GESOL:

Gaussian External Solvation Module Containing The SMD Solvation Model

Users Manual

Version 2008

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1. Licensing

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2. Executive summary

GESOL is a set of Fortran subroutines and C-Shell scripts that carries out liquid-phase electronic structure calculations using a charge-density (D) based solvation model (SM) called the SMD model. The SMD model in GESOL is based on the Polarizable Continuum Model (PCM) of the Gaussian 03 electronic structure package for the bulk electrostatic component of the solvation free energy and on the Analytical Surface Area (ASA) algorithm (originally developed for the AMSOL program, but also contained in full in the GESOL program) for the first-solvation-shell component. To run an SMD calculation GESOL employs the External option of Gaussian 03. It requires the user to have a Gaussian 03 executable (Revisions D or later) installed. It does not require Gaussian 03 source code, nor does it make any modifications to Gaussian 03 code. Gaussian 03 licenses are available from Gaussian, Inc., and GESOL licenses are available from the University of Minnesota.

3. Theory

3.1. Introduction to the SMD model

The SMD model is a universal continuum solvation model where "universal" denotes applicable to all solvents, and "continuum" denotes that the solvent is not represented explicitly but rather as a dielectric fluid with surface tensions at the solute-solvent interface ("continuum" solvation models are sometimes called "implicit" solvation models). SMD is applicable to any charged or uncharged solute in any solvent or liquid medium for which a few key descriptors are known, and it directly calculates the standard-state free energy of solvation at 298 K and 1 atmosphere of pressure (the user may, if desired, use the standard-state free energy of solvation to calculate free energies of solvation under other conditions, free energies of transfer, partition coefficients, and solubilities). The calculations also yield the polarized solute wave function in solution from which various properties, such as liquid-phase partial charges, may be calculated.

The model separates the standard-state free energy of solvation into three components, as discussed in the next three paragraphs.

The first component is the bulk electrostatic contribution arising from a self-consistent reaction field (SCRF) treatment that involves an integration of the nonhomogeneous Poisson equation for electrostatics in terms of the Polarizable Continuum Model (PCM), more specifically, in terms of the Integral-Equation-Formalism Polarizable Continuum Model (IEFPCM) implemented in *Gaussian 03*. The cavities for the bulk electrostatics calculation are defined by superpositions of nuclear-centered spheres whose sizes are determined by parameters called intrinsic atomic Coulomb radii. The SMD Coulomb radii have been optimized for H, C, N, O, F, Si, P, S, Cl, and Br. For any other atom the SMD model uses the van der Waals radius of Bondi for those atoms for which Bondi defined radii; in cases where the atomic radius is not given in Bondi's paper (Bondi, A. "Van der Waals volumes and radii," *J. Phys. Chem.* **1964**, *68*, 441) a radius of 2.0 Å is used. The bulk electrostatic term is sometimes called the electrostatic term, but it should be emphasized that it is calculated from the bulk dielectric constant (bulk relative permittivity), which is not a completely valid description of the solvent in the first solvation shell.

The second contribution to the free energy of solvation is the contribution arising from short-range interactions between the solute and solvent molecules in the first solvation shell. This contribution is sometimes called the cavity—dispersion—solvent-structure (CDS) term, and it is a sum of terms that are proportional (with geometry-dependent proportionality constants called atomic surface tensions) to the solvent-accessible surface areas (SASAs) of the individual atoms of the solute. The SASA of the solute molecule is the area of a surface generated by the center of a spherical effective solvent molecule rolling on the van der Waals surface of the solute molecule. The SASA is calculated with the Analytic Surface Area (ASA) algorithm (see Liotard, D. A.; Hawkins, G. D.; Lynch, G. C.; Cramer, C. J.; Truhlar, D. G. "Improved methods for semiempirical solvation models," *J. Comput. Chem.* 1995, 16, 422). The van der Waals radii of

Bondi are used in this procedure when defined; in cases where the atomic radius is not given in Bondi's paper (Bondi, A. "Van der Waals volumes and radii," *J. Phys. Chem.* **1964**, *68*, 441) a radius of 2.0 Å is used. The solvent radius is set to 0.40 Å for any solvent. Note that the CDS term includes any aspects of solvent structure that are not described by bulk electrostatics, for example, cavitation, dispersion, the partial covalent character of hydrogen bonding, exchange repulsion, and the deviation of the effective dielectric constant in the first solvation shell from its bulk value. The sum of the latter three effects is called the solvent-structure contribution. The semiempirical nature of the CDS term also makes up for errors due to (i) assuming fixed and model-dependent values of the intrinsic Coulomb radii and (ii) any systematic errors in the description of the solute-solvent electrostatic interaction by the nonhomogeneous Poisson equation in terms of the PCM model.

The third component is the concentration component. This is zero if the standard state concentration of the solute is the same in the gas phase and solution (for example, if it is one mole per liter in the gas as well as in the solution), and it can be calculated from the ideal-gas formulas when they are not equal. The SMD solvation free energy is output at 298 K for a standard-state concentration of 1 M in both the gaseous and liquid-phase solution phases. Solvation free energies in the literature are often tabulated using a standard-state-gas phase pressure of 1 atm. To convert 1-molar-to-1-molar solvation free energies at 298 K to a standard state that uses a gas-phase pressure of 1 atm and solute standard state concentration of 1 M, add +1.89 kcal/mol to the computed solvation free energy. Note: we use "liquid phase" and "solution phase" as synonyms in this documentation.

3.2. Applicability of the SMD model implemented in GESOL

The SMD model employs a single set of parameters optimized over six electronic structure methods, namely, M05-2X/MIDI! 6D, M05-2X/6-31G(d), M05-2X/6-31+G(d,p), M05-2X/cc-pVTZ, B3LYP/6-31G(d), and HF/6-31G(d). The model parameters are intrinsic Coulomb radii for the IEFPCM bulk electrostatics and so-called atomic surface tension coefficients for the CDS contribution to the free energy of solvation. The SMD model implemented in GESOL may be used for liquid-phase single-point energy calculations, geometry optimizations, and Hessian evaluations with any of the ground-electronic-state electronic structure methods implemented in Gaussian 03 for which the IEFPCM model is available. In particular, GESOL has been tested for single-point energy calculations using the semiempirical AM1 and PM3 methods, Hartree-Fock (HF) theory, density functional theory (DFT), Møller-Plesset perturbation theory (MP2, MP3, MP4SDQ), coupled cluster theory (CCD, CCSD), configuration interaction (QCISD), and the complete active space self-consistent field (CASSCF) for ground electronic states. Analytical gradients can be computed using HF, DFT, MP2, and CASSCF. Analytical second-order derivatives over the bulk-electrostatic contribution to the free energy of solvation can be computed using HF, DFT, and MP2. Note that in all cases when an analytical Hessian is requested the second-order derivatives over the bulk-electrostatic

contribution is analytical, but the smaller contribution from CDS terms is computed by numerical differentiation of the corresponding analytical first-order derivatives.

Liquid-phase geometry optimizations can be carried out using analytical gradients.

3.3. A note on Poisson solvers

IEFPCM is an algorithm for solving the nonhomogeneous Poisson equation for continuum solvation calculations in which the solute is represented by its electronic density in real space.

The nonhomogeneous Poisson equation is the Poisson equation for a nonhomogeneous dielectric constant.

In particular, the dielectric constant is taken as unity inside the solute (because polarization of the solute is included explicitly) and as the bulk dielectric constant outside the solute (in the solvent, which is treated as a continuum (as opposed to discrete medium).

Although the SMD model was parameterized⁴ for the IEFPCM algorithm, it may also be used with other algorithms for solving the nonhomogeneous Poisson equation for continuum solvation calculations in which the solute is represented by its electron density in real space. This includes, for example, the conductor-like screening algorithm⁵ (variously called COSMO, GCOSMO, and C-PCM, but here called CPCM). CPCM solves the nonhomogeneous Poisson equation for an infinite dielectric constant (corresponding to the solvent being a conductor rather than a dielectric) and then uses one or another scaling relation to estimate the result for a finite dielectric constant; this is a better approximation at high dielectric constant (e.g., 80) than at low dielectric constant (e.g., below 10). Even for a very low dielectric constant (e.g., 2), the difference between IEFPCM and CPCM is probably less than the errors in either due to the unrealistic treatment of dielectric response at the solute-solvent boundary (discontinuous change in dielectric constant from 1 to the bulk value at a fixed boundary whose location is somewhat arbitrary) and due to some solute change lying outside the solute cavity; 6 nevertheless the atomic surface tensions were parameterized using IEFPCM, and so that model is preferred when available. We have tested CPCM against IEFPCM using the SMD default parameters for both algorithms (both algorithms are implemented in Gaussian 03). The typical difference between IEFPCM and CPCM in Gaussian 03 for solutes in solvents with dielectric constants greater than or equal to 32 is less than 0.2 kcal/mol for ions and less than 0.1 kcal/mol for neutrals. The typical difference between IEFPCM and CPCM for neutral solutes in solvents with dielectric constants less than 32 is less than 0.5 kcal/mol.

¹ Cancès, E.; Mennucci, B.; Tomasi, J. J. Chem. Phys. **1997**, 107, 3032.

² Wangsness, R. K. *Electromagnetic Fields*; Wiley: New York, **1979**; p 179.

³ Mennucci, B.; Cancès, E.; Tomasi, J. J. Phys. Chem. B **1997**, 101, 10506.

⁴ Marenich, A. V.; Cramer, C. J.; Truhlar, D. G. J. Phys. Chem. B 2008 (submitted).

⁵ Klamt, A.; Schüürmann, G. J. Chem. Soc., Perkin Trans. 2 **1993**, 799; Truong, T. N.; Stefanovich, E. V. Chem. Phys. Lett. **1995**, 240, 253; Baldridge, K.; Klamt, A. J. Chem. Phys. **1997**, 106, 6622; Barone, V.; Cossi, M. J. Phys. Chem. A **1998**, 102, 1995.

⁶ Marenich, A. V.; Cramer, C. J.; Truhlar, D. G. J. Chem. Theory Comput. 2008, 4, 877.

The SMD model should not be used with the generalized Born approximation. The generalized Born approximation (for which many references are given elsewhere⁷) is based on the partial atomic charges of the solute (rather than the solute electronic density in real space), and it has different systematic errors than the models based on the nonlinear Poisson equation. Just as the SMD solvation model was developed for models based on the nonlinear Poisson equation, an earlier model called SM8⁸ was developed for use with the generalized Born approximation.

⁷ Cramer, C. J.; Truhlar, D. G. Chem. Rev. **1999**, 99, 2161.

⁸ Marenich, A. V.; Olson, R. M.; Kelly, C. P.; Cramer, C. J.; Truhlar, D. G. J. Chem. Theory Comput. 2007, 3, 2011.

4. Description of GESOL subprograms

The hierarchy of the GESOL program is given below:

Subprogram	Description
gesol	This C-Shell script reads the <i>GESOL</i> input file provided by the user, checks it for errors, initializes the <i>GESOL</i> program, and terminates the <i>GESOL</i> program. It creates the <i>GESOL</i> scratch directory, the <i>GESOL</i> work files containing the SMD parameters, and the <i>Gaussian 03</i> input file called g03 shuttle.com that contains the solute's geometry and
	the "External" keyword to invoke an external program called gesol_external. Upon terminating the 'g03 g03_shuttle.com' command this script retrieves the computational results from the <i>Gaussian 03</i> output file called g03_shuttle.log and passes the information to the <i>GESOL</i> output file.
gesol_header	This C-Shell script outputs the <i>GESOL</i> version information.

gesol_init_f	This Fortran code reads the \$GESOL namelist in the <i>GESOL</i> input file, sets up the SMD model parameters, and passes this information to <code>gesol</code> , with the solvent's descriptors being retrieved from a file called <code>gesol_solvent_t</code> (this file is included in the <i>GESOL</i> distribution).
g03	This is a <i>Gaussian 03</i> executable. It is called twice (see a footnote): one time by the <code>gesol</code> script (the g03 parent process), another time by <code>gesol_external</code> (the g03 child process).
	The g03 parent process reads the input information from the g03_shuttle.com file and writes the computational results into the g03_shuttle.log file. The same process generates an input file with the name Gau-\$PID.EIn for running an external program called gesol_external. The g03 parent process reads an output file with the name Gau-\$PID.EOu generated by gesol_external upon its termination. The format of the Gau* files is described at http://www.gaussian.com/g ur/k external.htm.
	The g03 child process called by gesol_external carries out a PCM electrostatic calculation using the g03_external.com input file and writes the results in the g03_external.log file.
	Note that <i>Gaussian 03</i> should be installed prior to execution of the <i>GESOL</i> program. The \$903root variable must be set up, otherwise the <i>GESOL</i> program will stop.
gesol_external	This C-Shell script creates the g03_external.com input file for the g03 child process. Upon the termination of the latter, this script collects the PCM electrostatic data (energies, gradients, and second-order derivatives if requested) from the g03_external.chk checkpoint file and the g03_external.log file generated by the g03 child process and passes the electrostatic data augmented with the CDS corrections to the Gau-\$PID.EOu file.
	In the case of geometry optimization and numerical calculation of gradients and frequencies, the gesol_external script is called once for each geometry.

<pre>gesol_external_inp_f</pre>	This Fortran code computes the intrinsic Coulomb radii and the CDS contributions to the PCM electrostatic data (energies, gradients, and second-order derivatives if requested) for gesol_external.
<pre>gesol_external_out_f</pre>	This Fortran code produces the <i>GESOL</i> solvation data output for gesol_external.

* If a gas-phase geometry optimization is requested, an additional *Gaussian* calculation will be carried out before a solvation calculation. In this case, the solvation calculation will use the optimized gas-phase geometry stored in the file called g03_optgas.log.

The typical structure of the g03 shuttle.com file:

The typical structure of the g03 external.com file:

```
%mem=500mb
%nproc=4
%chk=g03_external
#P CIS(Root=1,50-50,Conver=7,EqSolv,full)/6-31G* SCF=TIGHT scrf=(cpcm,read)
# force
title

      0.0000000000
      0.0000000000
      -0.5425000026

      0.0000000000
      0.0000000000
      0.6775000032

      0.0000000000
      0.9353070044
      -1.0825000051

      0.0000000000
      -0.9353070044
      -1.0825000051

    6
    1
 scfvac pcmdoc nodis norep nocav rsolv=0 epsinf=1.00001 surface=sas noaddsph
 EPS=78.35000
 RADII=UFF MODIFYSPH
          1.850000 [1.0]
      2 1.520000 [1.0]
         1.200000 [1.0]
      3
            1.200000 [1.0]
```

This is a brief description of *GESOL* subprograms. In most of the cases, a more detailed description is given in the comment cards in the Fortran code or C-Shell script for each subprogram.

5. Citation of the GESOL program and the methods used by GESOL

Publications including work performed with *GESOL* should cite the *GESOL* software package: Marenich, A. V.; Hawkins, G. D.; Liotard, D. A.; Cramer, C. J.; Truhlar, D. G. GESOL – version 2008, University of Minnesota, Minneapolis, 2008.

Publications including work performed with *GESOL* should also cite the *Gaussian* software package:

Frisch, M. J.; Trucks, G. W.; Schlegel, H. B.; Scuseria, G. E.; Robb, M. A.; Cheeseman, J. R.; Montgomery, J. A., Jr.; Vreven, T.; Kudin, K. N.; Burant, J. C.; Millam, J. M.; Iyengar, S. S.; Tomasi, J.; Barone, V.; Mennucci, B.; Cossi, M.; Scalmani, G.; Rega, N.; Petersson, G. A.; Nakatsuji, H.; Hada, M.; Ehara, M.; Toyota, K.; Fukuda, R.; Hasegawa, J.; Ishida, M.; Nakajima, T.; Honda, Y.; Kitao, O.; Nakai, H.; Klene, M.; Li, X.; Knox, J. E.; Hratchian, H. P.; Cross, J. B.; Bakken, V.; Adamo, C.; Jaramillo, J.; Gomperts, R.; Stratmann, R. E.; Yazyev, O.; Austin, A. J.; Cammi, R.; Pomelli, C.; Ochterski, J. W.; Ayala, P. Y.; Morokuma, K.; Voth, G. A.; Salvador, P.; Dannenberg, J. J.; Zakrzewski, V. G.; Dapprich, S.; Daniels, A. D.; Strain, M. C.; Farkas, O.; Malick, D. K.; Rabuck, A. D.; Raghavachari, K.; Foresman, J. B.; Ortiz, J. V.; Cui, Q.; Baboul, A. G.; Clifford, S.; Cioslowski, J.; Stefanov, B. B.; Liu, G.; Liashenko, A.; Piskorz, P.; Komaromi, I.; Martin, R. L.; Fox, D. J.; Keith, T.; Al-Laham, M. A.; Peng, C. Y.; Nanayakkara, A.; Challacombe, M.; Gill, P. M. W.; Johnson, B.; Chen, W.; Wong, M. W.; Gonzalez, C.; Pople, J. A. *Gaussian 03*, *Revisions D.01* or *E.01*; Gaussian, Inc.: Wallingford, CT, 2004.

In addition, as usual, the user should give literature references for any methods used. A convenient collection of literature references is provided next.

SMD model

Marenich, A. V.; Cramer, C. J.; Truhlar, D. G. "Universal solvation model based on solute electron density and on a continuum model of the solvent defined by the bulk dielectric constant and atomic surface tensions," *J. Phys. Chem. B* **2009** (in press).

ASA algorithm

Liotard, D. A; Hawkins, G. D.; Lynch, G. C.; Cramer, C. J.; Truhlar, D. G. "Improved methods for semiempirical solvation models," *J. Comp. Chem.* **1995**, *16*, 422.

Derivatives of CDS terms

Tunón, I.; Ruiz-López, M. F.; Rinaldi, D.; Bertrán, J. "Computation of hydration free energies using a parameterized continuum model: study of equilibrium geometries and reactive processes in water solution," *J. Comp. Chem.* **1996**, *17*, 148.

Zhu, T.; Li, J.; Liotard, D. A.; Cramer, C. J.; Truhlar, D. G. "Analytical gradients of a self-consistent reaction-field solvation model based on CM2 atomic charges," *J. Chem. Phys.* **1999**, *110*, 5503.

IEFPCM algorithm

Cancès, E.; Mennucci, B.; Tomasi, J. "A new integral equation formalism for the polarizable continuum model: Theoretical background and applications to isotropic and anisotropic dielectrics," *J. Chem. Phys.* **1997**, *107*, 3032.

Mennucci, B.; Tomasi, J. "Continuum solvation models: a new approach to the problem of solute's charge distribution and cavity boundaries," *J. Chem. Phys.* **1997**, *106*, 5151.

Mennucci, B.; Cancès, E.; Tomasi, J. "Evaluation of solvent effects in isotropic and anisotropic dielectrics and in ionic solutions with a unified integral equation method: theoretical bases, computational implementation, and numerical applications," *J. Phys. Chem. B* **1997**, *101*, 10506.

Tomasi, J.; Mennucci, B.; Cancès, E. "The IEF version of the PCM solvation method: an overview of a new method addressed to study molecular solutes at the QM ab initio level," *J. Mol. Struct. (Theochem)* **1999**, *464*, 211.

CPCM algorithm

Barone, V.; Cossi, M. "Quantum calculation of molecular energies and energy gradients in solution by a conductor solvent model," *J. Phys. Chem. A* **1998**, *102*, 1995.

Cossi, M.; Rega, M.; Scalmani, G.; Barone, V. "Energies, structures, and electronic properties of molecules in solution with the C-PCM solvation model," *J. Comp. Chem.* **2003**, *24*, 669.

CASSCF PCM algorithm

Cossi, M.; Barone, V.; Robb, M. A. "A direct procedure for the evaluation of solvent effects in MC-SCF calculations," *J. Chem. Phys.* **1999**, *111*, 5295.

6. GESOL input description

This section describes the structure of a *GESOL* input file. Various examples of the *GESOL* input are given in the section entitled "*GESOL* test suite".

In general, the *GESOL* input is subject to the same syntax rules as used by any *Gaussian 03* input file as described at http://www.gaussian.com/g_ur/m_input.htm. However, the *GESOL* input has the following features and limitations:

- 1. The user should use a Unix editor (for instance, vi) to construct a GESOL input file.
- 2. The \$GESOL namelist must be placed in the end of the input file (a type case of the \$GESOL content is not critical). The \$GESOL namelist keywords are described further in this section.
- 3. The \$GESOL keyword should be followed by the \$END word.
- 4. Input sections should be separated by a blank line.
- 5. There should be no link command in the input.
- 6. A route section (# line) must be presented, but it cannot occupy more than one line.
- 7. A route section (# line) cannot contain more than six keywords.
- 8. The *geom* keyword in the route section as well as reading the geometry from a checkpoint file is not permitted.
- 9. The *scrf* keyword in the route section is not permitted.
- 10. The keywords in the route section should be separated by at least one space.
- 11. There should be no space between the options within the same keyword used in the route group. For instance, "opt= (path=7, trustupdate, addredun, qst3)" is correct.
- 12. A title section must be present, but it cannot occupy more than one line.
- 13. The use of Cartesian coordinates for molecular geometry specification is recommended. However, the use of redundant internal coordinates through the *Gaussian 03* options *ModRedundant*, *QST2*, and *QST3* is still permitted unless the *gen* or *genecp* keywords are specified.
- 14. The user should avoid basis set definitions with the use of asterisk. For instance, use "6-31G (d)" instead of "6-31G*".

Keyword in \$GESOL	Description
EGAS=0	calculates the free energy of solvation relative to the gas-phase total
	energy computed for each new geometry (default)
EGAS=1	calculates the free energy of solvation relative to the gas-phase total
	energy computed for the input geometry (this is equivalent to EGAS=0 if
	only a single-point energy calculation is requested)
EGAS=EGAS_Value	calculates the free energy of solvation relative to EGAS_Value provided
	by the user

IGAS=0 does not optimize the gas-phase geometry (default)

IGAS=1 optimizes the gas-phase geometry

LCDS=.TRUE. turns on the CDS corrections (default)

LCDS=.FALSE. turns off the CDS corrections

LVERB=.TRUE. turns on the verbose output

LVERB=.FALSE. turns off the verbose output (default)

PCM='IEFPCM' invokes the IEFPCM model for bulk electrostatics (default)

PCM='CPCM' invokes the CPCM model for bulk electrostatics

PCM='NONE' skips solvation

READRAD='file_name' requires that the intrinsic Coulomb radii should be read in for each atom

in the molecule from the file provided by the user (this option can

override the SMD default settings)

READPCM='file_name' requires that the PCM keywords should be read in from the file provided

by the user (this option can override the SMD default settings); by default *GESOL* uses the following PCM keywords: scfvac, pcmdoc, nodis, norep, nocav, rsolv=0, epsinf=1.00001, surface=sas, noaddsph

SOLVENT='solvent_name' defines the solvent by solvent name (default: SOLVENT='WATER')

In addition to SOLVENT='WATER', GESOL supports the following solvent keywords:

1,1,1-TRICHLOROETHANE	ACETONITRILE	ETHYLBENZENE
1,1,2-TRICHLOROETHANE	ACETOPHENONE	FLUOROBENZENE
1,2,4-TRIMETHYLBENZENE	ANILINE	FORMAMIDE
1,2-DIBROMOETHANE	ANISOLE	FORMICACID
1,2-DICHLOROETHANE	BENZALDEHYDE	N-HEPTANE
1,2-ETHANEDIOL	BENZENE	N-HEXADECANE
1,4-DIOXANE	BENZONITRILE	N-HEXANE
1-BROMO-2-METHYLPROPANE	BENZYLALCOHOL	HEXANOICACID
1-BROMOOCTANE	BROMOBENZENE	IODOBENZENE
1-BROMOPENTANE	BROMOETHANE	IODOETHANE
1-BROMOPROPANE	BROMOFORM	IODOMETHANE
1-BUTANOL	BUTANAL	ISOPROPYLBENZENE
1-CHLOROHEXANE	BUTANOICACID	P-ISOPROPYLTOLUENE
1-CHLOROPENTANE	BUTANONE	MESITYLENE
1-CHLOROPROPANE	BUTANONITRILE	METHANOL
1-DECANOL	BUTYLETHANOATE	METHYLBENZOATE
1-FLUOROOCTANE	BUTYLAMINE	METHYLBUTANOATE
1-HEPTANOL	N-BUTYLBENZENE	METHYLETHANOATE
1-HEXANOL	SEC-BUTYLBENZENE	METHYLMETHANOATE

1-HEXENE	TERT-BUTYLBENZENE	METHYLPROPANOATE
1-HEXYNE	CARBONDISULFIDE	N-METHYLANILINE
1-TODOBUTANE	CARBONTETRACHLORIDE	METHYLCYCLOHEXANE
1-IODOHEXADECANE	CHLOROBENZENE	N-METHYLFORMAMIDE (E/ZMIXTURE)
1-IODOPENTANE	CHLOROFORM	NITROBENZENE
1-IODOPROPANE	A-CHLOROTOLUENE	NITROBENZENE
1-NITROPROPANE	O-CHLOROTOLUENE	NITROMETHANE
1-NONANOL	M-CRESOL	O-NITROTOLUENE
1-NONANOL 1-OCTANOL	O-CRESOL	N-NONANE
1-PENTANOL	CYCLOHEXANE	N-OCTANE
1-PENTENE	CYCLOHEXANONE	N-PENTADECANE
		PENTANAL
1-PROPANOL	CYCLOPENTANO	
2,2,2-TRIFLUOROETHANOL	CYCLOPENTANOL	N-PENTANE
2,2,4-TRIMETHYLPENTANE	CYCLOPENTANONE	PENTANOICACID
2,4-DIMETHYLPENTANE	DECALIN (CIS/TRANSMIXTURE)	PENTYLETHANOATE
2,4-DIMETHYLPYRIDINE	CIS-DECALIN	PENTYLAMINE
2,6-DIMETHYLPYRIDINE	N-DECANE	PERFLUOROBENZENE
2-BROMOPROPANE	DIBROMOMETHANE	PROPANAL
2-BUTANOL	DIBUTYLETHER	PROPANOICACID
2-CHLOROBUTANE	O-DICHLOROBENZENE	PROPANONITRILE
2-HEPTANONE	E-1,2-DICHLOROETHENE	PROPYLETHANOATE
2-HEXANONE	Z-1,2-DICHLOROETHENE	PROPYLAMINE
2-METHOXYETHANOL	DICHLOROMETHANE	PYRIDINE
2-METHYL-1-PROPANOL	DIETHYLETHER	TETRACHLOROETHENE
2-METHYL-2-PROPANOL	DIETHYLSULFIDE	TETRAHYDROFURAN
2-METHYLPENTANE	DIETHYLAMINE	TETRAHYDROTHIOPHENE-S, S-DIOXIDE
2-METHYLPYRIDINE	DIIODOMETHANE	TETRALIN
2-NITROPROPANE	DIISOPROPYLETHER	THIOPHENE
2-OCTANONE	CIS-1,2-DIMETHYLCYCLOHEXANE	THIOPHENOL
2-PENTANONE	DIMETHYLDISULFIDE	TOLUENE
2-PROPANOL	N, N-DIMETHYLACETAMIDE	TRANS-DECALIN
2-PROPEN-1-OL	N, N-DIMETHYLFORMAMIDE	TRIBUTYLPHOSPHATE
E-2-PENTENE	DIMETHYLSULFOXIDE	TRICHLOROETHENE
3-METHYLPYRIDINE	DIPHENYLETHER	TRIETHYLAMINE
3-PENTANONE	DIPROPYLAMINE	N-UNDECANE
4-HEPTANONE	N-DODECANE	XYLENE (MIXTURE)
4-METHYL-2-PENTANONE	ETHANETHIOL	M-XYLENE
4-METHYLPYRIDINE	ETHANOL	O-XYLENE
5-NONANONE	ETHYLETHANOATE	P-XYLENE
ACETICACID	ETHYLMETHANOATE	
ACETONE	ETHYLPHENYLETHER	

The free energy of solvation for a given solute in a particular medium depends on the values of the solvent descriptors defined for the medium. The SMD model uses the following set of solvent descriptors for any nonaqueous solvent:

DIELEC dielectric constant, ε , of solvent

SOLN index of refraction at optical frequencies at 293 K, n_{20}^D

SOLA Abraham's hydrogen bond acidity, Σα₂^H
 SOLB Abraham's hydrogen bond basicity, Σβ₂^H
 SOLG γ = γ_m / γ⁰ (default is 0.0), where γ_m is the macroscopic surface tension at air/solvent interface at 298 K, and γ⁰ is 1 cal mol⁻¹ Å⁻² (1 dyne/cm = 1.43932 cal mol⁻¹ Å⁻²)
 SOLC aromaticity, φ: the fraction of non-hydrogenic solvent atoms that are aromatic carbon atoms
 SOLH electronegative halogenicity, ψ: the fraction of non-hydrogenic solvent atoms

In the case of water, there is only one solvent descriptor, the dielectric constant (DIELEC=78.35), which defines the bulk-electrostatics contribution to the free energy of solvation. If the solvent is specified, the program will use the values of the solvent descriptors (DIELEC, SOLA, SOLB, SOLC, SOLG, SOLH, and SOLN), which are stored in a file called gesol_solvent_t. However, the user can override the default values by specifying the new (floating-point) values of these descriptors in the namelist \$GESOL in the *GESOL* input file. For a desired solvent, these values can be derived from experiment or from interpolation or extrapolation of data available for other solvents. Solvent parameters for common organic solvents are tabulated in the *Minnesota Solvent Descriptor Database*. The latest version of this database is available at: http://comp.chem.umn.edu/solvation/mnsddb.pdf.

that are F. Cl or Br

By default for a single-point energy calculation in the liquid phase the free energy of solvation is defined as a difference between the liquid-phase total energy and the gas-phase total energy calculated at the input geometry unless the EGAS=EGAS_Value option is used. In the latter case GESOL uses the gas-phase total energy (EGAS_Value) provided by the user.

If a liquid-phase geometry optimization is requested, it is recommended to use the equilibrium gas-phase geometry as an initial geometry and the EGAS=1 option in the GESOL input file. The user can exploit the IGAS=1 option to optimize the gas-phase geometry using GESOL (this option can be applied only if the input geometry is given in Cartesian coordinates). If the IGAS=1 option fails to work, the gas-phase geometry should be obtained separately using the original Gaussian. If the gas-phase geometry is not a good approximation to the liquid-phase geometry, the user may exploit any other initial geometry, provided the total energy corresponding to the equilibrium gas-phase geometry is specified via the EGAS keyword in the GESOL input file. In either case the final free energy of solvation is calculated as a difference between the liquid-phase total energy obtained at the liquid-phase equilibrium geometry and the gas-phase total energy obtained at the gas-phase equilibrium geometry. Therefore, the final energy of solvation contains the nuclear reorganization term (in other words, an energy term corresponding to the change in the solute's geometry upon solvation). If the EGAS=0 option is used, the gas-phase energy will be updated for each optimization step and, therefore, the nuclear reorganization contribution to the free energy of solvation will be omitted.

7. GESOL output description

This section describes the *GESOL* output structure. Each output file is a concatenation of the following outputs:

- 1. Header
- 2. Table with the *GESOL* keywords
- 3. File q03 shuttle.com
- 4. Beginning of g03 shuttle.log
- 5. File q03 external.com
- 6. File g03 external.log if verbose output is requested (LVERB=.TRUE.)
- 7. *GESOL* solvation summary
- 8. End of g03 shuttle.log

Note that in the case of geometry optimization sections 5, 6, 7 are printed for each optimization cycle.

If a gas-phase geometry optimization is requested (IGAS=1), an additional *Gaussian* calculation will be carried out before a solvation calculation. An additional file (g03_optgas.log) containing the output of the gas-phase geometry optimization will be generated. The gas-phase optimization will be followed by a solvation calculation using the optimized gas-phase geometry.

GESOL exploits the scfvac option in Gaussian 03 for a PCM bulk-electrostatics calculation unless the READPCM keyword in the GESOL input file is applied to specifically override the default setting. If the scfvac option is used in the Gaussian calculation, the liquid-phase SCRF is preceded by a gas-phase SCF. When the gas-phase SCF has converged, Gaussian continues the same SCF procedure to the liquid-phase SCRF. GESOL can exploit the scfvac option with any of the following electronic structure methods: AM1, PM3, HF, DFT, and CASSCF. For other available methods (MP2, MP3, MP4SDQ, CCD, CCSD, QCISD) the scfvac option cannot be used. For any of these post-HF methods Gaussian 03 equilibrates the solvent reaction field calculated at a given level of theory to the solute electronic density obtained at the HF level, skipping the gas-phase energy calculation at the post-HF level of theory. Nevertheless, in those cases when the scfvac option is not used (for instance, when the user overrides the default GESOL setting) or cannot be used (like with the methods above), GESOL creates an additional file called g03_externalgas.com to carry out a separate gas-phase single-point energy calculation. However, this calculation will be skipped if the user provides the gas-phase total energy in the GESOL input file using the EGAS=EGAS_Value keyword.

The typical *GESOL* solvation summary lists the values of Coulomb atomic radii used for a bulk-electrostatics calculation, van der Waals radii used for a CDS calculation, CDS contributions to the gradients in Cartesian coordinates (if requested), atomic contributions to the solvent accessible surface area and to the CDS energy term, and solvation energy components split over bulk-electrostatics and non-bulk-electrostatics contributions.

An example of solvation energy components is given below for the case when the scfvac option is used:

```
(0) E-EN(g) gas-phase elect-nuc energy
                                                          -286.236405 a.u.
(1) E-EN(liq) elect-nuc energy of solute
                                                          -286.235727 a.u.
(2) G-P(liq) polarization free energy of solvation
                                                             -35.517 kcal/mol
(3) G-ENP(lig) elect-nuc-pol free energy of system
                                                         -286.292326 a.u.
(4) G-CDS(liq) cavity-dispersion-solvent structure
                                                                0.000 kcal/mol
   free energy
(5) G-P-CDS(liq) = G-P(liq) + G-CDS(liq) = (2) + (4)
                                                              -35.517 kcal/mol
(6) G-S(liq) free energy of system = (1) + (5)
                                                          -286.292326 a.u.
(7) DeltaE-EN(liq) elect-nuc reorganization
   energy of solute molecule (7) = (1) - (0)
                                                              0.425 kcal/mol
(8) DeltaG-ENP(lig) elect-nuc-pol free energy
   of solvation (8) = (3) - (0)
                                                             -35.091 kcal/mol
(9) DeltaG-S(liq) free energy of solvation
    (9) = (6) - (0)
                                                              -35.091 kcal/mol
```

The ENP term refers to the electronic-nuclear-polarization (ENP) contribution to the free energy of solvation. The nuclear relaxation (N) component of the ENP term is equal to the difference between the gas-phase total energy calculated at the gas-phase equilibrium structure and the gas-phase total energy calculated at the *liquid*-phase equilibrium structure. If the geometry is assumed to be the same in the gas phase and in the liquid phase (see the EGAS=0 option in the section entitled "GESOL input description"), then the ENP term becomes just an electronic polarization (EP) term. The CDS term refers to the cavity–dispersion–solvent-structure contribution.

If the scfvac option is not used the *GESOL* output of energy components is simplified to the following:

If verbose output is requested (LVERB=.TRUE.) the *GESOL* program will generate two checkpoint files: g03_geom.chk (with geometry parameters, forces, and a computed Hessian if requested) and g03_morb.chk (with computed molecular orbitals after the last SCF calculation).

8. GESOL installation and execution

The *GESOL* software package comes as a single tar file (gesol.tar) that should be placed in the user's directory and then untarred by executing the following command:

```
>tar xvf gesol.tar
```

There will be a directory called gesol containing two subdirectories (gesol/bin and gesol/tests). The subdirectory gesol/bin contains the following files:

```
-rwxr-x---
                    comp gesol
-rwxr-x---
                    gesol
                    gesol external
-rwxr-x---
                    gesol external inp f.F
-rw-r----
                    gesol external out f.F
-rw-r----
                    gesol header
-rwxr-x---
                    gesol init f.F
-rw-r--r--
-rw-r----
                    gesol solvent t
```

The user should set the working directory to gesol/bin and then compile the Fortran codes (*.F) by executing the following command:

```
>./comp gesol
```

The user should define the full path to <code>gesol/bin/gesol</code> through the \$PATH environment variable in a dot-file called .bashrc or in .cshrc (depending on which shell is used), for instance, by adding a line:

```
export PATH=$PATH:$HOME/gesol/bin
or
setenv PATH ${PATH}:$HOME/gesol/bin
```

The user should also assign the \$DIR_GESOL variable to the full path to the gesol/bin directory by adding a line in .bashrc or in .cshrc:

```
export DIR_GESOL=$HOME/gesol/bin
or
setenv DIR GESOL $HOME/gesol/bin
```

It is recommended to define the scratch space through the \$SCR_GESOL variable. If \$SCR_GESOL is not set up by the user, the program will set it to '/scratch*/\$USER/' if such a directory exists (otherwise it will set the scratch space to the current directory).

The user can run the *GESOL* program by executing the following command: >gesol <input> <output>

To assure that the *GESOL* kit has been properly installed, the user is encouraged to run the whole *GESOL* test suite that can be found in gesol/tests. This directory contains 42 input examples (*.inp). The corresponding output files (*.out) are located in

gesol/tests/output. A Perl script called compare.pl can be used to compare the user-obtained output files against those in gesol/tests/output by executing the following command:

>./compare.pl *.out

A difference in the last digit is acceptable. Test18, Test19, Test23, and Test27 may produce a difference in the second-third digit that is acceptable too. All the tests using the Minnesota (M05) suite of density functionals will fail if *GESOL* is run with a revision of *Gaussian 03* earlier than Revision E.01.

Note that *Gaussian 03* should be installed prior to execution of the *GESOL* program. The \$903root variable must be set up, otherwise the *GESOL* program will stop.

9. GESOL test suite

The *GESOL* test suite contains 42 representative input/output files located in gesol/tests. This test suite includes single-point energy calculations, local minimum and transition state geometry optimizations, and Hessian calculations for the ground electronic states in the liquid phase. The tested electronic structure methods include AM1, PM3, HF, DFT, MP2, MP3, MP4SDQ, CCD, CCSD, QCISD, and CASSCF. The open-shell electronic systems $Ru(H_2O)_6^{3+}$ and CH_3O^{\bullet} are tested using spin-unrestricted Hartree-Fock (UHF) wavefunctions.

test1.inp

HF/STO-3G single-point solvation energy and analytical gradients for the cyclohexanamine cation in water

test1.am1.inp

AM1 single-point solvation energy for the cyclohexanamine cation in water

test1.pm3.inp

PM3 single-point solvation energy for the cyclohexanamine cation in water

test1.ccd.inp

CCD single-point solvation energy for the cyclohexanamine cation in water

test1.ccsd.inp

CCSD single-point solvation energy for the cyclohexanamine cation in water

test1.mp3.inp

MP3 single-point solvation energy for the cyclohexanamine cation in water

test1.mp4.inp

MP4(SDQ) single-point solvation energy for the cyclohexanamine cation

test1.qcisd.inp

QCISD single-point solvation energy for the cyclohexanamine cation in water

test2.inp

B3LYP/3-21G analytical geometry optimization and analytical Hessian calculation in the liquid phase for the cyclohexanamine cation using the CalcFC option (the initial Hessian is calculated), LCDS=.FALSE. (no CDS terms are included), READRAD='radii.dat' (Coulomb radii are read in from the file called radii.dat)

test3.inp

B3LYP/6-31+G(d,p) analytical Hessian calculation for methanol in the gas phase

test3.m052x.inp

M05-2X/6-31+G(d,p) analytical Hessian calculation for methanol in the gas phase

test4.inp

B3LYP/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in benzene using the IGAS=1 option (the gas-phase geometry is optimized first)

test4.m052x.inp

M05-2X/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in benzene using the IGAS=1 option (the gas-phase geometry is optimized first)

test5.inp

B3LYP/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in methylene chloride using the IGAS=1 option (the gas-phase geometry is optimized first)

test5.m052x.inp

M05-2X/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in methylene chloride using the IGAS=1 option (the gas-phase geometry is optimized first)

test6.inp

B3LYP/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in methanol using the IGAS=1 option (the gas-phase geometry is optimized first)

test6.m052x.inp

M05-2X/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in methanol using the IGAS=1 option (the gas-phase geometry is optimized first)

test7.inp

B3LYP/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in water using the PCM keywords provided in the file pcm.dat (option READPCM) and the EGAS=-115.734872 option (it means that the free energy of solvation at each step of the liquid-phase geometry optimization is calculated relative to the user-provided gas-phase total energy value that is -115.734872; the gas-phase SCF calculation is skipped)

test7.m052x.inp

M05-2X/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in water using the PCM keywords provided in the file pcm.dat (option READPCM) and the EGAS=-115.706492 option (it means that the free energy of solvation at each step of the liquid-phase geometry optimization is calculated relative to the user-provided gas-phase total energy value that is -115.706492; the gas-phase SCF calculation is skipped)

test8.inp

MP2(Full)/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in water using the EGAS=0 option (it means that the free energy of solvation at each step of the liquid-phase geometry optimization is calculated relative to the gas-phase total energy updated for each step during the optimization)

test9.inp

MP2(Full)/6-31+G(d,p) analytical geometry optimization and analytical Hessian calculation for methanol in water using the EGAS=1 option (it means that the free energy of solvation at each step of the liquid-phase geometry optimization is calculated relative to the gas-phase total energy obtained at the first optimization step for the input geometry which in this example is the equilibrium gas-phase geometry)

test10.inp

HF/3-21G analytical gradients for methanol in acetonitrile

test11.inp

HF/3-21G numerical gradients for methanol in acetonitrile using the default *Gaussian 03* value for differentiation step

test12.inp

HF/6-31G(d) single-point energy for dimethyl 4-bromo-2,5-dichlorophenyl thiophosphate in water

test13.inp

HF/6-31G(d) single-point energy for dimethyl 4-bromo-2,5-dichlorophenyl thiophosphate in octanol

test14.inp

HF/6-31G(d) single-point energy for tetramethylsilane in water using LVERB=.TRUE. (verbose output) in the \$GESOL namelist and '# P' in the Gaussian 03 route line (for more verbose output)

test15.inp

HF/6-31G(d) single-point energy for tetramethylsilane in water using the PCM='CPCM' option (CPCM model for electrostatics)

test16.inp

HF/6-31G(d) single-point energy for tetramethyl silane in water using the CPCM model for electrostatics (option PCM='CPCM') and the PCM keywords provided in the file pcm.dat (option READPCM) as well as LVERB=.TRUE. (verbose output) in the \$GESOL namelist and '# P' in the *Gaussian 03* route line (for more verbose output)

test17.inp

HF/6-31G(d) single-point energy for 1-heptanol in ortho-dichlorobenzene with the solvent parameters (DIELEC, SOLA, SOLB, SOLC, SOLG, SOLH, SOLN) defined by the user in the \$GESOL namelist

test18.inp

BLYP/6-31B(d) single-point energy for aniline in carbontet using the GEN keyword in the *Gaussian 03* route line and the 6-31B(d) basis set stored externally in the file basis.dat

test19.inp

BLYP/6-31B(d) single-point energy for aniline in carbontet using the GEN keyword in the *Gaussian 03* route line and the 6-31B(d) basis set entered in the *GESOL* input file as a separate section

test20.inp

Spin-unrestricted BLYP single-point energy for the Ru(III) hexaaqua complex using the GEN keyword in the *Gaussian 03* route line and the effective core potential on Ru

test21.inp

HF analytical Hessian calculation for the Ru(II) hexaaqua complex in the gas phase using LVERB=.TRUE. to obtain the checkpoint file g03_geom.chk with the initial Hessian for the next test

test22.inp

HF analytical geometry optimization for the Ru(II) hexaaqua complex in water using the initial Hessian obtained in the previous test (option opt=ReadFC) and analytical calculation of frequencies for the liquid-phase equilibrium geometry

test23.inp

 $\mathrm{HF/6-31+G(d)}$ analytical optimization of the transition state of the $\mathrm{NH_3+CH_3Cl}$ reaction in water using internal coordinates defined with the ModRedundant option and analytical Hessian calculation

test24.inp

HF/6-31+G(d) analytical optimization of the transition state of the NH₃ + CH₃Cl reaction in water using Cartesian coordinates (no ModRedundant) and analytical Hessian calculation

test25.inp

HF/3-21G analytical optimization of the $SiH_2 + H_2$ transition state (*Gaussian 03* Test Job 302) using the opt=qst2 option and testing the IEFPCM bulk electrostatics only (LCDS=.FALSE.)

test26.inp

HF/3-21G analytical optimization of the SiH₂ + H₂ transition state (*Gaussian 03* Test Job 302) using the opt=qst2 option and the SMD default settings for aqueous solution (LCDS=.TRUE., SOLVENT='WATER')

test27.inp

Spin-unrestricted HF/3-21G analytical optimization of the transition state of the CH₂OH \rightarrow CH₃O isomerization (*Gaussian 03* Test Job 413) in n-hexane using the opt=qst3 option

test28.inp

HF/STO-3G single-point energy for CH₂O in water (*Gaussian* Test Job 616) using LVERB=.TRUE. to obtain the checkpoint file g03_morb.chk which contains the molecular orbital guess for the next test

test29.inp

CASSCF/STO-3G analytical gradients for the ground electronic state of CH_2O in water (Gaussian Test Job 616) using the guess=read keyword in the route line to read the initial molecular orbitals from test28 and using the PCM keywords provided in the file pcm.dat (option READPCM)

test30.inp

CASSCF/STO-3G numerical gradients for the ground electronic state of CH_2O in water (Gaussian Test Job 616) with the iop(1/39=-1) keyword in the route line to use a user-provided value of differentiation step as well as using the guess=read keyword in the route line to read the initial molecular orbitals from test28, using the PCM keywords provided in the file pcm. dat (option READPCM), and using the EGAS=1 option

10. Platforms on which GESOL has been tested

The current version of *GESOL* has been tested with *Gaussian 03* (Revisions D.01 and E.01) on the following platforms:

- IBM pSeries 690 and pSeries 655 Nodes (Power 4 processors), running AIX version 5.3
- SGI Altix Intel Itanium 2, running SUSE Linux 2.6.5
- IBM Blade Center AMD Opteron Linux Cluster, running SUSE Linux 2.6.5
- SGI Altix XE 1300, running SUSE Linux 2.6.16

11. Revision history

Version 2008 is the first version.