atom.

= n, I1, I2, ..., In (case 2, when n > 10)
= explicitly define n MM atoms in $FFDATA to be active site atoms. This rather lengthy array is always generated (and printed into the .dat file) by using LACTMM with n =< 10 for restart jobs. Default n=0 means that all MM atoms are active site atoms. Maximum n=2000.

LACTQM = n, K1, R1, ..., Kn, Rn (case 1, when n =< 10)
= define sphere radii in angstrom for n QM atoms in $DATA. All MM and QM atoms sitting in these spheres are defined as active site atoms. At most 2000 QM and MM atoms can be active site atoms so R should be typically < 17.0 A. Default n=0 means that all QM atoms are active site atoms but note that LACTMM may also invoke some active site QM atoms. Use the automatically generated LACTQM for restart jobs. For example, LACTQM=2, 5 15.0, 8 15.0 is to define all QM and MM atoms within 15.0 A to the 5th QM atom and those within 15.0 A to the 8th QM atom as active site atoms. To explicitly define n (n=<10) QM atoms as active site atoms, one can give a series of small radii such as 0.1 A after each atom.

= n, I1, I2, ..., In (case 2, when n > 10)
= explicitly define n QM atoms in $DATA to be active site atoms. This rather lengthy array should be generated by using LACTQM with n =< 10 for restart jobs. Default n=0 means that all QM atoms are active site atoms. Maximum n=2000.

Active site QM and MM atoms defined using LACTMM and LACTQM will move in geometry optimization, Hessian calculation, and MD simulation. Nonactive site atoms will be absolutely fixed in their input Cartesian coordinates (even IRATLLE and JRATTLE cannot move them). However, active site QM and MM atoms can still be explicitly fixed by using NFIXMM and NFIXQM.

IHESS = request Hessian guided geometry optimization.

```
          Works for all MM and QM/MM cases but is limited
          to 2000 movable atoms.  This keyword is
          irrelevant to RUNTYP=HESSIAN.
          Default = 1 for QM/MM systems.  Otherwise 0.
        = 0   no Hessian, use steepest descent.  It can
              converge, but very slow and may require
              $QUANPO NSTEP=30000 or more.  This is
              recommended for pure MM systems because
              Hessian methods are very time consuming.
              In addition, for large pure MM systems, we
              suggest the use of $STATPT OPTTOL=1.0D-05.
        = 1   use Hessian.  Hessian is usually
              good for ~100 optimization steps.  After
              that, the Hessian may become wrong and
              lose its guiding power.  Use $STATPT to
              input Hessian options.  If $HESS is from
              a previous pure MM run, MMHESS=1 must be
              used.  IHESS=1 is recommended for QM/MM
              because steepest descent method converges
              very slowly.  Typically the default $STATPT
              OPTTOL=1.0D-04 is good, but occasionary
              for very flat potential energy surfaces,
              such as H transfer from one O to another O,
              1.0D-05 should be used to avoid false
              identifications of minima.  When IHESS=1
              is selected, the $HESS at each optimization
              step is alternatively printed out in the
              .hs1 and .hs2 files.

JOUT    = report simulation information such as energies
          and temperature to the log file every JOUT steps.
          Default=1.

KOUT    = in RUNTYP=MD write coordinates and velocity to
          the trj file every KOUT steps (default=100).
        = in RUNTYP=OPTIMIZE coordinates are written to
          the trj file every KOUT steps (default=1).

CENTX   =
CENTY   =
CENTZ   = define the center of the PBC master box or the
          sphere center.  If not found, it is
          automatically calculated.  Use the same CENTX,
          CENTY, CENTZ for restart jobs.
```

```
XBOX   =
YBOX   =
ZBOX   = size of the periodic box in angstrom.
         Default 1.0D+30 means no PBC is imposed.

IADDWAT= add water molecules to the system
       = 0   no adding water (default)
       = 1   add water in PBC master box
       = 2   add water in a sphere
         When MMFF94 is used, it is better to add water
         with ITYPWAT=301 and obtain a good $FFDATA,
         then use LOUT=1 and NFFTYP=50000 to apply the
         MMFF94 force field to all atoms in $FFDATA.

ITYPWAT= select the water model.  Rigid water models
         should use IRATTLE=10 or 20 in MD.  For 5-point
         water models the following (real) masses are
         implemented:
              O=14.000, H=1.008, M=1.000 (amu)
         Users can also define their own water models.
         One way is to add new water models to the library
         file path/gamess/auxdata/QUANPOL/WATERIONS.LIB,
         the other is to directly modify the parameters in
         $FFDATA and $FFDATB groups already generated by
         QuanPol for one of the built-in models (use a
         similar one). ITYPWAT=300 and 500 should be used
         for user defined 3-point and 5-point models.
         4-point and 6-point models are not supported.
       =   0  no specification (default)
       = 301  flexible nonpolarizable 3-point model
       = 302  flexible polarizable 3-point model
       = 303  flexible SPC/Fw model by Wu/Tepper/Voth,
                        J.Chem.Phys. 124, 024503 (2006).
       = 304  rigid TIP3P (LJ terms for H atoms, CHARMM)
       = 305  rigid TIP3P (no LJ term for H atoms, AMBER)
       = 306  rigid SPC
       = 307  rigid SPC/E (extended SPC)
       = 308  rigid POL3, J.Phys.Chem.99,6208 (1995)
       = 504  rigid TIP5P-E, J.Chem.Phys.120,6085 (2004)
       = 505  rigid TIP5P, J.Chem.Phys.112,8910 (2000)
       = 300  user defined 3-point model. See IRATTLE.
       = 500  user defined 5-point model. See IRATTLE.

JADDNA1= add Na+ ions to DNA/RNA PO4- sites.
JADDK1 = add K+  ions to DNA/RNA PO4- sites.
```

```
       = 0   skip (default)
       = 1   add NA+/K+ ions to all possible PO4- sites

IADDNA1= number of Na+  ions randomly added. Default=0.
IADDK1 = number of K+   ions randomly added. Default=0.
IADDCA2= number of Ca2+ ions randomly added. Default=0.
IADDMG2= number of Mg2+ ions randomly added. Default=0.
IADDCL1= number of Cl-  ions randomly added. Default=0.

KOUTPBC= request coordinates be printed in PBC master box.
       = 0   no PBC print out (default)
       = 1   $PBCDATA and $PBCFFDATA and $PBCFFDATB are
             printed to the dat file every KOUT steps.
             These coordinates should not be used to
             restart jobs.

KOUTACT= n, R
         n specifies the n-th atom in $FFDATA;
         R is a radius, typically 10 A.
         Active site atoms within R to the n-th atom are
         printed out in log file for visualization.
         default n=0 and R=0.0.

ITSTAT = enable the thermostat (velocity scaling)
       = 0   no thermostat (default)
       = 1   Berendsen. Scale all velocities at every MD
             step so that
                 T' = (1-(DT/TT))*T + (DT/TT)*T0
             Eq (11) in J.Chem.Phys. 81, 3684 (1984).
                 T  = temperature
                 T0 = target or bath temperature TEMP0
                 TT = BERENDT (default 200 fs).
                      If TT>>DT, virtually no scaling.
                      If TT =DT, complete scaling to T0.
                      If T-T0 > 100 K, TT=10*DT is used.
                      If T-T0 > 200 K, TT=   DT is used.
             Berendsen thermostat tends to give an average
             T slightly (0.01~0.3 K) lower than T0.
       = 2   Andersen. Reassign Maxwell-Boltzmann
             velocities to 20% randomly selected atoms
             at every MD step. The velocity components
             of all selected atoms are assigned as:
                 v  = sigma*SQRT(-2*Ln(u1))*Cos(2*Pi*u2)
                 u1 = random number in (0,1)
                 u2 = random number in (0,1)
```

```
              sigma  = SQRT(k*T0/m)
                  k  = Boltzmann constant
                  T0 = target or bath temperature TEMP0
                  m  = mass of the atom
              Andersen thermostat is not good for time-
              dependent properties such as diffusion
              coefficient and vibrational spectrum.

IPSTAT = enable the barostat (volume scaling)
       = 0   no barostat (default)
       = 1   Berendsen barostat at every MD step:
                  mu = [1 - (BETA*DT/TP)*(P0-P)]**(1/3)
              Eq (21) in J.Chem.Phys. 81, 3684 (1984)
              misses the BETA.
                  P    = pressure, could be 1000 bar.
                  P0   = target or bath pressure PRES0
                  BETA = 4.9D-05  bar-1
                  TP   = BERENDP (default 200 fs)
              To enhance MD stability, mu larger than
              1.0001 is set to be 1.0001, smaller than
              0.9999 is set to be 0.9999.
       = 3   Berendsen barostat at every MD step, but
              separately in x, y, z directions.  This
              is necessary for anisotropic simulation
              systems such as lipids in water.  This
              has little effect on isotropic systems.
         A barostat is meaningful only for PBC system.

BEREND = BERENDT, BERENDP
       = Berendsen thermostat coupling time for ITSTAT=1,
         Berendsen barostat coupling time for IPSTAT=1,3.
         Default = 200.0D-15 second (200 fs) for both.

TEMP0  = bath temperature in K.  For MD jobs, there is no
         default, and must be input by user.  For other
         jobs, the default=298.15 K.
         This is the temperature for Hessian
         thermochemistry calculation.

PRES0  = bath pressure in bar.  Default=1.0 bar.
         A pre-equilibrium system may show huge positive
         or negative pressures like 100,000 bar.
         An equilibrium system may show pressures
         fluctuating by several tens or hundreds bar.
         When IPSTAT=1,3 is used, the average pressure
```

```
         converges slowly to PRESO in ~100,000 fs.

INTALG = MD integrator algorithm.
       = 1   Beeman algorithm (default)
             This Beeman algorithm does not require a
             step back.  Instead, its first step is simply
             a velocity verlet step.
       = 2   velocity verlet algorithm

NRANDOM= selects the seed for QuanPol's random number
         generator:
       = 0   use fixed seeds (default)
       = 1   use time/date to generate seeds
         QuanPol uses a 16-bit pseudo-random integer
         generator with a cycle length 6953607871644.  See
         Wichmann & Hill, Appl.Statist. 31, 188-190 (1982)
         Fixed and time/date seeds should give the same
         randomness.

IRATTLE= apply RATTLE to constrain bond lengths in MD.
         It is irrelevant to geometry optimization or
         Hessian vibration calculation.
         Good for all MM, QM/MM and QM/<MM> systems, but
         QM atoms will not be rattled unless IRATQM=1.
         RATTLE does not affect atoms fixed by NFIXMM,
         NFIXMMB, NFIXQM, NFIXQMB, or nonactive site
         atoms defined by LACTMM.
         IRATTLE=1 is recommended because it is fast.
         Others are relatively slow.  See SCALRAT.
         QuanPol does not distinguish between 1-3
         Urey-Bradley terms and regular 1-2 bond terms:
         terms with force constants < 100 kcal/mol/A**2
         are not constrained by RATTLE (except for zero-
         strength bond between two H atoms).
         QuanPol RATTLE recognizes H atoms by the
         nuclear charge (NUC=1.0), which does not affect
         any interaction potential.  So, any point can
         be given NUC=1.0 (and also a mass), and treated
         like an H atom by RATTLE.  Five-point water
         models have 4 points given NUC=1.0 in order to
         use IRATTLE options 10 and 20.  It is not
         recommended to use NUC=1.0 for other atoms
         because some calculations, such as FIXSOL, also
         rely on NUC to recognize atoms.
       = 0   skip (default).
```

= 1 constrain bonds that involve H atoms and have bond constants larger than 100 kcal/mol/A**2. If water models are involved, this will constrain the O-H and O-M bonds in 3-point and 5-point models because they are usually 500 kcal/mol/A**2 strong. The H-H, H-M and M-M distances will not be constrained if their strengths are 0.0, but will be constained if their strengths are > 100 kcal/mol/A**2.

= 10 constrain bonds that involve H atoms and have bond constants larger than 100 kcal/mol/A**2, and bonds that involve two H atoms and have zero bond constants. This option is designed for systems involving rigid 3-point and 5-point water models: it will constrain the O-H and O-M bonds, as well as the H-H, H-M and M-M distances.

= 2 constrain all bonds that have bond constants larger than 100 kcal/mol/A**2. This option can be used for any rigid molecules when 3N-6 (3N-5 for linear molecule, N=number of mass points) independent bonds are defined. Rigid solvent models must use RATTLE. If water models are involved, this will constrain the O-H and O-M bonds in 3-point and 5-point models because they are usually 500 kcal/mol/A**2 strong. The H-H, H-M and M-M distances will not be constrained if their strengths are 0.0, but will be constained if their strengths are > 100 kcal/mol/A**2.

= 20 constrain all bonds that have bond constants larger than 100 kcal/mol/A**2, and bonds that involve two H atoms and have zero bond constants. This option is designed for systems involving rigid 3-point and 5-point water models: it will constrain the O-H and O-M bonds, as well as the H-H, H-M and M-M distances.

JRATTLE= n, I1, J1, R1, ..., In, Jn, Rn
n specifies the number of atom pairs to be constrained using the RATTLE scheme, or some additional bonds (especially some coordinate

bonds that are significantly longer than normal covalent bonds) to be used by LOUT=1 in generating a force field (in this case, Rn must be given but will not be used).
I1, J1, R1 are the sequential numbers and target distance (A) of the 1st pair of atoms. Must give n pairs. n can be 0 - 10.
When both IRATTLE and JRATTLE are used, JRATTLE pairs (if new after check) are added to IRATTLE pairs. JRATTLE does not affect atoms fixed by NFIXMM, NFIXMMB, NFIXQM, NFIXQMB. Default=0.

IRATQM = specify the rattle of QM atoms in a QM/MM system when IRATTLE and/or JRATTLE are used.
= 0 use no rattle for QM atoms, and no rattle between QM atoms and MM atoms.
= 1 use rattle for QM atoms. QM atoms will be rattled if and only if they appear as rattled MM atoms in $FFDATA. This option must be used (thus the default) for QM/MM jobs when the QM part contains TIP5P style water molecules.
The defaults should not be changed unless one really knows the working mechanism of rattle in QM/MM MD.

RATOLC =
RATOLV = convergence criteria in RATTLE step 1 for coordinate and step 2 for velocity.
Default RATOLC=1.0D-05 and RATOLV=1.0D-08.
Loose criteria may destroy energy conservation while tight criteria are costly.

MXRATT = maximum iterations in RATTLE steps 1 and 2.
Usuaully 4 iterations are enough for IRATTLE=1.
For rigid 5-point water models (IRATTLE=10 or 20) it requires ~30 iterations when SCALRAT=1.5 is used (defautl=200).

SCALRAT= scaling factor in RATTLE correction to coordinate and velocity. Default is:
1.0 for IRATTLE=1
1.3 for IRATTLE=10 or 20 and 3-point water models
1.5 for IRATTLE=10 or 20 and 5-point water models

```
NFIXQM = specifies QM atoms in $DATA to be fixed in MD
         simulation and geometry optimization.  If any of
         these fixed QM atoms appear in $FFDATA as MM
         atoms, these MM atoms will also be fixed.
         To fix 2 QM atoms, 5 and 18, give:
             NFIXQM = 2, 5, 18
         At most 200 QM atoms can be fixed.  Default=0.
         If this input is lengthy, use multiple lines
         and '>' at the end of each line to glue them
         together.

NFIXQMB= similar to NFIXQM, but for atoms in QM state B,
         which are input in $DATA and specified by
         MATOMB, MCHARGB and MULTB.
         At most 200 QM atoms can be fixed.  Default=0.
         If both NFIXQM and NFIXQMB are used, the total
         number cannot exceed 200.

NFIXMM = specifies MM atoms in $FFDATA to be fixed in MD
         simulation and geometry optimization.  If any of
         these fixed MM atoms appear in $DATA as QM atoms,
         these QM atoms will also be fixed.  To fix 4
         MM atoms, 100, 1234, 9999 and 70012, give:
             NFIXMM = 4, 100, 1234, 9999, 70012
         At most 200 MM atoms can be fixed.  Default=0.

NFIXMMB= similar to NFIXMM, but for atoms in $FFDATB.
         At most 200 MM atoms can be fixed.  Default=0.
         If both NFIXMM and NFIXMMB are used, the total
         number cannot exceed 200.

NFIXQM, NFIXQMB, NFIXMM, NFIXMMB are absolutely enforced,
even IRATTLE and JRATTLE cannot affect them.  They also
fix active site atoms defined using LACTMM and LACTQM.

SCFTYP2, TDDFT2, CITYP2, MPLEVL2, MULT2, ICHARG2
       = similar and default to the keywords SCFTYP,
         TDDFTYP, CITYP, MPLEVL, MULT and ICHARG in group
         $CONTRL, but to define a different QM calculation
         on the MD trajectory. For example, when DFT/MM MD
         is performed, one can use TDDFT2=EXCITE to
         request a TDDFT calculation and obtain vertical
         excitation energies.  Apply only to MD.
         The results are printed out as '2ND' potential
         energies in the log file.
```

```
          Defaults are their counterparts in $CONTRL,
          meaning no additional QM calculation.

   **** MD free energy simulation ****

MATOMA =,MATOMB=,MCHARGA=,MCHARGB=,MULTA=,MULTB=
       = specify the numbers of atoms, the charges, and
         the multiplicities of QM state A and state B in
         QM/MM and QM/<MM> style free energy calculations.
         MATOMB can be smaller but never be greater than
         MATOMA. Defaults:
             MATOMA  = the number of atoms in $DATA
             MCHARGA = ICHARG in $CONTRL
             MULTA   = MULT in $CONTRL
             MATOMB  = 0
             MCHARGB = 0
             MULTB   = 1
         The input in $DATA must have all the atoms for
         state A defined before the atoms for state B.
         If QM state A is listed in $FFDATA, QM state B
         must also be listed in $FFDATB.  For IFEPTYP=2,
         the coordinates of MATOMB atoms may be
         different from those of MATOMA.
         (1) The sum of MATOMA and MATOMB must equal
             to the total number of atoms in the $DATA.
         (2) The sum of MCHARGA and MCHARGB must
             equal to the total charge defined by
             ICHARG in $CONTRL.
         (3) MULTA and MULTB must be reasonable for
             state A and state B, respectively.

IFEPTOP= specify single or dual topology MD simulation.
         Single topology QM/MM system can also run OPT
         for IFEPTOP=1 and IFEPTYP=1.
         Both IFEPTOP=1 and 2 need $FFDATB to define
         state B (the second or target state in FEP), and
         need KFREEA and KFREEB to specify the alchemical
         atoms in $FFDATA and $FFDATB.
         When QM atoms are involved, only IFEPTOP=1 is
         allowed, and MATOMA and MATOMB are required to
         define QM states A and B.
         For IFEPTYP=1, the coordinates of MATOMB atoms
         must be the same as those in MATOMA, but may be
         less in number (e.g., deprotonated) or smaller
         in atomic numbers (e.g., F atoms become H atoms)
```

to define an alchemical perturbation.
For IFEPTYP=2, the coordinates of MATOMB atoms may be different from those of MATOMA to form a geometric perturbation, but A and B must be the same molecule with the same number and types of atoms. In any case, MATOMB cannot be greater than MATOMA.

= 0 use single topology in $FFDATA (default).

= 1 use single topology scheme, in which only one set of atoms is used to run MD and sample the phase space, but the solute atoms in the KFREEA and KFREEB lists can have different force field parameters or different (fixed) coordinates for states A and B.

= 2 use dual topology scheme, in which two sets of solute atoms coexist in the MD (but those of A not seeing those of B) and sample different phase spaces. Soft-core charge and LJ potentials are usually used to avoid sampling difficulty arising from singularity. Dual topology is only implemented for pure MM systems (no induced dipole) and IFEPTYP=1.

IFEPTYP= specify the type of free energy perturbation (FEP) calculation (i.e. what free energy or free energy change to be calculated).
When NFIXMM and NFIXMMB are used to fix two, three, or more atoms in states A and B, state B can differ from A in coordinates of the atoms in NFIXMM and NFIXMMB (all of the other atoms must have the same coordinates).
Note it is almost meaningless to use different settings in switching and shifting functions in relative free energy calculation.

= 0 use no potential energy (default). This null option gives zero free energy change, so no FEP will be performed.

= 1 For pure MM, use solvation potential energy of the solute molecules (i.e. the KFREEA and KFREEB atoms). This is equivalent to excluding the internal potential energy of the solute molecules from the total energy. For pure MM systems, this option is usually called solvation free energy perturbation, and both IFEPTOP=1 and 2 can be used.

```
       = 1   For regular QM/MM, the total QM/MM potential
             energy (including solvation and QM internal
             energy) is used.  The coordinates of MATOMB
             atoms must be the same as those of MATOMA.
       = 1   For mean-field QM/<MM>, the solvation free
             energy change is derived from MM simulation,
             and corrected by the QM internal energy and
             QM/<MM> mean-field electrostatic potential.
             The coordinates of MATOMB atoms must be the
             same as those of MATOMA.
       = 2   For pure MM, use solvation potential energy
             of the solute molecules (i.e. the KFREEA and
             KFREEB atoms), the covalent potential energy
             within the KFREEA atoms (and KFREEB atoms for
             B), and the noncovalent potential energy
             within the KFREEA atoms (and KFREEB atoms for
             B).  Require NFIXMM and NFIXMMB.
             The following settings are enforced:
               WSIMUL=0.0,WPERT1=1.0,WPERT2=1.0,ISOFTCR=0
             Only IFEPTOP=1 can be used for IFEPTYP=2.
             For pure MM systems, this option is usually
             called potential of mean force (PMF).
       = 2   For regular QM/MM, the total QM/MM potential
             energy (including solvation and QM internal
             energy) is used.  The coordinates of MATOMB
             atoms may be different from those of MATOMA.
       = 2   For mean-field QM/<MM>, the solvation free
             energy change is derived from MM simulation,
             and corrected by the QM internal energy and
             QM/<MM> mean-field electrostatic potential.
             The coordinates of MATOMB atoms may be
             different from those of MATOMA.

KFREEA = n, K1, K2, ..., Kn
         n specifies the number of atoms in $FFDATA
         included in FEP calculation,
         K1 - Kn are the sequencial number of the n atoms
         in $FFDATA. The limit of n is 500.
         If this input is lengthy, use multiple lines
         and '>' at the end of each line to glue them
         together.

KFREEB = m, K1, K2, ..., Km
         m specifies the number of atoms in $FFDATB
         included in FEP calculation,
```

```
          K1 - Km are the sequencial number of the m atoms
          in $FFDATB.  The limit of m is 500.
          For IFEPTOP=1 KFREEB is the same
          as KFREEA (it is not necessary to input KFREEB).
          If this input is lengthy, use multiple lines
          and '>' at the end of each line to glue them
          together.

WSIMUL =, WPERT1=, WPERT2=
       = three weights (i.e., coupling coefficient
          lambda) of the target state B in an FEP
          calculation. All values must be from 0.0 to 1.0.
          Defaults=0.0, 1.0, 1.0.
          Usually a series of values are used to build a
          perturbation route forth and back. The system is
          simulated in the state defined with WSIMUL, and
          the free energy differences are calculated for
          the two states defined with WPERT1 and WPERT2.
          The default value of WPERT2 = WPERT1. Examples:
            WSIMUL=0.5  WPERT1=0.0  WPERT2=1.0
            WSIMUL=0.5  WPERT1=0.6  WPERT2=0.7
            WSIMUL=1.0  WPERT1=0.9  WPERT2=0.8

ISOFTCR= specify the use of soft-core potentials for
          Lennard-Jones, charge-charge interactions in
          alchemical free energy perturbation simulation
          (only for IFEPTOP=2).
       = 0   do not use soft-core (default).
       = 1   use soft-core LJ and CH potentials:
             LJ=lambda*4*EPS*
                {1/[SOFTALJ*(1-lambda)**2+(R/SIG)**6]**2
                +1/[SOFTALJ*(1-lambda)**2+(R/SIG)**6]}
             CH=lambda*QI*QJ/
                SQRT[SOFTACH*(1-lambda)**2+R**2]
             lambda = WSIMUL, WPERT1, or WPERT2

SOFTALJ= soft-core parameter alpha for Lennard-Jones.
          Default=0.3.

SOFTACH= soft-core parameter alpha for charge-charge.
          Default=2.8 A**2.

For IFEPTOP=1, KFREEB must be the same as KFREEA, and
$FFDATB must have the same topology as $FFDATA: same
atoms with the same coordinates (except for atoms fixed
```

```
by NFIXMM and NFIXMMB for IFEPTYP=2 jobs), same number
of bonds, angles, dihedrals and other covalent terms.
The parameters (e.g., mass, charge, LJ potential, bond
constant, angle bending constant and others) associated
with alchemical atoms in the KFREEA (=KFREEB) list can be
different in order to define two different states.
IFEPTOP=1 MD is performed on the potential energy
surface (PES) for that the covalent potential parameters
(e.g. bond lengths and constants) are combined using
F(W)=(1-W)*F(A)+W*F(B), charge and LJ potential energies
are combined using E(W)=(1-W)*E(A)+W*E(B).
The best way to create the $FFDATB for IFEPTOP=1 is to
modify the $FFDATA by changing the names, masses, bond
constants, charges and LJ parameters (but never the
coordinates) of the solute atoms in the KFREEA list.

For IFEPTOP=2, KFREEB can be different from KFREEA.
$FFDATB must be very similar to $FFDATA: only the atoms
in KFREEA and KFREEB can be different, and all other
atoms must be the same with the same coordinates.
IFEPTOP=2 MD is performed on the potential energy
surface (PES) for that the covalent potential parameters
(e.g. bond lengths and constants) are in full strength
for both A and B (i.e. ideal-gas-molecule end states),
while charge and LJ potential energies are combined using
E(W)=(1-W)*E(A)+W*E(B).  Soft-core charge/LJ potentials
are generally required to achieve better sampling.
The best way to create the $FFDATB for IFEPTOP=2 is to
modify the $FFDATA by changing and/or inserting atoms and
their covalent and noncovalent potentials.  The KFREEB
atoms and all of their covalent/noncovalent potentials
specified in $FFDATB are identified and added to
$FFDATA.  Since other parts in $FFDATB are not used,
it is not necessary to change them (even though they may
look wrong).  One may also use two similar $FFPDB to
create two similar $FFDATA and rename one as $FFDATB.

JUMBUP =  0  no action. (default)
       = -1  adjust the R0 value on the fly for
             JUMBPOT=12 when RUNTYP=OPTIMIZE so that the
             energy is minimized.  This is useful when
             JUMBPOT=12 is used to locate a minimum point
             on the potential energy surface.  If the
             adjustment and optimization are not
             converging, there is unlikely a minimum
```

point in the given region of the potential energy surface. The convergence criterion of R0 is that the bias potential energy be less than 1.6D-6 hartree.

= 1 adjust the R0 value on the fly for JUMBPOT=12 when RUNTYP=OPTIMIZE so that the energy is maximized. This is useful when JUMBPOT=12 is used to locate a saddle point on the potential energy surface. If the adjustment and optimization are not converging, there is unlikely a saddle point in the given region of the potential energy surface. Saddle points sometimes are difficult to locate so a few trials with the bias potential on different bonds may be required. The convergence criterion of R0 is that the bias potential energy be less than 1.6D-6 hartree.

JUMBPOT= NTYP, I1, I2, I3, I4, FC, R0
= apply umbrella sampling bias (harmonic) potential to a reduced or combined MM internal coordinate:
V_bias = 0.5*FC*(R - R0)**2
1D histograms are printed out to the .log file every JOUT steps, with 61 bins and bin size of either 0.01 A or 1.0 degree.

JUM2POT= NTYP, I1, I2, I3, I4, FC, R0
= apply a second umbrella sampling bias potential to a reduced or combined MM internal coordinate. 2D histograms are printed out to the .trj file every KOUT steps, with 3721 bins and bin size of either 0.01 A or 1.0 degree.

If selected, these bias potentials are added to all MM, QM/MM and QM/<MM> calculations (MD, OPT). So, they can also be used for transition state search. A transiton state can often be located by using RUNTYP=OPTIMIZE and a single bias potential JUMBPOT=12 with a FC value such as 300 to 3000 kcal/mol/A**2. JUMBUP=1 can be used to automatically adjust R0 values on-the-fly to precisily determine the transition state geometry. The FC value may heavily affect the convergency of the R0 value and the optimization

process.

The QuanPol Weighted Histogram Analysis (QPWHA) program can be used to obtain 1D and 2D PMF profiles. For NTYP=12 (e.g. for Na+ and Cl- ions), the 1D PMF obtained from QPWHA program must be corrected by a relative volume-entropy term, which is kT*Ln((R/R0)**2). Here k is Boltzmann constant, T is temperature, R is the distance, and R0 is the reference distance at which the PMF is set to be zero.

To obtain good 1D PMF, at least 100,000 MD steps are required for each window (i.e. each R0). To obtain good 2D PMF, at least 1000,000 MD steps are required for each 2D window. Therefore, 2D umbrella sampling is very expensive.

```
NTYP= define the internal coordinate R
    = 0      nothing (default)
    = 12     R = R12 (needs kT*Ln((R/R0)**2) )
    = 1212   R = R12 - R'12
    = 123    R = angle 123           (0-180 deg)
    = 1234   R = dihedral angle 1234 (0-360 deg)
Ii  = atoms in $FFDATA. Must give four integers,
      but some or all can be 0.
FC  = force constant, either in kcal/mol/A**2 or
      kcal/mol/deg**2, depending on NTYP
R0  = equilibrium R, either in A or degree
```

Six examples for setting up 1D umbrella sampling:

```
  JUMBPOT= 12     8  5  0  0   120.000     3.00
  JUMBPOT= 1212   3  4  4  5    80.000    -0.20
  JUMBPOT= 1212   3  5  7  8   100.000     1.50
  JUMBPOT= 123    6  2  7  0     0.010   120.00
  JUMBPOT= 1234   2  6  9  4     0.010   340.00
```

An example for setting up 2D umbrella sampling:

```
  JUMBPOT= 12     8  5  0  0   120.000     2.20
  JUM2POT= 12    10 25  0  0   120.000     1.50
```

An example for setting up 2D umbrella sampling:

```
  JUMBPOT= 12     8  5  0  0   120.000     1.20
  JUM2POT= 1234  10 11 19 20     0.010   120.00
```

```
IRMDF  = I1, I2, R1, R2, N
       = apply thermodynamic integration in MD simulation
         to evaluate the mean force between two atoms,
         the distance between which is constrained via a
         RATTLE-like scheme. Can coexist with RATTLE, but
         the IRMDF atoms will not be affected by RATTLE.
         Works for MM and QM/MM MD simulations.  The two
         atoms can be MM or QM, both or either.

         I1  = MM atom in $FFDATA.
         I2  = MM atom in $FFDATA.
         R1  = starting distance between I1 and I2 in A,
               must be between 0-100 A.
         R2  = ending distance between I1 and I2 in A,
               must be between 0-100 A.  R2 can be larger
               or smaller than R1.
         N   = the number of evenly distributed distances
               in between R1 and R2 for that the MD
               simulation will be consecutively run,
               NSTEP/N steps for each distance.
               N must be an integer between 1-100. If N=1,
               the simulation will be run for (R1+R2)/2.

           For example, inputing
             IRMDF= 98, 100, 2.0, 3.0, 10
         will evaluate the mean force between MM atoms
         98 and 100 for 10 distances from 2.05 to 2.95 A:
             2.05, 2.15, 2.25, ..., 2.85, 2.95
           If NSTEP=1000000, for each distance 100000 MD
         steps will be run to obtain the mean force.
           The mean force will be multiplied by 0.10 A,
         which is (R2-R1)/N, to produce the free
         energy change for the 10 distance bins:
             delta G from 2.00 to 2.10
             delta G from 2.10 to 2.20
             ...
             delta G from 2.90 to 3.00
         Adding these 10 values up will give the
         free energy change from 2.00 to 3.00 A.
           The system should have been equilibrated
         with the distance restricted at 2.05 A via
         RATTLE or IRMDF.
           If MM atoms 98 and 100 are defined as QM atoms
         in $DATA, the mean force is for two QM atoms.
```

```
   **** mean field QM/<MM> MD simulation ****

MEANFLD= average position mean field QM/<MM> calculation:
         Cui and Li, J. Chem. Phys. 138, 174114 (2013)
       = 0   normal QM/MM, no mean field (default)
       = n   run MM MD simulation for n steps in the
             presence of a rigid MM image of the QM
             region, store and use the n sets of the MM
             coordinates to run a mean field QM/<MM>
             calculation to obtain QM wavefunction and
             energy.  For polarizable MM, the (n+1)/2 step
             coordinates from the n sets are used to run a
             QM/MMpol calculation to obtain polarization
             energy.  Only energy can be run for QM
             atoms in the MM mean field.
             MEANFLD can vary from 1 to 20,000, or even
             larger if there is enough computer memory.
             MEANFLD=10000 and MFMERGE=20 work very well.

MFMERGE= specify how the n (n = MEANFLD) sets of MM
         coordinates are merged (averaged) to reduce
         the computing time in evaluating QM 1-electron
         integrals of the MM charges that are more than
         SWRAQ angstrom away from the QM center point.
         For MM charges within SWRAQ angstrom, MIN(n,10)
         will be used to replace MFMERGE.
       = 1   no mergence, so the n sets of MM coordinates
             are used explicitly (but very slow).
       = m   merge every m sets (m<n, e.g. m=20, n=10000)
             of MM coordinates into one set (i.e. the
             average coordinate of the m sets for each
             MM atom), which is then used to perturb the
             QM wavefunction (via 1-electron integral).
             Default=20 should not be changed unless one
             really understands the method.

MFQMCHG= specify how the charges are created for the
         QM region in mean field QM/<MM>.
       = 1    use the force field atomic charges.
              This method can be very inaccurate.
       = 10   use multipole points at each atom (default).
              The multipole points are generated with a
              density based 3D grid point expansion
```

```
              method.  The solution phase wavefunction is
              optimized using the FixSol model.
              This option does not need IFIXSOL=1.

QuanPol QM/<MM> MD simulation using MEANFLD=10000:
**  QM/<MM> MD step 0  **
1. Initial: (x0_QM, v0_QM, x0_MM, v0_MM)
2. IMMM MD 0 and 1-10000
   a. Create an MM image (e.g. charges and LJ potential)
      of the QM region using pure QM method (no MM).  The
      image does not contain polarizability.
   b. Using the rigid MM image of the QM, obtain E_IMMM
      and forces on all MM atoms.  If induced dipoles are
      used, they are used only for the MM region, not
      for the QM region (i.e. no polarizability for the
      image of the QM).
   c. MM atoms move.  Record 10000 sets of MM coordinates.
      Record LJ interaction energy and forces between QM
      and MM atoms as E0_<QMMMLJ>.  For LJQMMM=1,
      E0_<QMMMLJ> is part of E0_<MM>.
   d. Report IMMM average energies:
        E0_<IMMM> =          E0_<IMMMES> + E0_<MM>
                           + E0_<QMMMLJ> + K0_<MM>
                           + E0_<MMpol>
                Tn = K0_QM  + Kn_MM (for T scaling)
   f. T and P scaling, but QM atoms are not scaled.
3. Run a QM/<MM> calculation to get E0_QM, E0_QM<MMES>
   and E0_QMMMpol.  If induced dipoles are used, the
   middle step MM coordinates are used to calculate
   polarization energy.  Now polarization is described
   for the QM region using QM method.
4. Report QM/<MM> MD energies:
        E0_QM<MM> = E0_QM  + E0_QM<MMES> + E0_<MM>
                  + K0_QM  + E0_<QMMMLJ> + K0_<MM>
                           + E0_QMMMpol
5. Print out all coordinates and velocity for restart:
     x0_QM, v0_QM, x0_MM, v0_MM

**  QM/<MM> MD step 1  **
1. No change: (x0_QM, v0_QM, x10000_MM, v10000_MM)
2. IMMM MD 10001-20000
   a. Using the rigid MM image of the QM, obtain E_IMMM
      and forces on all MM atoms.
   b. MM atoms move. Record 10000 sets of MM coordinates.
      Record LJ interaction energy and forces between QM
```

```
      and MM atoms as E1_<QMMMLJ>.  For LJQMMM=1,
      E1_<QMMMLJ> is part of E1_<MM>.
   c. Report IMMM average energies:
        E1_<IMMM> =          E1_<IMMMES> + E1_<MM>
                           + E1_<QMMMLJ> + K1_<MM>
                           + E1_<MMpol>
                Tn = K0_QM  + Kn_MM (for T scaling)
   d. TP scaling.  QM atoms are not scaled.
3. Run a QM/<MM> calculation to get E1_QM, E1_QM<MMES>
   and E1_QMMMpol.
4. Report QM/<MM> MD energies:
        E1_QM<MM> = E1_QM  + E1_QM<MMES> + E1_<MM>
                  + K0_QM  + E1_<QMMMLJ> + K1_<MM>
                           + E1_QMMMpol
5. Print out all coordinates and velocity for restart:
      x0_QM, v0_QM, x10000_MM, v10000_MM
6. T and P scaling, but QM atoms are not scaled.


   **** cell-list and fast-list ****

QuanPol uses a standard cell-list scheme to generate a
large neighbor list, which is typically 2.0 times larger
than the small neighbor list and has a long updating
cycle like 55 fs.  The small list can be efficiently and
frequently (e.g. every 11 fs) generated from the large
list.  QuanPol uses an automatic method to determine when
to update a neighbor list.  The atoms displace more than
0.2 and less than 0.9 of the buffer width are stored in
7 lists called fast-lists.  When there are ~100 atoms in
the 4th fast-list, which stores atoms that have displaces
between 0.5 and 0.6 of the buffer width, it is fairly
quick to check the pair distances between the atoms in all
fast-lists.  New atom pairs are added to the current list
to avoid an immediate update, unless the number of atoms
in the 4th fast-list exceeds MXCHECK (typically 300).

For an equilibrium system, the frequencies of updating
the large and small neighbor lists are almost constants.
QuanPol identifies the frequencies and skips unnecessary
checking of the fast-lists.  For example, when BUFWID1
=1.0 A and BUFWID2=4.0 A are used, the lists update every
~55 and ~11 MD steps (DT=1 fs) for a PBC system with 9121
protein atoms, 45 ions, and 60759 water atoms at T=310 K,
P=1 bar and V=88.77**3 A**3.  In this case, it is safe to
```

```
skip the first 48 steps [estimated as NINT(55-SQRT(55))]
for the large list and the first 8 steps for the small
list.

Fast-list updating information is printed in the dat file
for the first 10,000 MD steps.

MXCHECK= maximum number of atoms to be checked for the
         4th fast-list, which stores atoms that have
         displaces between 0.5 and 0.6 of the buffer
         width.  Default=100, maximum=300.
         MXCHECK=1 is essentially the CHARMM heuristic
         method.

MXLIST2= maximum number of neighbor MM atoms around a
         given MM atom in the large neighbor list.
         Default=3400 is good for SWRB=12.0 and BUFWID2
         =4.0 A.  MXLIST2 can be estimated as
         ((SWRB+BUFWID2)**3)*3/4.

BUFWID2= The width of the buffer region for the large
         neighbor list.  This width is added to SWRB to
         define the sphere.  Default=4.0 A is good for
         water and biological systems consisting of water.
         3.0-6.0 A are reasonable values for SWRB=12.0 A.
         It is good to have BUFWID2 > BUFWID1 + 3.0 A.
         If BUFWID2 equals to BUFWID1, only one neighbor
         list (with MXLIST2) will be used.

MXLIST1= maximum number of neighbor MM atoms around a
         given MM atom in the small neighbor list.
         Default=1700 is good for SWRB=12.0 and BUFWID1
         =1.0 A.  MXLIST1 can be estimated as
         ((SWRB+BUFWID1)**3)*3/4.

BUFWID1= The width of the buffer region for the small
         neighbor list.  This width is added to SWRB to
         define the sphere.  Default=1.0 A is good for
         water and biological systems consisting of water.
         1.0-2.0 A are reasonable values for SWRB=12.0 A.

   **** long-range interactions ****

ISWITCH= selects switching function (default=1).
         Switching functions work in the tail region,
```

```
          from SWRA to SWRB.
        = 0   no switching function
        = 1   atom-atom switching function for LJ;
              QMcenter-MMatom switching function for
              QM-rep, QM-charge and QM-pol interactions;
              If IPOLSHF=0 is specified, atom-atom
              switching function is also used for
              charge-pol and pol-pol interactions.
          The switching function implemented in QuanPol is
              W(r) = 1 - 10*D**3 + 15*D**4 - 6*D**5
          with
              D=(r**2 - SWRA**2)/(SWRB**2 - SWRA**2)

ISHIFT = selects shifting function (default=4). The order
          of aggressiveness in shifting is 1 > 2 > 3 > 4.
          Shifting functions operate on the range zero to
          SWRB for charge-charge interaction. If IPOLSHF=1
          is specified, shifting function is also used for
          charge-pol and pol-pol interactions.
        = 0   no shifting function
        = 1   use the atom-atom shifting function
                  S(r)=(1-r/SWRB)**2
              This shifting function is used by the ENCAD
              and ilMM codes.
        = 2   use the atom-atom shifting function
                  S(r)=1-[3*RXNEPS/(2*RXNEPS+1)]*(r/SWRB)+
                  [(RXNEPS-1)/(2*RXNEPS+1)]*[(r/SWRB)**3]
              to mimic a dielectric reaction field.
              RXNEPS is required. This shifting function is
              Eq (5) in Rick, J.Chem.Phys. 120, 6085 (2004)
        = 3   use the simple atom-atom level shifting:
                  S(r)=(1-r/SWRB)
              This is not a smooth function.
        = 4   use the atom-atom shifting function
                  S(r)=[1-(r/SWRB)**2]**2
              This is one of the CHARMM shifting functions.

For dipolar bulk systems, if Ewald summation is not used,
a shifting function (rather than a switching function)
should be used (otherwise structures and energies may be
wrong).  Many force fields, especially water models, are
optimized for particular shifting functions, switching
functions, and cutoff distances.  Very different results
may be obtained when different shifting and switching
functions are used.
```

```
For relative energy or free energy calculations, it is
almost meaningless to use different settings in switching
and shifting functions.

IPOLSHF= select atom-atom shifting function for
         charge-pol and pol-pol interactions.
       = 0   use switching function (default)
       = 1   use shifting function. This is not
             recommended because induced dipole energy is
             sensitive to shifting functions.  Induced
             dipole energy is much less sensitive to
             switching functions because they only work
             at far distances.

SWRA   =
SWRB   = distance cutoffs for the switching function
         that gradually drops the interactions from full
         strength at SWRA to zero at SWRB.  In angstrom.
         For MM atoms only.  SWRB is also the cutoff for
         shifting functions.
         Default SWRA=10 A, SWRB=12 A when PBC is used.
         Defaults are huge values when PBC is not used.

SWRAQ  =
SWRBQ  = same as SWRA and SWRB, but for QM-MM interaction.
         SWRAQ and SWRBQ should be as large as possible.
         The defaults are 10 A and 12 A.  For protein
         calculations, 22 A and 32 A are good.

IEWALD = request Ewald summation for PBC charge-charge
         interaction.  Only charge-charge is implemented,
         with the tin-foil conductor boundary condition.
         Works only for neutral and pure MM systems.
         Also works for MM IFEPTYP=1,2 (with IFEPTOP=1).
       = 0    no Ewald summation (default)
       = 1    use cubic Ewald summation
       = 2    use near-spherical Ewald summation, 2~3
              times faster than IEWALD=1 (recommended)

KEWALD = the number of cubic or spherical shells in Ewald.
         Often called K-vector in the literature.
         Default=10 (should increase for XBOX > 30 A).
         Maximum 100.
         When 10 shells are used, there are 9261 boxes
```

```
          for IEWALD=1 and 5833 boxes for IEWALD=2,
          including the master box.  The direct charge-
          charge interaction (i.e. real space sum) is
          calculated within the master box (i.e. minimum
          image convention) and with a cutoff = SWRB,
          which is typically 12.0 A (22.68 bohr).  See:
          KEWALD          =     5      10      20      40
          IEWALD 1 # boxes=  1331    9261   68921  531441
          IEWALD 2 # boxes=   967    5833   39913  293621

SPLIT  = the Ewald splitting parameter in the Gauss error
          function ERF(SPLIT*R).  Default 0.15 bohr**(-1)
          is good for SWRB = 12.0 A (22.68 bohr) because
          ERFC(0.15*22.68) = 1.5D-06.
          Larger  SPLIT, smaller SWRB, larger  KEWALD.
          Smaller SPLIT, larger  SWRB, smaller KEWALD.

For bulk water, when IEWALD=2 SWRB=12 SPLIT=0.15 are used,
the following settings can likely converge the Ewald
energy to within 0.1 kcal/mol:
  XBOX   =    25    50    75   100   125   150  (in Ang)
  KEWALD =     6    14    22    31    41    51
For a given system, inclreasing KEWALD by 2 can typically
decrease the error of its Ewald energy by 10 times.

   **** continuum solvation models ****

RXNEPS = dielectric constant in ISPHSOL, IFIXSOL and
          ISHIFT=2 calculations.  Default=78.39.

IFIXSOL= enable the FixSol solvation model
          calculation, which is available for QM/MM and
          pure MM systems. FixSol paper:
          Thellamurege and Li, JCP 137, 246101 (2012)
          FixSol is equivalent to CPCM or COSMO, but uses
          the FIXPVA2 tessellation scheme.  FixSol works
          for HF, DFT, GVB, MCSCF, TDDFT, and MP2.
        = 0   skip (default)
        = 1   perform FixSol calculation
          When FixSol is used, PBC and switching/shifting
          functions are turned off automatically.

FIXTOL = convergency criterion in FixSol iterative
          calculation of surface charges.
          Default=1.0D-10 e is almost always good.
```

For large systems, FIXTOL=1.0D-06 e may be used.

MXFFTS = maximum number of surface tesserae to be used in FixSol calculation. Default is usually enough.

NTSATM = number of surface tesserae per atom to be used in FixSol calculation. Only 60, 240 and 960 are allowed. Default=60. FixSol uses the FIXPVA2 tessellation method.

By default, FixSol uses a set of simplified united atomic radii (SUAR):

H	0.000 A
Li - B	1.400 A
C	2.100 A
N	2.000 A
O	1.900 A
F - Al	1.800 A
Si	2.000 A
P	2.200 A
S	2.400 A
Cl	2.760 A
Ar	3.000 A
All others	2.400 A

NRADQM and NRADMM values override the RALLQM, RALLMM or SUAR defaults, and NRADQM overrides NRADMM. The override order is:
NRADQM > NRADMM > RALLQM > RALLMM > SUAR

RALLMM = FixSol radii for all heavy MM atoms in $FFDATA. Default = 0.0 A, use SUAR.

RALLQM = FixSol radii for all heavy QM atoms in $DATA. The capping QM H atoms in QM/MM systems will be treated as heavy atoms. Default = 0.0 A, use SUAR.

NRADMM = n, I1, R1, I2, R2, ... In, Rn
= specify the FixSol radii (in angstrom) for up to 200 MM atoms in $FFDATA.
n = number of atoms (default=0)
In = MM atom sequential number in $FFDATA
Rn = radius (e.g. 0.001, 1.80, 500.0)
For example, NRADMM=2 500 2.0 502 2.5 is to

```
          assign the 500th MM atom with 2.0 A radius and
          the 502nd MM atom with 2.5 A radius.

NRADQM = n, I1, R1, I2, R2, ... In, Rn
       = specify the FixSol radii (in angstrom) for up
         to 200 QM atoms in $DATA.
         n   = number of atoms (default=0)
         In  = QM atom sequential number in $DATA
         Rn  = radius (e.g. 0.001, 1.80, 500.0)
         For example, NRADQM=2 5 1.7 6 1.9 is to
         assign the 5th QM atom with 1.7 A radius and
         the 6th QM atom with 1.9 A radius.


          ** Spherical boundary condition and  **
          ** SphSol have strong surface effect **
          **          Do not use them          **

SPHRAD = radius of the sphere containing the QM/MM system.
         Default is a huge value, meaning no sphere.
         A Lennard-Jones type potential is applied to keep
         the heavy atoms in the sphere.  For each atom:
       V=4*SPHEPS*{[SPHSIG/(r-R)]**12 - [SPHSIG/(r-R)]**6}
       R=  SPHRAD + [2**(1/6)-1]*SPHSIG
       V= -SPHEPS when r = SPHRAD - SPHSIG

SPHEPS = Lennard-Jones epsilon parameter for SPHRAD.
         Default=0.15 kcal/mol is good for water.
         Proper values should be determined empirically.

SPHSIG = Lennard-Jones sigma parameter for SPHRAD.
         Default=1.5 A is good for water.
         Proper values should be close to the radii of
         the solvent atoms, which are usually around 1.5.

ISPHSOL= enable spherical solvation model (SphSol)
       = 0   no SphSol (default)
       = 1   image charge method, currently only for
             pure MM system
       = 60, 240, 960, 3840 to choose surface charge
             method and define the number of surface
             elements.  Available for MM and QM/MM.
         When SphSol is used, PBC and switching/shifting
         functions are turned off automatically.
```

```
RSPHSOL= radius of sphere in angstrom (default=1.0D+30)
         used in the SphSol calculation.
         SPHRAD is also required.  For water solvent,
             RSPHSOL = SPHRAD + 0.60 A
             RXNEPS  = 78.39
             SPHEPS  =  0.15
             SPHSIG  =  1.50
         are strongly suggested.

   **** MD properties ****

NRDF   = n, NAME1, NAME2, ...
       = specifies the number of pairs for the radial
         distribution function calculation, and the names
         of the atoms.  Must give n pairs of names.
         This option works for both periodic and spherical
         boundaries (defined by XBOX and SPHRAD).
         Default n = 0.
         The RDF is calculated at every MD step but
         printed out every JOUT steps.

NRDEN  = n, NAME1, NAME2, ...
       = specifies the number of atoms for the radial
         density profile calculation, and the names of
         the atoms.  Must give n names (default n = 0).
         The profile is calculated at every MD step but
         printed out every JOUT steps.

DELRDF = specifies the radial increment in the radial
         distribution function calculation (NRDF) and the
         radial density profile (NRDEN) calculation.
         Default=0.05 angstrom.

DIFFUSE= n, NAME1, NAME2, ...
       = specifies the number of atoms for diffusion
         coefficient calculation, and the names of the
         atoms.  Must give n names.  Default n=0.

TIMDFS = time interval for diffusion coefficient
         calculation.
         Default=3.0D-12 second is good for water.
         Can be larger, but should not be smaller.
         There must be sufficient displacement in order to
         apply the statistical formula.
```

```
NATPDB = number of atoms in the PDB file (but waters in
         PDB are excluded).  If $FFPDB is used, NATPDB
         will be automatically determined.  The main use
         is for restart jobs in which only $FFDATA is
         provided.

NRIJMM = NRIJMM, I1, J1, I2, J2, ...
       = specifies up to 100 pairs of MM atoms to print
         out their distances at every JOUT steps.
         Works for both MD and OPTIMIZE.  Useful when one
         wants to monitor H-bond distances.  Default
         NRIJMM = 0.

NRIJQM = NRIJQM, I1, J1, I2, J2, ...
       = specifies up to 100 pairs of QM atoms to print
         out their distances at every JOUT steps.
         Default NRIJQM = 0.

NAIJKMM= NAIJKMM, I1, J1, K1, I2, J2, K2, ...
       = specifies up to 100 sets of MM atoms to print
         out their angles (IJK) at every JOUT steps.
         Default NAIJKMM = 0.

NAIJKQM= NAIJKQM, I1, J1, K1, I2, J2, K2, ...
       = specifies up to 100 sets of QM atoms to print
         out their angles (IJK) at every JOUT steps.
         Default NAIJKQM = 0.

NRMSD  = root-mean-square-displacement calculation
         for all NATPDB atoms in $FFPDB or $FFDATA.
         Works for both MD and OPTIMIZE.
       = 0   skip (default)
       = 1   calculate RMSD from the initial coordinates
             at every JOUT steps. The average unsigned
             displacement is also printed out.

NGYRA  = radius of gyration calculation for all
         NATPDB and non-hydrogen NATPDB atoms in $FFPDB
         or $FFDATA(see TIMGYRA).
         Works for both MD and OPTIMIZE.
       = 0   skip (default)
       = 1   calculate radius of gyration using formula:
                 R=SQRT[sum(m*r*r)/sum(m)]
                    r: distance from COM
                    m: atom mass
```

```
            So R is mass-weighted RMS distance from COM.

TIMGYRA= time interval for radius of gyration calculation.
         Default=1.0D-12 s.  Can be larger or smaller.
         For OPTIMIZE, it is every JOUT steps.

NRALL  = activate internuclear distance calculation
         for all NATPDB atoms in $FFPDB or $FFDATA
         (see TIMRALL).  Works for both MD and OPTIMIZE.
       = 0   skip (default)
       = 1   calculate internuclear distances and compare
             to those in the initial structure.  RMS
             deviation is printed out at every JOUT steps.

TIMRALL= time interval for internuclear distance
         calculation.  Default=1.0D-12 second.  Can be
         larger or smaller, but frequent calculation
         slows down the MD.  For OPTIMIZE, it is every
         JOUT steps.

NDIEL  = MD simulation of dielectric constant.
       = 0   skip
       = 1   calculate dielectric constant for the whole
             system, including all QM and MM atoms
             (default).
             If NATPDB>0, it also calculates dielectric
             constant for the subsystem defined by NATPDB
             (i.e. a protein or DNA/RNA molecule).
         The following formula in atomic units is used:
             Eps = 1 + 4*Pi*(<M**2> - <M>**2)/(3kTV)
               M = total dipole moment of the system or
                   the subsystem (including induced atomic
                   dipoles) at the center of mass.
               k = Boltzmann constant
               T = average temperature
               V = average volume. For NATPDB atoms, V is
                   estimated as 6.72 A**3 per atom.
         For open systems, the volume is infinite, so the
         dielectric constant is 1.

IVIBMM = n, I1, I2, I3, ... In
       = specifies up to 200 atoms in $FFDATA to calculate
         their center of mass and dipole moment at each MD
         step.  In addition, the velocities of these MM
         atoms and the velocity sum will be printed out
```

at every MD step.
Default n=0.
If this input is lengthy, use multiple lines
and '>' at the end of each line to glue them
together.
Note that in any case, the dipole moment of all
MM or QM or QM/MM atoms, the velocities of all
QM and IVIBMM atoms, the velocity sums of all MM,
QM, QM/MM, and IVIBMM atoms are always printed
out at every MD step.
The QuanPol Vibrational Spectrum Program can be
used to analyze the time dependence of the dipole
moment and velocities, and generate IR and
vibrational spectra.

**** preparation tools ****

NFOLD = this is used only for $FFDATA to duplicate the
input molecule in 3D space NFOLD times.
Reasonable values are 0, 3, 6, 9, 12 and 15,
which leads to 1, 8, 64, 512, 4096 and 32768
copies. 0, 1, 2, 3, ..., 14, 15 can be used.
Default=0, no action.

RFOLD = specifies the spacing when NFOLD is active.
The value should be typically the cubic root of
the volume of the duplicated molecule, and should
be calculated using density. For example, 3.1,
4.7 and 4.9 A are good for H2O, CH2Cl2 and
CH3COCH3, respectively. Default=0.0 A.

ICOMBIN= combine $FFDATA and $FFDATB to be a new $FFDATA.
This can be used to combine solutes with a box
of solvent molecules prepared using NFOLD, or
to combine two molecules with a covalent bond
between them.
See IDELETE if overlap atoms need to be deleted.
= 0 skip (default)
= 1 combine $FFDATA and $FFDATB, both remain
in their original Cartesian coordinates.
= 2 combine $FFDATA and $FFDATB, and translate
$FFDATB so its geometric center coincides
with that of $FFDATA (move B to match A).
= 3 combine $FFDATA and $FFDATB, between that
there is one covalent bond specified via

```
             the keyword MATCHAB.

MATCHAB= IA1, IA2, IB1, IB2
       = specify the sequence numbers of a pair of atoms
         forming a covalent bond in $FFDATA and $FFDATB
         when ICOMBIN=3 is used.
         IA1 and IA2 for the two bonded atoms in $FFDATA.
         IB1 and IB2 for the two bonded atoms in $FFDATB.
         Atoms IA1 and IB1 should have the same Cartesian
         coordinates, so do atoms IA2 and IB2.
         When ICOMBIN=3 is used, atoms in $FFDATA are all
         deleted if they are on the IA2 side, atoms in
         $FFDATB are all deleted if they are on the IB1
         side.  Covalent terms across this bond is
         estimated using existing values in $FFDATA and
         $FFDATB.

IDELETE= check the atoms in $FFDATA and delete those
         are within 1.0 A to any one of the first n atoms
         (n=IDELETE).  The atoms forming covalent bonds
         with any deleted atoms will also be deleted
         (molecule deletion).  Default=0, no action.
         This can be used to remove overlaping atoms in a
         $FFDATA generated from ICOMBIN=1 and 2 (not 3).

ISCOOP = scoop out a subset of atoms/molecules from
         a given $FFDATA.  The scooped-out atoms are
         centered at CENTX, CENTY, CENTZ, which are either
         given or determined from the input $FFDATA.
       = 0   skip (default)
       = 1   scoop out a rectangular box with side lengths
             XBOX, YBOX, ZBOX.
       = 2   scoop out a sphere with radius = SPHRAD

   **** force field files ****

NFFFILE= select force field parameter and topology files
       = 0   use no such files (default)
       = 2   use parameter and topology files from CHARMM
       = 3   use parameter and topology files from AMBER

TOPFILE= path/name of a CHARMM or AMBER GAFF topology
         file, in single quotes.  For example, if
         yyy=/home/user,
      'yyy/gamess/auxdata/QUANPOL/top_all27_prot_na.rtf'
```

```
      'yyy/gamess/auxdata/QUANPOL/top_all36_na.rtf'
      'yyy/gamess/auxdata/QUANPOL/top_all36_prot.rtf'
      'yyy/gamess/auxdata/QUANPOL/top_amber_cornell.inp'
      'yyy/gamess/auxdata/QUANPOL/top_opls_aa.inp'
      'yyy/amber-gaff.mol2'
         The amber-gaff.mol2 file must be generated by
         using AmberTools (http://ambermd.org/), and in
         the mol2 format.

         There must be no space between 'TOPFILE' & '=',
         and the path/name must be in single quotes,
         and less than 60 characters.
         * Correct examples:
              TOPFILE='yyy/gamess/auxdata/QUANPOL/xxx'
              TOPFILE=  'yyy/xxx'
         * Wrong examples:
              TOPFILE ='yyy/gamess/auxdata/QUANPOL/xxx'
              TOPFILE='~/gamess/auxdata/QUANPOL/xxx'
              TOPFILE=yyy/gamess/auxdata/QUANPOL/xxx

TOPAMIA= path/name of an AMBER topology file for amino
         acids, in single quotes.  For example, if
         yyy=/home/user,
         'yyy/gamess/auxdata/QUANPOL/all_amino94.in'
         'yyy/gamess/auxdata/QUANPOL/all_amino02.in'
         'yyy/gamess/auxdata/QUANPOL/amino10.in'
         'yyy/gamess/auxdata/QUANPOL/amino12.in'
         See TOPFILE for correct input format.

TOPCTER= path/name of an AMBER topology file for
         C-terminal amino acids, in single quotes.
         For example, if yyy=/home/user,
         'yyy/gamess/auxdata/QUANPOL/all_aminoct94.in'
         'yyy/gamess/auxdata/QUANPOL/all_aminoct02.in'
         'yyy/gamess/auxdata/QUANPOL/aminoct10.in'
         'yyy/gamess/auxdata/QUANPOL/aminoct12.in'
         See TOPFILE for correct input format.

TOPNTER= path/name of an AMBER topology file for
         N-terminal amino acids, in single quotes.
         For example, if yyy=/home/user,
         'yyy/gamess/auxdata/QUANPOL/all_aminont94.in'
         'yyy/gamess/auxdata/QUANPOL/all_aminont02.in'
         'yyy/gamess/auxdata/QUANPOL/aminont10.in'
         'yyy/gamess/auxdata/QUANPOL/aminont12.in'
```

```
         See TOPFILE for correct input format.

TOPNUCA= path/name of an AMBER topology file for nucleic
         acids, in single quotes.  For example, if
         yyy=/home/user,
         'yyy/gamess/auxdata/QUANPOL/all_nuc94.in'
         'yyy/gamess/auxdata/QUANPOL/all_nuc02.in'
         'yyy/gamess/auxdata/QUANPOL/nucleic10.in'
         See TOPFILE for correct input format.

PARFILE= path/name of a CHARMM/AMBER/MMFF parameter file,
         in single quotes.  For example, if
         yyy=/home/user,
       'yyy/gamess/auxdata/QUANPOL/par_all27_prot_na.prm'
       'yyy/gamess/auxdata/QUANPOL/par_all36_prot.prm'
       'yyy/gamess/auxdata/QUANPOL/par_all36_na.prm'
       'yyy/gamess/auxdata/QUANPOL/par_amber_cornell.inp'
       'yyy/gamess/auxdata/QUANPOL/par_amber_98.inp'
       'yyy/gamess/auxdata/QUANPOL/par_opls_aa.inp'
       'yyy/gamess/auxdata/QUANPOL/parm91.dat'
       'yyy/gamess/auxdata/QUANPOL/parm94.dat'
       'yyy/gamess/auxdata/QUANPOL/parm96.dat'
       'yyy/gamess/auxdata/QUANPOL/parm98.dat'
       'yyy/gamess/auxdata/QUANPOL/parm99.dat'
       'yyy/gamess/auxdata/QUANPOL/parm10.dat'
       'yyy/gamess/auxdata/QUANPOL/gaff.dat'
       'yyy/gamess/auxdata/QUANPOL/MMFF-I_AppendixB.ascii'
         See TOPFILE for correct input format.

PARFIL2= path/name of a second AMBER parameter file
         frcmod.* that is to add and replace parameters
         in regular parameter file parm**.dat.
         For example, if yyy=/home/user,
         'yyy/gamess/auxdata/QUANPOL/frcmod.ff99SB'
         'yyy/gamess/auxdata/QUANPOL/frcmod.ff12SB'
         'yyy/gamess/auxdata/QUANPOL/frcmod.ff02pol.r1'
         'yyy/gamess/auxdata/QUANPOL/frcmod.parmbsc0'
         See TOPFILE for correct input format.

PARFIL3= path/name of a third AMBER parameter file
         frcmod.* that is to add or replace parameters
         in regular parameter file parm**.dat and
         PARFIL2.  This is seldom used.

LJSIGMA= select the use of sigma or Rmin/2 for LJ in the
```

```
         input and output $FFDATA (and $FFDATB).  This is
         only for I/O purposes.
       = 0   use Rmin/2 (default)
       = 1   use sigma, which is 1.781797436280679*Rmin/2

WT14LJ = scaling factor for 1-4 Lennard-Jones interaction.
         Default=1.00.
         For CHARMM, QuanPol uses an additional set of
         parameters for 1-4 LJ interaction.  In this case
         WT14LJ must be 1.00.  If not, only the first set
         of LJ parameters will be used, and scaled by
         WT14LJ for 1-4 cases.
         For AMBER and OPLSAA, QuanPol has two ways to
         scale the 1-4 LJ interaction by 0.50:
         1. Use WT14LJ = 1.00 but an additional set of
            pre-scaled LJ parameters. (default)
         2. Use WT14LJ = 0.50.  The additional set of LJ
            parameters is not used.
         For MMFF94, the default 1.00 should be used.
         Users can input WT14LJ to override the defaults.

WT14CH = scaling factor for 1-4 charge-charge interaction.
         Default=1, 1/1.2, 1/2, 3/4 for CHARMM, AMBER,
         OPLSAA, MMFF94, respectively, and = 1 for other
         cases.
         Users can input WT14CH to override the defaults.

   **** others ****

IDOCHG = include MM charges
IDOLJ  = include MM Lennard-Jones
IDOCMAP= include CHARMM CMAP for proteins
         For all of these,
       = 1   include (default)
       = 0   exclude

IDOPOL = specify how to include induced dipoles.  For
         large systems, IDOPOL=1 is ~2 times slower than
         IDOPOL=0, and IDOPOL=100 is ~10 times slower
         than IDOPOL=0.  Most induced dipole models are
         parameterized using IDOPOL=100, and must use
         IDOPOL=100.  Only those parameterized using
         IDOPOL=1 can use IDOPOL=1.  For the same system,
         IDOPOL=1 gives 85%~90% of the polarization
         energy as compared to IDOPOL=100.
```

```
       = 0    do not include
       = 1    dipoles are induced by external field due
              to MM charges, QM nuclei and electrons, and
              induced surface charges.  No interaction
              between induced dipoles are considered and
              no iteration is required, thus very fast.
       = 100  Dipoles are induced by external field and
              the field due to other induced dipoles.
              It requires many iterations (maximum=100).
              ITYPWAT=302 and NFFTYP=30000 (polarizable
              version from 2002) should use IDOPOL=100
              (default).

POLTOL = convergency criterion in induced dipole iterative
         calculation when IDOPOL=100.  Default=1.0D-09
         e*bohr.

IPODAMP= specify methods for damping interactions between
         induced dipoles at short distances.  Damping is
         necessary only for IPO1213=1.
       = 0    no damping (default)
       = 1    linear Thole model (energy not conserved)
       = 2    exponential Thole model
       = 3    Tinker-exponential model (Thole-Amoeba)
         For details of these methods, see Eq 41, 42, 43
         in J. Phys.: Condens. Matter 21 (2009) 333102

APODAMP= the unitless factor a in the damping formulas
         for IPODAMP=1, 2, and 3.  Defaults are 2.500,
         2.000, and 0.300, respectively.

IPO1213= specify inclusion of 1-2 and 1-3 interactions
         of induced dipoles.
       = 0    exclude 1-2 and 1-3 pairs (default)
       = 1    include 1-2 and 1-3 pairs
         Inclusion of 1-2 and 1-3 interactions often
         requires the use of IPODAMP=1,2,3 and is
         typically 2~3 times slower than excluding them,
         due to the stronger couplings between induced
         dipoles.  Induced dipoles may have difficulty
         to converge if the factor a (see APODAMP) is too
         small for IPODAMP=1 or too large for IPODAMP=
         2 and 3.

Use $END or a $END line to end $QUANPO.
```

==========

==========

$FFDATA group (optional, relevant if QuanPol is used)
$FFDATB group (optional, relevant if QuanPol is used)

The input is given in subsections with a keyword at the start of the subsection, and STOP at its end.

It is free format, but each line shall not exceed 79 characters, including space.

```
COORDINATES
NAME, NUC, X, Y, Z
         NAME    = The name of the atom.
         NUC     = nuclear charge of the atom
         X,Y,Z   = Cartesian coordinates in angstrom
STOP

MMVELOCITY
NAME, VX, VY, VZ
         NAME    = The name of the atom.
         VX,VY,VZ= velocity in atomic unit, which is
                   2187691.2633 m/s.
STOP

QMVELOCITY
NAME, VX, VY, VZ
         NAME    = The name of the QM atom.
         VX,VY,VZ= velocity in atomic unit, which is
                   2187691.2633 m/s.
STOP

         MMVELOCITY and QMVELOCITY are required for
         restarting jobs, and should be copied together
         with COORDINATES from the *.trj file of a
         previous job.

PARAMETERS
NAME, MASS, Q, POL, SIGMA, EPSILON, SIGMA2, EPSILON2
         NAME    = The name of the atom.
         Q       = Force field charge (e) on the atom.
         POL     = Polarizability of the atom, in A**3
         SIGMA   = Lennard-Jones parameter in angstrom.
                   When LJSIGMA=0, input RMIN/2.
```

```
                When LJSIGMA=1, input SIGMA.
        EPSILON = Lennard-Jones parameter in kcal/mol
        SIGMA2, EPSILON2
                = the LJ parameters for select 1-4 cases
                  in CHARMM. Give zeros if not these.

        Give the same number of lines as specified in
        the COORDINATES section
STOP

QMMMREP
N, C1, Z1, C2, Z2, C3, Z3, C4, Z4
        N       = number of Gaussian type potentials.
                  currently only 4 is allowed.
        C1 - C4 = strength factor of the potential
        Z1 - Z4 = radial factor of the potential

        give the same number of lines as specified in
        the COORDINATES section
STOP

BOND
SERIAL#, ATOM1, ATOM2, BFC, R0
        SERIAL# = serial number of the bond.
                  this is only for notation purpose.
        ATOM1   = serial number in COORDINATES section
                  for the first atom in the bond.
        ATOM2   = same as ATOM1, but for the second atom.
        BFC     = bond force constant in kcal/mol/A**2.
                  note QuanPol uses E = BFC*(R-R0)**2.
        R0      = equilibrium bond length in angstrom.
STOP

ANGLE
SERIAL#, ATOM1, ATOM2, ATOM3, AFC, ANGLE0
        SERIAL# = serial number of the angle.
                  this is only for notation purpose.
        ATOM1   = serial number in COORDINATES section
                  for the first atom in the angle.
        ATOM2   = same as ATOM1, but for the second atom.
        ATOM3   = same as ATOM1, but for the third atom.
        AFC     = angle bending force constant in
                  kcal/mol/rad**2.
                  note QuanPol uses E = AFC*(A-A0)**2.
        ANGLE0  = equilibrium angle in degree.
```

```
STOP

STRBEND
SERIAL#, BOND1, BOND2, FC1, FC2
         SERIAL# = serial number of the angle.
                   Must be the same as in ANGLE section.
         BOND1   = serial number of the bond in the BOND
                   section for the first bond (atoms 1
                   and 2) in the angle.
         BOND2   = serial number of the bond in the BOND
                   section for the second bond (atoms 2
                   and 3) in the angle.
         FC1     = stretch-bend force constant in
                   kcal/mol/rad/angstrom, for BOND1
         FC2     = stretch-bend force constant in
                   kcal/mol/rad/angstrom, for BOND2
STOP

DIHROT
SERIAL#, ATOM1, ATOM2, ATOM3, ATOM4, VROT, N, GAMMA
         SERIAL# = serial number of the dihedral rotation
                   angle. This is only for notation
                   purpose.
         ATOM1   = serial number in COORDINATES section
                   for the first atom in the dihedral
                   rotation angle.
         ATOM2   = same as ATOM1, but for the second atom.
         ATOM3   = same as ATOM1, but for the third atom.
         ATOM4   = same as ATOM1, but for the fourth atom.
         VROT    = rotational barrier in kcal/mol
         N       = multiplicity, an integer.
         GAMMA   = the phase factor in degree.
STOP

DIHR3V
SERIAL#, ATOM1, ATOM2, ATOM3, ATOM4, VROT1, VROT2, VROT3
         Similar to DIHROT, but for MM2, MM3 and MMFF94
         style torsion potential.
         VROT1,2,3 are rotational barrier in kcal/mol
STOP

DIHBND
SERIAL#, ATOM1, ATOM2, ATOM3, ATOM4, DBFC, DIHB0
         SERIAL# = serial number of the dihedral bending
                   (improper torsion) angle. this is only
```

```
                for notation purpose.
        ATOM1   = serial number in COORDINATES section
                for the first atom in the dihedral
                bending angle.
        ATOM2   = same as ATOM1, but for the second atom.
        ATOM3   = same as ATOM1, but for the third atom.
        ATOM4   = same as ATOM1, but for the fourth atom.
        DBFC    = dihedral bending force constant in
                kcal/mol/rad**2
        DIHB0   = equilibrium dihedral bending angle in
                degree.
STOP

CMAP
SERIAL#, ATOM1, ATOM2, ATOM3, ATOM4, ATOM5, ITYPE
        SERIAL# = serial number of the CHARMM correction
                map phi,psi couples. this is only
                for notation purpose.
        ATOM1   = serial number in COORDINATES section
                for the first atom in the phi angle
                (the carbonyl carbon of an amino acid
                residue) of the peptide backbone in a
                phi,psi couple.
        ATOM2   = serial number in COORDINATES section
                for the second atom in the phi angle
                (peptide N atom) of a phi,psi couple.
                this is the first atom of the psi angle.
        ATOM3   = serial number in COORDINATES section
                for the third atom in the phi angle
                (the alpha C atom) of a phi,psi couple.
                this is the 2nd atom of the psi angle.
        ATOM4   = serial number in COORDINATES section
                for the fourth atom in the phi angle
                (a carbonyl carbon) of a phi,psi couple.
                this is the third atom of the psi angle.
        ATOM5   = serial number in COORDINATES section
                for the fourth atom in the psi angle
                (the next peptide N atom).
        ITYPE   = specifies the map potential a phi,psi
                couple belongs to.
                =1 alanine map (all except for pro/gly)
                =2 proline map
                =3 glycine map
STOP
```

```
When $FFPDB is given, CMAP is automatically generated for
restart jobs, via $FFDATA input.  The CMAP group could be,
but should not be, input by a user.

WAGGING
SERIAL#, ATOM2, ATOM3, ATOM4, ATOM1, WFC
         SERIAL# = serial number of the wagging angle.
                   this is only for notation purpose.
         ATOM2   = serial number in COORDINATES section
                   for the second atom in the wagging
                   angle.
         ATOM3   = same as ATOM2, but for the third atom.
         ATOM4   = same as ATOM2, but for the fourth atom.
         ATOM1   = same as ATOM2, but for the first atom.
         WFC     = wagging force constant kcal/mol/rad**2
STOP

MMTYPE
NATOM
N01 N02 N03 ... N18 N19 N20
N21 N22 N23 ... N(NATOM)
         NATOM   = total number of atoms in MMTYPE
                   section.  This must be accurate and
                   occupy a line.
         N(I)    = atom type in force field such as
                   MMFF94.  In MMFF94, there are 95
                   types of atoms.  Each line must have
                   exactly 20 atoms except for the last
                   line, which may have 1-20 atoms.  A
                   line should not exceed 79 characters
                   (including space).  The MMTYPE section
                   is always generated by using LOUT=1.
                   If 0 is seen, one can manually change
                   0 to a real MMFF94 type.  For example,
                   one can change the heme bound Oxygen
                   atom to MMFF94 type 6.  A real type
                   number is required when the LJ
                   potential is needed.
STOP

MMFFLJ
NMMTP
I,J,RIJ,EPSIJ,   I,J,RIJ,EPSIJ,   I,J,RIJ,EPSIJ
         NMMTP   = total number of types in MMFFLJ
                   section.  This must be accurate and
```

```
                occupy a line.
        I, J    = atom types in force field such as
                  MMFF94.  In MMFF94, there are 95
                  types of atoms.  J must be equal to
                  or greater than I.
        RIJ     = the minimum Lennard-Jones energy
                  distance (angstrom) between two atoms
                  of type I and type J.
        EPSIJ   = the well depth (kcal/mol) of the LJ
                  term between two atoms of type I and
                  type J.  Each line must have 1, 2, or
                  3 sets, and cannot exceed 79 characters
                  (including space).  The MMFFLJ section
                  is always generated by using LOUT=1.
STOP

Use a $END line to end $FFDATA or $FFDATB.

=============================================================
```

==========

$FFPDB group (optional, relevant if QuanPol is used)

Simply pasting a PDB text file into $FFPDB may work.

(1). H atoms must be added beforehand, and must appear
at the correct places in the PDB file. Currently
QuanPol cannot add any missing atoms. The CHIMERA
program from UCSF can be used to add H atoms and
generate PDB files for QuanPol use.
(2). PDB format is enforced. Sequential numbers are not
used by QuanPol. Chemical symbols are used.
(3). Multiple chains are allowed. 'TER' lines can be used,
but not necessary.
(4). SSBOND lines are required to define S-S bonds.
(5). Most PDB metal ions can be processed by QuanPol and
assigned integer charges, Lennard-Jones potential and
effective QMREP potential. No bonds, angles and
dihedral angles will be assigned to them by QuanPol.
(6). Water section must be the last section of the PDB.
The potential of these waters is set by ITYPWAT.
A hydroxyl group can be obtained by manually editing
a water (can be purposely moved to be the last atom
of the PDB file) in the QuanPol generated $FFDATA.
(7). Small molecules in PDB should be processed separately
and recombined using ICOMBIN=1, 2, or 3.

Use a $END line to end $FFPDB.

==========

The remaining groups apply only to MCSCF and CI runs.

```
* * * * * * * * * * * * * * * * * * * *
 For hints on how to do MCSCF and CI
see the 'further information' section
* * * * * * * * * * * * * * * * * * * *
```

==========

$CIINP group (optional, relevant for any CITYP)

This group is the control box for Graphical Unitary Group Approach (GUGA) CI calculations or determinant based CI. Each step which is executed potentially requires a further input group described later.

NRNFG = An array of 10 switches controlling which steps of a CI computation are performed.
1 means execute the module, 0 means don't.

- NRNFG(1) = Generate the configurations. See either $CIDRT or $CIDET input. (default=1)
- NRNFG(2) = Transform the integrals. See $TRANS. (default=1)
- NRNFG(3) = determinants: skip the CI iterations.
  GUGA: Sort integrals and calculate the Hamiltonian matrix, see $CISORT and $GUGEM. (default=1)
- NRNFG(4) = determinants: meaningless
  GUGA: Diagonalize the Hamiltonian matrix, see $GUGDIA or $CIDET. (default=1)
- NRNFG(5) = Construct the one electron density matrix, and generate NO's. See $GUGDM or $CIDET. (default=1)
- NRNFG(6) = Construct the two electron density matrix. See $GUGDM2 or $CIDET. (default=0 normally, but 1 for CI gradients)
- NRNFG(7) = Construct the Lagrangian of the CI function. Requires DM2 matrix exists. See $LAGRAN. (default=0 normally, but 1 for CI gradients) This does not apply to determinants.
- NRNFG(8-10) are not used.

Users seldom need to input NRUNFG, as the defaults are quite reasonable.

```
NPFLG = An array of 10 switches to produce debug printout.
        There is a one to one correspondence to NRNFG, set
        to 1 for output. (default = 0,0,0,0,0,0,0,0,0,0)

        The most interesting may be NPFLG(2)=1 to see the
        transformed 1e- integrals.  NPFLG(2)=2 adds the
        very numerous transformed 2e- integrals to this.

IREST = n    Restart the -CI- at stage NRNFG(n).
=========================================================
```

==========

$DET group (required by MCSCF if CISTEP=ALDET or ORMAS)
$GEN group (required by MCSCF if CISTEP=GENCI)
$CIDET group (required if CITYP=ALDET, ORMAS, or FSOCI)
$CIGEN group (required if CITYP=GENCI)

This group describes the determinants to be used in a MCSCF or CI wavefunction:

a) For full CI calculations (ALDET) the $DET/$CIDET will generate a full list of determinants. If the CI is part of an MCSCF, this means the MCSCF is of the FORS type (which is also known as CASSCF).
b) For Occupation Restricted Multiple Active Space (ORMAS) CI, the input in $ORMAS will partition the active orbitals defined here into separate spaces, that is, provide both $DET/$CIDET and $ORMAS.
c) For Full Second Order CI, provide $CIDET and $SODET inputs.
d) For a general CI (meaning user specified space orbital products) provide $DET/$CIDET plus $GEN/$CIGEN and most likely $GCILST (according to the keyword GLIST).

In the above, group names for MCSCF/CI jobs are separated by a slash.

Determinants contain several spin states, in contrast to configuration state functions. The Sz quantum number of each determinant is the same, but the Hamiltonian eigenvectors will have various spins S=Sz, Sz+1, Sz+2, ... so NSTATE may need to account for states of higher spin symmetry. In Abelian groups, you can specify the exact spatial symmetry you desire.

GLIST = general determinant list option
The keyword GLIST must not be given in a $DET or $CIDET input group! These both generate full determinant lists, automatically.
= INPUT means $GCILST input will be read.
= EXTRNL means the list will be read from a disk file GCILIST generated in an earlier run.
= SACAS requests generation of sevaral CAS spaces of different space symmetries, specified by

the input IRREPS. This option is intended for state averaged calculations for cases of high symmetry, where degenerate irreps of the true group may fall into different irreps of the Abelian subgroup used.

* * * The next four define the orbital spaces * * *
There is no default for NCORE, NACT, and NELS:

NCORE = total number of orbitals doubly occupied in all determinants.

NACT = total number of active orbitals.

NELS = total number of active electrons.

SZ = azimuthal spin quantum number for each of the determinants, two times SZ is therefore the number of excess alpha spins in each determinant. The default is SZ=S, extracted from the MULT=2S+1 given in $CONTRL.

* * * The following determine the state symmetry * * *

GROUP = name of the point group. The default is to copy this from $DATA, if that group is Abelian (C1, Ci, Cs, C2, C2v, C2h, D2, or D2h). If not, the point group used will be C1 (no symmetry).

STSYM = specifies the spatial symmetry of the state. Of course these names are the standard group theory symbols for irreducible representations:

```
     C1   A
     Ci   Ag  Au
     Cs   AP  APP   (P stands for prime, i.e. ')
     C2   A   B
     C2v  A1  A2  B1  B2
     C2h  Ag  Bu  Bg  Au
     D2   A   B1  B2  B3
     D2h  Ag  B1g B2g B3g Au  B1u B2u B3u
```

Default is STSYM being the totally symmetric state, listed as the first column above.
The free format scanner is not able to read quotes

so the letters "P" must be used in Cs.

IRREPS = specifies the symmetries of the GLIST=SACAS space determinant list. This variable should always be an array, as a single symmetry is more quickly obtained by the regular full CI code. The values given are more primitive than STSYM, being the following integers, not strings:

IRREPS=	1	2	3	4	5	6	7	8 meaning
C1	A							
Ci	Ag	Au						
Cs	A'	A''						
C2	A	B						
C2v	A1	A2	B1	B2				
C2h	Ag	Bu	Bg	Au				
D2	A	B1	B2	B3				
D2h	Ag	B1g	B2g	B3g	Au	B1u	B2u	B3u

* * * the following control the diagonalization * * *

NSTATE = Number of CI states to be found, including the ground state. The default is 1, meaning ground state only. The maximum number of states is 100. See also IROOT below (two places).

PRTTOL = Printout tolerance for CI coefficients, the default is to print any larger than 0.05.

ANALYS = a flag to request analysis of the CI energy in terms of single and double excitation pair correlation energies. This is normally used in CI computations, rather than MCSCF, and when the wavefunction is dominated by a single reference, as the analysis is done in terms of excitations from the determinant with largest CI coefficient. The defalt is .FALSE.

ITERMX = Maximum number of Davidson iterations per root. The default is 100. A CI calculation will fail if convergence is not obtained before reaching the limit. MCSCF computations will not bomb if the iteration limit is reached, instead the last CI vector is used to proceed into the next orbital update. In cases with very large active

spaces, it may be faster to input ITERMX=2 or 3 to allow the program to avoid fully converging the CI eigenvalue problem during the early MCSCF iterations. For small active spaces, it is best to allow the CI step to be fully converged on every iteration.

CVGTOL = Convergence criterion for Davidson eigenvector routine. This value is proportional to the accuracy of the coefficients of the eigenvectors found. The energy accuracy is proportional to its square. The default is 1.0E-5, but 1E-6 if gradients, MPLEVL, CITYP, or FMO selected).

NHGSS = dimension of the Hamiltonian submatrix which is diagonalized to obtain the initial guess eigenvectors. The determinants forming the submatrix are chosen on the basis of a low diagonal energy, or if needed to complete a spin eigenfunction. The default is 300.

NSTGSS = Number of eigenvectors from the initial guess Hamiltonian to be included in the Davidson's iterative scheme. It is seldom necessary to include extra states to obtain convergence to the desired states. The default equals NSTATE.

MXXPAN = Maximum number of expansion basis vectors in the iterative subspace during the Davidson iterations before the expansion basis is truncated. The default is the larger of 10 or 2*NSTGSS. Larger values might help convergence, do not decrease this parameter below 2*NSTGSS.

CLOBBR = a flag to erase the disk file containing CI vectors from the previous MCSCF iteration. The default is to use these as starting values for the current iteration's CI. If you experience loss of spin symmetry in the CI step, reverse the default, to always take the CI from the top. Default = .FALSE.

* * * the following control the 1st order density * * *

The following pertain to CI calculations by CITYP=xxx (not to the CI step within MCSCF jobs). Similar keywords apply to MCSCF runs, see just below.

PURES = flag to say that IROOT and NGFLGDM just below should count only those states whose S value is a match to that implied by MULT in $CONTRL. Thus, PURES=.TRUE. (the default) allows selection of S1 as IROOT=2 (the second singlet), even if there is a T1 state (and maybe others!) between S0 and S1. Of course, NSTATE must be large enough to reach S1 (at least 3, if there is a T1 between S0 and S1).
Setting PURES to .FALSE. ignores the spin of each state when using IROOT and NFLGDM.

IROOT = the root whose density is saved on the disk file for subsequent property analysis. Only one root can be saved, and the default value of 1 means the ground state. Be sure to set NFLGDM to form the density of the state you are interested in!
IROOT has a similar meaning for MCSCF, see below.

NFLGDM = Array controlling each state's density formation.
0 -> do not form density for this state.
1 -> form density and natural orbitals for this state, print and punch occ.nums. and NOs.
2 -> same as 1, plus print density over MOs.
3 -> same as 2, plus print properties for this state (see $ELMOM, $ELPOT, et cetera).
The default is NFLGDM(1)=1,0,0,...,0 meaning only ground state NOs are generated.

SAFLG = is a logical flag that determines whether or not state averaged CI density matrices and natural orbitals should be evaluated. Setting SAFLG=.TRUE. will result in the evaluation of the state averaged density matrix and NOs. The default .FALSE. means generate state-specific densities according to the NFLGDM input. See also WSTATE.

WSTATE = An array of up to 100 weights to be given to the densities of each state in forming the average density matrix. The default is to optimize a pure ground state, WSTATE(1)=1.0,0.0,...,0.0.

Note that values given for WSTATE (during a CI calculation) will only be used if SAFLG=.TRUE. It should also be noted that any electronic state that has a nonzero value for WSTATE but a zero for NFLGDM will reset its value for NFLGDM to 1.

FSTATE = An array of up to 100 weights to be given to the densities of each state in forming the average density matrix used for QM-EFP polarization. FSTATE is ignored unless PMTD1=.FALSE. in $CONTRL. See also PURES. The default is to set FSTATE from WSTATE if only the latter is given.

* * * the following control the state averaged * * *
* * * 1st and 2nd order density matrix computation * * *

The following keywords apply to the CI step within the MCSCF iterations. See just above for similar inputs pertaining to CITYP=xxx calculations.

PURES = a flag controlling the spin purity of the state averaging. If true, the WSTATE array pertains to the lowest states of the same S value as is chosen by the MULT keyword in $CONTRL. In this case, the value of NSTATE will need to be bigger than the total number of weights given as WSTATE if there are other spin states present at low energies. If .FALSE., it is possible to state average over more than one S value, which might be of interest in spin-orbit coupling jobs. State-averaged MCSCF gradient runs must use .TRUE. The default is .TRUE.

WSTATE = An array of up to 100 weights to be given to the densities of each state in forming the average. The default is to optimize a pure ground state, WSTATE(1)=1.0,0.0,...,0.0
A small amount of the ground state can help the convergence of excited states greatly.
Gradient runs are possible only with pure states.
Be sure to set NSTATE above appropriately!
See also IDWREF just below.

IDWREF = The target state K used to control dynamically

adjusted MCSCF state weights. This keyword may only be used for CISTEP=ALDET or CISTEP=ORMAS. The default is 0, to use static WSTATE values.

Dynamic weights are updated every MCSCF iteration by the formula:

WSTATE(n) = sech^2[-DWPARM*(E(n)-E(K))].

for n= state K and any other weighted states, followed by a normalization to sum to unity. The formula gives the largest weight to state K, with decreasing weight given to states farther away in energy. See Deskevich, Nesbitt, and Werner, J.Chem.Phys. 120, 7281(2004).
If IDWREF is given, the values given in WSTATE are used only to specify which roots should have non-zero weights.
The target state is often the ground state, K=1, but any other state may be used: often K=IROOT!
Converged dynamic weights will be passed to the determinant MCQDPT program (becoming its default WPTST) and to the state-averaged gradient/NACME program.

DWPARM = the value of the energy parameter used by IDWREF. The default is 2.0 eV.

IROOT = the MCSCF state whose energy will be used as the desired value. (default=0)
The default means to use the average (according to WSTATE) of all states as the FINAL energy, which is not a physically meaningful quantity.
When given as non-zero, IROOT chooses a specific state, ignoring any states with undesired spins, see PURES above, and also ignoring any states of the correct spin which were given no weight.
Any run doing either analytic state-specific gradients in state-averaged runs, or a gradient by numerical differentiation must pick the desired specific IROOT value!
IROOT has a similar meaning for CI, see above.

FSTATE = An array of up to 100 weights to be given to the densities of each state in forming the average density matrix used for QM-EFP polarization.
FSTATE is ignored unless PMTD1=.FALSE. in $CONTRL.

See also PURES. The default is to set FSTATE from WSTATE if only the latter is given.

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$ORMAS group (required by MCSCF if CISTEP=ORMAS) (required for CITYP=ORMAS)

This group partitions an active space, defined in $DET or $CIDET, into Occupation Restricted Multiple Active Spaces (ORMAS). All possible determinants satisfying the occupation restrictions (and of course the space symmetry restriction given in $DET/$CIDET) will be generated. This group's usefulness lies in reducing the large number of determinants present in full CI calculations with large active spaces.

There are no sensible defaults for these inputs, but if the group is entirely omitted, a full CI calculation will be performed. That is, the defaults are
NSPACE=1, MSTART(1)=NCORE+1, MINE(1)=NELS, MAXE(1)=NELS
meaning all active orbitals are in one partition.

NSPACE = number of orbital groups you wish to partition the active space (NACT in $DET/$CIDET) into.

MSTART = an array of NSPACE integers. These specify where each orbital group starts in the full list. You must not overlook the NCORE core orbitals in computing MSTART values. Space I runs from orbital MSTART(I) up to orbital MSTART(I+1)-1, or NACT+NCORE if I is the last space, I=NSPACE.

IMPORTANT !!!! Remember to make sure your orbitals have been reordered to suit MSTART, using NORDER in $GUESS.

MINE = an array of NSPACE integers. These specify the minimum numbers of electrons that must always occupy the orbital groups. In other words, MINE(I) is the minimum number of electrons that can occupy space I in any of the determinants.

MAXE = an array of NSPACE integers. These specify the maximum numbers of electrons that must always occupy the orbital groups. In other words, MAXE(I) is the maximum number of electrons that can occupy space I in any of the determinants.

The number of active electrons is NELS in $DET or $CIDET, and the program will check that MINE/MAXE values are consistent with this total number.

Input for Coupled Electron Pair Approximations

These two keywords provide size-extensivity corrections for singly and doubly excited CI calculations. At present, these approximate corrections may only be applied to a single state. The CISD may follow RHF (single reference, SR) or complete active space (multireference, MR) calculations. Usually, the final ORMAS orbital space will be the entire external space of the SR-CISD or MR-CISD calculations. The excitation level (MAXE) into this space should only be two. The number of electrons being correlated (NELS in $CIDET) is denoted Ne. The value of a parameter G determines the weight of the approximate size-extensivity correction, with the literature containing several possible choices: GVAL here sometimes is written as -(1-G) in the literature. The first order density matrix for the chosen CEPA-style correction will be generated, and used for property calculation.

```
CEPA    = NONE  ordinary SR-CISD or MR-CISD (default)
        = CEPA0 Coupled Electron Pair Approximation,
                whose GVAL= 1.0
        = ACPF  Averaged Coupled Pair Functional,
                whose GVAL= (Ne-2)/Ne
        = AQCC  Averaged Quadratic Coupled-Cluster,
                whose GVAL= (Ne-3)(Ne-2)/[Ne(Ne-1)]
        = READ  user will supply the desired GVAL.

GVAL    = is given only when CEPA=READ
```

An example of the SR-AQCC size-extensivity correction for a molecule with 10 chemical cores, 8 occupied valence orbitals, and 163 total MOs is

```
 $CONTRL SCFTYP=RHF CITYP=ORMAS RUNTYP=ENERGY
 $CIDET  NCORE=10 NACT=153 NELS=16
 $ORMAS  CEPA=AQCC NSPACE=2
         MSPACE(1)=11,19 MINE(1)=14,0 MAXE(1)=16,2
```

A MR-CEPA case with N active electrons and M electrons in filled valence orbitals should use three spaces, with NELS M+N; MINE M-2,N-2,0; and MAXE M,N+2,2.

Review: P.G.Szalay, in Modern Ideas in Coupled-Cluster methods, R.J.Bartlett (ed), World Scientific, Singapore (1997), pp 81-123.

* * * * *

BLOCK = a flag to request that natural orbital generation for CISTEP=ORMAS MCSCF or CITYP=ORMAS CI runs should prevent mixing between the NSPACE orbital subspaces. This means the NOs only diagonalize the diagonal blocks of the density, and are thus not the genuine NOs. However, these approximate NOs can be used with MOREAD to exactly reproduce the ORMAS energy, which is invariang to rotations within the orbital subspaces. (Default=.FALSE.)

QCORR = a flag to request Davidson-style +Q corrections. If this is not sensible for your CI choice, the program will not print this correction, anyway. The default is .TRUE.

FDIRCT = a flag to choose storage in memory of some intermediates. This is very large, and slower in the case of many occupied orbitals, but helpful with a smaller number of orbitals. Therefore the default for this is .TRUE. for MCSCF runs, but .FALSE. during CI computations.

*** See REFS.DOC for more information on using ORMAS ***

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$CEEIS group (optional, for extrapolation to FCI limit)

The method termed Correlation Energy Extrapolation by Intrinsic Scaling (CEEIS) allows one to extrapolate sequences of CI energies, computed with the ORMAS program, to what is effectively the full CI limit for a given basis set. Typically, the energy for SD and SDT excitation levels using all orbitals (m=M, meaning occupied + all virtuals) is combined, using certain scaling relations, with explicit computations using m orbitals for quadruple, quintuple... excitations (x), using a smaller m for each higher excitation, to obtain the extrapolated FCI limit, within an estimated error bar. When this is done for several basis sets, it is possible to extrapolate the individual full CI energies to the limit of the complete basis set.

A series of papers combines complete basis set CEEIS energies with scalar relativistic, spin-orbit, and long range electrostatic corrections to produce a very accurate rotational-vibrational spectrum of F2, see

L.Bytautas, T.Nagata, M.S.Gordon, K.Ruedenberg
J.Chem.Phys. 127, 164317/1-20 (2007)
L.Bytautas, N.Matsunaga, T.Nagata, M.S.Gordon, K.Ruedenberg
J.Chem.Phys. 127, 204301/1-12 (2007)
L.Bytautas, N.Matsunaga, T.Nagata, M.S.Gordon, K.Ruedenberg
J.Chem.Phys. 127, 204313/1-19 (2007)
L.Bytautas, K.Ruedenberg
J.Chem.Phys. 130, 204101/1-14 (2009)

The input description below is quite terse. A full description of how to use CEEIS with ORMAS is provided in a separate file (a Word document) named

~/gamess/tools/ci-tools/ceeis/CEEIS.doc

containing a much more detailed description of how to do this kind of calculation. This document explains how to use an Excel spreadsheet to allow visual checking of the energy data that are being extrapolated. Several input examples are given in the same directory.

ENREF = reference energy, usually either a zero-excited ORMAS reference wavefunction, or some SCF level energy (if the reference is one determinant).

```
ISTPEX = highest excitation level considered by the CEEIS,
         the default is 8 (octuple excitations).

M1M2EX = an array to specify the various ORMAS computations
         to be performed, at each excitation level x.
         0's start the specification of m values for each
         level x=3,4,...ISTPEX.  Some examples follow,
  M1M2EX(1)= 0,0,0,
             0,7,10,-14,20
             0,7,10,-14   ISTEPX=5
The final two zero's on the first (SDT) line mean do the
SDT computations with the entire virtual space, and also
for all m values used at the higher excitations.  The SDTQ
energies are found for m=7,10,11,12,13,14,20, that is, the
minus sign implies all values in the range 10-14.  The
SDTQ5 computations do not include m=20.  If there is not
enough memory to do the entire SDT calculation, this can be
extrapolated (losing accuracy in the entire CEEIS process),
by input such as
  M1M2EX(1)= 0,7,10,-14,20,27,
             0,7,10,-14,20
             0,7,10,-14   ISTEPX=5
Changing the 0,0 part of the triples line to what is shown
extrapolates from m=27.  Note that it is an error not to
include the same m values that higher excitations will use.
There is no input for doubles, as in all cases the program
will generate the SD energy for the entire virtual space,
and additional SD energies for the m values chosen for use
by the higher excitation levels.
  M1M2EX(1)= all 0's will carry out a fully automated CEEIS
using MMIN to MMIN+4, testing convergence, possibly adding
MMIN+5 to MMIN+9 and so forth.

IDELTM = range increment for the m1,m2 ranges given as
         {m1,-m2} in M1M2EX.  Default=1.

ISCHME = extrapolation choice (the default is 1) for energy
         increments (DEMAT = differences of EMAT values):
       = 1 means extrapolate excitation level "x" by
             DEMAT(m,x) = a*DEMAT(m,x-2) + b
       = 2 means extrapolate quadruples as above, but
           x=5+6 or x=7+8,... are extrapolated together:
             DEMAT(m,x) = A*DEMAT(m,2) + B*DEMAT(m,3) + C
           In this case energies for odd excitation levels
```

are not needed, and their computation can be avoided by making the odd levels in M1M2EX be the same input for 5+6, 7+8, ...

MMIN = "m" value of the lowest virtual orbital to be considered in the extrapolation. The default is NCORE + 1 + MAX(no. valence e-, no. valence orbs), which is in fact the lowest "m" that should ever be used.

XTRTOL = an array of thresholds for each extrapolated energy E(x), if the automated CEEIS is being used. default = 2D-4 Hartree for all levels x.

NSEXT = an array containing NSPACE entries. Each entry corresponds to an ORMAS orbital group defined by MSTART in $ORMAS, and can be either 0 or 1. An entry of 1 means include excitations from this space during the CEEIS. 0 means do not include any such excitations, meaning electrons in this subspace are NOT being correlated, apart from the correlation built into the original ORMAS. The final entry in the list is the virtual space, and must be given as 1. The default is all 1's.

RESTRT = a flag to say that the CEEIS calculation is being restarted, in which case energies provided in the $CEDATA input are read, and only the missing energies will be calculated. Default = .FALSE.

IEXPND = expands the excitation level in restarts, e.g. if the previous data was computed for ISTPEX=6, and you now wish to use ISTPEX=8, enter IEXPND=2 to add two more columns to the matrix EMAT(m,x) being read in $CEDATA.

==========

$CEDATA group (optional restart data for CEEIS runs)

This group contains previously computed ORMAS energies, forming the EMAT array, to be used to restart CEEIS runs. It is required if RESTRT in $CEEIS is true.

==========

==========

$GCILST group (required by MCSCF if CISTEP=GENCI) (required if CITYP=GENCI)

This group defines space products to be used in the general CI calculation, or in a MCSCF wavefunction. The input is free format.

Line 1: NSPACE ISYM

The first line gives the total number of space products to be entered in the second lines. The option ISYM can be omitted, or given as 0, in which case the program will verify that all space products typed in the second lines indeed have the spatial symmetry defined by STSYM in the $GEN or $CIGEN input groups. If ISYM is 1, the user is indicating that more than one space symmetry is known to be in the list, that this is intentional, and the program should proceed with the calculation. This might be of use in state averaging two representations in a group that has more than two total representations, and therefore faster than turning symmetry off completely by GROUP=C1. ISYM=2 has the same meaning but turns on additional printing.

Line 2 is repeated NSPACE times. Each line 2 contains NACT integers, which must be 0, 1, or 2, and therefore tells the occupation of each of the active orbitals in each space product. An example input is:

```
 $GEN     GLIST=INPUT NELS=6 NACT=4 SZ=0.0 $END
 $GCILST
5
2 2 2 0
2 1 2 1
2 0 2 2
2 2 0 2
0 2 2 2
 $END
```

which generates 6 Ms=0 determinants, much less than the 16 determinants in a C1 symmetry full list for 6 e- in 4 MOs.

The second space product above generates two determinants. All space products with singly occupied orbitals are used to form all possible determinants, to ensure that the final

states are eigenfunctions of the S**2 operator (meaning they will be pure spin states).

Note that there is no way at present to generate lists such as singles and doubles from a single reference.

Convergence of MCSCF calculations with arbitrary lists of space products will depend on how well chosen your list is, and may very well require the use of FULLNR or JACOBI convergers.

A utility program to pre-select the important part of CI expansions with high excitation levels, based on information from CI-SDT calculations, is distributed with the source code. See the file

~/gamess/tools/ci-tools/select/readme.1st

for more information.

==========

==========

$GMCPT group (relevant if CISTEP=GMCCI in $MCSCF) (relevant if MRPT=GMCPT in $MRMP)

This group specifies the determinants to be used in a general MCSCF wavefunction. Additional inputs give the necessary information to compute a 2nd order perturbation energy correction to the MCSCF energy of such a MCSCF reference, by choosing MPLEVL=2 in $CONTRL and MRPT=GMCPT.

The PT is of quasidegenerate type, in which several MCSCF states can be perturbed simultaneously. After 2nd order correction to both its diagonal and off-diagonal matrix elements, this model Hamiltonian is diagonalized to give the GMC-QDPT energies. The diagonalization also yields some information about the remixing of the reference states at 2nd order. Of course, the program can also be used to obtain the 2nd order correction to the energy of just one state.

GMC-QDPT is therefore analogous to the two equivalent MCQDPT programs (MRPT=MCQDPT or DETMRPT) for CAS-type references, but allows more general types of MCSCF reference. Compared to those programs, there are also choices for the 0-th order states, for the orbital energies, and for the treatment of external excitations.

The letters GMCPT should be understood as standing for GMC-QDPT, and have been shortened only because of the constraints on input group names to 6 or fewer letters.

At the present time, this program does not support EXETYP=CHECK. It is enabled for parallel execution.

1. data to specify active space and electronic state:

NMOFZC: number of frozen core orbitals, during the PT the shape of these orbitals will be optimized in the MCSCF stage, so they are "frozen" in the sense of not being correlated in the PT. The default is the number of chemical core orbitals.

NMODOC: number of orbitals restricted to double occupancy

during MCSCF, but which are correlated in the PT calculation. In other words, the filled valence orbitals. (no default). (It is possible to enter a different keyword NMOCOR which is the total number of doubly occupied orbitals, and NMOFZC. In this case the program will obtain NMODOC by subtraction, namely NMODOC = NMOCOR - NMOFZC).

NMOACT: number of active orbitals in the MCSCF (no default)

NMOFZV: number of virtual orbitals to be omitted from the PT step. The default is 0, retaining all virtuals.

NELACT: number of active electrons. Since the default is computed from the total number of electrons given in $DATA and $CONTRL's ICHARG, minus 2*NMOFZC minus 2*NMODOC, there is little reason to input this.

MULT: multiplicity of the state, with the default being taken from MULT in $CONTRL.

SZ: spin projection quantum number for determinants, default is (MULT-1)/2

STSYM: The symmetry of the electronic state. See $DET for possible values: use AP/APP in Cs, not primes. Default is the totally symmetric representation.

If you are treating a system with degenerate states in an appropriate Abelian subgroup of the true group, up to three STSYM values can be given, to specify all components of that originally degenerate state. For example,

```
     STSYM(1)=b1u,b2u,b3u
```

generates all P states for an atom running in the Abelian subgroup D2h.

2. data to specify the MCSCF CI (and PT's reference CI):

The type of general MCSCF reference is specified by REFTYP, which can be MRX, ORMAS, or RAS:

REFTYP= MRX means multi-reference determinant list, plus excitations (default). The determinants will be

given by $PDET input, and the keywords NPDET and NEXCIT defined below are required.

REFTYP= RAS means the active space is divided into three subspaces, known as RAS1, RAS2, and RAS3. Keywords MSTART and NEXCIT defined below are required. For example, MSTART(1)=4,6,9 defines a RAS with three orbitals in the NMOFZC/NMODOC spaces, while the RAS1, RAS2, and RAS3 subspaces contain 2, 3, and NMOACT-5 orbitals. It remains only to specify the excitation level NEXCIT between these spaces.

REFTYP= ORMAS defines even more general subspaces than RAS, and requires inputs NSPACE, MSTART, MINE, and MAXE. These have the same meaning as the $ORMAS keywords.

NPDET is the number of parent determinants, to be given as NPDET lines in the $PDET input. A value is required for REFTYP=MRX.

NEXCIT is an excitation level. A value is required for REFTYP=MRX or REFTYP=RAS.

NSPACE is the number of subspaces into which the active space is divided. Required for REFTYP=ORMAS.

MSTART is an array telling the starting MO of each orbital space. It is required for REFTYP=RAS and ORMAS.

MINE is an array giving the minimum number of electrons occupying each subspace. Required for REFTYP=ORMAS.

MAXE is an array giving the maximum number of electrons occupying each subspace. Required for REFTYP=ORMAS.

NSPACE, MSTART, MINE, and MAXE have the same meaning as in the $ORMAS input. See the 'how to do MCSCF/CI' section of REFS.DOC, for help in understanding the power of the ORMAS type of reference determinant list.

3. data to define the reference CI states:

KSTATE is an array of states to be used. As an example, KSTATE(1)=0,1,0,1 means use states 2 and 4. The

default is the ground state, KSTATE(1)=1,0,0...

WSTATE is a set of weights for each state. The default is equal weight assigned to every state selected by KSTATE (WSTATE(1)=1.0, 1.0, 1.0, ...)

IROOT specifies which state's energy should be saved for use in numerical gradient evaluation. IROOT counts only for those states included by KSTATE, so KSTATE(1)=0,1,0,1 and IROOT=2 refers to the second root computed (4th overall). Default: IROOT=1.

ISPINA spin adaptation (default=0)
0 means off, 1 means on (strictly), -1 means on (loosely). Proper spin states are picked up automatically so this input is usually skipped. See NSOLUT in this context.

KNOSYM a flag to turn off space symmetry use, i.e. STSYM. .FALSE. will ignore symmetry (default=.TRUE.)

KNOSPN a flag to ignore spin symmetry, i.e. MULT. Give as .FALSE. to ignore the spin (default=.TRUE.)

The next few influence the Davidson CI diagonalization, and are quite similar to $MCQDPT keywords, so the description here is terse.

NSOLUT is the number of roots to be obtained. If there are not enough states of the correct spin found in the first NSOLUT states to satisfy KSTATE/WSTATE, increase this parameter to find enough.

MXITER is the maximum number of Davidson iterations to find the states (default=200)

THRCON is the convergence criterion on the CI coefficient convergence (default= 1.0d-6)

THRENE is a convergence criterion on the total energy of the states. This is ignored if given as a negative number. (default = -1.0d-12 Hartree)

MAXBAS maximum expansion space size in the Davidson diagonalization subspace (default=100)

MDI dimension of the initial guess subspace used to initiate the Davidson iterative CI solver. See NHGSS in $DET for more information (default=300).

4. data to define perturbation theory computation:

KXGMC a flag to choose the 0-th order Hamiltonian used, when more than one state is included by KSTATE and WSTATE. KXGMC has no impact on single state runs. .TRUE. selects Granovsky's XMCQDPT equations for the zero-th order Hamiltonian, see
A.A.Granovsky, J.Chem.Phys. 134, 214113(2011).
.FALSE. selects the original definition of the unperturbed Hamiltonian. The default is .TRUE.

IWGT selects wavefunction analysis (default=1)
0 means off, 1 means on (external), -1 means on (internal orbitals). This will compute the approximate weight of the MCSCF reference CI in the first order wavefunction. It is therefore a very useful diagnostic for the quality of the calculation, as the MCSCF state should be a high percentage. The formula for the decomposition is changed from the original CAS-type MCQDPT (REFWGT in $MCQDPT), see Miyajima, Watanabe, and Nakano's reference cited below.
Select IWGT=0 if the fastest speed is desired.

KFORB flag to request canonicalization (default=.TRUE.) Canonicalization within the core, virtual, and any rotationally invariant active subspaces yields a well defined theoretical model. You would not normally turn this option off.

KROT flag for treating (ij)->(ab) excitations
.TRUE. means treating this type of term by the traditional MCQDPT formulae
.FALSE. uses a MP2-type formula when this type of term arises between two identical determinants, while using zero otherwise. This is thought to be better in terms of size-consistency. (default)
KROT has an impact on run times and on the numerical result. See the paper cited below by

Ebisuzaki, Watanabe, and Nakano for details.

THRWGT threshold weight on the square of CI coefficients, for determinant selection. Any determinants that are excluded from the reference list due to THRWGT are treated in the outer space of the perturbation. Give as a negative number to retain all of the determinants, even those of very little importance, in the reference of the perturbation treatment. The default is 1.0d-8.

KSZDOE flag to use spin (Sz) dependent orbital energies. This variable is ignored for singlet state(s), or if SZ is chosen as 0.
If .TRUE., alpha and beta orbital energies are not the same,

```
Ealp(i) = h(i,i) + sum_kl { Dalp(k,l)[(ii|kl)-(il|ki)]
                           +Dbet(k,l) (ii|kl)}
Ebet(i) = h(i,i) + sum_kl { Dbet(k,l)[(ii|kl)-(il|ki)]
                           +Dalp(k,l) (ii|kl)}
```

If .FALSE. both sets use the energies

```
E(i) = h(i,i) + sum_kl D(k,l)[(ii|kl)-1/2*(il|ki)]
     = [Ealp(i)+Ebet(i)]/2
```

from the total density D(k,l)=Dalp(k,l)+Dbet(k,l)
Default=.TRUE.

THRGEN threshold on generator constants. Default=1.0d-9 Raising lowers accuracy but produces speedups. Lowering to 1.0d-12 should give full accuracy for benchmarking purposes.

THRHDE threshold to ignore |<I|V|nu>/dE|, which is not a very effective screening, and its use is thus not recommended. Default is 1.0 which should not screen anything. Possible values are 0.05-0.10, since many |<I|V|nu>/dE| are around 0.02-0.03.

The next two deal with the so-called "intruder state avoidance". There are theoretical difficulties with either one. THRDE just drops terms, so the potential surface may have small discontinuities. EDSHFT always shifts results a little bit, even if no small denominators (aka intruder states) are actually present. Clearly both are "band-

aids"! Note that the first ISA technique is turned on, by default.

THRDE is a threshold to simply drop out any term whose energy denominator is too small. The default for this is 0.005 Hartree. Change to zero to turn this option off.

EDSHFT is the same as the same keyword in $MCQDPT. The denominators D are changed to D + EDSHFT/D. Turn off THRDE if you select this option. A reasonable value to try is 0.02, the default is 0.0.

5. miscellaneous data

CEXCEN = string defining the units for the excitation energy. Choose from these 4 strings (any case):
eV (default), cm-1, Kcal/mol, KJ/mol

DDTFPT = a flag requesting the distributed data integral transformation be used, if the run is parallel. This option requires MEMDDI in $SYSTEM. If there is not enough memory to allow this, turn this option off to use an alternate parallel transformation (DEFAULT=.TRUE.).

Note: There are additional technical parameters for $GMCPT, documented only in the source code file gmcpt.src.

In case it is desirable for the GMC-QDPT program to reproduce results obtained by the DETMRPT/MCQDPT programs:

a) use a CAS-SCF reference in the MCSCF step
b) select REFTYP=ORMAS here, and enter NSPACE=1, giving only one value for MSTART, MINE, MAXE
c) retain the entire CAS reference in the internal determinant's perturbation space, THRWGT=-1.0
d) select the original external determinant space's perturbation treatment, KROT=.FALSE.
e) use equal alpha/beta orbital energies, KSZDOE=.FALSE.
f) in multi-state mode, select KXGMC off, to reproduce those program's 0-th order reference states
g) ensure ISA is turned off, THRDE= -1.0

h) perhaps adjust numerical parameters to full accuracy, to increase the no. of decimals: THRGEN=1D-12, THRHDE=1D+10.

References for GMC-QDPT:

a) H.Nakano, R.Uchiyama, K.Hirao
J.Comput.Chem. 23, 1166-1175(2002)
b) M.Miyajima, Y.Watanabe, H.Nakano
J.Chem.Phys. 124, 044101/1-9(2006)
c) R.Ebisuzaki, Y.Watanabe, H.Nakano
Chem.Phys.Lett. 442, 164-169(2007)

The first paper introduced the theory, with further developments including reference state weights given in the second. The present computer code is based on the efficient formulation involving ionized intermediate determinants, as described in the third paper.

==========

==========

$PDET group (required if NPDET>0 in $GMCPT)

This group defined the "parent" determinants, which will be excited to excitation level NEXCIT. There must be a total of NPDET determinants given in the group. Each determinant may have spaces at the front or rear, but not embedded within the string. An example, presuming NPDET=3, is

```
 $PDET
    2200
    2+-0
    2-+0
 $END
```

==========

$ADDDET group (optional, if NPDET>0 in $GMCPT)
$REMDET group (optional, if NPDET>0 in $GMCPT)

These two groups add (or remove) determinants from the reference list. The first line in the group tells how many determinants are contained in the group.

```
 $ADDDET/$REMDET
   2
   2002
   +-02
 $END
```

These two determinants would be generated if the $PDET list was used with NEXCIT=2 (or higher), but this $REMDET would remove them from the generated total reference CI.

==========

==========

$SODET group (required if CITYP=FSOCI)

This group controls a full second order CI calculation using determinants (see also the keyword SOCI in $CIDRT). Most of the characteristics of the active space (such as NCORE, NACT, NELS) must be given by $CIDET input, as a preliminary full CI according to $CIDET will be made. The FCI states will then used as the initial guess for the full second order CI. A few additional parameters may be given in this group, but many runs will not need to give any of these.

NEXT = the number of external orbitals to be included.
The default is the entire virtual MO space.

NSOST = the number of states to be found in the SOCI.
The default is copied from NSTATE in $CIDET.

MAXPSO = maximum expansion space size used in the SOCI.
The default is copied from MXXPAN in $CIDET.

ORBS = MOS means use the MCSCF orbitals, which should be allowed to undergo canonicalization (see the CANONC keyword in $MCSCF), or the input $VEC group in case SCFTYP=NONE. (default)
NOS means to instead use the natural orbitals of the MCSCF.

==========

==========

$DRT group (required by MCSCF if CISTEP=GUGA)
$CIDRT group (required if CITYP=GUGA)

This group describes the Configuration State Functions (CSFs) used by the MCSCF or CI calculation. The Distinct Row Table (DRT) is the means by which the Graphical Unitary Group Approach (GUGA) specifies configurations. The group is spelled $DRT for MCSCF runs, and $CIDRT for CI runs. The main difference in these is NMCC versus NFZC.

There is no default for GROUP, and you must choose one of FORS, FOCI, SOCI, or IEXCIT.

GROUP = the name of the point group to be used. This is usually the same as that in $DATA, except for RUNTYP=HESSIAN, when it must be C1. Choose from the following: C1, C2, CI, CS, C2V, C2H, D2, D2H, C4V, D4, D4H. If your $DATA's group is not listed, choose only C1 here.

FORS = flag specifying the Full Optimized Reaction Space set of configuration should be generated. This is usually set true for MCSCF runs, but if it is not, see FORS in $MCSCF. (Default=.FALSE.)

FOCI = flag specifying first order CI. In addition to the FORS configurations, all singly excited CSFs from the FORS reference are included. Default=.FALSE.

SOCI = flag specifying second order CI. In addition to the FORS configurations, all singly and doubly excited configurations from the FORS reference are included. (Default=.FALSE.)

IEXCIT= electron excitation level, for example 2 will lead to a singles and doubles CI. This variable is computed by the program if FORS, FOCI, or SOCI is chosen, otherwise it must be entered.

INTACT= flag to select the interacting space option. See C.F.Bender, H.F.Schaefer J.Chem.Phys. 55, 4798-4803(1971). The CI will include only those

CSFs which have non-vanishing spin couplings with the reference configuration. Note that when the Schaefer group uses this option for high spin ROHF references, they use Guest/Saunders orbital canonicalization.

* * the next variables define the single reference * *

The single configuration reference is defined by filling in the orbitals by each type, in the order shown. The default for each type is 0.

Core orbitals, which are always doubly occupied:
NMCC = number of MCSCF core MOs (in $DRT only).
NFZC = number of CI frozen core MOs (in $CIDRT only).

Internal orbitals, which are partially occupied:
NDOC = number of doubly occupied MOs in the reference.
NAOS = number of alpha occupied MOs in the reference, which are singlet coupled with a corresponding number of NBOS orbitals.
NBOS = number of beta spin singly occupied MOs.
NALP = number of alpha spin singly occupied MOs in the reference, which are coupled high spin.
NVAL = number of empty MOs in the reference.

External orbitals, occupied only in FOCI or SOCI:
NEXT = number of external MOs. If given as -1, this will be set to all remaining orbitals (apart from any frozen virtual orbitals).
NFZV = number of frozen virtual MOs, never occupied.

* * the next two help with state symmetry * *

STSYM= The symmetry of the electronic state. See $DET for possible values: use AP/APP in Cs, not primes. Default is the totally symmetric representation.

note: This option overwrites whatever symmetry is implied by NALP/NAOS/NBOS. It is easier to pick STSYM than to allow its inference from the singly occupied orbitals, which is a relic of ancient input files.

NOIRR= controls labelling of the CI state symmetries.
= 1 no labelling (default)

```
     = 0 usual labelling.  This can be very time consuming
         if the group is non-Abelian.
     =-1 fast labelling, in which all CSFs with small CI
         coefficients are ignored. This can produce weights
         quite different from one, due to ignoring small
         coefficients, but overall seems to work OK.
         Note that it is normal for the weights not to sum
         to 1 even for NOIRR=0 because for simplicity the
         weight determination is focused on the relative
         weights rather than absolute.  However weight do
         not sum to one only for row-mixed MOs.
     = -2,-3... fast labelling and sets SYMTOL=10**NOIRR
         for runs other than TRANSITN.  All irreps with
         weights greater than SYMTOL are considered.

       * * * the final choices are seldom used * * *

MXNINT = Buffer size for sorted integrals. (default=20000)
         Adjust this upwards if the program tells you to,
         which may occur in cases with large numbers of
         external orbitals.

MXNEME = Buffer size for energy matrix.  (default=10000)

NPRT   = Configuration printout control switch.
         This can consume a HUMUNGUS amount of paper!
         0 = no print (default)
         1 = print electron occupancies, one per line.
         2 = print determinants in each CSF.
         3 = print determinants in each CSF (for Ms=S-1).

=========================================================
```

==========

$MCSCF group (for SCFTYP=MCSCF)

This group controls the MCSCF orbital optimization step. The difference between the five convergence methods is outlined in the Further Information chapter, which you should carefully study before trying MCSCF computations.

--- the next chooses the configuration basis ---

CISTEP = ALDET chooses the Ames Lab. determinant full CI, and requires $DET input. (default)
= ORMAS chooses an Occupation Restricted Multiple Active Space determinant CI, requiring both $DET and $ORMAS inputs.
= GUGA chooses the graphical unitary group CSFs, and requires $DRT input. This is the only value usable with the QUAD converger.
= GENCI chooses the Ames Laboratory general CI, and requires $GEN input.
= GMCCI chooses the Kyushu University general CI, and requires $GMCPT input.

--- the next five choose the orbital optimizer ---

FOCAS = a flag to select a method with a first order convergence rate. (default=.FALSE.)
Parallel runs with FOCAS do not use MEMDDI.

SOSCF = a flag selecting an approximately second order convergence method, using an approximate orbital hessian. (default=.TRUE.)
Parallel runs with SOSCF do not use MEMDDI.

FULLNR = a flag selecting a second order method, with an exact orbital hessian. (default=.FALSE.)
Parallel runs with FULLNR require input of MEMDDI.

QUAD = a flag to pick a fully quadratic (orbital and CI coefficient) optimization method, which is applicable to FORS or non-FORS wavefunctions. QUAD may not be used with state-averaging. (default = .FALSE.)
This converger can be used only in serial runs.

```
JACOBI = a flag to pick a program that minimizes the
         MCSCF energy by a sequence of 2x2 Jacobi
         orbital rotations.  This is very systematic in
         forcing convergence, although the number of
         iterations may be high and the time longer
         than the other procedures.  This option does
         not compute the orbital Lagrangian, hence at
         present nuclear gradients may not be computed.
         (default = .FALSE.)
         This converger can be used only in serial runs.

Note that FOCAS must be used only with FORS=.TRUE. in $DRT.
The other convergers are usable for either FORS or non-FORS
wavefunctions, although convergence is always harder in the
latter case, when FORS below must be set .FALSE.


   --- the next apply to all convergence methods ---
Keywords specific to each converger are described below.

ACURCY = the major convergence criterion, the maximum
         permissible asymmetry in the Lagrangian matrix.
         (default=1E-5, but 1E-6 if MPLEVL, CI, or FMO
         is selected.)

ENGTOL = a secondary convergence criterion, the run is
         considered converged when the energy change is
         smaller than this value. (default=1.0E-10)

MAXIT  = Maximum number of iterations (default=100 for
         FOCAS, 60 for SOSCF, 30 for FULLNR or QUAD)

MICIT  = Maximum number of microiterations within a
         single MCSCF iteration. (default=5 for FOCAS
         or SOSCF, or 1 for FULLNR or QUAD)

NWORD  = The maximum memory to be used, the default is
         to use all available memory.  (default=0)

FORS   = a flag to specify that the MCSCF function is of
         the Full Optimized Reaction Space type, which is
         sometimes known as CAS-SCF.  .TRUE. means omit
         active-active rotations from the optimization.
         Since convergence is usually better with these
```

```
          rotations included, the default is sensible:
          for FOCAS: .TRUE.,
          for FULLNR or QUAD: .FALSE. for FULLNR or QUAD,
          and for SOSCF: .TRUE. for ALDET/GUGA
                     but .FALSE. for ORMAS/GENCI)
          It is seldom a good idea to enter this keyword.


   Some keywords that apply after convergence is obtained:

CANONC = a flag to cause formation of the "standard
          Fock operator", used to generate canonical core
          and virtual orbitals.  This may reorder the core
          by orbital energies.  If the active space is also
          canonicalized, the active orbitals may also be
          reordered by energy.  Whenever possible, the
          program will also attempt to canonicalize the
          active orbitals.  (default=.TRUE.)

VVOS   = Valence Virtual Orbital generation, akin to the
          same keyword in $SCF, for MCSCF runs.  The same
          restrictions (no core potentials, atoms H-Xe)
          apply.  (default= .FALSE.)

FINCI  = NONE means skip regeneration of CAS-CI states over
               final converged orbitals.  (default)
       = MOS  use the final MOS, including any final
               canonicalization by CANONC, to regenerate
               the CAS-CI states matching the MOs.
       = NOS  use the final NOS to regenerate the CAS-CI
               states.  Note that CISTEP=ORMAS' natural
               orbital process will mix active subspaces,
               so an ORMAS natural orbital CI will not
               reproduce the MCSCF energies.
This keyword is not implemented for CISTEP=GENCI or GMCCI.

DIABAT = flag controlling construction of diabatic states,
          from the final MCSCF adiabatic states.
          This is presently programmed only for CISTEP=GUGA.
          See the $DIABAT input.   (default is .FALSE.)

EKT    = a flag to cause generation of extended Koopmans'
          theorem orbitals and energies.  (Default=.FALSE.)
    For this option, see R.C.Morrison and G.Liu,
    J.Comput.Chem., 13, 1004-1010 (1992).  Note that
```

```
    the process generates non-orthogonal orbitals, as
    well as physically unrealistic energies for the
    weakly occupied MCSCF orbitals.  The method is
    meant to produce a good value for the first I.P.

NPUNCH = MCSCF punch option (analogous to $SCF NPUNCH)
         0  do not punch out the final orbitals
         1  punch out the occupied orbitals
         2  punch out occupied and virtual orbitals
             The default is NPUNCH = 2.

NPFLG  = an array for debug printing control.  This is
         analogous to the same variable in $CIINP.
         Elements 1,2,3,4,6,8 make sense, the 8th step
         controlling debugging of the orbital optimization.
         In case you want to see normal output from all
         steps during all iterations, set NPFLG(10)=1.
         This may help trace problems that occur only
         after the first iteration.


     --- the next apply to SOSCF optimizations ---

NOFO   = number of FOCAS iterations before switching to the
         SOSCF converger.  May be 0, 1, ... (default=1).
         One FOCAS iteration at the first geometry permits
         a canonicalization of the virtual space to occur,
         which is likely to be crucial for convergence.

MCFMO  = set to 1 to remove redundant orbital Lagrangian
         elements in FMO-MCSCF.  Note that corresponding
         orbital rotations will still be optimised but not
         considered when deciding whether a run converged.
         This option is only in effect if detached bonds
         are present (for which redundant orbitals exist).
         Default: 1.
         (This variable is irrelevant except to FMO runs)

   --- the next three refer to FOCAS optimizations ---

CASDII = threshold to start DIIS (default=0.05)

CASHFT = level shift value (default=1.0)

NRMCAS = renormalization flag, 1 means do Fock matrix
```

```
         renormalization, 0 skips (default=1)

    --- the next applies to the QUAD method ---
 (note that all FULLNR input is also relevant to QUAD)

QUDTHR = threshold on the orbital rotation parameter,
         SQCDF, to switch from the initial FULLNR
         iterations to the fully quadratic method.
         (default = 0.05)

   --- The JACOBI converger accepts FULLNR options ---
      --- NORB, NOROT, MOFRZ, and FCORE as input ---

   --- all remaining input applies only to FULLNR ---
        except that JACOBI obeys four of these!

     Freezing any orbitals (FCORE, MOFRZ, NORB, NOROT)
     is incompatible with gradients, as the orbitals will
     not be fully optimized.  Use frozen orbital options
     only with RUNTYP=ENERGY!

DAMP   = damping factor, this is adjusted by the program
         as necessary.  (default=0.0)

METHOD = DM2 selects a density driven construction of the
         Newton-Raphson matrices.  (default).
       = TEI selects 2e- integral driven NR construction.
         See the 'further information' section for more
         details concerning these methods.  TEI is slow!

LINSER = a flag to activate a method similar to direct
         minimization of SCF.  The method is used if
         the energy rises between iterations.  It may in
         some circumstances increase the chance of
         converging excited states.  (default=.FALSE.)

FCORE  = a flag to freeze optimization of all filled
         orbitals, which is useful in preparation for
         RUNTYP=TRANSITN jobs.  Filled orbitals means not
         only chemical core, but also any inert valence
         orbitals below the active space. Setting FCORE
         automatically forces CANONC false. It may be
         useful to decrease TOLZ and TOLE in $GUESS by two
         orders of magnitude to ensure the filled orbitals
         are unchanged during MOREAD.  (default=.FALSE.)
```

```
MOFRZ  = an array of orbitals to be frozen out of the
         orbital optimization step (default=none frozen).
         This list may contain active orbitals, as well
         as the filled orbitals.
         No more than 15 orbitals may be frozen.
         You probably want to toggle CANONC off too!

   --- the last few FULLNR options are seldom used ---

NORB   = the number of orbitals to be included in the
         optimization. The default is to optimize with
         respect to the entire basis.  Give NORB as two
         smaller than the number of MOs if you want to
         freeze out the top two virtual orbitals.
         (default=all orbitals present in the run).

NOROT  = an array of up to 250 orbital rotation pairs
         to be omitted from the optimization process.
         The program automatically deletes all core-core
         rotations, all act-act rotations if FORS=.TRUE.,
         and all core-act and core-virt rotations if
         FCORE=.TRUE.  Additional rotations are input as
         I1,J1,I2,J2... to exclude rotations between
         orbital I running from 1 to NORB, and J running
         up to the smaller of I or NVAL in $TRANS.

DROPC  = a flag to include MCC core orbitals during the
         CI computation.  The default is to drop them
         during the CI, instead forming Fock operators
         which are used to build the correct terms in
         the orbital hessian. (default = .TRUE.)

=============================================================
```

==========

$MRMP group (relevant if SCFTYP=MCSCF, MPLEVL=2)

This group allows you to specify which second order multi-reference perturbation theory program is executed. See REFS.DOC for more details about multireference PT.

Results from these programs should never be referred to as "CASPT2". That method is similar in spirit, but is a different set of equations, whose numerical results will not be identical to those used for MRMP/MCQDPT. When the reference wavefunction is CAS-SCF, the perturbation energies from either DETMRPT or MCQDPT programs should be called MRMP when applied to a single state, and MCQDPT when applied to more than one state. GMCPT is a different method, also not "CASPT2".

Diabatic state generation is permitted only through the CSF-based CAS-reference perturbation program (MCQDPT).

MRPT = DETMRPT requests a determinant program.
The MCSCF may use CISTEP=ALDET, using a CAS-SCF reference, in which case the run produces results equivalent to MCQDPT.
The MCSCF may also use CISTEP=ORMAS to use more general references.
In either case, the reference must be given by $DET (and possibly $ORMAS) inputs.
See $DETPT for perturbation specific input.
(default for most runs)

= MCQDPT requests a CSF (GUGA based) program. Its advantages compared to DETMRPT are that it can do spin-orbit MRPT, and find the weight of the MCQDPT zeroth order state.
CISTEP can be ALDET or GUGA, your choice.
See $MCQDPT for related input.
(default for RUNTYP=TRANSITN)
(default for DIABAT=.TRUE. in $MCSCF)

= GMCPT requests a determinant based program that can use non-CAS type reference functions, including ORMAS or user defined lists.

See $GMCPT for related input and more info.

Both the DETMRPT and MCQDPT programs produce numerically identical results, if you select a tight value of THRGEN=1D-12 for the latter program (in some cases you may also need to tighten their CI convergence criteria). Eight or more decimal place energy agreement between the two codes has been observed, when being careful about these cutoffs. This is true whether the codes are running in single state mode, which the literature calls MRMP, or in multi-state mode, which the literature calls MCQDPT.

Generally speaking, the determinant code uses direct CI technology to avoid disk I/O, and is much faster when used with larger active spaces (particularly above 12 active orbitals). The determinant code uses essentially no disk space beyond that required by the MCSCF itself. The determinant code uses native integral transformation codes, including the distributed memory parallel transformation. However, the determinant code is perhaps a bit slower when there is a small active space and very many filled valence orbitals included in the PT. Both codes exploit distributed memory parallelization (MEMDDI).

The determinant program lacks complete control of orbital canonicalization. Be careful to read in only canonicalized core, active, and virtual MOs if you pick RDVECS=.TRUE. with this program.

RDVECS = a flag controlling whether the orbitals should be MCSCF optimized in this run. A value of .TRUE. means that your converged MCSCF orbitals are being given in $VEC, and the program will branch to the perturbation treatement. (default=.FALSE.)

notes:
If you select RDVECS, and are not doing spin-orbit coupling with the CSF program, $GUESS method GUESS=MOREAD is used to process the orbitals. Its options such as NORB and PURIFY will apply to reading the $VEC input, and as always, MOREAD in $GUESS will orthogonalize.
If you are using the CSF program for spin-orbit coupling, $GUESS is ignored, and the $VEC or $VECn group must contain all virtuals. The orbitals will not be reorthogonalized unless you select the MODVEC option.

```
In either case, if your orbitals are not orthogonal, you
are better off repeating MCSCF with RDVECS=.FALSE.!

MODVEC = 0 skip orthogonalization (default)
       = 1 do orthogonalization in the SO-MCQDPT program.

================================================================
```

==========

$DETPT group (relevant if SCFTYP=MCSCF and MPLEVL=2)

This input group applies to the determinant-based multi-reference perturbation theory program, if chosen by MRPT=DETMRPT in $MRMP.

When applied to only one state, the theory is known as multi-reference Moller-Plesset (MRMP), but the term MCQDPT is used when this theory is used in its multi-state form. Please note that this perturbation theory is not the same thing as the CASPT2 theory, and should -NEVER- be called that. A more complete discussion may be found in the 'Further Information' chapter.

NVAL = number of filled valence orbitals in the MCSCF to be included in the dynamic correlation treatment. This is analogous to NMODOC in the $MCQDPT input. The number of frozen cores orbitals is found by subtracting NVAL from NCORE in $DET, so that you need not specify the chemical core's size. Also, there is no input for specifying the active space, which is inherited from $DET. The default for NVAL correlates valence orbitals, but freezes any chemical cores.

NEXT = number of external orbitals to use. The default means to use all of them (default=-1).

NOS = a flag to use MCSCF natural orbitals rather than canonicalized orbitals as the basis of the PT. This changes the numerical results!!!

Omitting NPTST, IPTST, and WPTST is the simplest option, meaning that any state with a non-zero WSTATE in $DET is included in the pertubation. Canonicalization of the orbitals is normally done by the MCSCF program, see CANONC in $MCSCF. However, if not, or if the state weights are changed, the canonicalization is done in the perturbation code, according to CANON in this group. The default is the most computationally efficient.

CANON = flag to request canonicalization. Default=.TRUE.

```
          Turning off canonicalization is for experimental
          purposes, so most runs should not avoid it.  The
          canonicalization will be done in the perturbation
          code under three circumstances,
              RDVECS=.TRUE. was used, at the first geometry,
              the MCSCF step skipped canonicalization, or
              you enter NPTST/IPTST/SPTST information.
          Canonicalization uses the state averaged density
          matrix to build the "standard Fock operator", and
          involves diagonalizing its diagonal sub-blocks.

NPTST  = the number of states to include in generation of
         the unperturbed CAS states.  If NPTST is chosen,
         spins of the states will be ignored, like using
         PURES=.F. in $DET, so you must be careful in your
         matching IPTST input.

IPTST  = an array of CAS-CI states to be included in the
         perturbation theory, give NPTST values.

WPTST  = an array of state weights.  Like NPTST/IPTST, the
         default for WPTST is derived from WSTATE in $DET.

example: NPTST=3 IPTST(1)=1,3,5 might be used to include
three singlets, S0,S1,S2 in a MCQDPT-type treatment, but
skip over T1 and T2.  You will have done an earlier CI or
MCSCF run, in order to know that you need NPTST five or
higher to capture the lowest three singlets, and that these
singlets appear where they do.  NSTATE in $DET must be at
least 5 in this example, to find enough roots.

EDSHFT  is the same as the same keyword in $MCQDPT.  The
        denominators D are changed to D + EDSHFT/D.
        Reasonable values are 0.02 to 1D-4, if you need
        any shift at all.  The default is 0.0.

=============================================================
```

==========

$MCQDPT group (relevant if SCFTYP=MCSCF and MPLEVL=2)

Controls 2nd order MCQDPT (multiconfiguration quasi-degenerate perturbation theory) runs, if requested by MPLEVL=2 in $CONTRL. MCQDPT2 is implemented only for FORS (aka CASSCF) wavefunctions. The MCQDPT method is a multistate, as well as multireference perturbation theory. The implementation is a separate program, interfaced to GAMESS, with its own procedures for determination of the canonical MOs, CSF generation, integral transformation, CI in the reference CAS, etc. Therefore some of the input in this group repeats data given elsewhere, particularly for $DET/$DRT.

Analytic gradients are not available. Spin-orbit coupling may be treated as a perturbation, included at the same time as the energy perturbation. If spin-orbit calculations are performed, the input groups for each multiplicity are named $MCQD1, $MCQD2, ... rather than $MCQDPT. Parallel calculation is enabled.

When applied to only one state, the theory is known as multi-reference Moller-Plesset (MRMP), but the term MCQDPT is used when this theory is used in its multi-state form. Please note that this perturbation theory is not the same thing as the CASPT2 theory, and should -NEVER- be called that. A more complete discussion may be found in the 'Further Information' chapter.

Most values will inherit sensible defaults for the state symmetry and the orbital space counts from the $DET or $DRT input defining the MCSCF: however for multi-state runs, the user probably has to supply the desired state and weighting information.

In case of diabatic state generation at the MCQDPT level, the settings for state selection and weights will be inherited from the $DIABAT input, to be the same as used for the Diabatic MO generation. Thus diabatization runs will probably not give any input here, although they might override NMOFZC/NMODOC defaults.

*** MCSCF reference wavefunction ***

```
NEL    =   total number of electrons, including core.
           (default from $DATA and ICHARG in $CONTRL)

MULT   =   spin multiplicity (default from $CONTRL)

NMOACT =   Number of orbitals in FORS active space
           (default is the active space in $DET or $DRT)
NMOFZC =   number of frozen core orbitals, NOT correlated
           in the perturbation calculation.  (default is
           number of chemical cores)
NMODOC =   number of orbitals which are doubly occupied in
           every MCSCF configuration, that is, not active
           orbitals, which are to be included in the
           perturbation calculation.  (The default is all
           valence orbitals between the chemical core and
           the active space)
NMOFZV =   number of frozen virtuals, NOT occupied during
           the perturbation calculation.  The default is
           to use all virtuals in the MP2.  (default=0)

If the input file does not provide a $DET or $DRT, the user
must give NMOFZC, NMODOC, and NMOACT correctly here.

STSYM = The symmetry of the target electronic state(s).
        See $DET for possible values: use AP/APP in Cs, not
        primes.  This must be given, and need not match the
        state symmetry used in optimizing the orbitals by
        $DET or $DRT, although it often does.
        Default is the totally symmetric representation.

NOSYM  = 0 use CSF symmetry (see the STSYM keyword).
           off diagonal perturbations vanish if states are
           of different symmetry, so the most efficient
           computation is a separate run for every space
           symmetry. (default)
         1 turn off CSF state symmetry so that all states
           are treated at once.  STSYM is ignored.
           Presently this option does not seem to work!!
        -1 Symmetry purify the orbitals.  Since $GUESS is
           not read by MCQDPT runs, this option can be used
           as a substitute for its PURIFY.  After cleaning
           the orbitals, they are reorthogonalised within
           each irrep and within each group (core, double,
           active, virtual) separately.  Since this occurs
```

without MCSCF optimization if you have chosen to use RDVECS in $MRMP, it is *your* responsibility to ensure that any purification of the orbitals is small enough that the CAS energies for the original CASSCF and the CAS-CI performed during the MCQDPT are the same!

*** perturbation specification ***

KSTATE= state is used (1) or not (0) in the MCQDPT2. Maximum of 20 elements, including zeros. For example, if you want the perturbation correction to the second and the fourth roots,
KSTATE(1)=0,1,0,1
See also WSTATE.
(normal default=1,0,0,0,0,0,0,...)
(default for DIABAT=.TRUE. will be from $DIABAT)

XZERO a flag to choose the 0-th order Hamiltonian used, when more than one state is included by KSTATE and WSTATE. XZERO has no impact on single state runs. .TRUE. selects Granovsky's XMCQDPT equations for the zero-th order Hamiltonian, see
A.A.Granovsky, J.Chem.Phys. 134, 214113(2011).
.FALSE. selects the original definition of the unperturbed Hamiltonian. The default is .FALSE.

*** Intruder State Removal ***

EDSHFT = energy denominator shifts. (default=0.0,0.0) See also REFWGT.

Intruder State Avoidance (ISA) calculations can be made by changing the energy denominators around poles (where the denominator is zero). Each denominator x is replaced by x + EDSHFT/x, so that far from the poles (when x is large) the effect of such change is small. EDSHFT is an array of two values, the first is used in spin-free MCQDPT, and the second is for spin-orbit MCQDPT. Both values are used if RUNTYP=TRNSTN, only the first is used otherwise. A suggested pair of values is 0.02,0.1, but experimentation with your system is recommended. Setting these values to zero is ordinary MCQDPT, whereas infinite collapses to the MCSCF reference.

Note that the energy denominators (which are ket-dependent in MCQDPT) are changed in a different way for each ket-vector, that is, for each row in MCQDPT Hamiltonian matrix. In other words, the zeroth order energies are not "universal", but state specific. This is strictly speaking an inconsistency in defining zeroth order energies that are usually chosen "universally".

In order to maintain continuity when studying a PES, one usually uses the same EDSHFT values for all points on PES. In order to study the potential surface for any extended range of geometries, it is recommended to use ISA, as it is quite likely that one or more regions of the PES will be unphysical due to intruder states.

For an example of how intruder states can appear at some points on the PES, see Figures 1,2,7 of
K.R.Glaesemann, M.S.Gordon, H.Nakano
Phys.Chem.Chem.Phys. 1, 967-975(1999)
and also
H.A.Witek, D.G.Fedorov, K.Hirao, A.Viel, P.-O.Widmark
J.Chem.Phys. 116, 8396-406(2002)
For a discussion of intruder state removal from MCQDPT, see
H.A.Witek, Y.-K.Choe, J.P.Finley, K.Hirao
J.Comput.Chem. 23, 957-965(2002)

REFWGT = a flag to request decomposition of the second order energy into internal, semi-internal, and external contributions, and to obtain the weight of the MCSCF reference in the 1st order wave function. This option significantly increases the run time! When you run in parallel, only the transformation steps will speed up, as the PT part of the reference weight calculation has not been adapted for speedups (default=.FALSE.)

The EDSHFT option does not apply if REFWGT is used. One purpose of using REFWGT is to try to understand the nature of the intruder states.

*** Canonical Fock orbitals ***

IFORB = 0 skip canonicalization (default when DIABAT=.TRUE.).
= 1 determine the canonical Fock orbitals.

(the usual default)
= 3 canonicalise the Fock orbitals averaged over all $MCQDx input groups.

IFORB=3 option pertains only to RUNTYP=TRANSITN. It is primarily meant to include spin-orbit coupling perturbation into the energy perturbation, but could also be used in conjunction with OPERAT=DM to calculate only the second order energy perturbation. IFORB=3 means that WSTATE is used as follows: In each $MCQDx group, the WSTATE weights are divided by the total number of states (sum(i) IROOTS(i)), so the sum over all WSTATE values in all $MCQDx groups is normalized to sum to 1. Thus there is no normalization to 1 within each $MCQDx group.
This option might be used to speed up an atomic MCQDPT, e.g. if computing the 3-P ground state of carbon, one would want to average over all three spatial components of the P term, to be sure of spatial degeneracy, but then run the perturbation using symmetry, separately on the B1g+B2g+B3g subspecies (within D2h) of a P term. It is very important to give weights appropriate for the symmetry, the input requires care.

WSTATE = weight of each CAS-CI state in computing the closed shell Fock matrix. You must enter 0.0 whenever the same element in KSTATE is 0.
In most cases setting the WSTATEs for states to be included in the MCQDPT to equal weights is the best, and this is the default.
Runs with DIABAT=.TRUE. default to the same weights used during the DMO generation step.

*** Miscellaneous options ***

ISELCT is an option to select only the important CSFs for inclusion into the CAS-CI reference states. Set to 1 to select, or 0 to avoid selection of CSFs (default = 0)
All CSFs in a preliminary complete active space CI whose CI coefficients exceed the square root of THRWGT are kept in a smaller CI to determine the zero-th order states. Note that the CSFs with smaller coefficients, while excluded from the reference states, are still used during the

perturbation calculation, so most of their energy contribution is still retained. This can save appreciable computer time in cases with large active spaces.

THRWGT = weight threshold for retaining CSFs in selected configuration runs. In quantum mechanics, the weight of a CSF is the square of its CI coefficient. (default=1d-6)

THRGEN = threshold for one-, two-, and three-body density matrix elements in the perturbation calculation. The default gives about 5 decimal place accuracy in energies. Increase to 1.0D-12 if you wish to obtain higher accuracy, for example, in numerical gradients (default=1D-8). Tightening THRGRN and perhaps CI diagonalization should allow 7-8 decimal place agreement with the determinant code.

THRENE = threshold for the energy convergence in the Davidson's method CAS-CI. (default=-1.0D+00)

THRCON = threshold for the vector convergence in the Davidson's method CAS-CI. (default=1.0D-06)

MDI = dimension of small Hamiltonian diagonalized to prepare initial guess CI states. (default=50)

MXBASE = maximum number of expansion vectors in the Davidson diagonalization subspace (e.g. MXXPAN). (default=50)

NSOLUT = number of states to be solved for in the Davidson's method, this might need to exceed the number of states in the perturbation treatment in order to "capture" the correct roots.

NSTOP = maximum number of iterations to permit in the Davidson's diagonalization.

LPOUT = print option, 0 gives normal printout, while <0 gives debug print (e.g. -1, -5, -10, -100) In particular, LPOUT=-1 gives more detailed

```
           timing information.  (default=0)

The next three parameters refer to parallel execution:

DOORD0 =   a flag to select reordering of AO integrals
           which speeds the integral transformations.
           This reduces disk writes, but increases disk
           reads, so you can try turning it off if your
           machine has slow writes.  (default=.TRUE.)

PARAIO =   access 2e- integral file on every node, at
           the same time.  This affects only runs with
           DOORD0 true, and it may be useful to turn
           this off in the case of SMP nodes sharing
           a common disk drive.  (default=.TRUE.)

DELSCR =   a flag to delete file 56 containing half-
           transformed integrals after it has been
           used.  This reduces total disk requirements
           if this file is big.  (default=.FALSE.)

Note that parallel execution will be more effective if you
use distributed memory, MEMDDI in $SYSTEM.  Using
AOINTS=DIST in $TRANS is likely to be helpful in situations
with relatively poor I/O rates compared to communication,
e.g. SMP enclosures forced to share a single scratch disk
system.  See PROG.DOC for more information on parallel
execution.

Finally, there are additional very specialized options,
described in the source code routine MQREAD: IROT, LENGTH,
MAXCSF, MAXERI, MAXROW, MXTRFR, THRERI, MAINCS, NSTATE

=============================================================
```

==========

$EXCORR group (compatible with CITYP=ORMAS)

This group prepares input data used to run the universal perturbative explicitly correlated basis set completeness correction (PT2R12). This sequence starts with a GAMESS multireference CI calculation, using ORMAS, and then passes information (basis set, orbitals, density matrix) to the Massively Parallel Quantum Chemistry (MPQC) program. The latter program's calculation uses R-12 methods to minimize basis set incompleteness errors.

PT2R12 = PT2R12 basis set incompleteness correction.
Selecting this flag generates ASCII data files that serve as MPQC's input.
(DEFAULT = .false.)

NFRZC = number of frozen core orbitals in the PT2R12 basis set incompleteness correction.
(DEFAULT = NCORE from $CIDET)

NINACT = number of inactive orbitals in the PT2R12 basis set incompleteness correction. (DEFAULT = 0)

NCORR = number of orbitals to be explicitly correlated.
(DEFAULT = NINACT + NACT from $EXCORR)

NFRZV = number of frozen valence orbitals in the PT2R12 basis set incompleteness correction.
(DEFAULT = 0)

PUNTOL = printing tolerance for the second order reduced density matrix (DEFAULT = 1.00E-11)

The following are used specifically for the MPQC interface to GAMESS.

DFBS = use density fitting for integral evaluation
Note: recomputed reference energy will be slightly different. (DEFAULT = .false.)

```
RUNR12  = compute [2]_R12 correction with MPQC interface.
          (DEFAULT = .false.)

SINGLS  = compute [2]_S correction with MPQC interface.
          (DEFAULT = .false.)

F12EXP  = f12 exponent. (default=1.0D+00)

NTHRDS  = number of threads that are spawned during the
          [2]_R12 and/or [2]_S computation. (DEFAULT = 1)

=============================================================
```

==========

$CASCI group (relevant to SCFTYP=RHF MPLEVL=2)

This group carries out the Improved Virtual Orbital - Complete Active Space CI method of Freed, Chaudhuri, and co-workers. IVO-CASCI starts with a RHF reference, and then generates IVOs, which are used in a CI computation within an active space chosen by the user. The input consists of this group, a $MCQDPT, and perhaps a $IVOORB input, along with SCFTYP=RHF and MPLEVL=2. MULT in $CONTRL applies to the SCF reference, while MULT in $MCQDPT selects the spin of the IVO-CASCI state(s). Doublets are treated by using a cation RHF reference.

IVOCAS = a flag to turn on IVO-CASCI computation. This is usually the only input required (default=.FALSE.)

MOLIST = a flag to request complete control over the active space specification. The default uses the parameters in $MCQDPT to select from the IVOs with the lowest energy. (default=.FALSE.)

DEGENR = a flag to indicate the HOMO is degenerate. The program should set this for you.

PRINT = a flag to print debugging info (default=.FALSE.)

The user should request IFORB=0 in $MCQDPT to suppress its generation of canonical orbitals, so that the IVOs are used. A Huckel guess is usually fine. The $MCQDPT should define the active orbitals taken from the IVO set by giving NMOFZC, NMODOC, and NMOACT, and the electronic state is specified by that group's MULT, NSTATE, and NSTSYM.

References:

D.M.Potts, C.M.Taylor, R.K.Chaudhuri, K.F.Freed
J.Chem.Phys. 114, 2592-2600(2001)
R.K.Chaudhuri, K.F.Freed, S.A.Abrash, D.M.Potts
J.Mol.Spectrosc. 547, 83-96(2001)
R.K.Chaudhuri, K.F.Freed
J.Chem.Phys. 126, 114103/1-6(2007)

A simple example follows,

```
 $contrl scftyp=rhf mplevl=2 runtyp=energy ispher=1 $end
 $casci  IVOCAS=.true. $end
 $mcqdpt mult=3 stsym=b1 nstate=1 iforb=0
         nel=8 nmofzc=1 nmodoc=2 nmoact=2 $end
 $basis  gbasis=ccd $end
 $guess  guess=huckel $end
 $data
Methylene...3-B-1 state...RHF/cc-pVDZ
Cnv  2

C   6.0   0.0  .0000000000  .0289123030
H   1.0   0.0  .9813851814  .4758735367
 $end
```

The result for the 1st order energy will be -38.9156231594, which is a full CI within a two orbital space, generated by the IVO process, rather than a more expensive MCSCF run.

==========

$IVOORB group (relevant if MOLIST=.T. in $CASCI)

In case the IVOs are not generated in the desired order, this group can fully specify the orbital counts in each irreducible representation.

line 1: NIRREP - gives the total number of irreps

line 2: NDIM, NCORE, NDOC, NUNOCC, NSING - for this irrep, gives its total dimension, the number of core MOs in the CASCI, and 3 parameters which define the active orbitals: filled, empty, and singly occupied (0,1 only) in the reference. Repeat NIRREP times. A 6 active e- example is

```
 $IVOORB
2
59 4 2 2 0
26 0 1 1 0
 $END
```

==========

The input groups $CISORT, $GUGEM, $GUGDIA, $GUGDM, $GUGDM2, $LAGRAN, and $TRFDM2 pertain only to GUGA CI, chosen by either $CONTRL's CITYP=GUGA or $MCSCF's CISTEP=GUGA. Equivalent values (using the same keywords) may be given for determinant runs in $DET or $CIDET input groups.

==========

$CISORT group (relevant for GUGA -CI- or -MCSCF-)

This group provides further control over the sorting of the transformed molecular integrals into the order the GUGA program requires.

NDAR = Number of direct access records.
(default = 2000)

LDAR = Length of direct access record (site dependent)

NBOXMX = Maximum number of boxes in the sort.
(default = 200)

NWORD = Number of words of fast memory to use in this step. A value of 0 results in automatic use of all available memory. (default = 0)

NOMEM = 0 (set to one to force out of memory algorithm)

==========

$GUGEM group (relevant for GUGA -CI- or -MCSCF-)

This group provides further control over the calculation of the energy (Hamiltonian) matrix.

CUTOFF = Cutoff criterion for the energy matrix.
(default=1.0E-8)

NWORD = not used.

==========

==========

$GUGDIA group (relevant for GUGA -CI- or -MCSCF-)

This group provides control over the Davidson method diagonalization step.

NSTATE = Number of CI states to be found, including the ground state. (default=1, ground state only.) You can solve for any number of states, but only 100 can be saved for subsequent sections, such as state averaging. See IROOT in $GUGDM/$GUGDM2.

PRTTOL = Printout tolerance for CI coefficients (default = 0.05)

MXXPAN = Maximum no. of expansion basis vectors used before the expansion basis is truncated. (default=30)

ITERMX = Maximum number of iterations (default=50)

CVGTOL = Convergence criterion for Davidson eigenvector routine. This value is proportional to the accuracy of the coefficients of the eigenvector(s) found. The energy accuracy is proportional to its square. (default=1.0d-5, but 1E-6 if gradients, MPLEVL, CITYP, or FMO selected).

NWORD = Number of words of fast memory to use in this step. A value of zero results in the use of all available memory. (default = 0)

MAXHAM = specifies dimension of Hamiltonian to try to store in memory. The default is to use all remaining memory to store this matrix in memory, if it fits, to reduce disk I/O to a minimum.

MAXDIA = maximum dimension of Hamiltonian to send to an incore diagonalization. If the number of CSFs is bigger than MAXDIA, an iterative Davidson procedure is invoked. Default=100

NIMPRV = Maximum no. of eigenvectors to be improved every iteration. (default = nstate)

```
NSELCT = Determines initial guess to eigenvectors.
         = 0 ->  Unit vectors corresponding to the NSTATE
                 lowest diagonal elements and any diagonal
                 elements within SELTHR of them. (default)
         < 0 ->  First abs(NSELCT) unit vectors.
         > 0 ->  use NSELCT unit vectors corresponding to
                  the NSELCT lowest diagonal elements.

SELTHR = Guess selection threshold when NSELCT=0.
         (default=0.01)

NEXTRA = Number of extra expansion basis vectors to be
         included on the first iteration.  NEXTRA is
         decremented by one each iteration.  This may be
         useful in "capturing" vectors for higher states.
         (default=5)
         On AXP processors, enter as 0 to avoid core dumps.

KPRINT = Print flag bit vector used when
         NPFLG(4)=1 in $CIINP.       (default=8)
         value  1 bit 0 print final eigenvalues
         value  2 bit 1 print final tolerances
         value  4 bit 2 print eigenvalues and tolerances
                        at each truncation
         value  8 bit 3 print eigenvalues every iteration
         value 16 bit 4 print tolerances every iteration

Inputs for a multireference Davidson correction, in case
the orbitals are from a MCSCF.

NREF   = number of CSFs in the MCSCF (full CI) job.

EREF   = the energy of the MCSCF reference.

=========================================================
```

==========

$GUGDM group (relevant for GUGA -CI-)

This group provides further control over formation of the one electron density matrix. See NSTATE in $GUGDIA.

NFLGDM = Array controlling each state's density formation.
0 -> do not form density for this state.
1 -> form density and natural orbitals for this state, print and punch occ.nums. and NOs.
2 -> same as 1, plus print density over MOs.
The default is NFLGDM(1)=1,0,0,...,0 meaning only ground state NOs are generated.
Note that forming the 1-particle density for a state is negligible compared to diagonalization time for that state.

IROOT = The root whose density matrix is saved on desk for later computation of properties. You may save only one state's density per run. By default, this is the ground state (default=1).

WSTATE = An array of up to 100 weights to be given to the 1 body density of each state. The averaged density will be used for property computations, as well as "state averaged natural orbitals". The default is to use NFLGDM/IROOT, unless WSTATE is given, when NFLGDM/IROOT are ignored.
It is not physically reasonable to average over any CI states that are not degenerate, but it may be useful to use WSTATE to produce a totally symmetric density when the states are degenerate.

IBLOCK = Density blocking switch. If nonzero, the off diagonal block of the density above row IBLOCK will be set to zero before the (now approximate) natural orbitals are found. One use for this is to keep the internal and external orbitals in a FOCI or SOCI calculation from mixing, where IBLOCK is the highest internal orbital. (default=0)

NWORD = Number of words of memory to use. Zero means use all available memory (default=0).

==========

==========

$GUGDM2 group (relevant for GUGA -CI- or -MCSCF-)

This group provides control over formation of the 2-particle density matrix.

WSTATE = An array of up to 100 weights to be given to the 2 body density of each state in forming the DM2. The default is to optimize a pure ground state. (Default=1.0,99*0.0)
A small amount of the ground state can help the convergence of excited states greatly.
Gradient runs are possible only with pure states.

IROOT = the MCSCF state whose energy will be used as the desired value. The default means to use the average (according to WSTATE) of all states as the FINAL energy, which of course is not a physically meaningful quantity. This is mostly useful for the numerical gradient of a specific state obtained with state averaged orbitals. (default=0).

Be sure to set NSTATE in $GUGDIA appropriately!

CUTOFF = Cutoff criterion for the 2nd-order density. (default = 1.0E-9)

NWORD = Number of words of fast memory to use in sorting the DM2. The default uses all available memory. (default=0).

NOMEM = 0 uses in memory sort, if possible.
= 1 forces out of memory sort.

NDAR = Number of direct access records. (default=4000)

LDAR = Length of direct access record (site dependent)

NBOXMX = Maximum no. of boxes in the sort. (default=200)

==========

==========

$LAGRAN group (relevant for GUGA -CI- gradient)

This group provides further control over formation of the CI Lagrangian, a quantity which is necessary for the computation of CI gradients.

```
 NOMEM =   0 form in core, if possible
       =   1 forces out of core formation

 NWORD =   0 (0=use all available memory)

 NDAR  = 4000

 LDAR  = Length of each direct access record
         (default is NINTMX from $INTGRL)
```

==========

==========

$TRFDM2 group (relevant for GUGA -CI- gradient)

This group provides further control over the back transformation of the 2 body density to the AO basis.

```
 NOMEM =   0 transform and sort in core, if possible
       =   1 transform in core, sort out of core, if poss.
       =   2 transform out of core, sort out of core

 NWORD =   0 (0=use all available memory)

 CUTOFF= 1.0D-9, threshold for saving DM2 values

 NDAR  = 2000

 LDAR  = Length of each direct access record
         (default is system dependent)

 NBOXMX= 200
```

==========

Usually neither $LAGRAN nor $TRFDM2 are given. Since these groups are normally used only for CI gradient runs, we list here the restrictions on GUGA CI gradients:

a) SCFTYP=RHF, only
b) no FZV orbitals in $CIDRT, all MOs must be used.
c) the derivative integrals are computed in the 2nd derivative code, which is limited to spd basis sets.
d) the code does not run in parallel.
e) Use WSTATE in $GUGDM2 to specify the state whose gradient is to be found. Use IROOT in $GUGDM to specify the state whose other properties will be found. These must be the same state!
f) excited states often have different symmetry than the ground state, so think about GROUP in $CIDRT.
g) the gradient can probably be found for any CI for which you have sufficient disk to do the CI itself. Time is probably about 2/3 additional.

See also $CISGRD for CI singles gradient

==========

$DIABAT group (relevant if DIABAT=.TRUE. in $MCSCF)

This group controls creation of diabatic states from adiabatic states using complete active space-type MCSCF wavefunctions. Diabatization is performed at a single geometry, during RUNTYP=ENERGY, if DIABAT=.TRUE. in $MCSCF. Diabatization is presently programmed only for CISTEP=GUGA, and may be performed at either the the CASSCF level or at the MCQDPT level.

Diabatization creates first the Diabatic Molecular Orbitals (DMOs), and then the diabatic states by rotation of the adiabatic CI states obtained with the DMOs. DMOs are a set of active orbitals evolving smoothly from a reference geometry (where the adiabatic states are cleanly separated, i.e. already diabatic in nature), through a region where several states might come close, or even undergo avoided crossings, and beyond to another region where adiabatic states are once again cleanly separable. Only one side is considered the reference geometry for DMO generation. The dominant CSFs in the diabatic reference states are taken from the adiabatic states at this reference geometry, possibly informed by user knowledge about the dominant CSFs at the other side of the crossing region.

If MPLEVL=2 is specified, the diabatization program will also produce diabatic states at the MCQDPT level, utilizing the CAS-level DMOs during the MCQDPT diabatization. This is a simpler procedure than was used prior to 2013. Note that $MCQDPT input need not be given, as DIABAT=.TRUE. will force the selection of the CSF-based MCQDPT program, and will pass orbital counts and state weights from this input group to the MCQDPT.

The method is described in:
H.Nakamura, D.G.Truhlar J.Chem.Phys. 115, 10353-10372(2001)
H.Nakamura, D.G.Truhlar J.Chem.Phys. 117, 5576-5593(2002)
H.Nakamura, D.G.Truhlar J.Chem.Phys. 118, 6816-6829(2003)
Z.H.Li, R.Valero, D.G.Truhlar
Theoret.Chem.Acc. 118, 9-24(2007)
K.R.Yang, X.Xu, D.G.Truhlar
Chem.Phys.Lett. 573, 84-89(2013)

REFMOS = a flag controlling reading of "order reference
orbitals" at a reference geometry, from $DFMVEC.
These are often obtained by the 3-fold way, or
perhaps the 4-fold way at a nearby geometry.
Default is .FALSE.
If not set, this run will use the 3-fold way to
prepare DMOs, and will also punch the DMOs for
possible use as the $DFMVEC for other geometries.
If set, this run will use the order reference
orbitals to help align the active orbitals of the
run to their order at the reference geometry.
This is normally a good idea!

REFGRP = a flag controlling reading of groups of CSFs
expected to dominate different diabatic states.
Default is .FALSE.
If not set, for a run at some chosen reference
geometry, the dominant groups are prepared and
punched as a $REFCSF group. See also SLCTTH,
which sets the threshold for "dominant".
If set, diabatization will be performed, using the
dominant CSF group information read from $REFCSF.

Note: real diabatization runs must set REFGRP=.TRUE. but in some cases diabatization might have no ambiguity in orbital ordering, so REFMOS might be .TRUE. or .FALSE.

SLCTTH = selection threshold for dominant configurations,
when REFGRP=.FALSE. Also used as a printing
threshold in adiabatic and diabatic states.
Default is 0.20; it pertains to CI coefficients.

* * * Keywords related to state selection * * *

The defaults are quite reasonable, so most runs might omit all of these! Let NWEIGHT be the number of states up to and including the highest weighted state in the MCSCF orbital optimization (according to WSTATE in $GUGDM2). NWEIGHT includes any states with zero weight below the highest weighted one. The defaults use NWEIGHT states during the DMO generation, all with equal weight in the DMO generation, and then diabatize NWEIGHT states.

```
NGRST  = number of low lying states to be excluded from the
         final diabatization.  Default = 0.

NDIAST = number of states above the first NGRST which are
         included in the final diabatization.
         Default = NWEIGHT - NGRST.

NEXST  = number of excited states above the states being
         dealt with.  One might set NSTATE in $GUGDIA
         fairly high, to monitor the position of states to
         ensure they don't come close in energy to the
         interesting states, which stop at NWEIGHT.
         Such extra states are ignored during generation of
         DMOs and during diabatization.
         Default = NSTATE - NGRST - NDIAST.

WBLOCK = array of three (3) weights for the GR/DIA/EX
         blocks of states, used during DMO generation.
         The default is to give all NGRST and NDIAST states
         equal weight in the DMO process, with no weight
         for the NEXST states, namely
           NGRST/(NGRST+NDIAST), NDIAST/(NGRST+NDIAST), 0.0
```

Suppose the system of interest has one state lying at very low energy, two excited states of interest that are close to each other, and the user monitors three states higher than these. The MCSCF might very well average only the two states that come close together,

```
 $GUGDIA NSTATE=6 $END
 $GUGDM2 WSTATE(1)=0,1,1,0,0,0 $END
```

The situation is thus NWEIGHT=3, so if no keywords are chosen here, both DMO generation and diabatization involve the first three states. The most reasonable non-default choice is NGRST=1, to omit the low-lying ground state from the diabatization, but keep it during the DMO generation. In case one also wishes to have the DMO step ignore the low lying state, enter the keyword WBLOCK(1)=0.0,1.0,0.0 which weights only the 2nd and 3rd states.

```
          * * * three-fold way parameters * * *

ALPHAN = weight of the state-averaged natural orbital term,
         default = 2.0

ALPHAR = weight of the state-specific occupation number
```

```
          term, default= 1.0

ALPHAT = weight of the transition density matrix term,
          default = 0.5


           * * * four-fold way parameters * * *

The four-fold way is used if NMLAP and/or NDLAP are given.

NDLAP  = number of "resolution orbitals".  Resolution DMOs
          are introduced to determine some of DMOs in the
          '2' (or DOC) block, as defined by MOSLAB below.
          Complex multi-arrangment reactions may use this
          resolution to avoid scrambling certain DMOs with
          others of smaller occupancy.  A typical use is for
          systems with nearly filled lone pair orbitals.
          If given, $DPSVEC orbitals must be given, and if
          ORIENT is chosen, also $LCLDC input.
          Default = 0.

NMLAP  = number of "reference orbitals" used by the
          maximum overlap reference MO (MORMO) criterion of
          the "4-fold way" method for DMO determination.
          Reference DMOs are obtained at some reference
          geometry, and advice about their selection can
          be gained from looking at successful applications
          in the literature.
          MORMO is used to the determine some of the DMOs in
          the '1' (or VAL) orbitals, see MOSLAB below.
          If given, $DIAVEC orbitals must be given, and if
          ORIENT is chosen, also $LCLVL input.
          Default = 0.

ORIENT = logical flag to rotate the "reference orbitals"
          and/or "resolution orbitals" from the reference
          geometry to the present coordinates.
          Default = .FALSE.

MOSLAB = array containing a character assessment of the
          active orbitals:
            DOC ('2') orbitals should have occupancies close
                      to two in all electronic states,
                      and be filled in all reference CSFs;
            VAL ('1') orbitals have variable occupancies
```

in different electronic state,
not necessarily close to 1.0, with
variable occupancy in reference CSFs;
VIR ('0') orbitals should be only weakly
occupied in all electronic states,
and be empty in all reference CSFs.
Only orbitals marked '2' are candidates for the "resolution orbital" step (see NDLAP), and only orbitals marked '1' are candidates for the 4-fold MORMO step (see NMLAP). The default treats the entire active space as the VAL block:
MOSLAB(1)=1,1,1,...,1,1
Typically the number of '2' or '1' orbitals would exceed NDLAP and NMLAP inputs.
See also THDOC and THVIR to let the program choose the 2's, 1's, 0's based on the active orbitals occupation number.

THDOC = threshold on the state-averaged occupation numbers to identify DOC orbitals. Default=1.8 electrons.

THVIR = threshold on the state-averaged occupation numbers to identify VIR orbitals. Default=0.2 electrons.

* * * three-fold and four-fold iterations * * *

MAXIT = number of D3 or MORMO Jacobi cycle iterations. The 3-fold way iterations seem very robust, but the MORMO 4-fold way iterations are less well convergent and more numerous (default=200)

CONVTH = threshold for convergence of D3 and MORMO. Default = 1.0E-6

* * *

DMOSYM = flag to allow lowering of symmetry during the DMO process. Default = .TRUE., preserving symmetry.

Note: it is probably safer to enter GROUP=C1 in $DRT, and NOSYM=1 in $CONTRL, and thus have symmetry off during the entire run, than to choose this keyword.

* * *

Diabatization runs can read additional input groups which are not well described here. The $REFCSF and $DFMVEC input groups are often given. They are usually prepared by a three-fold DIABAT=.TRUE. run at some reference geometry, using both REFGRP=.FALSE. and REFMOS=.FALSE.

$REFCSF: list of dominant configurations at the reference geometry, which is created by a REFGRP=.FALSE. run. Note that the SLCTTH threshold assists in deciding how many CSFs are placed in the reference groups. The $REFCSF data is then read by all REFGRP=.TRUE. runs at the various other geometries, in the same format as it is generated.

$DFMVEC: a set of temporary DMOs for ordering the DMOs at the current geometry. Usually these are DMOs prepared by a 3-fold way calculation at one reference geometry, but could be from a 4-fold way calculation at a geometry very close to the current one. This contains only active MOS, namely NDOC+NALP+NAOS+NBOS+NVAL from $DRT.

$DPSVEC contains NDLAP resolution DMOs.

$DIAVEC contains NMLAP reference DMOs.

Note: $DFMVEC, $DPSVEC, $DFMVEC are typical $VEC type inputs. Each is read ignoring the MO index, so you might prepare the order reference MOs from converged natural orbitals by simply deleting all doubly occupied orbitals, and keeping all active orbitals. Similarly, reference or resolution orbitals may be plucked from any desired orbital set: natural, canonical, localized...

At present, there is no way for GAMESS to generate the orientation information, although this can be read in. Therefore their contents are not well described:

$LCLDC and $LCLVL are orientation data for DPSVEC and DIAVEC, respectively, required if ORIENT=.TRUE.

==========

==========

$TRANST group (relevant for RUNTYP=TRANSITN) (only for CITYP=GUGA or MPLEVL=2)

This group controls the evaluation of the radiative transition moment, or spin orbit coupling (SOC). An SOC calculation can be based on variational CI wavefunctions, using GUGA CSFs, or based on 2nd order perturbation theory using the MCQDPT multireference perturbation theory. These are termed SO-CI and SO-MCQDPT below. The orbitals are typically obtained by MCSCF computations, and since the CI or MCQDPT wavefunctions are based on those MCSCF states, the zero-th order states are referred to below as the CAS-CI states. SOC jobs prepare a model Hamiltonian in the CAS-CI basis, and diagonalize it to produce spin-mixed states, which are linear combinations of the CAS-CI states. If scalar relativistic corrections were included in the underlying spin-free wavefunctions, it is possible either to include or to neglect similar corrections to the spin-orbit integrals, see keyword NESOC in $RELWFN.

An input file to perform SO-CI will contain

```
 SCFTYP=NONE CITYP=GUGA MPLEVL=0 RUNTYP=TRANSITN
```

while a SO-MCQDPT calculation will have

```
 SCFTYP=NONE CITYP=NONE MPLEVL=2 RUNTYP=TRANSITN
```

The SOC job will compute a Hamiltonian matrix as the sum of spin-free terms and spin-orbit terms, H = H-sf + H-so. For SO-CI, the matrix H-sf is diagonal in the CAS-CI state basis, with the LS-coupled CAS-CI energies as the diagonal elements, and H-so contains only off-diagonal couplings between these LS states,

H-sf = CAS-CI spin-free E
H-so = CAS SOC Hamiltonian (e.g. HSO1, HSO2P, HSO2)

For SO-MCQDPT, the additional input PARMP defines these matrices differently. For PARMP=0, the spin-free term has diagonal and off-diagonal MCQDPT perturbations:

H-sf - CAS-CI spin-free E + 2nd order spin-free MCQDPT
H-so - CAS SOC Hamiltonian

For PARMP not equal to 0, the spin orbit operator is also included into the perturbing Hamiltonian of the MCQDPT:

H-sf - CAS-CI spin-free E + 2nd order spin-free MCQDPT
H-so - CAS SOC Hamiltonian + 2nd order SO-MCQDPT

Pure transition moment calculations (OPERAT=DM) are presently limited to CI wavefunctions, so please use only CITYP=GUGA MPLEVL=0. The transition moments computed by SO-MCQDPT runs (see TMOMNT flag) will form the transition density for the CAS-CI zeroth order states rather than the 1st order perturbed wavefunctions.

Please see REFS.DOC for additional information on what is actually a fairly complex input file to prepare.

OPERAT selects the type of transition being computed.

- = DM calculates radiative transition moment between states of same spin, using the dipole moment operator. (default)
- = HSO1 one-electron Spin-Orbit Coupling (SOC)
- = HSO2P partial two electron and full 1e- SOC, namely core-active 2e- contributions are computed, but active-active 2e- terms are ignored. This generally captures >90% of the full HSO2 computation, but with spin-orbit matrix element time similar to the HSO1 calculation.
- = HSO2 one and two-electron SOC, this is the full Pauli-Breit operator.
- = HSO2FF one and two-electron SOC, the form factor method gives the same result as HSO2, but is more efficient in the case of small active spaces, small numbers of CAS-CI states, and large atomic basis sets. This final option applies only to SO-CI.

PARMP = controls inclusion of the SOC terms in SO-MCQDPT, for OPERAT=HSO1 (default=1) or for HSO2P/HSO2 (default=3) only.

- 0 - no SOC terms should be included in the MCQDPT corrections at 2nd order, but they will be included in the CAS states on which the MCQDPT (i.e. up to 1st order)
- 1 - include the 1e- SOC perturbation in MCQDPT
- -1 - defined under "3", read on...
- 3 - full 1-electron and partial 2-electron in the form of the mean field perturbation (this is very similar to HSO2P, but in the MCQDPT2 perturbation). Only doubly occupied orbitals

(NMODOC) are used for the core 2e terms.
If the option is set to -1, then all core
orbitals (NMOFZC+NMODOC) are used. Neither
calculation includes extra diagrams including
filled orbitals, so both are "partial".
PARMP=3 (or -1) has almost no extra cost compared to
PARMP=1, but can only be used with OPERAT=HSO2 or HSO2P.
The options -1 and 3 are not rigorously justified, contrary
to HOS2P for a SO-CI, as 2e integrals with 2 core indices
appear in the second order in two ways. There is a mean-
field addition to 1e integrals, which is included when you
choose PARMP=3 or -1. But, there are separate terms from
additional diagrams that are not implemented, so that there
is some imbalance in including the partial 2e correction.
Nevetheless, it may be better to include such "partial"
partial 2e contributions than not to. Note that at first
order in the energy (the CAS-CI states) the N-electron
terms are treated exactly as specified by OPERAT.

NFFBUF = sets buffer size for form factors in SO-MCQDPT.
(applies only to OPERAT = HSO1, HSO2 or HSO2P).
This is a very powerful option that speeds up
SO-MCQDPT calculations by precomputing the total
multiplicative factor in front of each diagram so
that the latter is computed only once (this is in
fact what happens in MCQDPT). It is not uncommon
for this option to speed up calculations by a
factor of 10. Since this option forces running
the SO-CASCI part twice (due to the SO-MCQDPT
Hamiltonian being non-Hermitian), it is possible
that in rare cases NFFBUF=0 may perform similarly
or better. The upper bound for NFFBUF is NACT**2,
where NACT=NOCC-NFZC. Due to the sparseness of
the coupling constants it is usually sufficient to
set NFFBUF to 3*NACT. To use the older way of
dynamically computing form factors and diagrams on
the fly, set NFFBUF to 0. Default: 3*(NOCC-NFZC)

It is advisable to tighten up the convergence criteria in
the $MCQDx groups since SOC is a fairly small effect, and
the spin-free energies should be accurately computed, for
example THRCON=1e-8 THRGEN=1e-10.

PARMP has a rather different meaning for OPERAT=HSO2FF:
It refers to the difference between ket and bra's Ms,

```
        -1 do matrix elements for ms=-1 only
         0 do matrix elements for ms=0 only
         1 do matrix elements for ms=1 only
        -2 do matrix elements for all ms (0, 1, and -1),
           which is the default.
        -3 calculates form factors so they can be saved


* * * next defines the orbitals and wavefunctions * * *

NUMCI  = For SO-CI, this parameter tells how many CI
         calculations to do, and therefore defines how
         many $DRTx groups will be read in.
         For SO-MCQDPT, this parameter tells how many
         MCQDPT calculations to do, and therefore defines
         how many $MCQDx groups will be read in.
         (default=1)
         IROOTS, IVEX, NSTATE, and ENGYST below will all
         have NUMCI values.  NUMCI may not exceed 64.
You may wish to define one $DRTx or $MCQDx group for each
spatial symmetry representation occurring within each spin
multiplicity, as the use of symmetry during these separate
calculations may make the entire job run much faster.

NUMVEC = the meaning is different depending on the run:
      a) spin-orbit CI (SO-CI),
         Gives the number of different MO sets.  This can
         be either 1 or 2, but 2 can be chosen only for
         FORS/CASSCF or FCI wavefunctions.  (default=1)
         If you set NUMVEC=2 and you use symmetry in any
         of the $DRTx groups, you may have to use STSYM
         in the $DRTx groups since the order of orbitals
         from the corresponding orbital transformation
         is unpredictable.
      b) spin-orbit perturbation (SO-MCQDPT),
         The option to have different MOs for different
         states is not implemented, so your job will have
         only one $VEC1 group, and IVEX will not normally
         be input.  The absolute value of NUMVEC should be
         be equal to the value of NUMCI above.  If NUMVEC
         positive, the orbitals in the $VEC1 will be used
         exactly as given, whereas if NUMVEC is a negative
         number, the orbitals will be canonicalized
         according to IFORB in $MCQDx.  Using NUMVEC=-NUMCI
         and IFORB=3 in all $MCQDx to canonicalize over all
```

states is recommended.
Note that $GUESS is not read by this RUNTYP! Orbitals must be in $VEC1 and possibly $VEC2 input groups.

NFZC = For SO-CI, this is equal to NFZC in each $DRTx group. When NUMVEC=2, this is also the number of identical core orbitals in the two vector sets.
For SO-MCQDPT, this should be NMOFZC+NMODOC given in each of the $MCQDx groups.
The default is the number of AOs given in $DATA, this is not very reasonable.

NOCC = the number of occupied orbitals. For SO-CI this should be NFZC+NDOC+NALP+NAOS+NBOS+NVAL, but add the external orbitals if the CAS-CI states are CI-SD or FOCI or SOCI type instead of CAS.
For SO-MCQDPT enter NUMFZC+NUMDOC+NUMACT.
The default is the number of AOs given in $DATA, which is not usually correct.

Note: IROOTS, NSTATE, ENGYST, IVEX contain NUMCI values.

IROOTS = array containing the number of CAS-CI states to be used from each CI or MCQDPT calculation.
The default is 1 for every calculation, which is probably not a correct choice for OPERAT=DM runs, but is quite reasonable for the HSO operators.
The total number of states included in the SOC Hamiltonian is the summation of the NUMCI values of IROOTS times the multiplicity of each CI or MCQDPT. See also ETOL/UPPREN.

NSTATE = array containing the number of CAS-CI states to be found by diagonalising the spin-free Hamiltonians. Of these, the first IROOTS(i) states will be used to find transition moments or SOC. Obviously, enter NSTATE(i) >= IROOTS(i).
The default for NSTATE(i) is IROOTS(i), but might be bigger if you are curious about the additional energies, or to help the Davidson diagonalizer.
NSTATE is ignored by SO-MCQDPT runs, and you must ensure that your IROOTS input corresponds to the KSTATE option in $MCQDx.

ETOL = energy tolerance for CI state elimination.

This applies only to SO-CI and OPERAT=HSO1,2,2P.
After each CI finds NSTATE(i) CI roots for each
$DRTx, the number of states kept in the run is
normally IROOTS(i), but ETOL applies the further
constraint that the states kept be within ETOL of
the lowest energy found for any of the $DRTx.
The default is 100.0 Hartree, so that IROOTS is
the only limitation.

UPPREN = similar to ETOL, except it is an absolute energy,
instead of an energy difference.

IVEX = Array of indices of $VECx groups to be used for
each CI calculation. The default for NUMVEC=2 is
IVEX(1)=1,2,1,1,1,1,1..., and of course for
NUMVEC=1, it is IVEX(1)=1,1,1,1,1...
This applies only to CITYP=GUGA jobs.

ENGYST = energy values to replace the spin-free energies.
This parameter applies to SO-CI only.
A possible use for this is to use first or second
order CI energies (FOCI or SOCI in $DRT) on the
diagonal of the Hamiltonian (obtained in some
earlier runs) but to use only CAS wavefunctions
to evaluate off diagonal HSO matrix elements.
The CAS-CI is still conducted to get CI coefs,
needed to evaluate the off diagonal elements.
Enter MXRT*NUMCI values as a square array, by the
usual FORTRAN convention (that is, MXRT roots of
$DRT1, MXRT roots of $DRT2 etc), in hartrees, with
zeros added to fill each column to MXRT values.
MXRT is the maximum value in the IROOTS array.
(the default is the computed CAS-CI energies)
See B.Schimmelpfennig, L.Maron, U.Wahlgren,
C.Teichteil, H.Fagerli, O.Gropen Chem.Phys.Lett.
286, 261-266(1998).

* * * the next pertain only to spin-orbit runs * * *

ISTNO if given as positive values:
an array of one or two state indices which govern
computation of the density matrix of one state,
or the transition density of two states.
if given as negative values:

one state-averaged density with equal weights.
ISTNO(1)=5 state-specific density of state 5
ISTNO(1)=1,2 transition density between 1 and 2
ISTNO(1)=-1,-6 state-average all states 1 to 6
The default is ISTNO(1)=0,0 meaning no density.

Computation of the density gives access to the full Gaussian property package, except Mulliken populations. At present, computation of the transition density does just that, without any oscillator strengths. If the computation is of SO-MCQDPT type, the density or transition density that is computed will be that for the unperturbed SO-CASCI states.

DEGTOL = array of two tolerances to help define what states are considered degenerate. This is ignored except for linear molecules or atoms. The purpose is to decide what states are grouped together during the determination of simultaneous eigenstates of the spin-orbit Hamiltonian and Jz. DEGTOL(1) is in wavenumbers, and defines which spin-orbit states have the same energy. DEGTOL(2) is in units of electrons, and defines which natural orbitals are considered to be degenerate. If the Jz values in your run seem incorrect, tighten or relax the two degeneracy tolerances to get the correct groupings of the states. Default= 0.02,0.002

RSTATE = sets the zero energy level
format: ndrt*1000+iroot for adiabatic state (root)
0000 sets zero energy to the lowest diabatic root
default: 1001 (1st root in $DRT1 or $MCQD1)

ZEFTYP specifies effective nuclear charges to use.
= TRUE uses true nuclear charge of each atom, except protons are removed if an ECP basis is being used (default).
= 3-21G selects values optimized for the 3-21G basis, but these are probably appropriate for any all electron basis set. Rare gases, transition metals, and Z>54 will use the true nuclear charges.
= SBKJC selects a set obtained for the SBKJC ECP

basis set, specifically. It may not be sensible to use these for other ECP sets. Rare gases, lanthanides, and Z>86 will use the true nuclear charges.

ZEFF = an array of effective nuclear charges, overriding the charges chosen in ZEFTYP.

Note that effective nuclear charges can be used for any HSO type OPERAT, but traditionally these are used mainly for HSO1 as an empirical correction to the omission of the 2e- term, or to compensate for missing core orbitals in ECP runs.

ONECNT = uses a one-center approximation for SOC integrals:
= 0 compute all SOC integrals without approximations
= 1 compute only one-center 1e and 2e SOC integrals
= 2 compute all 1e, but only one-center 2e integrals
Numerical tests indicate the error of the one-center approximation (ONECNT=1) is usually on the order of a few wavenumbers for Li-Ne (a bit larger for F) and its errors appear to become negligible for anything heavier than Ne. ONECNT=1 appears to give a better balanced description than ONECNT=2. Very careful users can check how well the approximation works for their particular system by using ONECNT=0, then ONECNT=1, to compare the results. One important advantage of ONECNT=1/2 is that this removes the dependence of SOC 2e integrals upon the molecular geometry. This means the program needs to compute SOC 2e integrals only once for a given set of atoms and then they can be read by using SOC integral restart. RUNTYP=SURFACE automatically takes advantage of this fact.

JZ controls the calculation of Jz eigenvalues
= 0 do not perform the calculation
= 1 do the calculation
By default, Jz is set to 1 for molecules that are recognised as linear (this includes atoms!). Jz cannot be computed for nonlinear molecules. The matrix of Jz=Lz+Sz operator is constructed between spin-mixed states (eigenvalues of Hso). Setting Jz to 1 can enforce otherwise avoided (by symmetry) calculations of SOC matrix elements.

```
         JZ applies only to HSO1,2,2P.

TMOMNT = flag to control computation of the transition
         dipole moment between spin-mixed wavefunctions
         (that is, between eigenvectors of the Pauli-Breit
         Hamiltonian).  Applies only to HSO1,2,2P.
         (default is .FALSE.)

SKIPDM = flag to omit(.TRUE.) or include(.FALSE.) dipole
         moment matrix elements during spin-orbit coupling.
         Usually it takes almost no addition effort to
         calculate <R> excluding some cases when the
         calculation of forbidden by symmetry spin-orbit
         coupling matrix elements <Hso> may have to be
         performed since <R> and <Hso> are computed
         simultaneously.  Applies only to HSO1,2,2P.
         Since the lack of a MCQDPT density matrix means
         there are no MCQDPT dipole moments at present,
         SO-MCQDPT jobs will compute the dipole matrix
         elements for the CAS-CI states only.  However,
         the dipole moments in the spin-mixed states will
         be computed with the MCQDPT mixing coefficients.
         (default is .TRUE.)

IPRHSO = controls output style for matrix elements (HSO*)
       =-1 do not output individual matrix elements
       otherwise these are accumulative:
       = 0 term-symbol like kind of labelling:
           labels contain full symmetry info (default)
       = 1 all states are numbered consequently within each
           spin multiplicity (ye olde style)
       = 2 output only nonzero (>=1e-4) matrix elements

PRTPRM = flag to provide detailed information about the
         composition of the spin-mixed states in terms of
         adiabatic states. This flag also provides similar
         information about Jz (if JZ set).
         (default is .FALSE.)

LVAL   =  additional angular momentum symmetry values:
         For the case of running an atom:
         LVAL is an array of the L values (L**2 = L(L+1))
         for each $MCQDx/$DRTx (L=0 is S, 1 is P, etc.)
         For the case of running a linear molecule:
         LVAL is an array that gives the |Lz| values.  Note
```

that real-valued wavefunctions (e.g. Pi-x, Pi-y) have Lz and -Lz components mixed, so you should input |Lz| as 1 and 1 for both Pi-x and Pi-y. This parameter should not be given for a nonlinear polyatomic system.

Default: all set to -1 (that is, do not use these additional symmetry labels. It is the user's responsibility to ensure the values' correctness.

Note that for SO-MCQDPT useful options in $MCQDPT are NDIAOP and KSTATE. They enable efficient separation of atomic/linear symmetry irreps).

It is acceptable to set only some values and leave others as -1, if only some groups have definite values. Note that normally Lz values are printed at the end of the log file, so its easy to double check the initial values for LVAL. For the case of atoms LVAL drastically reduces the CPU time, as it reduces a square matrix to tridiagonal form. For the case of linear molecules the savings at the spin-orbit level are somewhat less, but they are usually quite significant at the preceding spin-free MCQDPT step.

MCP2E = Model Core Potential SOC 2e contributions.
Note that MCP 1e contributions are handled as in case of all-electron runs because MCP orbitals contain all proper nodes).
= 0 do not add the MCP 2e core-active contribution, but add any other 2e- terms asked for by OPERAT.
= 1 add this contribution, but no other 2e SOC term. This is recommended, and the default.
= 2 add this contribution and the 2e- contributions requested by OPERAT, for any e- which are being treated by quantum mechanics (not MCP cores).

Note that for MCP2E=0 and 2, HSO2, HSO1, HSO2P values of OPERAT are supported for the explicit 2e- contributions. The recommended approach is to assume that MCP alone can capture all the 2e SOC, for this use MCP2E=1 OPERAT=HSO2P. The entire 2e- contribution is achieved with MCP2E=2 OPERAT=HSO2. If your MCP leaves out many core electrons as

```
          particles, MCP2E=2 OPERAT=HSO2P can be tested to
          see if it adds a sizable amount to SOC, compared
          to MCP2E=1 OPERAT=HSO2P).
          MCP2E=2 OPERAT=HSO1 is an illegal combination.
          MCP2E=1 OPERAT=HSO1 is illogical since the MCP 2e
          integrals are computed but not used anywhere.

          The following table explains MCP2E and gives all
          useful combinations:

          MCP2E/OPERAT  2e SOC contributions     SOC 2e ints
            2 HSO2   MCPcore-CIact + CIcore-CIact  MCP+basis
                                   + CIact-CIact
            2 HSO2P  MCPcore-CIact + CIcore-CIact  MCP+basis
            1 HSO2P  MCPcore-CIact                 MCP
          using the following orbital space definitions:
            MCPcore orbitals whose e- are replaced by MCP
            CIcore  always doubly occupied
            CIact   MOs allowed to have variable occupation

      * * * expert mode HSO control options * * *

MODPAR =    parallel options, which are independent bit
            options, 0=off, 1=on.  Bit 1 refers only to
            HSO2FF, bit 2 to HSO1,2,2P.  Enter a decimal
            value 0, 1, 2, 3 meaning binary 00, 01, 10, 11.
 bit 1 = 0/1 (HSO2FF) uses static/dynamic load balancing in
            parallel if available, otherwise use static
            load balancing.  Dynamic algorithm is usually
            faster but may utilize memory less efficiently,
            and I/O can slow it down.  Also, dynamical
            algorithm forces SAVDSK=.F. since its
            unique distribution of FFs among nodes implies
            no savings from precalculating form factors.
 bit 2 = 0/1 (HSO1,2,2P) duplicate/distribute SOC integrals
            in parallel.  If set, 2e AO integrals and the
            four-index transformation are divided over
            nodes (distributed), and SOC MO integrals are
            then summed over nodes.
 The default is 3, meaning both bits are set on (11)

PHYSRC = flag to force the size of the physical record to
         be equal to the size of the sorting buffers.
         This option can have a dramatic effect on the
         efficiency.  Usually, setting PHYSRC=.TRUE. helps
```

```
          if the code complains that low memory enforces
          SLOWFF=.TRUE., or you set it yourself. For large
          active spaces and large memory (more precisely, if
          RECLEN is larger than the physical record size)
          PHYSRC=.TRUE. can slow the code down.  Setting
          PHYSRC to .true. forces SLOWFF to be .false.
          See MODPAR. (default .FALSE.) (only with HSO2FF)

RECLEN =  specifies the size of the record on file 40,
          where form factors are stored. This parameter
          significantly affects performance.
          If not specified, RECLEN have to be guessed,
          and the guess will usually be either an
          overestimate or underestimate. If the former
          you waste disk space, if the latter the program
          aborts. Note that RECLEN will be different for
          each pair of multiplicities and you must specify
          the maximum for all pairs.  The meaning of this
          number is how many non-zero form factors are
          present given four MO indices.  You can decrease
          RECLEN if you are getting a message "predicted
          sorting buffer length is greater than needed..."
          Default depends on active space. (only HSO2FF)

SAVDSK =  flag to repeat the form factor calculation twice.
          This avoids wasting disk space as the actually
          required record size is found during the 1st run.
          (default=.FALSE.) (only with HSO2FF)

SLOWFF =  flag to choose a slower FF write-out method.
          By default .FALSE., but this is turned on if:
          1) not enough memory for the fast way is available
          2) the maximum usable memory is available, as when
             the buffer is as large as the maximum needed,
             then the "slow FF" algorythm is faster.
          Generally SLOWFF=.true. saves up to 50% or so of
          disk space.  See PHYSRC.  (only with HSO2FF)

ACTION            controls disk file DAFL30 reuse.
        = NORMAL  calculate the form factors in this run.
        = SAVE    calculate, and store the form factors on
                  disk for future runs with the same active
                  space characteristics.
        = READ    read the form factors from disk from an
                  earlier run which used SAVE.
```

```
          (default=NORMAL) (only with HSO2FF)
          Note that currently in order to use ACTION =
          SAVE or READ you should specify MS= -1, 0, or 1


         * * * some control tolerances * * *

NOSYM= -1 forces use of symmetry-contaminated orbitals
           symmetry analysis, otherwise the same as NOSYM=0
     =  0 fully use symmetry
     =  1 do not use point group symmetry, but still use
           other symmetries (Hermiticity, spin).
     =  2 use no symmetry.   Also, include all CSFs for
           HSO1, 2, 2P.
     =  3 force the code to assume the symmetry specified
           in $DATA is the same as in all $DRTx groups, but
           is otherwise identical to NOSYM=-1.  This option
           saves CPU time and money(memory).  Since the $DRT
           works by mapping non-Abelian groups into their
           highest Abelian subgroup, do not use NOSYM=3 for
           non-Abelian groups.

SYMTOL = relative error for the matrix elements.  This
          parameter has a great impact upon CPU time, and
          the default has been chosen to obtain nearly
          full accuracy while still getting good speedups.
          (default=1.0E-4)

* * * the remaining parameters are not so important * * *

PRTCMO = flag to control printout of the corresponding
          orbitals.  (default is .FALSE.)

HSOTOL = HSO matrix elements are considered zero if they
          are smaller than HSOTOL.  This parameter is used
          only for print-out and statistics.
          (default=1.0E-1 cm-1)

TOLZ   = MO coefficient zero tolerance (as for $GUESS).
          (default=1.0E-8)

TOLE   = MO coefficient equating tolerance (as for
          $GUESS).  (default=1.0E-5)

=======================================================
```

```
* * * * * * * * * * * * * * * * * * * *
 For information on RUNTYP=TRANSITN,
see the 'further information' section
* * * * * * * * * * * * * * * * * * * *
```

Here is an alphabetical listing of all input group names:

ADDDET, 469
AFOMOD, 359
ALPDR, 144
AUXBAS, 103

BASIS, 28

CASCI, 494
CCINP, 104
CCRES, 381
CEDATA, 458
CEEIS, 456
CIDET, 445
CIDRT, 471
CIGEN, 445
CIINP, 443
CIMATM, 388
CIMFRG, 388
CIMINP, 382
CIS, 92
CISORT, 496
CISVEC, 95
COMP, 220
CONTRL, 7, 167
COSGMS, 309
CPHF, 137
CPMCHF, 138

DAMP, 270
DAMPGS, 273
DANDC, 371
DATA, 40
DATAL, 40
DATAS, 40
DCCORR, 377
DET, 445
DETPT, 483
DFT, 65
DFTB, 86
DFTBSK, 91
DIABAT, 503
DIPDR, 144
DISBS, 298
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