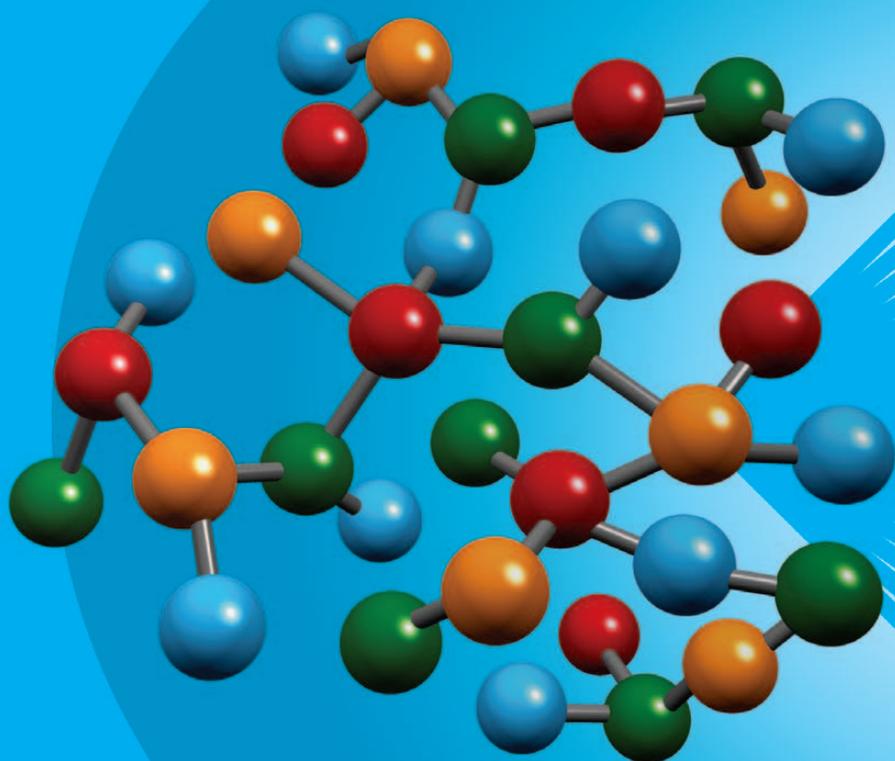


10

USER MANUAL



PARASURE™

Impressum

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PROGRAM HISTORY

Release Date	Version	Platforms
1 st July 2005	ParaSurf'05™ initial release (Revision A1)	32-bit Windows 32-bit Linux Irix
1 st January 2006	ParaSurf'05™ Revision B1 (customer-feedback release)	
1 st July 2006	ParaSurf'06™ Revision A1	32-bit Windows 32-bit Linux 64-bit Linux Irix
1 st July 2007	ParaSurf'07™ Revision A1	
1 st July 2008	ParaSurf'08™ Revision A1	
22 nd August 2008	ParaSurf'08™ Revision A2 (minor bug fix release)	
16 th December 2008	ParaSurf'08™ Revision A3 (minor bug fix release)	
1 st July 2009	ParaSurf'09™ Revision A1	32-bit Windows 64-bit Windows 32-bit Linux 64-bit Linux
1 st September 2009	New Vhamil.par file including PM6 and first-row transition metals in AM1*	
1 st February 2010	ParaSurf'09™ Revision B1 (additional atom-centred descriptors)	
1 st July 2010	ParaSurf'10™ Revision A1	

1 INTRODUCTION

ParaSurf™ is a program to generate isodensity or solvent-excluded surfaces from the results of semiempirical molecular orbital calculations, either from VAMP [1] or a public-domain version of MOPAC modified and made available by Cepos InSilico. [2] The surface may be generated by shrink-wrap [3] or marching-cube [4] algorithms and the former may be fit to a spherical harmonic series. [5] The principles of these two techniques are explained below, but for comparison Figure 1 shows default isodensity surfaces calculated by ParaSurf™ for a tetracycline derivative. The surfaces are color-coded according to the electrostatic potential at the surface.

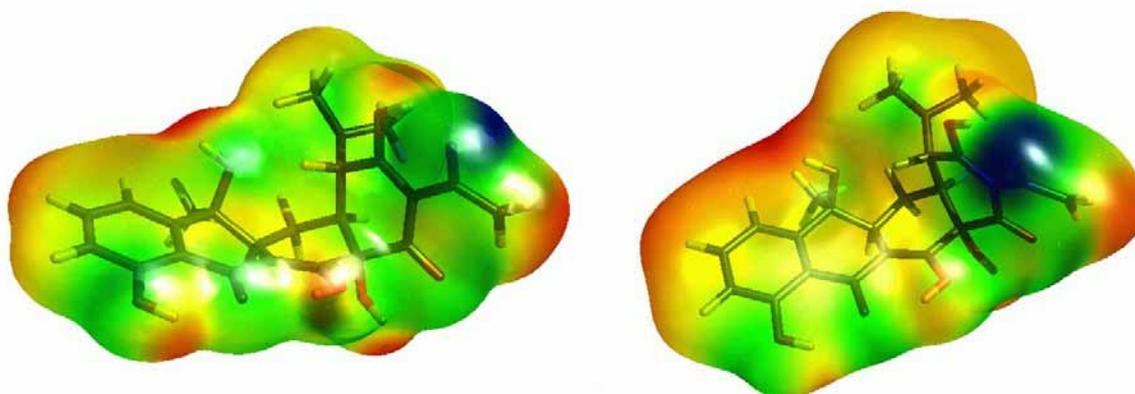


Figure 1 Marching-cube (left) and shrink-wrap (right, fitted to a spherical-harmonic approximation) isodensity surfaces calculated with ParaSurf™ using the default settings

Four local properties, the molecular electrostatic potential (MEP), [6] the local ionization energy (IE_L), [7] the local electron affinity (EA_L), [8] and the local polarisability (α_L) [8] are calculated at the points on the surface. Two further properties, the local hardness (η_L), [8] and the local electronegativity (χ_L) [8] can be derived from IE_L and EA_L .

The local properties can be used to generate a standard set of 81 descriptors [9] appropriate for quantitative structure-property relationships (QSPRs) for determining physical properties.

ParaSurf™ can also generate local enthalpies and free energies of solvation [10] and integrate them over the entire molecular surface to give the enthalpy or free energy of solvation. ParaSurf™ can read so-called *Surface-Integral Model* (SIM) files that allow it to calculate properties such as, for instance, the enthalpy and free energy of hydration and the free energies of solvation in *n*-octanol and chloroform. The surface-integral models are expressed as summations of local solvation energies over the molecular surface. These local solvation energies can be written to the ParaSurf™ surface file.

ParaSurf™ is the first program to emerge from the ParaShift collaboration between researchers at the Universities of Erlangen, Portsmouth, Southampton, Oxford and Aberdeen. It is intended to provide the molecular surfaces for small molecules (i.e. non-proteins) for subsequent quantitative structure-activity relationship (QSAR), QSPR, high-throughput virtual screening (HTVS), docking and scoring, pattern-recognition and simulation software that will be developed in the ParaShift project.



1.1 Changes relative to ParaSurf⁰⁹TM

ParaSurf¹⁰TM has been enhanced relative to its predecessor in order to provide improved flexibility and a more comprehensive range of descriptors and features. The changes are outlined below:

1.1.1 Local electron affinity for AM1* and other Hamiltonians with *d*-orbitals as polarisation functions

Calculating the local electron affinity with AM1* led to spurious results with ParaSurf⁰⁹TM because the *d*-polarisation functions dominated the summation. A new technique [11] has been introduced to fix this problem in ParaSurf¹⁰TM. A new command-line option requests that the local electron affinity be calculated exactly as in ParaSurf⁰⁹TM to ensure continuity.

1.1.2 The PM6 Hamiltonian

ParaSurf¹⁰TM can be used with PM6. [12] This was also the case with parSurf⁰⁹ if the post-release Vhamil.par file were used. PM6 is available for 70 elements.

1.1.3 Second generation surface-integral models; local hydrophobicity

The binned surface descriptors for local hydrophobicity and the logP_{OW} models associated with them are now available in ParaSurf¹⁰TM. [13, 14] The descriptors can be written to a comma-separated table for model generation.

1.1.4 Molecular fragments

ParaSurf¹⁰TM can now divide molecules up into predefined fragments and output their surfaces and the descriptors derived from them.

1.1.5 Atom-centred descriptors

Since ParaSurf⁰⁹TM release B1, ParaSurfTM has been able to calculate and output a new series of descriptors that relate to the properties of single atoms. These properties have proven to be useful in models of H-bonding and chemical reactivity. [15, 16]

1.2 Isodensity surfaces

Isodensity surfaces [17] are defined as the surfaces around a molecule at which the electron density has a constant value. Usually this value is chosen to approximate the van der Waals' shape of the



molecule. ParaSurf™ allows values of the isodensity level down to $0.00001 \text{ e}^{-\text{\AA}^{-3}}$. Lower values than this may result in failures of the surface algorithms for very diffuse surfaces.

1.3 Solvent-excluded surfaces

The solvent-excluded surface is obtained by rolling a spherical solvent molecule of radius r_{solv} over the surface of the molecule as shown in Figure 2. The surface of the solvent molecule defines the molecular surface, so that the yellow volume in Figure 2 becomes part of the molecule.

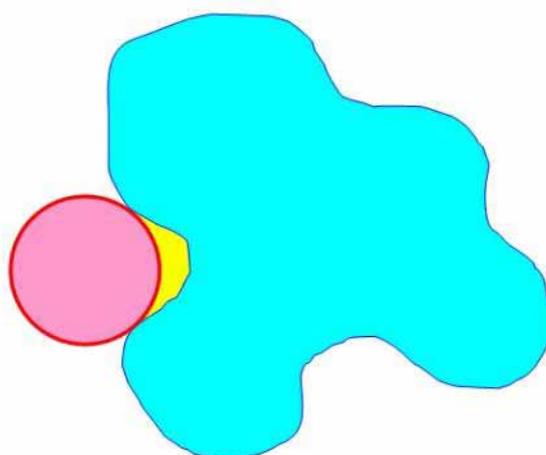


Figure 2 2D-representation of a solvent-excluded surface.

1.4 Solvent-accessible surfaces

Solvent-accessible surfaces are obtained in the same way as solvent-excluded surfaces but the outer surface of the solvent sphere is used to define the molecular surface, as shown in Figure 3.

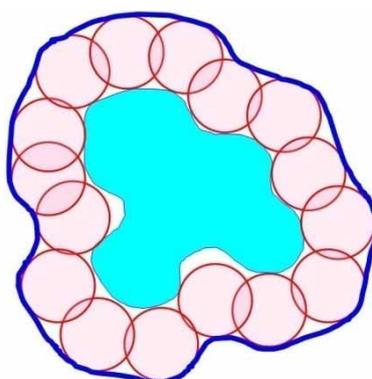


Figure 3 The solvent-accessible surface is obtained by rolling a spherical "solvent molecule".

1.5 Shrink-wrap surface algorithm

Shrink-wrap surface algorithms [3] are used to determine single-valued molecular surfaces. Single-valued in this case means that for any given radial vector from the centre of the molecule the surface is only crossed once (vectors **A** and **B** in Figure 4) and not multiply (vectors **C** and **D** in Figure 4):

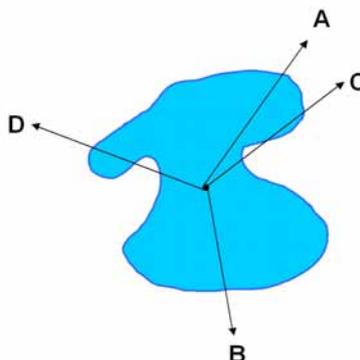


Figure 4 2D-representation of a molecular surface with single-valued (A and B) and multiply valued (C and D) radial vectors from the centre.

Single-valued surfaces are necessary for spherical-harmonic fitting (see 1.4). Thus, spherical-harmonic fitting is only available for shrink-wrap surfaces in ParaSurf™. The shrink-wrap algorithm works by starting outside the molecule (point **a** in Figure 5) and moving inwards along the radial vector until it finds the surface (in our case defined by the predefined level of the electron density, point **b** in Figure 5). Thus, the shrink-wrapped surface may contain areas (marked by dashed lines in Figure 5) for which the surface deviates from the true isodensity surface.

These areas of the surface, however, often have little consequence as they are situated above indentations in the molecule that are poorly accessible to solvents or other molecules. The shrink-wrapped surfaces generated by ParaSurf™ should normally be fitted to a spherical-harmonic series for use in HTVS, similarity, pattern-recognition or high-throughput docking applications. The default molecular centre in ParaSurf™ is the centre of gravity (CoG). In special cases in which the CoG lies outside the molecule, another centre may be chosen.

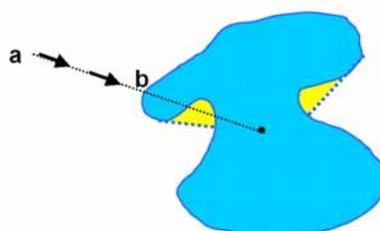


Figure 5 2D-representation of the shrink-wrap algorithm. The algorithm scans along the vector from point **a** towards the centre of the molecule until the electron density reaches the preset value (point **b**). The algorithm results in enclosures (marked yellow) for multi-valued radial vectors.

Figure 6 shows a spherical-harmonically fitted shrink-wrap surface for a difficult molecule. The areas shown schematically in Figure 5 are clearly visible.

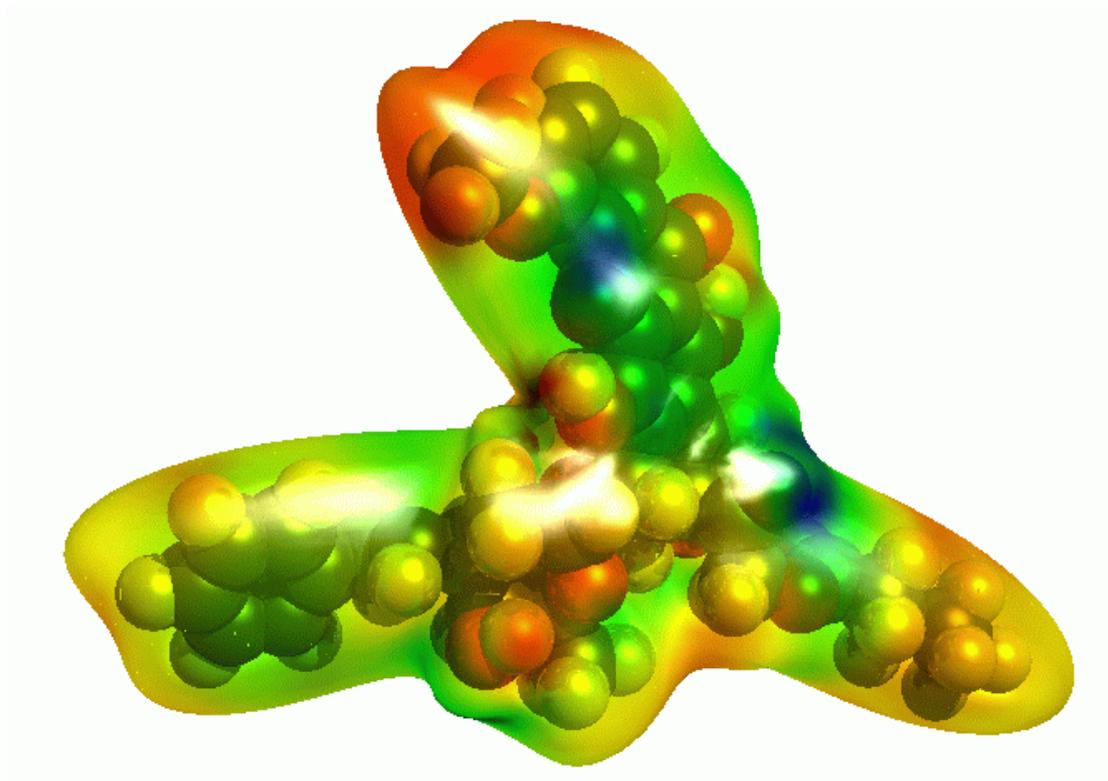


Figure 6 Spherical-harmonic approximation of a shrink-wrap isodensity surface. Note the areas where the surface does not follow the indentations of the molecule.

1.6 Marching-cube algorithm

The marching-cube algorithm [4] implemented in ParaSurf™ does not have the disadvantage of being single-valued like the shrink-wrap surface. It cannot, therefore, be fitted to a spherical harmonic series and is used as a purely numerical surface primarily for QSPR applications or surface-integral models. [10] The algorithm works by testing the electron density at the corners of cubes on a cubic lattice laid out through the molecular volume. The corners are divided into those “inside” the molecule (i.e. with a higher electron density than the preset value) and those “outside”. The surface triangulation is then generated for each surface cube and the positions of the surface points corrected to the preset electron density.

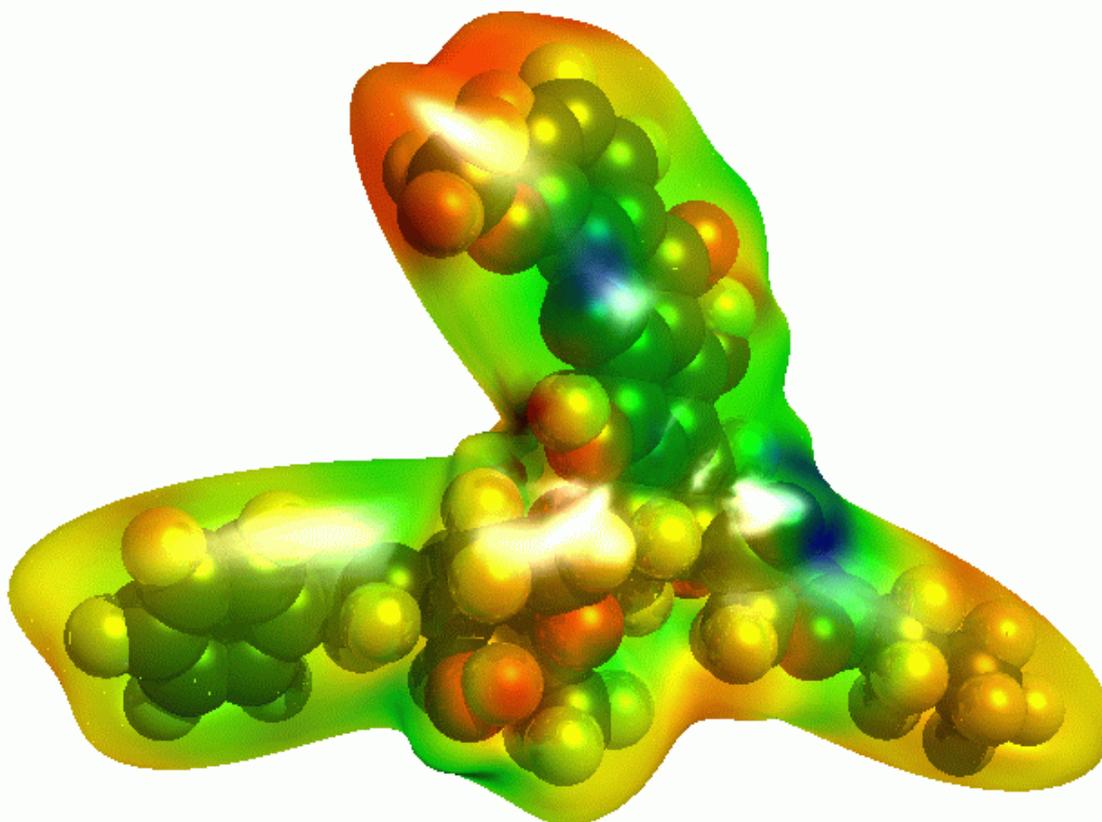


Figure 7 Spherical-harmonic approximation of a shrink-wrap isodensity surface. Note the areas where the surface does not follow the indentations of the molecule.

1.7 Spherical-harmonic fitting

Complex surfaces can be fitted to spherical harmonic series to give analytical approximations of the surface. [5] The surfaces are fit to a series of distances $r_{\alpha,\beta}$ from the centre along the radial vector defined by the angles α and β as:

$$r_{\alpha,\beta} = \sum_{l=0}^N \sum_{m=-l}^l c_l^m Y_l^m \quad (1)$$

Where the distances $r_{\alpha,\beta}$ are linear combinations of spherical harmonics Y_l^m defined as:

$$Y_l^m(\alpha, \beta) = \sqrt{\frac{(2l+1)(l-m)!}{4\pi(l+m)!}} P_l^m(\cos \alpha) e^{im\beta} \quad (2)$$

where $P_l^m(\cos \alpha)$ are associated Legendre functions and l and m are integers such that $-l \leq m \leq l$. In the above form, spherical harmonics are complex functions. Duncan and Olson [18] have used the real functions

$$Y_l^m(\alpha, \beta) = N_{lm} P_l^m(\cos \alpha) \cos |m| \beta \quad (3)$$

where N_{lm} are normalization factors, to describe molecular surfaces using spherical harmonics.

ParaSurfTM not only fits the surface itself (i.e. the radial distances) to spherical harmonic expansions, but also the four local properties (see 1.8). In this way, a completely analytical description of the shape of the molecule and its intermolecular binding properties is obtained. [19] This description can be truncated at different orders l depending on the application and the precision needed. Thus, a simple description of the molecular properties (shape, MEP, IE_L, EA_L and α_L) to order 2 consists of only five sets of nine coefficients each, or 45 coefficients. These coefficients can be rotated, overlaps calculated etc. [5] to give fast scanning of large numbers of compounds.

Note that, because of the approximate nature of the spherical-harmonic fits, the default isodensity level for the shrink-wrapped surface ($0.00002 \text{ e}^{-\text{\AA}^{-3}}$) is lower than that ($0.0003 \text{ e}^{-\text{\AA}^{-3}}$) appropriate for an approximately van der Waals' surface using the marching-cube algorithm. The lower value avoids the surface coming too close to atoms. Note also that the fits are incremental, which means that the order chosen for a given application can be obtained by ignoring coefficients of higher order in the spherical-harmonic series.

In some cases, the default resolution of the molecular surface does not allow fitting the spherical-harmonic expansion to very high orders without introducing noise ("ripples") on the fitted surface. In this case, the calculated RMSD becomes larger at higher orders of the spherical-harmonic expansion. ParaSurf¹⁰TM recognizes this condition and truncates the fitting procedure at the optimum value. This can be recognized in the output because the RMSD for later cycles remains constant and the coefficients of the higher order spherical harmonics are all zero. This guarantees the optimum fit in each case and is important for applications that use either the spherical-harmonic coefficients themselves or the hybridization coefficients.

The choice of centre for fitting to a spherical-harmonic expansion is critical. ParaSurf'10™ therefore goes through a multi-step procedure in order to find a suitable centre. This procedure is retained for all molecules for which the ParaSurf'08™ found a suitable centre. However, if the algorithms implemented in ParaSurf'08™ fail to find a suitable centre, the additional technique implemented in ParaSurf'10™ will probably work.

The problem with many molecules is that, for instance, the centre of mass does not lie within the molecular volume. This can easily be the case for, for instance, U- or L-shaped molecules. The procedure implemented in ParaSurf'10™ works as follows:

1. The program first calculates the centre of mass and tests whether it lies within the volume of the molecule. If it does, it is used as the molecular centre. If not, the program moves on to the next step.
2. ParaSurf™ calculates the principal moments of inertia of the molecule and derives a centre from them by assuming that the molecule is U- or V-shaped. The procedure tries to place the centre at the base centre of the molecule. This procedure was implemented in ParaSurf'08™ as a fallback if the centre of mass proved unsuitable. If it also fails to find a suitable centre, ParaSurf'10™ moves on to a third option, which finds a centre for all but the most difficult molecules.
3. The new procedure first searches for the largest plane in the molecule (i.e. the one that contains the most atoms). This search has some leeway, so that the atoms must not all lie exactly in the plane. As a second step, the second largest plane is sought. The molecular centre is then placed in the hinge area between the two planes, as illustrated in Figure 8:

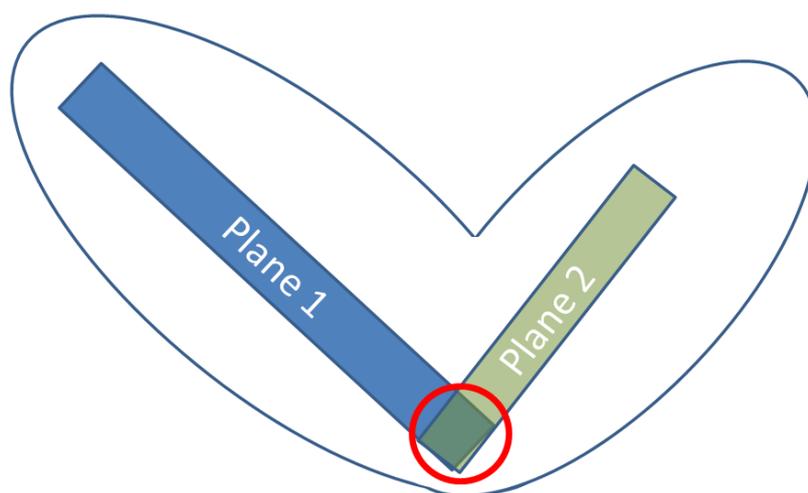


Figure 8 Schematic representation of the planes and hinge area used to determine the centre for spherical-harmonic expansions.



1.8 Local properties

The local properties calculated by ParaSurf™ are those related to intermolecular interactions. Local properties, sometimes inaccurately called fields in QSAR work, are properties that vary in space around the molecule and therefore have a distribution of values at the molecular surface. The best known and most important local property in this context is the molecular electrostatic potential, which governs Coulomb interactions, but the MEP only describes a part of the intermolecular interaction energy, so that further local properties are needed.

1.8.1 Molecular electrostatic potential

The MEP is defined in ParaSurf™ as the energy of interaction of a single positive electronic charge at the position \mathbf{r} with the molecule. Within quantum mechanical (semiempirical or *ab initio* molecular orbital (MO) theory, density functional theory (DFT)) the MEP ($V(\mathbf{r})$) is described [6] as:

$$MEP(\mathbf{r}) = \sum_{i=1}^n \frac{Z_i}{|\mathbf{R}_i - \mathbf{r}|} - \int \frac{\rho(\mathbf{r}') d\mathbf{r}'}{|\mathbf{r}' - \mathbf{r}|} \quad (4)$$

where n is the number of atoms in the molecule, Z_i is the nuclear charge of atom i located at \mathbf{R}_i and $\rho(\mathbf{r})$ is the electron-density function of the molecule. This expression, however, involves integrating the electron density, a time-consuming calculation. ParaSurf™ therefore uses two different approximate models for calculating the MEP.

1.8.1.1 The natural atomic orbital/PC (NAO-PC) model

The NAO-PC model [20, 21] uses a total of nine point charges, one positive charge at the nucleus and eight negative ones distributed around it, to describe the electrostatics of a non-hydrogen atom with a valence-only s - and p -basis set for the semiempirical Hamiltonians MNDO, [22] AM1 [23] and PM3. [24] The negative charges are located at the charge centres of each lobe of the natural atomic orbitals, which are obtained by diagonalising the one-atom blocks of the density matrix. [20] The NAO-PC charges are calculated by VAMP and output in the .sdf file for use in ParaSurf™. The NAO-PC model is therefore only available when using ParaSurf™ with VAMP .sdf input. NAO-PC charges are also not available for semiempirical Hamiltonians such as MNDO/d [25] or AM1* [26] that use d -orbitals in the basis set.

1.8.1.2 The multipole model

The integrals needed to evaluate equation (4) in MNDO-type methods use a multipole approximation [22, 25] that extends to quadrupoles. We can therefore also use this approximation to calculate atom-centred monopoles, dipoles and quadrupoles for each atom in the molecule. [27] This multipole model is applicable to all methods, including those with d -orbitals, and can be used with MOPAC output files as input to ParaSurf™.



1.8.2 Local ionization energy, electron affinity, hardness and electronegativity

The local ionization energy $IE_L(\mathbf{r})$ is defined [7] as a density-weighted Koopmans' ionization potential at a point \mathbf{r} near the molecule:

$$IE_L(\mathbf{r}) = \frac{-\sum_{i=1}^{HOMO} \rho_i(\mathbf{r})\varepsilon_i}{\sum_{i=1}^{HOMO} \rho_i(\mathbf{r})} \quad (5)$$

where $HOMO$ is the number of the highest occupied MO, $\rho_i(\mathbf{r})$ is the electron density at point \mathbf{r} due to MO i and ε_i is its Eigenvalue. The local ionization energy describes the tendency of the molecule to interact with electron acceptors (Lewis acids) in a given region in space. [7, 8]

The definition of the local electron affinity is a simple extension of **equation (5)** to the virtual MOs: [8]

$$EA_L(\mathbf{r}) = \frac{-\sum_{i=LUMO}^{norbs} \rho_i(\mathbf{r})\varepsilon_i}{\sum_{i=LUMO}^{norbs} \rho_i(\mathbf{r})} \quad (6)$$

The local electron affinity is the equivalent of the local ionization energy for interactions with electron donors (Lewis bases). [8]

Equation (6) requires that the occupied and virtual orbitals be approximately equivalent to each other. This is not the case for semiempirical Hamiltonians (such as AM1*) that include d -orbitals as polarisation functions or for extensive basis sets in Hartree-Fock *ab initio* or in Density-Functional theory (DFT) calculations. A new technique has therefore been defined [11] to exclude pure polarisation functions from the summation in **equation (6)**. This technique is now default in ParaSurf'10™ and gives reliable results. For continuity, a new command-line option (EAL09) has been introduced to request that the calculation of the local electron affinity be performed exactly as in ParaSurf'09™ and earlier versions.

Two further, less fundamental local properties have been defined. [8] These are the local hardness, η_L :

$$\eta_L = \frac{(IE_L - EA_L)}{2} \quad (7)$$

and the local electronegativity, χ_L :

$$\chi_L = \frac{(IE_L + EA_L)}{2} \quad (8)$$



1.8.3 Local polarisability

Within the NDDO, the molecular electronic polarisability is easily accessible using the parameterized version [28] of the variational technique introduced by Rivail, [29] which can also be partitioned into an additive polarisability scheme. [30] This allows us to define the local polarisability, α_L , at a point near the molecule as

$$\alpha_L(\mathbf{r}) = \frac{\sum_{j=1}^{norbs} \rho_j^1(\mathbf{r}) q_j \bar{\alpha}_j}{\sum_{j=1}^{norbs} \rho_j^1(\mathbf{r}) q_j} \quad (9)$$

where q_j is the Coulson occupation and $\bar{\alpha}_j$ the isotropic polarisability attributed to atomic orbital j . The density ρ_j^1 is defined as the electron density at the point in question due to an exactly singly occupied atomic orbital j . The sum is now over atomic orbitals, rather than MOs as for the other local properties. Thus, the local polarisability is a simple occupation-weighted sum of the orbital polarisabilities in which the contribution of each AO is determined by the density of the individual AO at the point being considered.

1.8.4 Field normal to the surface

The electrostatic field (the first derivative of the potential) normal to the molecular surface is closely related to the electrostatic solvation energy in implicit solvation models. [31, 32] This field also has the advantage that it is largely independent of the total molecular charge, so that charged molecules can be compared with neutral ones. If the molecular electrostatic potential is used for this purpose, the charge of ions leads a shift in the potential descriptors, so that molecules and ions with different charges cannot be compared directly. The direction of the normal field (inwards or outwards) also defines, for instance hydrogen-bond donors and acceptors specifically.

1.9 Descriptors

A set of 81 molecular descriptors derived from the MEP, local ionization energy, IE_L , electron affinity, EA_L , electronegativity, χ_L , hardness, η_L , and polarisability, α_L has been defined for QSPR-studies. [9] These and several related descriptors calculated and output by ParaSurf™ are defined in the following table.



Table 1: The descriptors calculated by ParaSurf™

Descriptor	Description	Formula/ Reference	Symbol in CSV file
μ	Dipole moment		dipole
μ_D	Dipolar density	[25]	dipden
α	Molecular electronic polarisability	[33]	polarizability
MW	Molecular weight		MWt
G	Globularity	[34]	globularity
A	Molecular surface area		totalarea
VOL	Molecular volume		volume
V_{\max}	Maximum (most positive) MEP	[35]	MEPmax
V_{\min}	Minimum (most negative) MEP	[35]	MEPmin
\bar{V}_+	Mean of the positive MEP values	[35]	meanMEP+
\bar{V}_-	Mean of the negative MEP values	[35]	meanMEP-
\bar{V}	Mean of all MEP values	[35]	meanMEP
ΔV	MEP-range	[35]	MEP-range
σ_+^2	Total variance in the positive MEP values	[35]	MEPvar+
σ_-^2	Total variance in the negative MEP values	[35]	MEPvar-
σ_{tot}^2	Total variance in the MEP	[35]	MEPvartot
v	MEP balance parameter	[35]	MEPbalance
$\sigma_{tot}^2 v$	Product of the total variance in the MEP and the balance parameter	[35]	var*balance
γ_1^V	Skewness of the MEP-distribution	$\gamma_1^{\alpha_L} = \frac{\sum_{i=1}^N (\alpha_L^i - \bar{\alpha}_L)^3}{(N-1)\sigma^3}$	MEPskew
γ_2^V	Kurtosis of the MEP-distribution	$\gamma_2^V = \frac{\sum_{i=1}^N (V_i - \bar{V})^4}{(N-1)\sigma^4} - 3$	MEPkurt
\int_V	Integrated MEP over the surface	$\int_V = \sum_{i=1}^N V_i a_i$	MEPint



Descriptor	Description	Formula/ Reference	Symbol in CSV file
IE_L^{\max}	Maximum value of the local ionization energy		IELmax
IE_L^{\min}	Minimum value of the local ionization energy		IELmin
\overline{IE}_L	Mean value of the local ionization energy	$\overline{IE}_L = \frac{1}{N} \sum_{i=1}^N IE_L^i$	IELbar
ΔIE_L	Range of the local ionization energy	$\Delta IE_L = IE_L^{\max} - IE_L^{\min}$	IELrange
σ_{IE}^2	Variance in the local ionization energy	$\sigma_{IE}^2 = \frac{1}{N} \sum_{i=1}^N \left[IE_L^i - \overline{IE}_L \right]^2$	IELvar
$\gamma_1^{IE_L}$	Skewness of the local ionization energy distribution	$\gamma_1^{IE_L} = \frac{\sum_{i=1}^N (IE_L^i - \overline{IE}_L)^3}{(N-1)\sigma^3}$	IELskew
$\gamma_2^{IE_L}$	Kurtosis of the local ionization energy distribution	$\gamma_2^{IE_L} = \frac{\sum_{i=1}^N (IE_L^i - \overline{IE}_L)^4}{(N-1)\sigma^4} - 3$	IELkurt
\int_{IE_L}	Integrated local ionization energy over the surface	$\int_{IE_L} = \sum_{i=1}^N IE_L^i a_i$	IELint
EA_L^{\max}	Maximum of the local electron affinity		EALmax
EA_L^{\min}	Minimum of the local electron affinity		EALmin
\overline{EA}_{L+}	Mean of the positive values of the local electron affinity	$\overline{EA}_{L+} = \frac{1}{N^+} \sum_{i=1}^{N^+} EA_{L+}^i$	EALbar+
\overline{EA}_{L-}	Mean of the negative values of the local electron affinity	$\overline{EA}_{L-} = \frac{1}{N^-} \sum_{i=1}^{N^-} EA_{L-}^i$	EALbar-
\overline{EA}_L	Mean value of the local electron affinity	$\overline{EA}_L = \frac{1}{N} \sum_{i=1}^N EA_L^i$	EALbar
ΔEA_L	Range of the local electron affinity	$\Delta EA_L = EA_L^{\max} - EA_L^{\min}$	EALrange
σ_{EA+}^2	Variance in the local electron affinity for all positive values	$\sigma_{EA+}^2 = \frac{1}{m} \sum_{i=1}^m \left[EA_i^+ - \overline{EA}^+ \right]^2$	EALvar+
σ_{EA-}^2	Variance in the local electron affinity for all negative values	$\sigma_{EA-}^2 = \frac{1}{n} \sum_{i=1}^n \left[EA_i^- - \overline{EA}^- \right]^2$	EALvar-
σ_{EAtot}^2	Sum of the positive and negative variances in the local electron affinity	$\sigma_{EAtot}^2 = \sigma_{EA+}^2 + \sigma_{EA-}^2$	EALvartot



Descriptor	Description	Formula/ Reference	Symbol in CSV file
v_{EA}	Local electron affinity balance parameter	$v_{EA} = \frac{\sigma_{EA+}^2 \cdot \sigma_{EA-}^2}{[\sigma_{EA}^2]^2}$	EALbalance
δA_{EA}^+	Fraction of the surface area with positive local electron affinity	$\delta A_{EA}^+ = \frac{A_{EA}^+}{A},$ A = total surface area	EALfraction+
A_{EA}^+	Surface area with positive local electron affinity		EALarea+
$\gamma_1^{EA_L}$	Skewness of the local electron affinity distribution	$\gamma_1^{EA_L} = \frac{\sum_{i=1}^N (EA_L^i - \overline{EA_L})^3}{(N-1)\sigma^3}$	EALskew
$\gamma_2^{EA_L}$	Kurtosis of the local electron affinity distribution	$\gamma_2^{EA_L} = \frac{\sum_{i=1}^N (EA_L^i - \overline{EA_L})^4}{(N-1)\sigma^4} - 3$	EALkurt
\int_{EA_L}	Integrated local electron affinity over the surface	$\int_{EA_L} = \sum_{i=1}^N EA_L^i a_i$	EALint
α_L^{\max}	Maximum value of the local polarisability		POLmax
α_L^{\min}	Minimum value of the local polarisability		POLmin
$\overline{\alpha_L}$	Mean value of the local polarisability	$\overline{\alpha_L} = \frac{1}{N} \sum_{i=1}^N \alpha_L^i$	POLbar
$\Delta\alpha_L$	Range of the local polarisability	$\Delta\alpha_L = \alpha_L^{\max} - \alpha_L^{\min}$	POLrange
σ_α^2	Variance in the local polarisability	$\sigma_\alpha^2 = \frac{1}{N} \sum_{i=1}^N [\alpha_L^i - \overline{\alpha_L}]^2$	POLvar
$\gamma_1^{\alpha_L}$	Skewness of the local polarisability distribution	$\gamma_1^{\alpha_L} = \frac{\sum_{i=1}^N (\alpha_L^i - \overline{\alpha_L})^3}{(N-1)\sigma^3}$	POLskew
$\gamma_2^{\alpha_L}$	Kurtosis of the local polarisability distribution	$\gamma_2^{\alpha_L} = \frac{\sum_{i=1}^N (\alpha_L^i - \overline{\alpha_L})^4}{(N-1)\sigma^4} - 3$	POLkurt
\int_{α_L}	Integrated local polarisability over the surface	$\int_{\alpha_L} = \sum_{i=1}^N \alpha_L^i a_i$	POLint
χ_L^{\max}	Maximum value of the local electronegativity		ENEGmax
χ_L^{\min}	Minimum value of the local electronegativity		ENEGmin



Descriptor	Description	Formula/ Reference	Symbol in CSV file
$\overline{\chi_L}$	Mean value of the local electronegativity	$\overline{\chi_L} = \frac{1}{N} \sum_{i=1}^N \chi_L^i$	ENEGbar
$\Delta\chi_L$	Range of the local electron electronegativity	$\Delta\chi_L = \chi_L^{\max} - \chi_L^{\min}$	ENEGrange
σ_{χ}^2	Variance in the local electronegativity	$\sigma_{\chi}^2 = \frac{1}{N} \sum_{i=1}^N \left[\chi_L^i - \overline{\chi_L} \right]^2$	ENEGvar
$\gamma_1^{\chi_L}$	Skewness of the local electronegativity distribution	$\gamma_1^{\chi_L} = \frac{\sum_{i=1}^N (\chi_L^i - \overline{\chi_L})^3}{(N-1)\sigma^3}$	ENEGskew
$\gamma_2^{\chi_L}$	Kurtosis of the local electronegativity distribution	$\gamma_2^{\chi_L} = \frac{\sum_{i=1}^N (\chi_L^i - \overline{\chi_L})^4}{(N-1)\sigma^4} - 3$	ENEGkurt
\int_{χ_L}	Integrated local electronegativity over the surface	$\int_{\chi_L} = \sum_{i=1}^N \chi_L^i a_i$	ENEGint
η_L^{\max}	Maximum value of the local hardness		HARDmax
η_L^{\min}	Minimum value of the local hardness		HARDmin
$\overline{\eta_L}$	Mean value of the local hardness	$\overline{\eta_L} = \frac{1}{N} \sum_{i=1}^N \eta_L^i$	HARDbar
$\Delta\eta_L$	Range of the local electron hardness	$\Delta\eta_L = \eta_L^{\max} - \eta_L^{\min}$	HARDrange
σ_{η}^2	Variance in the local hardness	$\sigma_{\eta}^2 = \frac{1}{N} \sum_{i=1}^N \left[\eta_L^i - \overline{\eta_L} \right]^2$	HARDvar
$\gamma_1^{\eta_L}$	Skewness of the local hardness distribution	$\gamma_1^{\eta_L} = \frac{\sum_{i=1}^N (\eta_L^i - \overline{\eta_L})^3}{(N-1)\sigma^3}$	HARDskew
$\gamma_2^{\eta_L}$	Kurtosis of the local hardness distribution	$\gamma_2^{\eta_L} = \frac{\sum_{i=1}^N (\eta_L^i - \overline{\eta_L})^4}{(N-1)\sigma^4} - 3$	HARDkurt
\int_{η_L}	Integrated local hardness over the surface	$\int_{\eta_L} = \sum_{i=1}^N \eta_L^i a_i$	HARDint
F_N^{\max}	Maximum value of the electrostatic field normal to the surface		FNmax
F_N^{\min}	Minimum value of the field normal to the surface		FNmin



Descriptor	Description	Formula/ Reference	Symbol in CSV file
$\overline{F_N}$	Mean value of the field normal to the surface	$\overline{F_N} = \frac{1}{N} \sum_{i=1}^N \chi_L^i$	FNmean
σ_F^2	Variance in field normal to the surface	$\sigma_F^2 = \frac{1}{N} \sum_{i=1}^N \left[F_N^i - \overline{F_N} \right]^2$	FNvartot
σ_{F+}^2	Variance in the field normal to the surface for all positive values	$\sigma_{F+}^2 = \frac{1}{m} \sum_{i=1}^m \left[F_N^{i+} - \overline{F_N^+} \right]^2$	FNvar+
σ_{F-}^2	Variance in the field normal to the surface for all negative values	$\sigma_{F-}^2 = \frac{1}{n} \sum_{i=1}^n \left[F_N^{i-} - \overline{F_N^-} \right]^2$	FNvar-
ν_F	Normal field balance parameter	$\nu_F = \frac{\sigma_{F+}^2 \cdot \sigma_{F-}^2}{\left[\sigma_F^2 \right]^2}$	FNbal
$\gamma_1^{F_N}$	Skewness of the field normal to the surface	$\gamma_1^{F_N} = \frac{\sum_{i=1}^N (F_N^i - \overline{F_N})^3}{(N-1)\sigma^3}$	FNskew
$\gamma_2^{F_N}$	Kurtosis of the field normal to the surface	$\gamma_2^{F_N} = \frac{\sum_{i=1}^N (F_N^i - \overline{F_N})^4}{(N-1)\sigma^4} - 3$	FNkurt
\int_{F_N}	Integrated field normal to the surface over the surface	$\int_{F_N} = \sum_{i=1}^N F_N^i a_i$	FNint
$\int_{F_N}^+$	Integrated field normal to the surface over the surface for all positive values	$\int_{F_N}^+ = \sum_{i=1}^N F_N^i a_i$ if $F_N^i \geq 0$	FN+
$\int_{F_N}^-$	Integrated field normal to the surface over the surface for all negative values	$\int_{F_N}^- = \sum_{i=1}^N F_N^i a_i$ if $F_N^i < 0$	FN-
$\int_{ F_N }$	Integrated absolute field normal to the surface over the surface	$\int_{ F_N } = \sum_{i=1}^N F_N^i a_i$	FNabs
Additionally if the Shannon Entropy is calculated			
H_{in}^{\max}	Maximum value of the internal Shannon Entropy		SHANImax
H_{in}^{\min}	Minimum value of the internal Shannon Entropy		SHANImin
$\overline{H_{in}}$	Mean value of the internal Shannon Entropy	$\overline{H_{in}} = \frac{1}{N} \sum_{i=1}^N H_{in}^i$	SHANImbar
$\sigma_{H_{in}}^2$	Variance in the internal Shannon Entropy	$\sigma_{H_{in}}^2 = \frac{1}{N} \sum_{i=1}^N \left[H_{in}^i - \overline{H_{in}} \right]^2$	SHANIvar



Descriptor	Description	Formula/ Reference	Symbol in CSV file
$\int_{H_{in}}$	Integrated internal Shannon Entropy over the surface	$\int_{H_{in}} = \sum_{i=1}^N H_{in}^i a_i$	SHANItot
And if the external Shannon Entropy is available			
H_{ex}^{max}	Maximum value of the external Shannon Entropy		SHANEmax
H_{ex}^{min}	Minimum value of the external Shannon Entropy		SHANEmin
$\overline{H_{ex}}$	Mean value of the external Shannon Entropy	$\overline{H_{ex}} = \frac{1}{N} \sum_{i=1}^N H_{ex}^i$	SHANEbar
$\sigma_{H_{ex}}^2$	Variance in the external Shannon Entropy	$\sigma_{H_{ex}}^2 = \frac{1}{N} \sum_{i=1}^N \left[H_{ex}^i - \overline{H_{ex}} \right]^2$	SHANEvar
$\int_{H_{ex}}$	Integrated internal Shannon Entropy over the surface	$\int_{H_{ex}} = \sum_{i=1}^N H_{ex}^i a_i$	SHANEtot

1.10 Surface-integral models (polynomial version)

The polynomial surface-integral models that can be calculated by ParaSurf™ are defined [10] using the expression

$$P = \sum_{i=1}^{ntri} f(V^i, IE_L^i, EA_L^i, \alpha_L^i, \eta_L^i) \cdot A^i \quad (10)$$

where P is the target property, usually a free energy, f is a polynomial function of the electrostatic potential V , the local ionization energy, IE_L , the local electron affinity, EA_L , the local polarisability, α_L and the local hardness, η_L . A^i is the area of the surface triangle i .

The molecular property P is printed to the output file and to the <filename>_p.sdf ParaSurf™ output SD-file. The individual values of the function f are added to the list of local properties written for each surface point to the .psf file if the surface details are output.

The surface-integral models themselves are not implemented directly in ParaSurf™, but are read in general form from the SIM file, whose format is given in 3.9. Thus, the users' own surface-integral models can be added to ParaSurf™. Data for generating surface-integral models can be derived simply from the .psf surface output for a normal ParaSurf™ run. Note that the program options given in the SIM file must be the same for all the models included in the file and that they override conflicting command-line options.

1.11 Binned surface-integral models

A more recent type of SIM model, binned SIM models, [13] is now implemented in ParaSurf¹⁰™ for the negative logarithm of the water-octanol partition constant, $\log P_{OW}$. These models divide the surface into bins according to the values of the local properties and use the total surface area assigned to each bin as descriptors for multiple linear regression models. These models have been implemented for marching cube surfaces using either the isodensity or solvent-excluded surfaces and for the AM1, AM1*, MNDO, MNDO/d, PM3 and PM6 Hamiltonians. In contrast to polynomial SIM models, they are encoded in the program and are output under the heading “ParaSurf™ ADMET Profiler”. A particular feature of the ParaSurf™ $\log P_{OW}$ models is that they are available in two versions. The first, denoted “conformationally averaged”, uses a standard calculational protocol in which the initial 3D structure is produced by CORINA [36] as the starting geometry for the semiempirical geometry optimization and uses only this one conformation to predict $\log P_{OW}$ for the compound. These models were trained on a large subset of the LogKOW dataset. [37] The second type of model, denoted “single conformation” was trained only on molecules without rotatable bonds (approximately 1,500 in all). These models should therefore be used in Boltzmann-weighted multi-conformational models, but are potentially very accurate. [13]

Table 2: The 28 local properties and products thereof used to construct binned area descriptors.

MEP	IE_L	EA_L	α_L	F_N	η_L	χ_L
	$MEP \times IE_L$	$MEP \times EA_L$	$MEP \times \alpha_L$	$MEP \times F_N$	$MEP \times \eta_L$	$MEP \times \chi_L$
		$IE_L \times EA_L$	$IE_L \times \alpha_L$	$IE_L \times F_N$	$IE_L \times \eta_L$	$IE_L \times \chi_L$
			$EA_L \times \alpha_L$	$EA_L \times F_N$	$EA_L \times \eta_L$	$EA_L \times \chi_L$
				$\alpha_L \times F_N$	$\alpha_L \times \eta_L$	$\alpha_L \times \chi_L$
					$F_N \times \eta_L$	$F_N \times \chi_L$
						$\eta_L \times \chi_L$

Local hydrophobicities and $\log P_{OW}$ models are available for the following combinations of Hamiltonians, surfaces and contours. The three letter model code is used to write the local hydrophobicity to the output .vmp file or to specify that the descriptors for the model are written out.



Table 3: Local hydrophobicity models and their model codes.

Hamiltonian	Surface	Contour	Training set	Model code
AM1	Marching Cube	Isodensity	CORINA Conformation	LP1
		Isodensity	Conformationally dependent	LS1
AM1*		Isodensity	Conformationally dependent	LS2
PM3		Isodensity	CORINA Conformation	LP3
		Isodensity	Conformationally dependent	LS3
MNDO		Isodensity	CORINA Conformation	LP4
		Isodensity	Conformationally dependent	LS4
MNDO/d		Isodensity	Conformationally dependent	LS5
PM6		Isodensity	Conformationally dependent	LS6

1.12 Spherical harmonic “hybrids”

Once the molecular shape or a local property have been fitted to a spherical-harmonic expansion, [17] the shape or property can be described succinctly as a series of spherical-harmonic “hybridization” coefficients analogous to the concept of hybrid atomic orbitals. Thus, for each value of l in **equation (1)** the “hybridization” coefficient H_l is given by:

$$H_l = \sum_{i=-m}^m (c_l^m)^2 \quad (11)$$

The hybridization coefficients H_l can be used as additional descriptors for fast QSPR screening.

1.13 Descriptors and moments based on polynomial surface-integral models

ParaSurf™ uses local properties defined in a surface-integral model (SIM, see 1.10) to calculate descriptors analogous to those listed in **Table 1**. Additionally, “dipolar moments” of the local property are calculated. These are gauge-independent moments calculated by first shifting values of the local property so that their sum is zero and then calculating moments according to

$$\mu = \sum_{i=1}^{ntri} P_i \mathbf{r}_i \quad (12)$$

where μ is the dipolar moment, P_i the value of the local property i situated at position \mathbf{r}_i .

The output for these properties derived from a SIM for $\log P_{OW}$ is shown below:

Descriptors calculated for $\log P$:

Dipolar moment	x:	-549.2	y:	-247.9	z:	-937.0
				Sum:	1114.	
Most positive value	:	1.407				
Most negative value	:	0.8325E-01				
Range	:	1.324				
Mean	:	0.1874				
Mean positive	:	0.1874				
Mean negative	:	0.000				
Total variance	:	0.2376E-01				
Positive variance	:	0.2376E-01				
Negative variance	:	0.000				
Balance parameter	:	0.000				
Balance*variance	:	0.000				

The values of these descriptors are often useful for deriving models directly related to the property modelled by the SIM. Note that no units are given in the output because they depend on the property modelled by the SIM.

1.14 Shannon entropy

The information content at the surface of the molecule can be defined based on the distribution of the four local properties over the surface using an approach analogous to that introduced by Shannon. [38]

Shannon defined the Shannon entropy, H , which corresponds to the amount of information (in bits) as

$$H = -\sum_{i=1}^n p_i \log_2(p_i) \quad (13)$$

where n is the number of possible characters and p_i is the probability that character i will occur. Note that, importantly, this definition of the amount of information is local (*i.e.* it only depends on the value of the probability of character i).

For a continuous property, X , **equation (1)** becomes



$$H = - \int_{-\infty}^{\infty} p(X) \log_2 p(X) dX \quad (14)$$

If we now assume that the Shannon entropy at a point in space near a molecule is defined by the values of the four continuous local properties described above, we obtain

$$H = - \iiint p(V, I, E, \alpha) \log_2 (V, I, E, \alpha) dV dI dE d\alpha \quad (15)$$

where $p(V, I, E, \alpha)$ is the probability of finding the values V, I, E and α . However, we can simplify this expression because the four properties are essentially independent of each other, [8, 9] so that we can write

$$H = - \int p(V) \log_2 p(V) dV - \int p(I) \log_2 p(I) dI \\ - \int p(E) \log_2 p(E) dE - \int p(\alpha) \log_2 p(\alpha) d\alpha \quad (16)$$

Transferring this definition to a molecule for which a triangulated surface of k triangles, where triangle i has area A_i and average values of the four local properties V_i, I_i, E_i and α_i we obtain

$$H = - \sum_{i=1}^k [p(V_i) \log_2 p(V_i) + p(I_i) \log_2 p(I_i) + p(E_i) \log_2 p(E_i) + p(\alpha_i) \log_2 p(\alpha_i)] \cdot A_i \quad (17)$$

where $p(X_i)$ is the probability that the value X_i of the property X , where X may be V, I, E or α , will occur.

ParaSurf™ offers two alternatives as sources for the probabilities $p(X_i)$. The first, known as the “external” Shannon entropy, is to use probabilities taken from an external dataset and defined in a separate statistics file. The default “external” statistics file is called **bins.txt** and is read from the ParaSurf™ root directory. The statistics defined in **bins.txt** were derived from AM1 calculations of all the bound ligands defined in the PDBbind database [39] in their correct protonation states and at geometries obtained by optimizing with AM1 starting from the bound conformation. [40]

Alternatively, the user can define a custom “external” statistics file using the ParaSurf™ module **binner** (available free of charge for ParaSurf™ users). The “external” Shannon entropy is useful for relating a series of molecules to each other, but is sensitive, for instance, to the total charge of the molecule.

The “internal” Shannon entropy is calculated using probabilities determined from the surface properties of the molecule itself, and therefore corresponds more closely to Shannon’s classical definition than the “external” Shannon entropy and the probabilities used are individual for each molecule. The “internal” Shannon entropy can be considered to represent the information content of the molecule. The properties of the two types of Shannon entropy will be described in a forthcoming paper.

1.15 Surface autocorrelations

Gasteiger et al. [40] introduced the concept of surface autocorrelations as powerful descriptions of molecular binding properties for quantitative structure-activity relationships (QSARs). In ParaSurf™, autocorrelations $A(R)$ are defined as:

$$A(R) = \frac{1}{ntri} \sum_{i=1}^{ntri} \sum_{j=i+1}^{ntri} \omega_{ij} e^{-\sigma(R-r_{ij})^2} \quad (18)$$

where r_{ij} is the distance between surface points i and j and ω_{ij} is a function of one or more local properties at the points i and j . The smoothing factor σ determines the steepness of the exponential function.

Four different autocorrelation functions are calculated by ParaSurf™. These are:

Shape autocorrelation	$\omega_{ij} = 1.0$	
Plus-plus MEP autocorrelation (V1)	$\omega_{ij} = V_i \times V_j$	$(V_i > 0 \text{ and } V_j > 0)$
	$\omega_{ij} = 0.0$	$(V_i < 0 \text{ or } V_j < 0)$
Minus-minus MEP autocorrelation (V1)	$\omega_{ij} = V_i \times V_j$	$(V_i < 0 \text{ and } V_j < 0)$
Plus-minus MEP autocorrelation (V2)	$\omega_{ij} = -V_i \times V_j$	$(V_i \times V_j < 0)$
	$\omega_{ij} = 0.0$	$(V_i \times V_j > 0)$

Autocorrelation functions based on the other three local properties correlate very strongly with the shape autocorrelation and are therefore not calculated.

ParaSurf™ calculates autocorrelations as vectors of $A(R)$ values 128 elements long starting at an R -value of 2.5 Å and increasing in steps of 0.06 Å (i.e. up to a maximum value of 10.12 Å). Figure 9 shows the four autocorrelation functions for trimethoprim calculated with AM1.

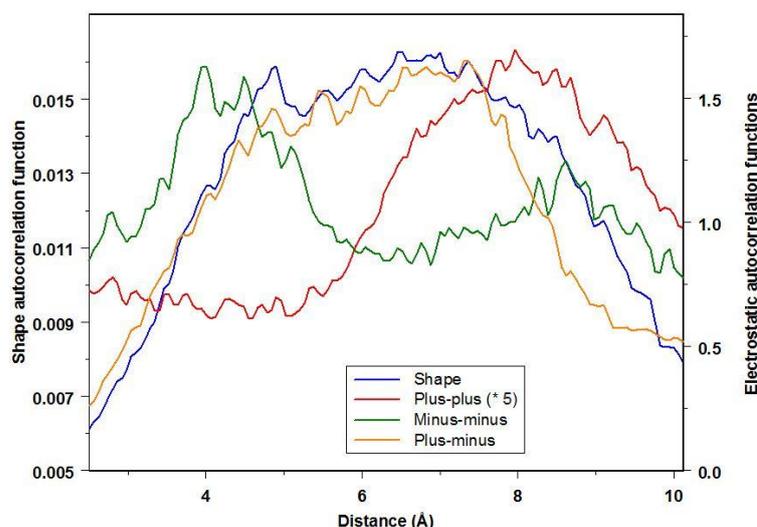


Figure 9 The four autocorrelation functions calculated using the AM1 Hamiltonian for trimethoprim.

The command-line argument `autocorr=<filename>` requests that similarities in the autocorrelation functions with the molecule described in `<filename>`, where `<filename>` must be a `ParaSurf.sdf` output file. The similarities S are defined as:

$$S = \frac{1}{N} \sum_{i=1}^N \frac{2 \cdot \min(A_1(R_i), A_2(R_i))}{(A_1(R_i) + A_2(R_i))} \quad (19)$$

where $A_1(R_i)$ is the value of the autocorrelation function for molecule 1 at distance R_i etc. To avoid division by zero, the summation ignores values of i for which the sum $A_1(R_i) + A_2(R_i)$ is zero. N is therefore the number of points within the defined range of R for which this sum is non-zero.

These similarities are calculated for the entire range of each of the three autocorrelation functions and also for the first, second, third and fourth quartal of the distance range for each of the autocorrelation functions (i.e. 2.5-4.42 Å, 4.426-6.34 Å, 6.346-8.26 Å and 8.266-10.12 Å). These individual similarities can be written to a table file (see 3.12) and are printed in the output file (see 3.4.4).

1.16 Standard Rotationally Invariant Fingerprints (RIFs)

Mavridis et al. [41] introduced standard rotationally invariant fingerprints (RIFs) based on the spherical-harmonic hybridization coefficients defined above. These fingerprints provide a detailed description of the molecular shape, electrostatics, donor/acceptor properties and polarisability as a standard series of 54 floating point numbers.

1.17 Maxima and Minima of the Local Properties

Jakobi et al. [42] have described the calculation and use of the most significant maxima and minima of the local properties on the surface of the molecule. These points were used in the ParaFrag procedure to detect scaffold hops with high similarity and can be viewed as pharmacophore points.

1.18 Atom-centred descriptors

Hennemann et al. [15, 16] have used atom-centred quantities calculated by ParaSurf™ as descriptors in order to calculate the strengths of hydrogen bonds [15] and for chemical reactivity models [16].



These descriptors (based on conventional solvent-accessible surface areas [43] using Bondi van der Waals radii [44] and a default solvent radius of 1.4 Å), C-H bond orders for hydrogen atoms, the constitution of the localized lone-pair orbitals on nitrogen atoms and the π -charges of carbon atoms in conjugated π -systems. These descriptors are now output by ParaSurf'10™.

1.19 Fragment analysis

ParaSurf'10™ can divide the input molecule into fragments (which must be defined in the input SDF file) and perform a full surface analysis for each fragment. This option and its output will be described in detail below.

2 PROGRAM OPTIONS

2.1 Command-line options

ParaSurf™ program options are given as command-line arguments. Arguments are separated by blanks, so that no single argument may contain a blank character. Arguments may be written in any combination of upper and lower case. The options are:

Table 4: ParaSurf™ command-line options

<name>		<p>Base name for the input file (must be the first argument).<name> is not required if the first argument is -version (see below)</p> <p>Using this option, the input file is assumed to be <name>_v.sdf if a file with this name exists.</p> <p>Otherwise the file <name>.sdf will be used as input.</p> <p>If neither of these files are found, the program will use an .sdf file written by the Cepos version of Mopac 6. These files are called <name>_m.sdf</p> <p>The output files are <name>_p.out <name>_p.sdf <name>.psf (optional) <name>.asd (optional) <name>_p.vmp (optional)</p>
surf=	wrap cube	Shrink-wrap surface (default) Marching-cube surface
contour=	isoden solvex	The surface is defined by the electron density A solvent-excluded surface is used.
fit=	sphh isod none	Spherical-harmonic fitting (default for surf=wrap) Smooth to preset isodensity value (default for surf=cube) No fitting
iso=	n.nn	Isodensity value set to n.nn e⁻³ (default for shrink-wrap surface = 0.00002 ; default for marching-cube surface = 0.0003 ; minimum possible value = 0.00001)
rsol=	n.nn	A solvent-probe radius of n.nn Å is used for calculating the solvent-excluded or solvent-accessible surface (default= 1.0 , allowed range is from 0.0 to 2.0 Å)

		not be centred and will correspond to the input coordinates and those in the SDF -output file.
shannon	=<filename>	Requests that Shannon entropies (both internal and external) be calculated. If no statistics file <filename> is given, the default file (bins.txt in the ParaSurf™ Root directory) will be used. If a statistics file is given that either does not exist, contains errors or is derived from ParaSurf™ runs using different options to the current one, only the internal Shannon entropy is calculated.
autocorr	=<filename>	Requests that the surface autocorrelation functions be calculated and written to the output .sdf file. <filename> must be a ParaSurf™ output .sdf file that contains the autocorrelation functions. In this case, similarities between the two molecules will be calculated and printed (see also aclist=).
table=	<filename>	An ASCII table of the ParaSurf™ descriptors will be written to the file <filename> . If <filename> exists, the values for the current molecule will be appended to the existing table, otherwise the file will be created.
aclist=	<filename>	An ASCII table of the calculated autocorrelation similarities will be written to the file <filename> . If <filename> exists, the values for the current molecule will be appended to the existing table, otherwise the file will be created.
riflist=	<filename>	An ASCII table of the calculated a standard rotationally invariant fingerprint (RIF) will be written to the file <filename> . If <filename> exists, the values for the current molecule will be appended to the existing table, otherwise the file will be created.
translate	=n.nn	Requests that ParaSurf™ performs low-resolution spherical-harmonic fits using translated centres at $(+n.nn, 0, 0)$, $(-n.nn, 0, 0)$, $(0, +n.nn, 0)$, $(0, -n.nn, 0)$, $(0, 0, +n.nn)$ and $(0, 0, -n.nn)$ relative to the original centre. The default value of n.nn is 0.5 Å. This value is obtained if translate is used alone. The maximum value of n.nn allowed is 1.0 Å. The translate option will be needed for later versions of ParaFit™ that allow translation of the molecule when overlaying.
translate 2	=n.nn	Requests that ParaSurf™ performs a more detailed translation scan with low-resolution spherical-harmonic fits using translated centres at $(+n.nn, 0, 0)$, $(+2n.nn, 0, 0)$, $(-n.nn, 0, 0)$, $(-2n.nn, 0, 0)$, $(0, +n.nn, 0)$, $(0, +2n.nn, 0)$, $(0, -n.nn, 0)$, $(0, -2n.nn, 0)$, $(0, 0, +n.nn)$, $(0, 0, +2n.nn)$, $(0, 0, -n.nn)$ and $(0, 0, -2n.nn)$ relative to the original centre. The default value of n.nn is 0.25 Å. This value is obtained if translate2 is used alone. The maximum value of n.nn allowed is 0.5 Å. The translate2 option will be needed for later versions of ParaFit™ that allow translation of the molecule when overlaying.
fragments		Perform a fragment analysis. The fragments must be defined in the input SDF file

<code>desfile= <filename></code>	Write the binned SIM descriptors to the file <code><filename></code> . If <code><filename></code> exists, the values for the current molecule will be appended to the existing table, otherwise the file will be created. The descriptors are written as a comma-separated table with headers. Note that <code>desmodel</code> must also be defined.
<code>desmodel= <code></code>	The bin definitions for the model denoted by <code><code></code> will be used to calculate the descriptors for the table of binned SIM descriptors. The possible values of <code><code></code> and their definitions are given in Table 2 .
<code>-version</code>	Must be the first argument. Requests that ParaSurf [™] prints the version number to the standard output channel and then stops without performing a calculation.
<code>eal09</code>	Do not use the selection procedure for virtual orbitals [11] when calculating the local electron affinity. This option provides continuity with earlier versions of ParaSurf [™]

Examples:

```
parasurf test surf=wrap fit=sphh iso=0.03 psf=on estat=naopc
```

Use the input file `test_v.sdf`, `test.sdf` or `test_m.sdf` to calculate a shrink-wrap surface with an isodensity value of $0.03 \text{ e}^{-\text{\AA}^{-3}}$, perform a spherical-harmonic fit, use NAO-PC electrostatics and write the spherical-harmonic coefficients to `test_P.sdf` and the entire surface to `test_P.psf`.

```
parasurf test surf=cube fit=none
```

Use the file `test_v.sdf`, `test.sdf` or `test_m.sdf` as input to perform a marching-cube surface determination without fitting and to calculate the descriptor set.

2.2 Options defined in the input SDF-file

2.2.1 Defining the centre for spherical-harmonic fits

The automatic determination of the molecular centre for spherical-harmonic fitting can be overridden by adding a field to the Input (usually VAMP) SDF-file with the tag:

`<SPHH_CENTER>`

The centre can be defined using Cartesian coordinates using an input line (immediately after the `SPHH_CENTER` tag) of the format:

Cartesian **x.xx** **y.yy** **z.zz**



where **x.xx**, **y.yy** and **z.zz** are the x, y, and z-coordinates, respectively. The capitalization of “**Cartesian**” is required.

Alternatively, a list of atoms can be given using the format

```
Atoms n1 n2 n3 n4 n5 n6 ...
```

where **n1** etc. are the numbers of the atoms to be used to calculate the centre of gravity. The capitalization of “**Atoms**” is required and the list of atoms is limited to one line.

2.2.2 Defining fragments

Molecular fragments can be defined in the input SDF file and fragments calculations requested using the fragments options, for instance

```
parasurf test surf=cube fragments
```

Figure 10 shows a sample <fragment> block from an SDF input file.

```
> <FRAGMENTS>
Start fragment
phenyl
  3  4  5 15 16 19 25 33
End fragment

Start fragment
methoxy1
  1  2 22 23 24
End fragment

Start fragment
methoxy2
 17 18 34 35 36
End fragment

Start fragment
methoxy3
 20 21 37 38 39
End fragment

Start fragment
methylene
  6 26 27
End fragment

Start fragment
thymine
  7  8  9 10 11 12 13 14 28 29 30 31 32
End fragment

Start fragment
everybody
  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
End fragment

> <END_FRAGMENTS>
```

Figure 10 A sample <FRAGMENTS> input block.

The first line after each "Start fragment" line (note the upper and lower case, which are necessary) defines the name given to the fragment. This is followed by the numbers of the atoms that make up the fragment (20i4, fixed format). Note that the fragments need not be mutually exclusive. The fragment "everybody" in the above example, for instance is the entire molecule. The fragment-definition block begins with

> <FRAGMENTS>

and ends with

> <END_FRAGMENTS>

tags.

Figure 11 shows the input molecule and the fragments.

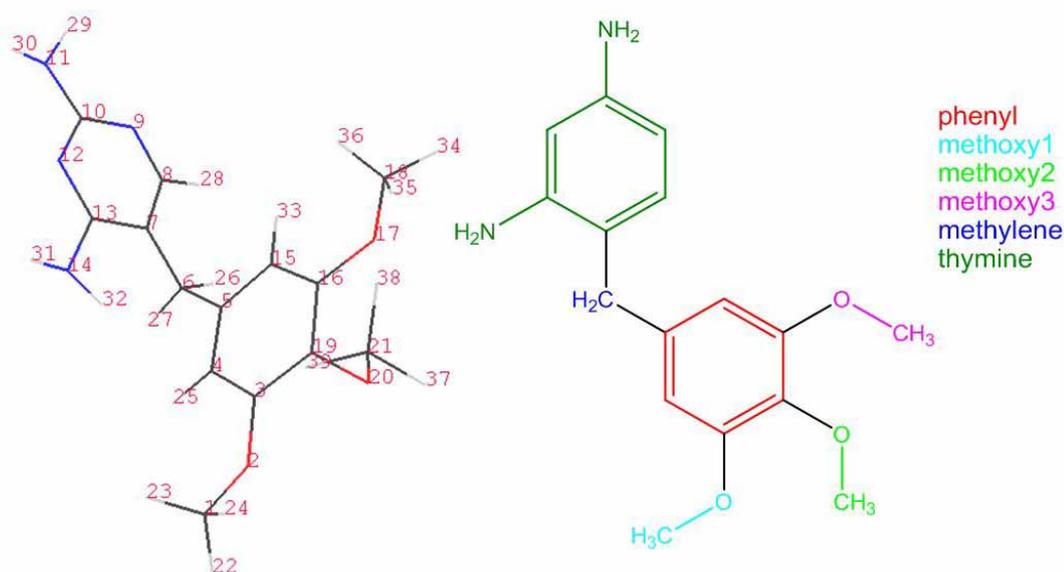


Figure 11 The fragments defined in the SDF input example.

In a FRAGMENTS run, ParaSurf™ first performs a calculation for the entire molecule and then analyses the molecular surface according to the standard ParaSurf™ technique used to assign surface triangles to individual atoms. The output for the phenyl fragment is shown in Figure 12. A similar output section is printed for each fragment. The results and the descriptors for each fragment are taken from the surface for the whole molecule and therefore refer to the fragment (both its electronic properties and the area of its surface) within the context of the molecule itself. The coordinates given for the maxima and minima of the local properties refer to the input geometry of the entire molecule.



```
<> Results for fragment number 1 : phenyl
Surface area   :      41.72 Angstrom**2
Fragment charge :      -0.01

      MEP      IEL      EAL      HARD      ENEG      F(N)      POL
Mean   :  -14.1   511.9   -70.5   291.2   220.7     0.0     0.30
Mean +ve:   10.4           0.0           3.0
Mean -ve:  -22.7          -70.5          -2.7
Maximum :   16.3   643.2   -29.1   371.3   279.1    18.9     0.33
Minimum  :  -64.8   427.1  -100.9   259.6   165.4   -15.0     0.25
Variance:  343.7  2538.6  439.1  445.7  1043.2    16.3    0.20E-03
Var. +ve:   15.1           0.0           13.0
Var. -ve:  172.8          439.1           4.1
Balance  :   0.074          0.000          0.181
Skew    :   -0.2     0.0     0.1     1.0    -0.5     2.3    -0.44
Kurtosis:  -0.5     -0.8    -1.3     0.9    -1.3     3.7    -0.41

IEL Maxima for this fragment
Number   x      y      z      IEL
1 :  -0.9431  -0.9603  -3.8285  641.0563
2 :  -0.3098  -1.4603  -0.4785  643.1733

EAL Maxima for this fragment
Number   x      y      z      EAL
1 :  -0.0931  -1.2270  -4.2285  -29.0852
2 :  -1.5231  -1.7186  -3.9785  -30.7426
3 :  -1.4098  -1.8603  -4.0285  -30.0862
5 :   0.7986  -1.0603  -0.4785  -29.7442

POL Maxima for this fragment
Number   x      y      z      POL
1 :  -0.2598  -2.4603  -4.3285   0.3300
2 :   0.0569  -2.3488  -4.3452   0.3301
3 :  -1.9431  -1.2153  -3.8285   0.3246
4 :  -0.3431  -0.0603  -4.0285   0.3211
5 :  -1.9431  -1.0853  -3.8118   0.3257
6 :   0.1286  -2.2603  -0.5285   0.3240
7 :   0.3569  -0.2936  -0.2285   0.3192

FN Maxima for this fragment
Number   x      y      z      FN
1 :   2.0819  -1.2803  -1.0452  13.4716
2 :  -1.5098  -3.7103  -0.7285  12.1519
3 :   0.2619  -0.0603  -0.1785  18.1139
```

Figure 12 ParaSurf10™ output for the phenyl fragment defined above.

The individual surfaces of the fragments are shown in Figure 13.

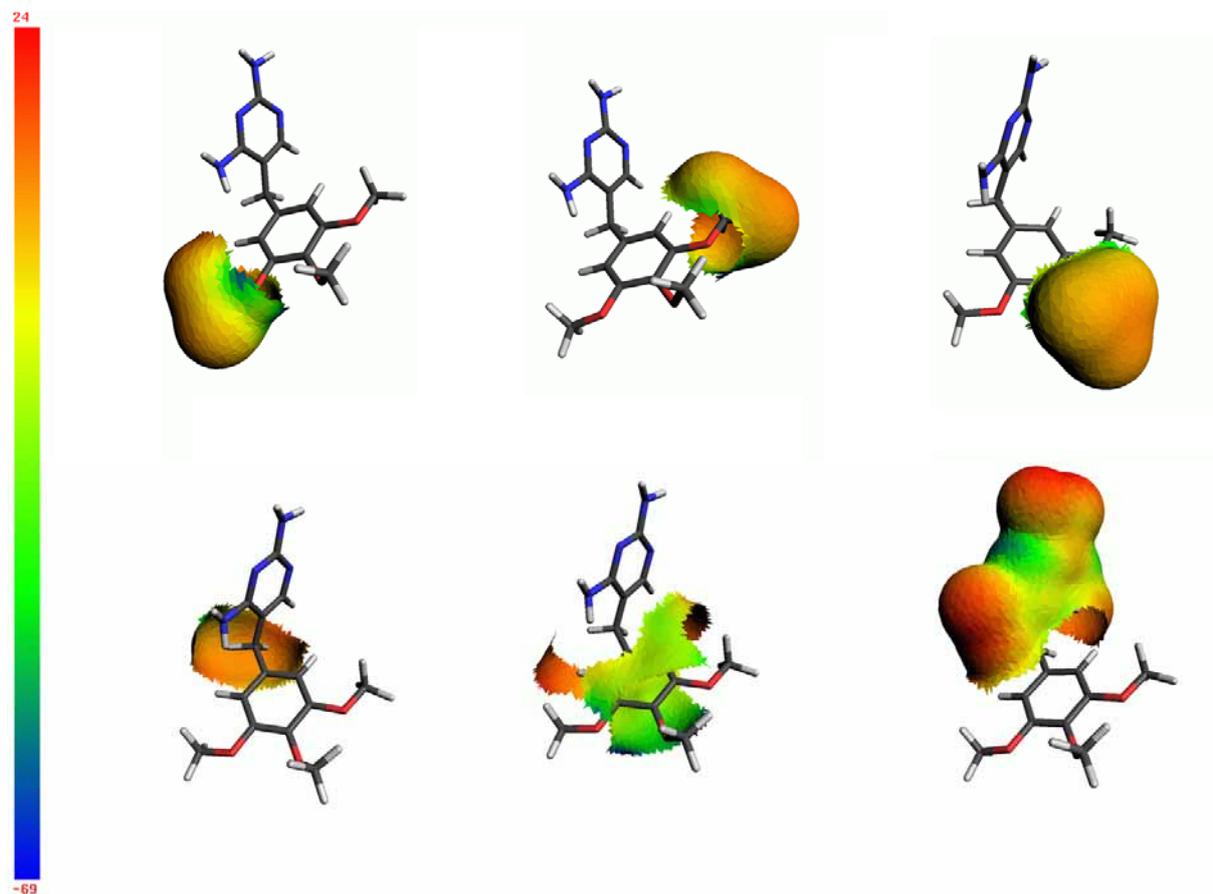


Figure 13 Surfaces calculated for the individual fragments, colour coded according to the MEP in kcal mol^{-1} . The fragments (clockwise from the top right) are methoxy1, methoxy2, methoxy3, thymine, phenyl and methylene.



3 INPUT AND OUTPUT FILES

ParaSurf™ uses the following files for input and output:

Table 5: ParaSurf™ input and output files

File	Name	Description
Input	<filename>_v.sdf or <filename>.sdf (if available) or <filename>_m.sdf	VAMP .sdf file output. VAMP must be run with the ALLVECT option to be able to calculate all the properties. The VAMP version used must be able to calculate AO-polarisabilities. If no VAMP .sdf file is found, ParaSurf™ defaults to a Cepas Mopac 6 .sdf file. It is strongly recommended to use the EF option for geometry optimizations in Mopac.
Hamiltonian	Vhamil.par	The VAMP parameters file (also found in the VAMP executable directory). This file must be copied to the ParaSurf™ executable directory.
Output	<filename>_p.out	Always written.
SD-file	<filename>_p.sdf	Always written.
ASD-file	<filename>.asd	Anonymous SD-file. Requested by the option asd=on
PSF-file	<filename>.psf	ParaSurf™ surface file. Requested by the option psf=on
VMP-file	<filename>_p.vmp	Debug file.
SIM-file	<filename>.sim	Surface-integral model definition. <filename> must have exactly three characters and the file must reside in the ParaSurf™ executable directory.
Descriptor table file	User defined	An ascii, comma-separated file that contains a line of descriptors for each molecule. This file will be created if it does not exist or an extra line will be appended if it does exist.
Binned SIM descriptor file	User defined	An ascii, comma-separated file that contains a line of the descriptors generated for the bin definitions used in the model defined by <code> in the desmodel= command-line option. A header defining the descriptors is printed as the first line.
Autocorrelation similarity file	User defined	An ascii, comma-separated file that contains a line of autocorrelation similarities for each molecule. This file will be created if it does not exist or an extra line will be appended if it does exist.
RIF table file	User defined	An ascii, comma-separated file that contains a line of the standard rotationally invariant fingerprint (RIF [41]) for each molecule. This file will be created if it does not exist or an extra line will be appended if it does exist.



3.1 The VAMP .sdf file as input

VAMP .sdf files, an extension of the MDL .sdf file format, [45] are the primary communication channel between VAMP and ParaSurf™. The atomic coordinates and bond definitions are given in the MDL format as shown in **Figure 14**. The remaining fields are indicated by tags with the form:

<FIELD_NAME>

FIELD_NAME is a predefined text tag used to locate the relevant data within the .sdf file.

Only the important fields for a ParaSurf™ calculation will be described here:

```
1-Bromo-3,5-difluorobenzene
OMVAMP81A04250313563D 1 0.00000 0.00000 0

12 12 0 0 0 0 1 v2000
-2.6274 0.2410 0.0003 F
-1.2738 0.2410 0.0003 C
-0.5810 1.4623 0.0003 C
0.8231 1.4389 0.0003 C
1.5096 2.6055 0.0004 F
1.5266 0.2198 0.0001 C
0.8142 -0.9793 0.0001 C
1.7431 -2.6055 -0.0004 Br
-0.5805 -0.9840 0.0002 C
-1.1264 2.4167 -0.0003 H
2.6274 0.2339 0.0003 H
-1.1515 -1.9253 0.0001 H

1 2 1
2 3 4
3 4 4
4 5 1
4 6 4
6 7 4
7 8 1
2 9 4
7 9 4
3 10 1
6 11 1
9 12 1
M END
```

Figure 14 The headers and titles, atomic coordinates and bond definitions from a VAMP .sdf file. The format follows the MDL definition. [29].

<HAMILTONIAN>

The Hamiltonian field defines the semiempirical Hamiltonian (model and parameters) used for the calculation. The Hamiltonian must be defined for ParaSurf™ to be able to calculate the electrostatics and the local polarisabilities. NAO-PC electrostatics and the local polarisability are not available for all methods. Quite generally, the multipole electrostatics model is to be preferred over the NAO-PC model, which can only be used if the VAMP .sdf file contains a block with the tag:

<NAO-PC>

NAO-PCs cannot be calculated for methods with *d*-orbitals. The local polarisability calculation has not yet been extended to these methods, but will be in a future release.

The following table gives an overview of the methods and their limitations:

Table 6: Hamiltonians and the available electrostatic and polarisability models.

Hamiltonian	Reference	Electrostatics		Local Polarisability
		NAO-PC	Multipole	
MNDO	[22]	YES	YES	YES
AM1	[23]	YES	YES	YES
PM3	[24]	YES	YES	YES
MNDO/c	[46]	YES	YES	NO
MNDO/d	[25]	NO	YES	NO
AM1*	[26]	NO	YES	NO

<VAMPBASICS>

The VAMPBASICS block contains the following quantities (FORTRAN format 6f13.6):

Heat of Formation	kcal mol ⁻¹
HOMO energy	eV
LUMO energy	eV
Dipole moment	
x-component	Debye
y-component	Debye
z-component	Debye

<TOTAL COULSON CHARGE>

The total charge of the molecule.

<DENSITY MATRIX ELEMENTS>

The DENSITY MATRIX ELEMENTS block contains the one-atom blocks of the density matrix for the non-hydrogen atoms. For an *sp*-atom, there are ten elements, for an *spd*-atom 45. The squares of the diagonal elements for hydrogen atoms are included in the <CHARGE ON HYDROGENS> block that follows the density matrix. The density-matrix elements are used in ParaSurf™ to calculate the local properties and are essential.

<ORBITAL VECTORS>

The ORBITAL VECTORS block contains the MO-eigenvectors and related information and is essential for calculating the local properties. VAMP must be run with the keyword **ALLVECT** in order to write all the MO vectors to the SDF file.



The entire SDF input file is echoed to the `<filename>_p.sdf` output file and the properties calculated by ParaSurf™ are added in additional blocks at the end.

3.1.1 Multi-structure SD-files

ParaSurf™ can read SD-files containing more than one molecule (e.g. those produced by the VAMP-QSAR model engine) and process them in one run. The command-line arguments apply to each molecule in the SD-file and the same semiempirical Hamiltonian must be used for each molecule or an error message will be printed and the program terminated.

As part of this enhancement, ParaSurf™ can use SD-files that do not contain the one-atom blocks of the density matrix explicitly. Thus, SD-files that only contain the molecular-orbital Eigenvectors and Eigenvalues give full ParaSurf™ functionality within the previous restrictions that:

- Polarisabilities are not yet available for Hamiltonians that use *d*-orbitals (MNDO/d and AM1*).
- NAO-PC electrostatics are only available if the NAO-PCs are present in the SD-file. Multipole electrostatics are available for all Hamiltonians.

The output SD-file written by ParaSurf™ also contains multiple molecules as in the input file. Other ParaSurf™ output files (.asd, .vmp etc.) are also concatenated.

Multiple SD-files can be used with a SIM file exactly as single molecules.

3.2 The Cepos MOPAC 6.sdf file as input

Cepos Mopac 6 writes an .sdf file containing the above blocks with the exception that the MOPACBASICS block replaces VAMPBASICS. No additional keywords are required to request the correct .sdf output for ParaSurf™.

3.3 The Vhamil.par file

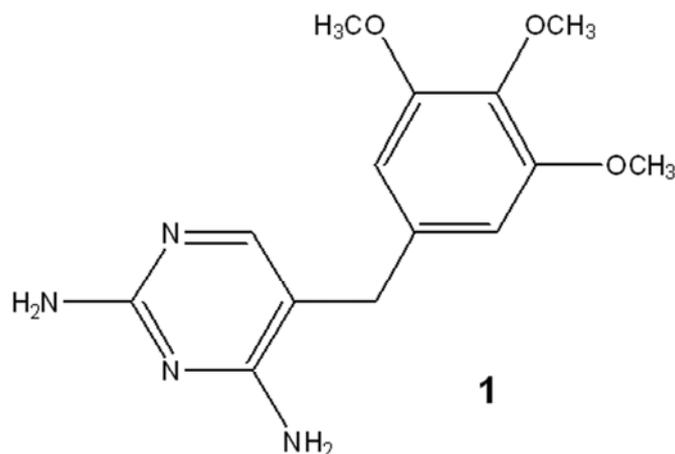
The file Vhamil.par is used by VAMP to define the available Hamiltonians and elements and supply the parameters. This file is also used by ParaSurf™ for the same purpose. A Vhamil.par file for standard Hamiltonians and elements is supplied with the ParaSurf™ program. In order to be sure that all Hamiltonians and elements available to VAMP can also be handled by ParaSurf™, however, the Vhamil.par file from the VAMP executable directory should be copied into the ParaSurf™ executable directory.

3.4 The ParaSurf™ output file

The ParaSurf™ output file provides the user with information about the calculation and the results. It is, however, not intended as the primary means of communication between ParaSurf™ and other programs. Thus, the essential information contained in the output file is also available from the ParaSurf™ output .sdf file.

3.4.1 For a spherical-harmonic surface

Figure 15 shows the output for a calculation using the options `surf=wrap fit=sphh translate` for trimethoprim, **1**.



```

<> ParaSurf'10, Revision A1
<> Copyright (c) 2006,2007,2008,2009,2010 Friedrich-Alexander-Universitaet
    Erlangen-Nuernberg and Cepos InSilico Ltd.
    All rights reserved.

<> Input = trimethoprim.sdf

<<>> Molecule    1 of    1 <<>>

<> Program options :

Using shrink-wrap isocontour surface
Fitting surface to spherical harmonics
Translations for spherical-harmonic fits: 1 step of    0.5000 Angstrom in each direction.
Using an isodensity surface contour
Isodensity value = 0.2000E-04 electrons/Angstrom**3
Triangulation mesh =    0.20 Angstrom
Using multipole electrostatics
    
```

Figure 15 ParaSurf® output for trimethoprim, **1**, using a spherical-harmonic surface.



Figure 15 continued

```
<> AM1 calculation for Trimethoprim

<> Translated spherical-harmonic fits:
dx      dy      dz      rmsd
0.0000  0.0000  0.0000  0.4034
0.5000  0.0000  0.0000  0.5684
-0.5000 0.0000  0.0000  0.5002
0.0000  0.5000  0.0000  0.5611
0.0000 -0.5000  0.0000  0.5193
0.0000  0.0000  0.5000  0.5689
0.0000  0.0000 -0.5000  0.4283

<> Fitting surface to spherical harmonics
<> Order(l)  RMSD

      0      1.92526847
      1      1.96114689
      2      1.55521125
      3      1.10609483
      4      0.93107676
      5      0.70605297
      6      0.63661488
      7      0.57077524
      8      0.52400109
      9      0.50050583
     10      0.47261493
     11      0.44416316
     12      0.41920775
     13      0.40320743
     14      0.39308983
     15      0.38341761
<> Spherical harmonic fit for MEP:
<> Order(l)  RMSD

      0      11.06621848
      1      11.02831889
      2      8.63330698
      3      6.86247364
      4      5.49824707
      5      4.58527334
      6      4.17139337
      7      3.45052537
      8      3.12581239
      9      2.77798689
     10      2.36033975
     11      2.07232627
     12      1.90441930
     13      1.72381187
     14      1.64582625
     15      1.46855812
     16      1.27875373
     17      1.07480393
     18      0.93507876
     19      0.88299081
     20      0.82791747
```



Figure 15 continued

```
<> Spherical harmonic fit for IE(1):
<> Order(1)   RMSD

    0    56.96181478
    1    50.08877418
    2    45.40744632
    3    43.50297274
    4    40.06772200
    5    35.49615651
    6    32.77544861
    7    26.87818719
    8    23.10705894
    9    19.60935653
   10    17.98417050
   11    16.21352138
   12    15.12917785
   13    14.62643122
   14    13.87383640
   15    13.44294950
   16    13.23244532
   17    12.62943635
   18    12.27106930
   19    12.27106930
   20    12.27106930

<> Spherical harmonic fit for EA(1):
<> Order(1)   RMSD

    0    12.18668274
    1    11.86538321
    2    11.74571609
    3     9.50312285
    4     8.72650603
    5     7.28921579
    6     7.13957211
    7     6.79022442
    8     6.48006338
    9     6.02636118
   10     5.73169119
   11     5.46777405
   12     5.18598187
   13     4.51689005
   14     4.11336321
   15     3.92017066
   16     3.68134487
   17     3.60264328
   18     3.40103297
   19     3.23507723
   20     3.10515890
```



Figure 15 continued

```
<> Spherical harmonic fit for Field(N):
<> Order(l)   RMSD
      0      1.69589564
      1      1.67583167
      2      1.55111880
      3      1.39253297
      4      1.20646876
      5      1.11340437
      6      0.99998080
      7      0.83247400
      8      0.80883259
      9      0.77684389
     10      0.72960436
     11      0.64461777
     12      0.59721766
     13      0.52631742
     14      0.51920158
     15      0.51920158
     16      0.51920158
     17      0.51920158
     18      0.51920158
     19      0.51920158
     20      0.51920158

<> Spherical harmonic fit for Alpha(l):
<> Order(l)   RMSD
      0      0.02367100
      1      0.01665303
      2      0.01371808
      3      0.01112413
      4      0.00912405
      5      0.00817327
      6      0.00769192
      7      0.00722555
      8      0.00694967
      9      0.00643212
     10      0.00588304
     11      0.00574182
     12      0.00531887
     13      0.00531378
     14      0.00521159
     15      0.00514920
     16      0.00514920
     17      0.00514920
     18      0.00514920
     19      0.00514920
     20      0.00514920

<> Property ranges:
Density   :   0.3567E-05 to   0.9969E-04
IE(l)     :   391.05 to     671.20
EA(l)     :   -108.56 to   -38.29
MEP       :   -48.50 to     16.80
Alpha(l)  :    0.2368 to    0.3374
Field(N)  :   -10.95 to     2.43
```



Figure 15 continued

```
<> Descriptors :

Dipole moment      :      1.2467 Debye
Dipolar density   :      0.1933E-02 Debye.Angstrom**-3
Molecular pol.    :      128.5408 Angstrom**3
Molecular weight  :      290.32
Globularity       :      0.7689
Total surface area :      469.51 Angstrom**2
Molecular volume  :      644.94 Angstrom**3

Most positive MEP :      16.80 kcal/mol
Most negative MEP :     -48.50 kcal/mol
Mean +ve MEP      :      5.59 kcal/mol
Mean -ve MEP      :     -10.80 kcal/mol
Mean MEP          :      -3.13 kcal/mol
MEP range         :      65.30 kcal/mol
MEP +ve Variance  :      10.80 (kcal/mol)**2
MEP -ve Variance  :      94.38 (kcal/mol)**2
MEP total variance :     105.18 (kcal/mol)**2
MEP balance parameter: 0.0921
MEP balance*variance : 9.6898 kcal/mol
MEP skewness      :     -1.1813
MEP kurtosis      :      1.3859
Integral MEP       :    -1166.52 kcal.Angstrom**2/mol

Maximum IE(1)     :      671.20 kcal/mol
Minimum IE(1)     :      391.05 kcal/mol
Mean IE(1)        :      475.70 kcal/mol
IE(1) range       :      280.15 kcal/mol
IE(1) variance    :     3233.28 (kcal/mol)**2
IE(1) skewness    :      0.6770
IE(1) kurtosis    :     -0.2281
Integral IE(1)    :     9650.55 eV.Angstrom**2

Maximum EA(1)     :     -38.29 kcal/mol
Minimum EA(1)     :    -108.56 kcal/mol
Mean +ve EA(1)    :      0.00 kcal/mol
Mean -ve EA(1)    :     -93.87 kcal/mol
Mean EA(1)        :     -93.87 kcal/mol
EA(1) range       :      70.27 kcal/mol
EA(1) +ve variance : 0.00 (kcal/mol)**2
EA(1) -ve variance : 142.48 (kcal/mol)**2
EA(1) total variance : 142.48 (kcal/mol)**2
EA(1) skewness    :      1.7822
EA(1) kurtosis    :      4.1719
Integral EA(1)    :    -1913.53 eV.Angstrom**2
EA(1) balance param. : 0.0000
Fraction pos. EA(1) : 1.0000 ( = 469.51 Angstrom**2)

Max. local Eneg.  :      299.60 kcal/mol
Min. local Eneg.  :      143.17 kcal/mol
Mean local Eneg.  :      190.92 kcal/mol
Local Eneg. range :      156.43 kcal/mol
Local Eneg. variance : 958.81 (kcal/mol)**2
Local Eneg. skewness : 0.82
Local Eneg. kurtosis : 0.02
Integral local Eneg. : 3868.51 eV.Angstrom**2

Max. local hardness : 371.59 kcal/mol
Min. local hardness : 247.44 kcal/mol
Mean local hardness : 284.79 kcal/mol
Local hard. range : 124.15 kcal/mol
Local hard. variance : 729.07 (kcal/mol)**2
Local hard. skewness : 0.58
Local hard. kurtosis : -0.48
Integral local Hard. : 5782.04 eV.Angstrom**2
```



Figure 15 continued

```
<> Standard rotationally invariant fingerprint:(L. Mavridis, B. D. Hudson
and D. W. Ritchie, J. Chem. Inf. Model., 2007, 47, 1787-1796.)
```

4.19237	1.05400	1.85764	1.68785	1.18769
1.26567	0.867227	3.63609	2.17574	5.11692
4.30008	3.74100	3.27509	2.68739	2.84994
2.15001	2.21810	2.09657	1.89247	1.59418
41.2102	9.49863	9.02058	7.90393	7.70216
7.38806	7.31984	18.0014	2.48822	3.58666
5.09562	3.73325	4.06352	2.92425	1.00675
0.228934	0.182796	0.173025	0.148046	0.122377
0.108944	1.72209	1.43605	1.73496	1.79099
1.73487	1.30824	1.34225	1.45904	1.09655
1.02302	0.924123	1.01307	0.859615	

```
<> Atomic surface properties:
```

Atom	Area	MEP		IE(l)		EA(l)		mean pol.	Field(N)		
		max	min	max	min	max	min		max	min	
C	1	0.000									
O	2	0.073	-38.63	-41.62	535.49	532.95	-77.41	-79.32	0.260	-6.89	-7.51
C	3	3.380	-6.38	-46.92	578.33	474.12	-41.12	-89.61	0.307	1.65	-7.54
C	4	1.259	-5.17	-15.60	573.38	498.18	-67.85	-90.38	0.322	-1.32	-2.72
C	5	0.699	-8.33	-13.90	573.55	531.88	-84.05	-92.54	0.320	-1.85	-3.05
C	6	0.000									
C	7	0.803	-9.81	-15.04	559.27	516.68	-71.66	-91.24	0.319	-0.88	-2.72
C	8	4.155	-1.37	-21.94	585.31	484.68	-48.35	-95.74	0.295	2.43	-1.73
N	9	4.183	-14.72	-32.41	535.55	452.61	-79.85	-104.91	0.279	1.59	-6.57
C	10	10.328	-1.84	-27.18	633.68	532.90	-38.86	-86.78	0.284	1.52	-2.98
N	11	0.000									
N	12	1.441	-14.69	-33.29	538.04	472.64	-74.72	-98.64	0.268	0.31	-5.93
C	13	6.263	-8.51	-26.51	637.06	512.83	-38.29	-82.55	0.286	2.16	-7.40
N	14	0.000									
C	15	2.104	-7.00	-15.39	589.73	496.41	-64.28	-92.21	0.316	-1.22	-10.76
C	16	3.888	-11.81	-43.40	569.55	479.96	-40.72	-85.82	0.310	-0.57	-8.44
O	17	0.000									
C	18	0.000									
C	19	6.191	-17.33	-48.50	583.22	465.65	-46.33	-86.05	0.315	-0.75	-7.77
O	20	2.039	-31.11	-44.39	532.30	445.05	-75.31	-93.15	0.247	-4.08	-7.49
C	21	0.000									
H	22	32.636	13.06	-39.48	560.92	405.94	-82.21	-99.66	0.297	1.30	-6.93
H	23	21.586	14.07	-20.13	561.93	408.35	-83.75	-96.08	0.294	1.53	-3.51
H	24	24.162	14.04	-30.19	567.47	407.17	-68.79	-95.29	0.292	1.32	-4.39
H	25	6.870	11.16	-5.32	527.12	425.97	-83.14	-95.64	0.288	1.11	-2.07
H	26	18.505	7.91	-7.43	535.39	400.22	-87.77	-100.66	0.299	1.23	-2.63
H	27	17.884	7.35	-20.62	543.64	399.67	-68.59	-100.81	0.303	1.04	-5.35
H	28	26.817	8.86	-27.87	536.84	413.57	-60.23	-103.43	0.284	1.94	-4.90
H	29	33.032	16.80	-28.67	671.20	474.61	-71.99	-107.85	0.248	2.20	-6.24
H	30	32.852	16.44	-28.20	669.03	476.76	-72.53	-107.92	0.241	2.18	-5.50
H	31	33.925	11.43	-28.95	657.35	471.32	-67.58	-108.56	0.244	2.17	-8.10
H	32	9.935	11.30	-27.11	642.05	472.51	-73.10	-99.96	0.259	2.29	-10.95
H	33	5.296	9.88	-13.60	504.92	434.61	-73.74	-96.58	0.295	1.34	-8.06
H	34	29.289	11.33	-40.37	565.02	406.91	-80.26	-99.68	0.291	1.32	-8.75
H	35	23.555	11.45	-33.33	567.66	407.69	-72.90	-95.65	0.292	1.33	-5.91
H	36	23.014	11.40	-13.11	563.89	407.56	-81.58	-99.03	0.295	1.28	-3.93
H	37	33.964	4.59	-38.61	554.62	394.98	-87.16	-108.55	0.294	0.57	-6.68
H	38	18.880	4.19	-40.99	558.72	396.48	-84.55	-108.23	0.298	0.50	-7.12
H	39	26.446	3.97	-34.03	550.48	391.05	-86.20	-107.61	0.296	0.55	-5.39
Total		465.455									



Figure 15 continued

```
<> Atomic surface properties:
```

Atom	Area	MEP		IE (l)		EA (l)		mean pol.	Field(N)		
		max	min	max	min	max	min		max	min	
C	1	0.000									
O	2	0.073	-38.63	-41.62	535.49	532.95	-77.41	-79.32	0.260	-6.89	-7.51
C	3	3.380	-6.38	-46.92	578.33	474.12	-41.12	-89.61	0.307	1.65	-7.54
C	4	1.259	-5.17	-15.60	573.38	498.18	-67.85	-90.38	0.322	-1.32	-2.72
C	5	0.699	-8.33	-13.90	573.55	531.88	-84.05	-92.54	0.320	-1.85	-3.05
C	6	0.000									
C	7	0.803	-9.81	-15.04	559.27	516.68	-71.66	-91.24	0.319	-0.88	-2.72
C	8	4.155	-1.37	-21.94	585.31	484.68	-48.35	-95.74	0.295	2.43	-1.73
N	9	4.183	-14.72	-32.41	535.55	452.61	-79.85	-104.91	0.279	1.59	-6.57
C	10	10.328	-1.84	-27.18	633.68	532.90	-38.86	-86.78	0.284	1.52	-2.98
N	11	0.000									
N	12	1.441	-14.69	-33.29	538.04	472.64	-74.72	-98.64	0.268	0.31	-5.93
C	13	6.263	-8.51	-26.51	637.06	512.83	-38.29	-82.55	0.286	2.16	-7.40
N	14	0.000									
C	15	2.104	-7.00	-15.39	589.73	496.41	-64.28	-92.21	0.316	-1.22	-10.76
C	16	3.888	-11.81	-43.40	569.55	479.96	-40.72	-85.82	0.310	-0.57	-8.44
O	17	0.000									
C	18	0.000									
C	19	6.191	-17.33	-48.50	583.22	465.65	-46.33	-86.05	0.315	-0.75	-7.77
O	20	2.039	-31.11	-44.39	532.30	445.05	-75.31	-93.15	0.247	-4.08	-7.49
C	21	0.000									
H	22	32.636	13.06	-39.48	560.92	405.94	-82.21	-99.66	0.297	1.30	-6.93
H	23	21.586	14.07	-20.13	561.93	408.35	-83.75	-96.08	0.294	1.53	-3.51
H	24	24.162	14.04	-30.19	567.47	407.17	-68.79	-95.29	0.292	1.32	-4.39
H	25	6.870	11.16	-5.32	527.12	425.97	-83.14	-95.64	0.288	1.11	-2.07
H	26	18.505	7.91	-7.43	535.39	400.22	-87.77	-100.66	0.299	1.23	-2.63
H	27	17.884	7.35	-20.62	543.64	399.67	-68.59	-100.81	0.303	1.04	-5.35
H	28	26.817	8.86	-27.87	536.84	413.57	-60.23	-103.43	0.284	1.94	-4.90
H	29	33.032	16.80	-28.67	671.20	474.61	-71.99	-107.85	0.248	2.20	-6.24
H	30	32.852	16.44	-28.20	669.03	476.76	-72.53	-107.92	0.241	2.18	-5.50
H	31	33.925	11.43	-28.95	657.35	471.32	-67.58	-108.56	0.244	2.17	-8.10
H	32	9.935	11.30	-27.11	642.05	472.51	-73.10	-99.96	0.259	2.29	-10.95
H	33	5.296	9.88	-13.60	504.92	434.61	-73.74	-96.58	0.295	1.34	-8.06
H	34	29.289	11.33	-40.37	565.02	406.91	-80.26	-99.68	0.291	1.32	-8.75
H	35	23.555	11.45	-33.33	567.66	407.69	-72.90	-95.65	0.292	1.33	-5.91
H	36	23.014	11.40	-13.11	563.89	407.56	-81.58	-99.03	0.295	1.28	-3.93
H	37	33.964	4.59	-38.61	554.62	394.98	-87.16	-108.55	0.294	0.57	-6.68
H	38	18.880	4.19	-40.99	558.72	396.48	-84.55	-108.23	0.298	0.50	-7.12
H	39	26.446	3.97	-34.03	550.48	391.05	-86.20	-107.61	0.296	0.55	-5.39
Total		465.455									



Figure 15 continued

```
<> Stationary points on the molecular surface (A. Jakobi, H. Mauser
and T. Clark, J. Mol. Model., 2008, 14, 547-558)

      x          y          z          value
<>      5 MEP Maxima      :
      4.7936      2.2899      -2.2084      11.45
      2.4965      4.0712      5.7445      12.67
      1.0770      5.8131      5.4602      16.80
      -2.2439     -2.1297      2.8572      11.43
      -5.5622     -3.4081     -0.8626      14.07
<>      3 MEP Minima      :
      -0.3945     -4.1333     -2.6456     -48.50
      1.9197     -2.8411     -3.4453     -42.54
      2.5161     -2.1045     -3.3008     -43.40
<>      3 IEL Maxima      :
      -1.4144      5.4218      3.9311      671.2
      -3.4005      1.4346      2.5848      657.3
      2.5158      3.2319      3.2339      642.2
<>      13 IEL Minima     :
      2.1418      1.5561     -4.5855      407.7
      0.4940     -4.6999      1.7295      391.5
      -4.0895     -2.9712      1.8500      408.4
      3.6525      1.2975      1.2233      407.6
      0.1300     -4.7857      1.5109      391.0
      -2.8688     -6.9328     -1.6690      405.9
      0.1327      5.3805     -2.2317      413.6
      -3.7288     -1.8541     -3.8279      407.2
      2.7277     -6.5570     -2.9447      395.0
      -4.8206      1.4292      0.2199      399.7
      4.7699     -2.4304      0.0000      396.5
      -1.4313      2.8849     -3.5503      400.2
      6.1623     -1.4832     -2.6349      406.9
<>      4 EAL Maxima      :
      -2.9928      2.6947      2.3379     -38.29
      0.4747     -0.8240     -3.7107     -40.72
      -1.6927      4.7425      3.2127     -38.86
      -0.8097     -1.8229     -3.5122     -41.12
<>      10 EAL Minima     :
      0.2649     -5.2698     -2.4638     -106.9
      1.8583      6.9358      2.6243     -107.9
      3.2295     -3.3153     -3.2557     -108.5
      -1.0575      0.1415      5.3927     -108.6
      0.7838     -3.6877      1.7626     -104.7
      0.1522     -5.6007     -1.7682     -108.0
      0.9842     -4.8653     -3.4860     -106.7
      0.4813      2.5816      6.0814     -107.9
      0.9630     -3.4415      1.7646     -104.7
      0.4219     -4.0142      1.6785     -104.7
<>      4 Alpha(l) Maxima :
      0.0000      0.0000     -3.4565      0.3237
      -1.3158     -0.7255     -3.2393      0.3286
      -2.9170      3.4094      0.9959      0.3259
      0.4062     -2.4010     -3.8398      0.3374
<>      5 Alpha(l) Minima :
      0.7758     -4.0667     -3.4739      0.2387
      0.0553     -4.3637     -2.7928      0.2397
      0.6923      3.3892      6.7598      0.2372
      -1.5392     -0.4236      5.3172      0.2411
      0.4406     -4.1863     -3.2471      0.2368
<>      0 F(N) Maxima      :
<>      0 F(N) Minima      :
<> ParaSurf used          15.97 seconds CPU time
```



After printing the program options, ParaSurf'10™ prints the shift in coordinates of the centre and the RMSD fits for the surface requested by the `translate` option. For speed, these fits use a lower number of surface points than the full fits that follow and are only calculated up to order six. The translated spherical-harmonic coefficients are printed in the output SDF file for use by ParaFit™. ParaSurf'10™ then moves on to fit the calculated shrink-wrap surface at full resolution for each of the local properties. It lists the root-mean-square deviations (RMSDs) for the surface points as a function of the order of the spherical-harmonic expansion, first for the geometry of the surface and then for each of the five local properties. The RMSD values give an idea of how well each order of the spherical-harmonic expansion fits the calculated shrink-wrap surface or the relevant property. The highest order used by ParaSurf™ is 15 for the surface itself and 20 for each property.

The descriptor table is then printed. For molecules with no surface areas with positive EA_L , $\sigma_{EA_L}^2$ is set to zero. The descriptors are those described in Table 1.

The spherical-harmonic hybridization coefficients are then listed for the shape and the five local properties. The coefficients are listed by increasing l starting from zero. The standard rotationally invariant fingerprint (RIF) [41] is printed. Note that the individual RIF-values correspond to the square roots of the hybridization coefficients from the tables above and that the RIF definition has been expanded to include hybridization coefficients of the field normal to the surface (the last 13 elements).

The table of atomic surface properties is derived by first finding the atom that contributes most (according to a Coulson analysis) to the electron density for each surface point. The point is then assigned to this atom and the maxima and minima in the MEP, IE_L , EA_L and F_N as well as the mean local polarisability for the points assigned to each atom are calculated. Note that, because of the fitting procedure, the values reported in this table may contain spurious ones if the fitted surface comes particularly close to an atom (or does not approach it). This situation is generally recognisable from the RMSD values printed for the fit. The surface used to calculate the descriptors and atomic-surface properties is the fitted spherical-harmonic surface of order 15.

The maxima and minima of the local properties selected according to the criteria outlined in reference 34 are then listed. These points are defined by their Cartesian coordinates and the corresponding values of the local property. In this example, no significant maxima and minima were found for the field normal to the surface. Generally, more maxima and minima are found for isodensity surfaces than for spherical-harmonic ones.



3.4.2 For a marching-cube surface

Figure 16 shows the output for a calculation using the options `surf=cube` for trimethoprim.

```
<> ParaSurf'10, Revision A1
<> Copyright (c) 2006,2007,2008,2009,2010 Friedrich-Alexander-Universitaet
    Erlangen-Nuernberg and Cepos InSilico Ltd.
    All rights reserved.

<> Input = trimethoprim.sdf

<<>> Molecule    1 of    1 <<>>

<> Program options :

    Using marching-cube isodensity surface
    Surface fitting turned off
    Using an isodensity surface contour
    Isodensity value = 0.3000E-03 electrons/Angstrom**3
    Triangulation mesh =    0.20 Angstrom
    Using multipole electrostatics

<> AM1 calculation for Trimethoprim
<> Number of triangles = 15024
<> Number of unique points : 7517

<> Property ranges:
Density : 0.2881E-03 to 0.3099E-03
IE(1)   : 392.35 to 654.76
EA(1)   : -109.82 to -29.09
MEP     : -69.88 to 24.82
Alpha(1) : 0.2288 to 0.3301
Field(N) : -29.18 to 18.88
```

Figure 16 ParaSurf™ output for trimethoprim using a marching-cube surface.



Figure 16 continued

```
<> Descriptors :

Dipole moment      :      1.2467 Debye
Dipolar density   :      0.3155E-02 Debye.Angstrom**-3
Molecular pol.    :      128.5408 Angstrom**3
Molecular weight  :      290.32
Globularity       :      0.7042
Total surface area :      369.79 Angstrom**2
Molecular volume  :      395.13 Angstrom**3

Most positive MEP :      24.82 kcal/mol
Most negative MEP :     -69.88 kcal/mol
Mean +ve MEP      :      9.05 kcal/mol
Mean -ve MEP      :     -18.72 kcal/mol
Mean MEP          :      -4.94 kcal/mol
MEP range         :      94.70 kcal/mol
MEP +ve Variance  :      31.60 (kcal/mol)**2
MEP -ve Variance  :     239.92 (kcal/mol)**2
MEP total variance :     271.53 (kcal/mol)**2
MEP balance parameter:      0.1028
MEP balance*variance :     27.9261 kcal/mol
MEP skewness      :     -1.0234
MEP kurtosis      :      0.6111
Integral MEP      :    -1674.26 kcal.Angstrom**2/mol

Maximum IE(1)     :      654.76 kcal/mol
Minimum IE(1)     :      392.35 kcal/mol
Mean IE(1)        :      486.30 kcal/mol
IE(1) range       :      262.41 kcal/mol
IE(1) variance    :     3584.97 (kcal/mol)**2
IE(1) skewness    :      0.4205
IE(1) kurtosis    :     -0.7616
Integral IE(1)    :     7764.76 eV.Angstrom**2

Maximum EA(1)     :     -29.09 kcal/mol
Minimum EA(1)     :    -109.82 kcal/mol
Mean +ve EA(1)    :      0.00 kcal/mol
Mean -ve EA(1)    :     -89.08 kcal/mol
Mean EA(1)        :     -89.08 kcal/mol
EA(1) range       :      80.74 kcal/mol
EA(1) +ve variance :      0.00 (kcal/mol)**2
EA(1) -ve variance :     276.47 (kcal/mol)**2
EA(1) total variance :     276.47 (kcal/mol)**2
EA(1) skewness    :      1.4621
EA(1) kurtosis    :      1.5753
Integral EA(1)    :    -1438.92 eV.Angstrom**2
EA(1) balance param. :      0.0000
Fraction pos. EA(1) :      1.0000 ( = 369.79 Angstrom**2)

Max. local Eneg.  :      290.14 kcal/mol
Min. local Eneg.  :      143.75 kcal/mol
Mean local Eneg.  :      198.61 kcal/mol
Local Eneg. range :      146.39 kcal/mol
Local Eneg. variance :     1205.84 (kcal/mol)**2
Local Eneg. skewness :      0.52
Local Eneg. kurtosis :     -0.78
Integral local Eneg. :     3162.92 eV.Angstrom**2

Max. local hardness :      371.30 kcal/mol
Min. local hardness :      247.91 kcal/mol
Mean local hardness :      287.69 kcal/mol
Local hard. range  :      123.39 kcal/mol
Local hard. variance :     724.88 (kcal/mol)**2
Local hard. skewness :      0.45
Local hard. kurtosis :     -0.66
Integral local Hard. :     4601.84 eV.Angstrom**2
```



Figure 16 continued

```

Maximum alpha(l)      : 0.3301      Angstrom**3
Minimum alpha(l)     : 0.2288      Angstrom**3
Mean alpha(l)        : 0.2830      Angstrom**3
Alpha(l) range       : 0.1013      Angstrom**3
Variance in alpha(l) : 0.4898E-03 Angstrom**6
Alpha(l) skewness    : -0.8040
Alpha(l) kurtosis    : -0.3752
Integral Alpha(l)    : 104.483      Angstrom**5

Maximum field normal  : 18.88 kcal/mol.Angstrom
Minimum field normal  : -29.18 kcal/mol.Angstrom
Mean field           : -0.85 kcal/mol.Angstrom
Field range          : 48.05 kcal/mol.Angstrom
Total field variance : 17.26 (kcal/mol.Angstrom)**2
+ve field variance   : 4.18 (kcal/mol.Angstrom)**2
-ve field variance   : 17.00 (kcal/mol.Angstrom)**2
Field balance param. : 0.16
Field skew           : 2.80
Field kurtosis       : 7.758
Integral F(N)        : -297.8      kcal.Angstrom/mol
Integral F(N +ve)    : 312.3      kcal.Angstrom/mol
Integral F(N -ve)    : -610.1     kcal.Angstrom/mol
Integral |F(N)|      : 922.4      kcal.Angstrom/mol

<> Atomic surface properties:

Atom  Area      MEP          IE(l)          EA(l)          mean      Field(N)
      max      min      max      min      max      min      pol.      max      min
C    1  0.257  -23.83  -46.81  569.04  546.04  -81.50  -92.65  0.268  -5.92  -12.94
O    2  3.658  -15.50  -69.70  594.61  456.71  -63.66  -81.53  0.269   9.41  -16.81
C    3  6.490   -7.36  -64.78  643.17  499.72  -30.09  -99.43  0.304  12.85  -9.93
C    4  2.166   -3.31  -19.76  632.00  493.47  -39.95 -100.75  0.316  -0.27  -5.07
C    5  1.600   -3.37  -18.28  633.56  547.00  -53.42 -100.30  0.313  -0.43  -3.87
C    6  0.000
C    7  2.042   -4.01  -22.33  605.70  512.44  -49.80  -91.06  0.317   6.32  -8.09
C    8  5.665    4.11  -28.25  638.27  488.34  -35.80  -88.30  0.288   6.91  -4.32
N    9  6.693  -19.84  -58.79  571.34  417.76  -54.71 -103.24  0.260   7.37  -19.27
C   10  9.411   -0.86  -46.23  654.76  543.32  -41.17  -81.09  0.279   5.81  -7.91
N   11  0.537  -46.53  -53.00  615.72  593.86  -60.28  -78.98  0.276  -2.51  -11.48
N   12  6.122  -16.63  -55.66  571.30  417.23  -51.01  -98.93  0.247  14.20  -19.99
C   13  7.570  -10.11  -44.07  644.87  527.82  -37.47  -82.80  0.284  12.28  -16.70
N   14  0.713  -41.89  -57.27  618.93  590.90  -64.88  -81.21  0.287 -11.29  -29.18
C   15  4.127   -8.07  -22.33  640.32  494.13  -30.91 -100.89  0.314  18.88  -6.00
C   16  5.886  -15.50  -60.73  641.06  507.48  -29.09  -94.41  0.307  14.49  -15.05
O   17  1.261  -18.70  -69.88  567.04  464.95  -64.27  -87.64  0.252  -4.23  -25.48
C   18  0.289  -16.74  -56.71  573.39  531.54  -74.34  -94.89  0.267  -5.84  -19.88
C   19  5.580  -15.52  -60.03  617.79  492.33  -39.25  -96.42  0.314   4.02  -5.35
O   20  3.960  -31.04  -63.94  579.08  438.53  -69.08  -94.47  0.265  -1.78  -13.88
C   21  0.543  -26.28  -54.82  563.68  530.83  -90.92 -106.12  0.269  -4.37  -10.55
H   22  20.848  22.24  -43.97  561.11  407.48  -83.45  -97.55  0.297   2.66  -13.21
H   23  16.018  22.21  -47.65  566.01  408.34  -70.47  -97.22  0.294   6.30  -5.56
H   24  16.235  22.21  -45.75  567.60  407.90  -66.77  -96.72  0.290   2.62  -9.87
H   25  7.143  16.35   -8.05  537.67  429.84  -70.41  -97.59  0.288   1.88  -4.03
H   26  13.545  13.09   -5.83  579.22  401.23  -85.87 -100.66  0.299   2.24  -3.30
H   27  13.114  11.65  -38.33  611.02  400.48  -74.22 -100.87  0.301   1.87  -13.51
H   28  17.462  13.34  -29.83  533.62  415.38  -56.04 -100.30  0.282   2.54  -5.68
H   29  20.093  24.36  -44.05  639.92  488.09  -72.40 -107.69  0.247   3.99  -15.00
H   30  20.380  24.82  -48.21  644.36  488.15  -70.42 -107.77  0.241   4.31  -17.04
H   31  20.025  22.73  -51.85  642.47  483.89  -67.45 -108.35  0.245   9.76  -27.09
H   32  10.792  22.31  -49.42  644.46  478.52  -79.21 -102.13  0.259   7.86  -26.66
H   33  7.935  15.01  -21.60  523.98  429.34  -65.58  -98.60  0.294   8.18  -7.77
H   34  20.353  17.51  -31.87  560.07  408.27  -87.93  -99.07  0.290   2.42  -12.17
H   35  16.221  17.81  -47.09  565.56  408.31  -66.99  -96.49  0.291   2.42  -12.12
H   36  16.250  17.77  -37.52  557.41  408.14  -69.22  -96.81  0.294  12.54  -6.31
H   37  20.708   8.06  -41.68  545.33  396.15  -95.89 -109.82  0.294   0.99  -9.80
H   38  16.217   8.06  -54.42  595.55  394.15  -82.57 -109.54  0.296   9.51  -11.25
H   39  18.651   7.90  -40.13  586.15  392.35  -74.89 -109.41  0.295   3.19  -4.47

Total  366.558

```



Figure 16 continued

```
<> Stationary points on the molecular surface (A. Jakobi, H. Mauser
and T. Clark, J. Mol. Model., 2008, 14, 547-558)

      x          y          z          value
<>    11 MEP Maxima      :
-3.2288    1.8355    -3.6285    7.168
 3.6569    1.8897    -3.0618    17.81
-1.7098    3.4897    -3.2285    12.76
-0.8648    3.3397    -3.2785    13.34
-5.4931   -3.9386    -2.2285    22.24
-4.2431    0.2897    -2.4285    9.660
 3.0069   -5.0936    -0.8285    8.063
-3.7931   -0.7603     0.1132    6.919
-1.9431   -1.8603     1.1798    19.01
-2.3764   -1.7103     1.7715    22.73
 1.0569    5.1397     4.3215    24.82
<>    12 MEP Minima      :
 1.4569   -3.0103    -3.9285   -63.17
 2.0184   -1.7936    -4.0285   -69.88
-1.4630   -4.0603    -3.4285   -69.70
-1.6931   -4.0603    -0.8285   -55.73
-0.7431    5.5397     0.1165   -53.25
-0.3431    5.5897     0.1498   -57.47
 0.6569    5.2397     0.2882   -54.40
 0.0569    5.5397     0.2082   -58.79
-3.7431    0.5680     1.3882   -55.54
-3.6931    0.7730     1.3265   -57.27
-1.5431    4.9397     2.9548   -53.00
-1.5431    2.1564     3.4715   -55.66
<>    10 IEL Maxima      :
-0.9431   -0.9603    -3.8285   641.1
-0.3098   -1.4603    -0.4785   643.2
 0.5569    2.1397     0.6548   654.8
-3.4431    1.4314     0.9715   625.4
-2.2931    3.5980     0.9515   650.5
-0.2431   -0.0103     1.0765   644.9
-1.1431    5.3397     1.6998   634.2
-3.0431    1.5397     2.1715   635.0
 1.4569    3.2397     2.3798   644.4
-1.7264    3.7397     3.1965   634.5
<>    17 IEL Minima      :
 1.2569    0.8230    -4.9285   411.0
 1.6501    1.3397    -4.9785   408.3
-4.2098   -2.2603    -4.4285   407.9
-1.9431    2.5980    -3.9785   401.2
 2.3236   -6.2603    -3.6285   396.2
 5.2069   -1.0936    -3.6285   408.3
-0.7431    3.9847    -3.2285   418.8
-3.7098   -6.3603    -2.6785   407.5
-0.3931    4.7397    -2.8285   415.4
 3.6569   -2.5603    -1.2285   394.2
-4.7598    1.1397    -1.0525   400.5
 2.9019    0.9397    -0.2452   408.2
 3.0402    1.1397    -0.3285   408.1
 0.0569   -4.8436     0.2715   392.3
 0.3069    5.4397     0.1632   417.8
-4.2014   -3.0603     0.4215   408.3
-0.9681    1.6564     3.4715   417.2
```



Figure 16 continued

<>	5 EAL Maxima	:		
	-0.0931	-1.2270	-4.2285	-29.09
	-1.5231	-1.7186	-3.9785	-30.74
	-1.4098	-1.8603	-4.0285	-30.09
	-2.7431	3.7564	-0.4835	-35.80
	0.7986	-1.0603	-0.4785	-29.74
<>	15 EAL Minima	:		
	0.8569	-4.9186	-3.9785	-106.5
	1.1736	-4.6853	-4.1285	-106.5
	1.6569	-4.3820	-4.1785	-106.7
	1.8319	-4.1770	-4.1285	-106.9
	2.0569	-3.9603	-4.0285	-107.7
	2.4819	-3.6270	-3.7785	-109.8
	-0.0431	-5.5103	-2.4178	-109.4
	3.9569	-3.9770	-2.0285	-106.9
	2.4569	-2.6270	-0.2785	-106.7
	0.0569	5.3397	-0.4285	-103.2
	0.7736	-5.7603	-0.0285	-104.7
	0.6286	-4.4603	0.5715	-104.6
	1.2768	6.2897	1.7715	-107.7
	-1.8024	-0.2436	3.7548	-108.4
	0.0569	2.9147	4.9548	-107.8
<>	9 Alpha(1) Maxima	:		
	-0.2598	-2.4603	-4.3285	0.3300
	0.0569	-2.3488	-4.3452	0.3301
	-1.9431	-1.2153	-3.8285	0.3246
	-0.3431	-0.0603	-4.0285	0.3211
	-1.9431	-1.0853	-3.8118	0.3257
	0.1286	-2.2603	-0.5285	0.3240
	0.3569	-0.2936	-0.2285	0.3192
	-3.1431	2.9397	-0.1785	0.3292
	0.5069	1.6814	-0.0285	0.3187
<>	9 Alpha(1) Minima	:		
	2.2569	-1.7603	-4.0285	0.2343
	-1.7523	-4.0603	-3.5285	0.2365
	-1.6931	-4.0603	-0.8285	0.2373
	2.1569	5.2990	2.5715	0.2441
	1.5402	6.3397	2.4475	0.2441
	1.0569	2.5397	3.1715	0.2409
	-2.0848	-0.4603	3.7215	0.2411
	-0.9681	1.6564	3.4715	0.2288
	0.0569	3.3147	5.1548	0.2372
<>	4 F(N) Maxima	:		
	2.0819	-1.2803	-1.0452	13.47
	-1.5098	-3.7103	-0.7285	12.15
	0.2619	-0.0603	-0.1785	18.11
	0.2069	1.1397	2.2048	13.48
<>	10 F(N) Minima	:		
	1.3069	-3.5820	-4.1285	-12.39
	2.1786	-1.8603	-3.9785	-24.61
	-0.1431	-4.6103	-3.4527	-13.19
	-1.7306	-4.2853	-3.4118	-16.57
	-1.7413	-4.6603	-1.2285	-10.34
	-0.5598	-0.9053	0.3882	-12.28
	-0.0848	5.5897	0.3715	-18.92
	-3.6931	0.7730	1.3265	-28.42
	-1.3431	5.2397	3.1439	-11.61
	-1.5431	2.4680	3.4715	-19.67



Figure 16 continued

```
<> Atomic contributions: :
Model No.      :      1      2
Sum over atoms :      0.3651  -0.5143

Atom      Area      Contributions
C1         0.2572     -0.0122     -0.0122
O2         3.6580     -0.2316     -0.2316
C3         6.4896      0.0378      0.0378
C4         2.1664      0.0325      0.0325
C5         1.5998      0.0298      0.0298
C6         0.0000      0.0000      0.0000
C7         2.0421      0.0255      0.0255
C8         5.6649      0.0637      0.0637
N9         6.6929     -0.3753     -0.3753
C10        9.4110      0.0658      0.0658
N11        0.5374     -0.0006     -0.0006
N12        6.1224     -0.2989     -0.2989
C13        7.5700      0.0522      0.0522
N14        0.7134     -0.0572     -0.0572
C15        4.1265      0.0564      0.0564
C16        5.8856      0.0539      0.0539
O17        1.2609     -0.1132     -0.1132
C18        0.2892     -0.0178     -0.0178
C19        5.5804     -0.0706     -0.0706
O20        3.9601     -0.3800     -0.3800
C21        0.5426     -0.0423     -0.0423
H22       20.8480      0.0546      0.0546
H23       16.0178      0.1067      0.1067
H24       16.2346      0.0611      0.0611
H25        7.1427      0.1142      0.1142
H26       13.5453      0.1275      0.1275
H27       13.1135      0.0458      0.0458
H28       17.4620      0.1426      0.1426
H29       20.0926      0.0337      0.0337
H30       20.3796     -0.0115     -0.0115
H31       20.0253     -0.0240     -0.0240
H32       10.7922      0.0704      0.0704
H33        7.9347      0.0810      0.0810
H34       20.3527      0.0876      0.0876
H35       16.2205      0.0739      0.0739
H36       16.2495      0.1174      0.1174
H37       20.7078      0.1297      0.1297
H38       16.2172      0.0457      0.0457
H39       18.6509      0.1700      0.1700
Constant                0.1209     -0.7584

<> ParaSurf used      12.12 seconds CPU time
```

The table of RMSD values is no longer printed and the range of the electron-density values for the surface points (a test for the quality of the surface) is closer to the target isodensity value (in this case $0.0003 \text{ e}^{-\text{\AA}^{-3}}$) than for the fitted surface. The internal precision used by the program is $\pm 2\%$ of the target isodensity value. The values of the descriptors and the atomic-surface properties are more consistent using the marching-cube surface and are recommended for QSPR and surface-integral applications.



3.4.3 For a job with Shannon entropy

Figures 17 and 18 show the relevant sections of the output for a calculation using the options `surf=cube` for trimethoprim with the extra `shannon` option, which requests internal and external Shannon entropies using the default `bins.txt` statistical background file from the `PARASURF_ROOT` directory. The output is identical to that shown in Figure 16 except that an additional Shannon entropy block is printed after the descriptors, as shown in Figure 17:

	internal	external	
Maximum Shannon H	: 0.4467	0.4786	bits Angstrom**2
Minimum Shannon H	: 0.0448	0.1570	bits Angstrom**2
Mean Shannon H	: 0.2296	0.3624	bits Angstrom**2
Variance Shannon H	: 0.0107	0.0068	bits Angstrom**2
Molecular Shannon H	: 86.24	135.04	bits

Figure 17 Shannon entropy section of the ParaSurf® output for trimethoprim, 1, using a marching-cube isodensity surface.

If the statistical background file is not found or does not have the correct format, only the “internal” Shannon entropy appears in this table.



The Shannon entropy is also analyzed based on the surfaces assigned to the individual atoms to give the table shown in Figure 18:

```

Shannon-entropy analysis :

                Shannon Entropy
Atom  Area  max      Internal      External
      min  mean  total  max  min  mean  total
C    1  0.257  0.2201  0.0790  0.1374  0.0353  0.3125  0.2335  0.2746  0.0707
O    2  3.658  0.2033  0.0587  0.1090  0.3986  0.3492  0.1882  0.2617  0.9572
C    3  6.490  0.1802  0.0583  0.1021  0.6629  0.3454  0.1696  0.2534  1.6442
C    4  2.166  0.1736  0.0780  0.1054  0.2283  0.3700  0.1607  0.2203  0.4773
C    5  1.600  0.1543  0.0847  0.1067  0.1707  0.3462  0.1729  0.2385  0.3815
C    6  0.000
C    7  2.042  0.1729  0.0868  0.1117  0.2282  0.3693  0.1673  0.2290  0.4677
C    8  5.665  0.2372  0.0859  0.1395  0.7901  0.4121  0.2460  0.3178  1.8003
N    9  6.693  0.1664  0.0789  0.1058  0.7084  0.3193  0.2207  0.2687  1.7987
C   10  9.411  0.1532  0.0539  0.1038  0.9767  0.3477  0.2101  0.2768  2.6047
N   11  0.537  0.0855  0.0588  0.0665  0.0358  0.2473  0.2256  0.2351  0.1263
N   12  6.122  0.2108  0.0756  0.1072  0.6566  0.2916  0.2197  0.2479  1.5178
C   13  7.570  0.1873  0.0591  0.1093  0.8277  0.3198  0.2162  0.2721  2.0596
N   14  0.713  0.1746  0.0629  0.1019  0.0727  0.2921  0.2318  0.2724  0.1943
C   15  4.127  0.1749  0.0879  0.1089  0.4492  0.3316  0.1837  0.2344  0.9674
C   16  5.886  0.1718  0.0600  0.0991  0.5832  0.3231  0.1854  0.2415  1.4211
O   17  1.261  0.1353  0.0614  0.0877  0.1105  0.3207  0.1928  0.2303  0.2904
C   18  0.289  0.2010  0.0734  0.1431  0.0414  0.3602  0.2089  0.2725  0.0788
C   19  5.580  0.1590  0.0558  0.0891  0.4971  0.2937  0.1669  0.2086  1.1643
O   20  3.960  0.1842  0.0648  0.0969  0.3836  0.3222  0.2104  0.2630  1.0415
C   21  0.543  0.1637  0.1057  0.1404  0.0762  0.3424  0.2627  0.2993  0.1624
H   22 20.848  0.4039  0.0796  0.3038  6.3337  0.4648  0.2564  0.4181  8.7168
H   23 16.018  0.4239  0.0765  0.3107  4.9767  0.4713  0.2101  0.4125  6.6078
H   24 16.235  0.4248  0.0749  0.3254  5.2820  0.4712  0.2231  0.4158  6.7503
H   25  7.143  0.3288  0.1404  0.2347  1.6761  0.4577  0.3210  0.4113  2.9376
H   26 13.545  0.3942  0.1235  0.2664  3.6089  0.4739  0.3284  0.4407  5.9700
H   27 13.114  0.3249  0.0891  0.2069  2.7131  0.4695  0.2296  0.4208  5.5177
H   28 17.462  0.3825  0.1071  0.2862  4.9975  0.4400  0.3017  0.3967  6.9266
H   29 20.093  0.2782  0.0527  0.1926  3.8688  0.3792  0.2132  0.3098  6.2241
H   30 20.380  0.2756  0.0540  0.1882  3.8360  0.3613  0.2121  0.2954  6.0205
H   31 20.025  0.3054  0.0541  0.2015  4.0361  0.3729  0.2176  0.3069  6.1449
H   32 10.792  0.2809  0.0715  0.1551  1.6743  0.4371  0.2328  0.3175  3.4264
H   33  7.935  0.3473  0.1138  0.2468  1.9586  0.4682  0.2585  0.4191  3.3252
H   34 20.353  0.4467  0.0991  0.3458  7.0389  0.4712  0.2812  0.4326  8.8037
H   35 16.221  0.4453  0.0718  0.3357  5.4460  0.4712  0.2381  0.4174  6.7712
H   36 16.250  0.4390  0.0836  0.3349  5.4415  0.4718  0.2623  0.4245  6.8976
H   37 20.708  0.3625  0.1214  0.2774  5.7443  0.4786  0.2938  0.4325  8.9554
H   38 16.217  0.3297  0.0776  0.2428  3.9373  0.4784  0.2562  0.4243  6.8809
H   39 18.651  0.3467  0.0890  0.2854  5.3230  0.4786  0.2533  0.4290  8.0007

<> ParaSurf used      7.96 seconds CPU time

```

Figure 18 Shannon entropy section of the ParaSurf® output for trimethoprim, 1, using a marching-cube isodensity surface.



3.4.4 For a job with autocorrelation similarity

In order to calculate, for instance, the autocorrelation similarities between captopril and trimethoprim, first calculate the reference compound (in this case captopril) and request that the autocorrelation functions be written to the ParaSurf™ SDF-output file:

```
parasurf captopril surf=cube autocorr
```

The calculate the autocorrelations for trimethoprim and their similarities to those of captopril:

```
parasurf trimethoprim surf=cube autocorr=captopril_p.sdf
```

This leads to the following additional output from ParaSurf™

```
<> Calculating autocorrelation similarities to captopril_p.sdf
<> Lead molecule = OC(=O)C1CCCN1C(=O)C(C)CS
```

Similarities :	Shape	+/+	-/-	+/-	IE (L)	EA (L)
Total :	0.8924	0.5535	0.6968	0.6675	0.3740	0.8364
1. Quartal :	0.9039	0.3785	0.6334	0.7132	0.3319	0.8695
2. Quartal :	0.8861	0.3713	0.6761	0.5637	0.3086	0.8366
3. Quartal :	0.9348	0.7294	0.8152	0.6597	0.3651	0.9109
4. Quartal :	0.8450	0.7349	0.6623	0.7334	0.4902	0.7286

Entropies :	Shape	+/+	-/-	+/-	IE (L)	EA (L)
Total :	0.0962	0.3210	0.3078	0.3348	0.3314	0.2225
1. Quartal :	0.0533	0.3390	0.3516	0.3261	0.3203	0.2007
2. Quartal :	0.1802	0.3338	0.3391	0.3632	0.3102	0.2354
3. Quartal :	0.1112	0.3010	0.2296	0.3382	0.3329	0.1431
4. Quartal :	0.0399	0.3103	0.3108	0.3118	0.3621	0.3107

Corr.Coeff. :						
(R) :	0.7914	-0.7041	0.5585	0.9201	0.9184	0.5880

Field Similarities :	Raw Data			Scaled		
+/+	-/-	+/-	+/+	-/-	+/-	
Total :	0.7497	0.6651	0.5998	0.7418	0.7024	0.5768
1. Quartal :	0.6836	0.5321	0.4983	0.7843	0.8004	0.6583
2. Quartal :	0.5508	0.6104	0.5652	0.9313	0.9307	0.9169
3. Quartal :	0.8520	0.7296	0.7738	0.5967	0.8438	0.5746
4. Quartal :	0.9125	0.7882	0.5617	0.6522	0.2349	0.1574

Field Entropies :	Raw Data			Scaled		
+/+	-/-	+/-	+/+	-/-	+/-	
Total :	0.2592	0.3223	0.3300	0.2458	0.1861	0.1858
1. Quartal :	0.3377	0.3606	0.3559	0.2370	0.2517	0.1957
2. Quartal :	0.3636	0.3573	0.3637	0.1105	0.1161	0.1326
3. Quartal :	0.1947	0.3109	0.2440	0.3357	0.2179	0.2426
4. Quartal :	0.1407	0.2606	0.3563	0.3000	0.1586	0.1722

Figure 19 Similarity output using autocorrelation functions. The lead molecule is captopril, which is defined in captopril_p.sdf using the SMILES string.



Similarities are calculated over the entire distance range (Total) and for each of the four quartals using the four different types of autocorrelation defined in 1.11. Often, for small molecules, the 4th quartal similarities are unity because the autocorrelations peter out at long range. Either the total similarities or the individual similarities for the quartals can be used for QSAR studies. Additionally, ParaSurf10™ calculates the “entropies” and the correlation coefficients between the two molecules for each of the autocorrelations. The “entropies” S are defined as

$$S = \frac{\sum_{i=1}^N p_i \log(p_i)}{N} \quad \text{where } p = \frac{a_2}{a_1} \quad (20)$$

where a_1 is the larger of the two autocorrelation values and a_2 is the smaller. N is the number of autocorrelation points considered. The “entropy” is zero for identical autocorrelations and has a maximum value of one.

A new feature in ParaSurf10™ is that autocorrelations are also calculated for the electrostatic field normal to the molecular surface. This field generally gives more highly resolved autocorrelations than the electrostatic potential and is less sensitive to the total charge of the molecule. The field autocorrelations are compared for +/+, +/- and -/- combinations of F_N , analogously to the potential. These comparisons are made both for the raw autocorrelations and for one that are shifted and scaled to occupy a range between zero and one.

3.5 ParaSurf™ SDF-output

The SDF output file (a fixed-format file) contains additional blocks with the information generated by ParaSurf™. These are:

<ParaSurf OPTIONS>

The ParaSurf™ OPTIONS block consists of one line giving the options used in the ParaSurf™ calculation. These are:

<surface> <fit> <electrostatic model> <isodensity level> (a4,2x,a4,2x,a5,2x,f8.3)

Where the individual variables can be:

<surface>	WRAP	Shrink-wrap surface
	CUBE	Marching-cube surface
<fit>	NONE	No fitting, unsmoothed marching-cube surface
	ISO	Marching-cube surface corrected to $\pm 2\%$ of the preset isodensity value
	SPHH	Spherical-harmonic surface fit



<code><electrostatic model></code>	NAOPC MULTI	NAO-PC electrostatics Multipole electrostatics
<code><isodensity level></code>	<i>n.nn</i>	The target isodensity value in $e\text{-}\text{\AA}^3$
<code><solvent probe radius></code>		The radius of the solvent probe used to calculate the SES or SAS
<code><triangulation mesh></code>		The mesh size used to triangulate the Surface

<MOLECULAR_CENTERS>

The molecular centres block appears only for calculations that use spherical harmonic fits. It includes two lines of the form:

```
"Spherical harmonic center = ", 3f12.6
```

```
"Center of gravity          = ", 3f12.6
```

These blocks give the x, y and z coordinates of the centre of the molecule used for the spherical-harmonic fit and the centre of gravity, respectively. These two centres are usually identical, but may be different if the centre of gravity lies outside the molecule (e.g. for U-shaped molecules).

<SPHERICAL_HARMONIC_.....>

The spherical harmonic fits are described in `<SPHERICAL_HARMONIC_....>` blocks. These blocks all have the same format and vary only in the property described. Each block has the form:

The spherical harmonic fits are described in `<SPHERICAL_HARMONIC_.....>` blocks. These blocks all have the same format and vary only in the property described. Each block has the form:

Order = nn	("Order = ",i4)
$l(c_l^m)$ m = -l to l	(I5, 10f8.4/5x,10f8.4/5x,10f8.4/5x,10f8.4) (One set of coefficients each for l = 1 to 15)
RMSDs : l, RMSD¹, RMSD²	("RMSDs:") (i8, 2f12.8) (One line for each l for l = 1 to 15, where RMSD ¹ is the area-weighted RMSD and RMSD ² the simple RMSD)

There are six such blocks, indicated by the tags:

<code><SPHERICAL_HARMONIC_SURFACE></code>	The fitted molecular surface (radial distances) in Angstrom
<code><SPHERICAL_HARMONIC_MEP></code>	The MEP values at the spherical-harmonic surface (l = 20) in kcal mol ⁻¹
<code><SPHERICAL_HARMONIC_IE(l)></code>	The IE _l values at the spherical-harmonic surface (l = 20) in kcal mol ⁻¹
<code><SPHERICAL_HARMONIC_EA(l)></code>	The EA _l values at the spherical-harmonic surface (l = 20) in kcal mol ⁻¹



<SPHERICAL_HARMONIC_ALPHA (L)> The α_L values at the spherical-harmonic surface ($l = 20$) in kcal mol⁻¹

<SPHERICAL_HARMONIC_FIELD (N)> The FN values at the spherical-harmonic surface ($l = 20$) in kcal mol⁻¹ Å⁻¹

<ParaSurf Descriptors>

The ParaSurf™ descriptors block lists the calculated descriptors in the following groups:

Molecular:	$\mu, \mu_D, \alpha, MW, G, A, VOL$ ("Molecular ", 5f10.4, 2f10.2)
MEP:	$V_{\max}, V_{\min}, \bar{V}_+, \bar{V}_-, \bar{V}, \Delta V, \sigma_+^2, \sigma_-^2, \sigma_{Tot}^2, v, \sigma_{Tot}^2 v, \gamma_1^V, \gamma_2^V, \int_V$ ("MEP ", 7f10.2/10x, f10.2, 5f10.4, 2x, g12.6)
IE(l):	$IE_L^{\max}, IE_L^{\min}, \overline{IE}_L, \Delta IE_L, \sigma_{IE}^2, \gamma_1^{IE}, \gamma_2^{IE}, \int_{IE}$ ("IE (l) ", 5f10.2, 2f10.4/12x, g12.6)
EA(l):	$EA_L^{\max}, EA_L^{\min}, EA_{L+}, EA_{L-}, EA_L, \Delta EA_L, \sigma_{EA+}^2, \sigma_{EA-}^2, \sigma_{EA}^2, v_{EA}, \delta A_{EA}^+, A_{EA}^+, \gamma_1^{EA}, \gamma_2^{EA}, \int_{EA}$ ("EA (l) ", 7f10.2/2f10.2, 2f10.4, f10.2, 2f10.4/12x, g12.6)
Eneg(l):	$\chi_L^{\max}, \chi_L^{\min}, \chi_L, \Delta \chi_L, \sigma_\chi^2, \gamma_1^\chi, \gamma_2^\chi, \int_\chi$ ("Eneg (l) ", 5f10.2, 2f10.4/12x, g12.6)
Hard(l):	$\eta_L^{\max}, \eta_L^{\min}, \eta_L, \Delta \eta_L, \sigma_\eta^2, \gamma_1^\eta, \gamma_2^\eta, \int_\eta$ ("Hard (l) ", 5f10.2, 2f10.4/12x, g12.6)
Alpha(l):	$\alpha_L^{\max}, \alpha_L^{\min}, \overline{\alpha}_L, \Delta \alpha_L, \sigma_\alpha^2, \gamma_1^\alpha, \gamma_2^\alpha, \int_\alpha$ ("Alpha (l) ", 5f10.2, 2f10.4/12x, g12.6)
F_N	$F_N^{\max}, F_N^{\min}, F_N, \sigma_F^2, \sigma_{F+}^2, \sigma_{F-}^2, v_F, \gamma_1^{F_N}, \gamma_2^{F_N}, \int_{F_N}^+, \int_{F_N}^-, \int_{F_N}$ ("Field desc", 7f10.4/" ", 6f10.4)

Jobs that include Shannon entropy give two extra sets of descriptors:

Shannon(i):	$H_{in}^{\max}, H_{in}^{\min}, H_{in}, \sigma_{H_{in}}^2, \int_{H_{in}}$ ("Shannon (i) ", 4f10.4, f10.2, f10.4)
Shannon(e):	$H_{ex}^{\max}, H_{ex}^{\min}, H_{ex}, \sigma_{H_{ex}}^2, \int_{H_{ex}}$ ("Shannon (e) ", 4f10.4, f10.2, f10.4)

For calculations using a spherical-harmonic fit, the hybridization coefficients are printed to the .sdf file as follows (tag line followed by as many lines with the coefficients as necessary):

<SHAPE HYBRIDS>

(15 coefficients, 6f12.6)

<MEP HYBRIDS>

(20 coefficients, 6f12.6)

<IE (L) HYBRIDS>

(20 coefficients, 6f12.2)

<EA (L) HYBRIDS>

(20 coefficients, 6f12.2)

<ALPHA (L) HYBRIDS>

(20 coefficients, 6f12.8)

<FIELD (N) HYBRIDS>

(20 coefficients, 6f12.4)

The hybridization coefficients are listed in order of increasing l from zero, exactly as in the output file.

The atomic surface properties are listed in the atomic order according to the following headings (tag line followed by as many lines with the surface properties as necessary):

<ATOMIC SURFACE AREAS>	Areas	(10f8.4)
<ATOMIC SURFACE MEP MAXIMA>	MEP maxima	(10f8.2)
<ATOMIC SURFACE MEP MINIMA>	MEP minima	(10f8.2)
<ATOMIC SURFACE IE(L) MAXIMA>	IE(l) maxima	(10f8.2)
<ATOMIC SURFACE IE(L) MINIMA>	IE(l) minima	(10f8.2)
<ATOMIC SURFACE EA(L) MAXIMA>	EA(l) maxima	(10f8.2)
<ATOMIC SURFACE EA(L) MINIMA>	EA(l) minima	(10f8.2)
<ATOMIC SURFACE MEAN POL>	Mean pol.	(10f8.4)
<ATOMIC SURFACE FIELD(N) MAXIMA>	FN maxima	(10f8.2)
<ATOMIC SURFACE FIELD(N) MINIMA>	FN minima	(10f8.2)

The properties correspond exactly to those printed in the table of surface properties in the output file.

<PROPERTY MAXIMA and MINIMA>

The ParaSurf™ block for the maxima and minima of the local properties is defined as follows for each property:

Header line (maxima)	Number of maxima for the property: N_{\max} , property {MEP, IEL, EAL or Alpha(L)}	(I3,a," Maxima")
Nmax maxima lines	x, y, z , property value	(3f12.4, 3x, g10.4)
Header line (minima)	Number of minima for the property: N_{\max} , property {MEP, IEL, EAL or Alpha(L)}	(I3,a," Minima")
N_{\min} minima lines	x, y, z , property value	(3f12.4, 3x, g10.4)

<STANDARD RIF>

The rotationally invariant fingerprint [41] is printed as a list of 54 floating point numbers (5g12.6). The first 41 are those defined in reference [41] and the last 13 are the square roots of the hybridization coefficients for the normal field from $l=0-12$.



3.5.1 Optional blocks in the SDF-output file

A calculation including Shannon entropy gives two extra lines in the descriptors block of the SDF-output file:

The maximum, minimum, mean, variance and total "internal" Shannon entropies.

"Shannon (i) "

(4f10.4, f10.2, f10.4)

The maximum, minimum, mean, variance and total "external" Shannon entropies (if these are calculated).

"Shannon (e) "

(4f10.4, f10.2, f10.4)

Additionally, extra blocks for the atomic Shannon entropy-related variables are added to the SDF-output after the other atomic-property blocks:

<ATOMIC SURFACE MAXIMUM H (internal)>

Maximum "internal" Shannon entropies

(10f8.4)

<ATOMIC SURFACE MINIMUM H (internal)>

Minimum "internal" Shannon entropies

(10f8.4)

<ATOMIC SURFACE MEAN H (internal)>

Mean "internal" Shannon entropies

(10f8.4)

<ATOMIC SURFACE TOTAL H (internal)>

Total "internal" Shannon entropies

(10f8.4)

If the external Shannon entropy is also calculated, the following blocks are also written:

<ATOMIC SURFACE MAXIMUM H (external)>

Maximum "external" Shannon entropies

(10f8.4)

<ATOMIC SURFACE MINIMUM H (external)>

Minimum "external" Shannon entropies

(10f8.4)

<ATOMIC SURFACE MEAN H (external)>

Mean "external" Shannon entropies

(10f8.4)

<ATOMIC SURFACE TOTAL H (external)>

Total "external" Shannon entropies

(10f8.4)



For calculations that include surface autocorrelations, these are written in the following blocks:

<SURFACE AUTOCORRELATION PARAMETERS>

The initial (lowest) value of the autocorrelation range in Å	("r _{low} = ", f12.6)
The number of autocorrelation points	("ncorr = ", i6)
The autocorrelation step length in Å	("corrstep = ", f12.6)
The smoothing parameter σ	("smooth = ", f12.6)

This block then contains a table that gives all the autocorrelations as a table with the following headings:

Table 7: Column headings and definitions for autocorrelation tables.

Column heading	Contents
R	Reference distance (R in equation (18))
SHAPE	Shape autocorrelation
VPP	MEP ++ autocorrelation
VPM	MEP +/- autocorrelation
VMM	MEP -- autocorrelation
IEL	IEL autocorrelation
EAL	EAL autocorrelation
FPP	Normal field ++ correlation (raw)
FPM	Normal field +/- correlation (raw)
FMM	Normal field -- correlation (raw)
FPP_s	Normal field ++ correlation (scaled)
FPM_s	Normal field +/- correlation (scaled)
FMM_s	Normal field -- correlation (scaled)

The format of the columns is (f10.3,4(1x,f10.6),2(1x,f10.3),3(1x,f8.1),3f8.3)

Calculations with spherical-harmonic fits that use the **TRANSLATE** or **TRANSLATE2** options, an additional block with the header

<TRANSLATED SPHERICAL HARMONIC FITS>

is printed. This block consists of nine sets of results (the original centre plus eight translated ones) for **TRANSLATE** and 16 for **TRANSLATE2**. The original centre is denoted by the header



Origin <shiftx><shifty><shiftz><RMSD>
("Origin :",3f12.4,f12.6)')

followed by the fitted coefficients (7f12.6). The shifted points are defined in the same way, but are denoted "Point N"

("Point ",i2,";",3f12.4,f12.6)

3.6 The surface (.psf) file

The .psf file can be used to derive properties and descriptors from the ParaSurf™ results. It includes the coordinates and properties of the atoms, surface points and surface triangles in the following format:

Number of atoms	(i6)
------------------------	------

One line per atom with the atomic surface properties:

Atomic number, x-coordinate, y-coordinate, z-coordinate, atomic surface area, V_{\max}, V_{\min}, IE_L^{\min}, EA_L^{\max}, mean polarisability	(i2, 3f10.5, f8.3, 4f8.2, f8.3)
--	---------------------------------

Number of surface points	(i6)
---------------------------------	------

One line per point with the local properties:

x-coordinate, y-coordinate, z-coordinate, MEP, IE_L, EA_L, α_L, atom_L	(3f10.5, 3f8.2, f8.4, i6)
---	---------------------------

(where atom_L is the atom to which the surface point is assigned)

Number of surface triangles	(i6)
------------------------------------	------

One line per triangle with the ID of the triangle and the local properties:

point #1, point #2, point #3, area, atom_{tri}, normal field	(3i6, f10.5, i6, g12.4)
---	-------------------------

(where point #1, 2 and 3 are the numbers of the surface points that make up the triangle and atom_{tri} is the atom to which the triangle is assigned)

3.7 Anonymous SD (.asd) files

The .asd file contains only those blocks from the ParaSurf™ output SD file that do not pertain directly to the 2D-molecular structure. Its purpose is to allow a full descriptions of the intermolecular bonding



properties of the molecule without revealing its structure. The .asd file can only be written from a ParaSurf™ calculation using spherical-harmonic fitting. Its form is:

The SD header line	(A molecular ID number etc.)
The program identifier line	(The normal second line of the SD-file)

And the blocks defined by the following tags:

<SPHERICAL_HARMONIC_SURFACE>
 <SPHERICAL_HARMONIC_MEP>
 <SPHERICAL_HARMONIC_IE(1)>
 <SPHERICAL_HARMONIC_EA(1)>
 <SPHERICAL_HARMONIC_FIELD(N)>
 <SPHERICAL_HARMONIC_ALPHA(1)>
 <SHAPE_HYBRIDS>
 <MEP_HYBRIDS>
 <IE(L) HYBRIDS>
 <EA(L) HYBRIDS>
 <FIELD(N) HYBRIDS>
 <ALPHA(L) HYBRIDS>
 <STANDARD_RIF>

<ParaSurf Descriptors>

(The molecular weight and the atomic surface properties are not included because they would allow the molecular formula to be reconstructed. The atoms assigned to each surface point or triangle are also not given.) The format of the descriptors is:

Molecular	$\mu, \mu_D, \alpha, MW, G, A, VOL$ ("Molecular ", 5f10.4, 2f10.2)
MEP	$V_{\max}, V_{\min}, \bar{V}_+, \bar{V}_-, \bar{V}, \Delta V, \sigma_+^2, \sigma_-^2, \sigma_{Tot}^2, v, \sigma_{tot}^2, \gamma_1^V, \gamma_2^V, \int_V$ ("MEP ", 7f10.2/10x, f10.2, 5f10.4, 2x, g12.6)
IE(I)	$IE_L^{\max}, IE_L^{\min}, \bar{IE}_L, \Delta IE_L, \sigma_{IE}^2, \gamma_1^{IE}, \gamma_2^{IE}, \int_{IE}$ ("IE(1) ", 5f10.2, 2f10.4/12x, g12.6)
EA(I)	$EA_L^{\max}, EA_L^{\min}, EA_{L+}, EA_{L-}, EA_L, \Delta EA_L, \sigma_{EA+}^2, \sigma_{EA-}^2, \sigma_{EA}^2, v_{EA}, \delta A_{EA}^+, A_{EA}^+, \gamma_1^{EA}, \gamma_2^{EA}, \int_{EA}$ ("EA(1) ", 7f10.2/2f10.2, 2f10.4, f10.2, 2f10.4/12x, g12.6)
Eneg(I)	$\chi_L^{\max}, \chi_L^{\min}, \chi_L, \Delta \chi_L, \sigma_\chi^2, \gamma_1^\chi, \gamma_2^\chi, \int_\chi$ ("Eneg(1) ", 5f10.2, 2f10.4/12x, g12.6)
Hard(I)	$\eta_L^{\max}, \eta_L^{\min}, \eta_L, \Delta \eta_L, \sigma_\eta^2, \gamma_1^\eta, \gamma_2^\eta, \int_\eta$ ("Hard(1) ", 5f10.2, 2f10.4/12x, g12.6)



Alpha(l)	$\alpha_L^{\max}, \alpha_L^{\min}, \overline{\alpha}_L, \Delta\alpha_L, \sigma_\alpha^2, \gamma_1^\alpha, \gamma_2^\alpha, \int_\alpha$	("Alpha (l) ", 5f10.2, 2f10.4/12x, g12.6)
F_N	$F_N^{\max}, F_N^{\min}, \Delta F_N, F_N, \sigma_F^2, \sigma_{F+}^2, \sigma_{F-}^2, \nu_F, \gamma_1^{F_N}, \gamma_2^{F_N}, \int_{F_N}^+, \int_{F_N}^-$	("Field desc", 7f10.4/" , 6f10.4)

Jobs that include Shannon entropy give two extra sets of descriptors:

Shannon(i)	$H_{in}^{\max}, H_{in}^{\min}, H_{in}, \sigma_{H_{in}}^2, \int_{H_{in}}$	("Shannon (i) ", 4f10.4, f10.2, f10.4)
Shannon(e)	$H_{ex}^{\max}, H_{ex}^{\min}, H_{ex}, \sigma_{H_{ex}}^2, \int_{H_{ex}}$	("Shannon (e) ", 4f10.4, f10.2, f10.4)

3.7.1 Optional blocks

For calculations that include surface autocorrelations, these are written in the following blocks:

<SURFACE AUTOCORRELATION PARAMETERS>

The initial (lowest) value of the autocorrelation range in Å	("rlow = ", f12.6)
The number of autocorrelation points	("ncorr = ", i6)
The autocorrelation step length in Å	("corrstep = ", f12.6)
The smoothing parameter σ	("smooth = ", f12.6)

This block then contains a table that gives all the autocorrelations as a table with the following headings:

Table 8: Column headings and definitions for the autocorrelation table in the output SDF file.

Column heading	Contents
R	Reference distance (R in equation (18))
SHAPE	Shape autocorrelation
VPP	MEP +/+ autocorrelation
VPM	MEP +/- autocorrelation
VMM	MEP -/- autocorrelation
IEL	IE _L autocorrelation
EAL	EA _L autocorrelation
FPP	Normal field +/+ correlation (raw)
FPM	Normal field +/- correlation (raw)
FMM	Normal field -/- correlation (raw)
FPP_s	Normal field +/+ correlation (scaled)



FPM_s	Normal field +/- correlation (scaled)
FMM_s	Normal field -/- correlation (scaled)

The format of the columns is (f10.3,4(1x,f10.6),2(1x,f8.3),3(1x,g10.4),3f8.3)

3.8 Grid calculations with ParaSurf™

3.8.1 User-specified Grid

The command

```
parasurf <filename> estat=multi grid=grid.dat
```

instructs ParaSurf™ to read a set of Cartesian coordinates from the file grid.dat and to calculate the four local properties (MEP, IEL, EAL, α L). The format of the file grid.dat (which must be in the same directory as the input) is one line per atom containing the x, y and z coordinates in free format, comma-separated, maximum line length 80. For instance, the following grid file:

```
-3.79480 , -7.06030 , 10.37150  
-3.79480 , -5.06030 , -7.62850  
-3.79480 , -5.06030 , -5.62850  
-3.79480 , -5.06030 , -3.62850  
-3.79480 , -5.06030 , 0.37150  
-3.79480 , -5.06030 , 2.37150  
-3.79480 , -5.06030 , 4.37150  
-3.79480 , -5.06030 , 6.37150  
-3.79480 , -5.06030 , 8.37150  
-3.79480 , -5.06030 , 10.37150  
-3.79480 , -3.06030 , -7.62850  
-3.79480 , -3.06030 , -5.62850  
-3.79480 , -3.06030 , 0.37150  
-3.79480 , -3.06030 , 2.37150
```

Figure 20 Sample grid file

*



gives the output shown in Figure 21.

```
<> ParaSurf'10, Revision A1
<> Copyright (c) 2006,2007,2008,2009,2010 Friedrich-Alexander-Universitaet
    Erlangen Nuernberg and Cepos InSilico Ltd.
    All rights reserved.

<> Input = trimethoprim.scr

<<>> Molecule 1 of 1 <<>>

<> Program options :
    Calculating local properties using grid file grid.txt
    Using multipole electrostatics

<> AM1 calculation for Trimethoprim

      X      Y      Z      density      MED      IE(1)      EA(1)      Pol(1)      Eneg(1)      Hard(1)      dv/dx      dv/dy      dv/dz
-3.79480 -7.06030 10.37150 0.1935E-21 0.30 492.13 -106.42 0.2415 192.86 299.28 -0.0097 -0.0048 0.0510
-3.79480 -5.06030 -7.62850 0.8566E-10 -2.55 473.54 -93.89 0.2930 189.83 283.71 1.4168 0.2745 0.3485
-3.79480 -5.06030 -5.62850 0.3544E-06 -2.70 486.77 -94.43 0.2950 196.17 290.60 3.7548 0.4931 -0.5285
-3.79480 -5.06030 -3.62850 0.1631E-02 4.92 443.77 -92.79 0.2977 175.49 268.28 10.4574 0.2186 -12.2912
-3.79480 -5.06030 0.37150 0.1922E-04 2.70 466.97 -92.67 0.2959 187.15 279.82 4.3028 -1.1509 0.9175
-3.79480 -5.06030 2.37150 0.9505E-08 2.02 430.72 -91.71 0.2962 169.51 261.21 0.6480 -0.7798 0.2082
 3.79480  5.06030 4.37150 0.4717E 11 1.44 481.91 96.47 0.2658 192.72 280.19 0.0152 0.3728 0.3406
-3.79480 -5.06030 6.37150 0.2516E-13 0.83 499.73 -104.69 0.2420 197.52 302.21 -0.0350 -0.0826 0.2489
-3.79480 -5.06030 8.37150 0.4712E-16 0.46 491.19 -106.70 0.2412 192.25 298.95 -0.0279 0.0127 0.1255
-3.79480 -5.06030 10.37150 0.3452E-19 0.29 487.33 -107.50 0.2411 189.91 297.41 -0.0236 0.0242 0.0576
-3.79480 -3.06030 -7.62850 0.4743E-09 -2.70 418.90 -92.36 0.2911 163.27 255.63 1.6378 -0.1542 0.4091
-3.79480 -3.06030 -5.62850 0.4080E-05 -2.68 415.57 -92.17 0.2909 161.70 253.87 4.6513 -0.4026 -1.0370
-3.79480 -3.06030 0.37150 0.4912E-03 8.26 409.49 -91.04 0.2960 159.23 250.27 3.9292 -2.7005 5.0951
-3.79400 -3.06030 2.37150 0.1305E-06 4.55 506.33 -90.94 0.2637 200.70 299.64 -1.2130 -1.6652 1.0520

<> ParaSurf used      0.14 seconds CPU time
```

Figure 21 Sample grid output file

The name and the extension (if any) of the grid file are free. Only the output file is written. The units of the local properties are those used in the normal output (i.e. V, IEL, and EAL in kcal mol⁻¹, α L in Ångstrom³).

3.8.2 Automatic grids

ParaSurf™ can generate grids automatically for lead compounds in ComFA®-like procedures. The `grid=auto` option generates a grid around the molecule (with a 4 Å margin around the positions of the atoms in each direction) and includes all points for which the electron density is lower than 10^{-2} (i.e. for points outside the molecule). The spacing of the grid is set to a default value of 1.0 Å, but can be set to any value up to a maximum of 2.0 Å by the command-line argument `lattice=n.n`, which sets the lattice spacing to $n.n$ Å. The grid thus generated is output (with the values of the local properties analogously to a calculation that uses an predefined grid and can be used for other molecules that have been aligned with the lead.

3.9 The SIM file format

SIM files must reside in the ParaSurf™ executable directory and are strictly fixed format. SIM files must be called `<filename>.sim`, where `<filename>` must have exactly three characters. A sample SIM file for a single model (the free energy of solvation in octanol) is shown in Figure 22:

```

> <OPTIONS>
surf=cube
fit=isod
estat=multi
iso=0.05
> <MODELS>
  1  3
> <DGO>
  3  1.61058
DeltaG (n-Octanol)
kcal/mol
-0.01107   F  1.0   0.0   0.0   1.0   0.0   1.0
 1.6793d-9 F  1.0   0.0   3.0   0.0   0.0   1.0
-2.0407d-10 T 1.0   0.0   1.0   0.0   1.0   1.5
  
```

Figure 22 Sample surface-integral model (SIM) file.

The first line, the OPTIONS tag, is compulsory and takes the form:

<OPTIONS>

The second to fifth lines, also compulsory in the order shown above, give the ParaSurf™ options to be used for the surface-integral model. These options are given in lower case and override conflicting command-line options.

Line 6 must be the MODELS tag with the format

<MODELS>



Line 7 contains the two integers (*Nmodels* and *Maxterms*) that define the number of models given in the file and the maximum number of terms for any one model. The format is:

<i>Nmodels</i>	<i>Maxterms</i>	(2i4)
----------------	-----------------	-------

The remainder of the SIM file consists of *Nmodels* blocks, each of which defines a single model and has the following format:

Model identifier tag

<MOD>

where MOD is a three-letter unique identifier for the model.

<i>Nterms</i> (the number of terms in the model), <i>constant</i> (the constant in the regression equation)	(i4,g12.6)
Model name (for output, maximum 20 characters)	(a20)
Units of the property <i>P</i> (for output, maximum 20 characters)	(a20)
<i>Nterms</i> lines, one per term, giving the definition of the model: <i>Coeff Abs m n o p q r</i>	(d12.6,13,6f8.4)

where each term is defined as:

$$\left[MEP^m \cdot IE_L^n \cdot EA_L^o \cdot \alpha_L^p \cdot \eta_L^q \right]^r \text{ if } \mathbf{Abs} \text{ is false and } \left[MEP^m \cdot IE_L^n \cdot EA_L^o \cdot \alpha_L^p \cdot \eta_L^q \right]^r \text{ if } \mathbf{Abs} \text{ is true.}$$

SIM files are only intended to be created by expert users.

3.10 Output tables

The command-line argument "`table=<filename>`" requests that the 41 descriptors written in the <ParaSurf DESCRIPTORS> block of the ParaSurf™ SD-file output are written, one line per molecule, in the file <filename>. If <filename> already exists, the line for the new molecules will be appended, otherwise a new file will be created and a header line including designations of the descriptors will be written as the first line. All lines in the table file are comma-separated with all blanks (including those in the Molecule ID) removed. The Descriptors in order are:

Table 9: Definitions and order of the descriptors printed to the descriptor table if requested.

Column Header	Symbol ¹	Descriptor
MolID		Molecular ID taken from the first line of the entry for each molecule with all blanks eliminated.
dipole	μ	Dipole moment
dipden	μ _D	Dipolar density



Column Header	Symbol ^a	Descriptor
polarisability	α	Molecular electronic polarisability
MWt	MW	Molecular weight
globularity	G	Globularity
totalarea	A	Molecular surface area
volume	VOL	Molecular volume
MEPmax	V_{\max}	Maximum (most positive) MEP
MEPmin	V_{\min}	Minimum (most negative) MEP
meanMEP+	\bar{V}_+	Mean of the positive MEP values
meanMEP-	\bar{V}_-	Mean of the negative MEP values
meanMEP	\bar{V}	Mean of all MEP values
MEPrange	ΔV	MEP-range
MEPvar+	σ_+^2	Total variance in the positive MEP values
MEPvar-	σ_-^2	Total variance in the negative MEP values
MEPvartot	σ_{tot}^2	Total variance in the MEP
MEPbalance	v	MEP balance parameter
var*balance	$\sigma_{tot}^2 v$	Product of the total variance in the MEP and the balance parameter
MEPskew	γ_1^V	Skewness of the distribution of the MEP
MEPkurt	γ_2^V	Kurtosis of the distribution of the MEP
MEPint	\int_V	Integral of the MEP*area over the surface
IELmax	IE_L^{\max}	Maximum value of the local ionization energy
IELmin	IE_L^{\min}	Minimum value of the local ionization energy
IELbar	\overline{IE}_L	Mean value of the local ionization energy
IELrange	ΔIE_L	Range of the local ionization energy
IELvar	σ_{IE}^2	Variance in the local ionization energy
IELskew	γ_1^{IE}	Skewness of the distribution of IE(L)
IELkurt	γ_2^{IE}	Kurtosis of the distribution of IE(L)
IELint	\int_{IE}	Integral of the IE(L)*area over the surface
EALmax	EA_L^{\max}	Maximum of the local electron affinity
EALmin	EA_L^{\min}	Minimum of the local electron affinity
EALbar+	\overline{EA}_{L+}	Mean of the positive values of the local electron affinity
EALbar-	\overline{EA}_{L-}	Mean of the negative values of the local electron affinity
EALbar	\overline{EA}_L	Mean value of the local electron affinity



Column Header	Symbol ^a	Descriptor
EALrange	ΔEA_L	Range of the local electron affinity
EALvar+	σ_{EA+}^2	Variance in the local electron affinity for all positive values
EALvar-	σ_{EA-}^2	Variance in the local electron affinity for all negative values
EALvartot	σ_{EAtot}^2	Sum of the positive and negative variances in the local electron affinity
EALbalance	v_{EA}	Local electron affinity balance parameter
EALfraction+	δA_{EA}^+	Fraction of the surface area with positive local electron affinity
EALarea+	A_{EA}^+	Surface area with positive local electron affinity
EALskew	γ_1^{EA}	Skewness of the distribution of the MEP
EALkurt	γ_2^{EA}	Kurtosis of the distribution of the MEP
EALint	\int_{EA}	Integral of the MEP*area over the surface
POLmax	α_L^{\max}	Maximum value of the local polarisability
POLmin	α_L^{\min}	Minimum value of the local polarisability
POLbar	$\overline{\alpha_L}$	Mean value of the local polarisability
POLrange	$\Delta \alpha_L$	Range of the local polarisability
POLvar	σ_α^2	Variance in the local polarisability
POLskew	γ_1^α	Skewness of the distribution of the local polarisability
POLkurt	γ_2^α	Kurtosis of the distribution of the local polarisability
POLint	\int_α	Integral of the $\alpha(L)$ *area over the surface
ENEGmax	χ_L^{\max}	Maximum of the local electronegativity
ENEGmin	χ_L^{\min}	Minimum of the local electronegativity
ENEGbar	$\overline{\chi_L}$	Mean value of the local electronegativity
ENEGrange	$\Delta \chi_L$	Range of the local electronegativity
ENEGvar	σ_χ^2	Variance in the local electronegativity
ENEGskew	γ_1^χ	Skewness of the distribution of the local electronegativity
ENEGkurt	γ_2^χ	Kurtosis of the distribution of the local electronegativity
ENEGint	\int_χ	Integral of the $\chi(L)$ *area over the surface
HARDmax	η_L^{\max}	Maximum of the local electronegativity
HARDmin	η_L^{\min}	Minimum of the local electronegativity
HARDbar	$\overline{\eta_L}$	Mean value of the local electronegativity
HARDrange	$\Delta \eta_L$	Range of the local electronegativity
HARDvar	σ_η^2	Variance in the local electronegativity
HARDskew	γ_1^η	Skewness of the distribution of the local electronegativity



Column Header	Symbol ^a	Descriptor
HARDkurt	γ_2^η	Kurtosis of the distribution of the local electronegativity
HARDint	\int_η	Integral of the $\chi(L)$ *area over the surface
FNmax	F_N^{\max}	Maximum value of the field normal to the surface
FNmin	F_N^{\min}	Minimum value of the field normal to the surface
FNrange	ΔF_N	Range of the field normal to the surface
FNmean	$\overline{F_N}$	Mean value of the field normal to the surface
FNvartot	σ_F^2	Variance in field normal to the surface
FNvar+	σ_{F+}^2	Variance in the field normal to the surface for all positive values
FNvar-	σ_{F-}^2	Variance in the field normal to the surface for all negative values
FNbal	ν_F	Normal field balance parameter
FNskew	$\gamma_1^{F_N}$	Skewness of the field normal to the surface
FNkurt	$\gamma_2^{F_N}$	Kurtosis of the field normal to the surface
FNint	\int_{F_N}	Integrated field normal to the surface over the surface
FN+	$\int_{F_N}^+$	Integrated field normal to the surface over the surface for all positive values
FN-	$\int_{F_N}^-$	Integrated field normal to the surface over the surface for all negative values
FNabs	$\int_{ F_N }$	Integrated absolute field normal to the surface over the surface

^aSymbols as used in section 1.9.

If the Shannon entropy is calculated, the following additional descriptors are added:

Table 10: Additional descriptors (Shannon entropy)

Column Header	Symbol	Descriptor
SHANImax	H_{in}^{\max}	Maximum internal Shannon entropy
SHANImin	H_{in}^{\min}	Minimum internal Shannon entropy
SHANlvar	$\sigma_{H(in)}^2$	Variance of the internal Shannon entropy
SHANlbar	\overline{H}_{in}	Mean internal Shannon entropy
SHANItot	H_{in}^{tot}	Total internal Shannon entropy
<i>and if the external Shannon entropy is also calculated</i>		
SHANEmax	H_{ex}^{\max}	Maximum external Shannon entropy
SHANEmin	H_{ex}^{\min}	Minimum external Shannon entropy



Column Header	Symbol	Descriptor
SHANEvar	$\sigma_{H(ex)}^2$	Variance of the external Shannon entropy
SHANEbar	\bar{H}_{ex}	Mean external Shannon entropy
SHANEtot	H_{ex}^{tot}	Total external Shannon entropy
SHANEtot	H_{ex}^{tot}	Total external Shannon entropy

3.11 Binned SIM descriptor tables

If the option "`desfile=<filename>`" is used, a user-defined file with binned SIM-descriptors is written. The bin limits are taken from installed models using the command-line option "`desmodel=<code>`", where `<code>` is the model code taken from **Table 3**. If the table file does not exist, a new one with a header line will be written, otherwise the results for the current molecule will be appended. The descriptors are denoted by a two- or three-letter code to denote the property followed by the number of the descriptor (currently 1-12). The letter codes are:

Table 11: Letter codes (Binned SIM descriptor tables)

Code	Property	Code	Property	Code	Property
MEP	MEP	IEL	IE _L	EAL	EA _L
POL	α_L	FN	F _N	HD	η_L
ENG	χ_L	MI	MEP \times IE _L	MA	MEP \times EA _L
MP	MEP \times α_L	MF	MEP \times F _N	MH	MEP \times η_L
ME	MEP \times χ_L	IA	IE _L \times EA _L	IP	IE _L \times α_L
IF	IE _L \times F _N	IH	IE _L \times η_L	IE	IE _L \times χ_L
AP	EA _L \times α_L	AF	EA _L \times F _N	AH	EA _L \times η_L
AE	EA _L \times χ_L	PF	α_L \times F _N	PH	α_L \times η_L
PE	α_L \times χ_L	FH	F _N \times η_L	FE	F _N \times χ_L
HE	η_L \times χ_L				

The descriptor file is comma-separated.



3.12 Autocorrelation similarity tables

If the option "`aclist=<filename>`" is used, a user-defined file with the autocorrelation similarities is written. If this file does not exist, it is created and the header line written, otherwise entries are appended. The ASCII file is comma-separated with the following header line:

```
MolID, shape, shapeQ1, shapeQ2, shapeQ3, shapeQ4, Vpp, VppQ1, VppQ2,
VppQ3, VppQ4, Vmm, VmmQ1, VmmQ2, VmmQ3, VmmQ4, Vpm, VpmQ1, VpmQ2,
VpmQ3, VpmQ4, IE, IEQ1, IEQ2, IEQ3, IEQ4, EAi, EAQ1, EAQ2, EAQ3,
EAQ4, Fpp, FppQ1, FppQ2, FppQ3, FppQ4, Fmm, FmmQ1, FmmQ2, FmmQ3,
FmmQ4, Fpm, FpmQ1, FpmQ2, FpmQ3, FpmQ4, Fspp, FsppQ1, FsppQ2,
FsppQ3, FsppQ4, Fsmm, FsmmQ1, FsmmQ2, FsmmQ3, FsmmQ4, Fspm, FspmQ1,
FspmQ2, FspmQ3, FspmQ4, Hshape, HshapeQ1, HshapeQ2, HshapeQ3,
HshapeQ4, HVpp, HVppQ1, HVppQ2, HVppQ3, HVppQ4, HVmm, HVmmQ1, HVmmQ2,
HVmmQ3, HVmmQ4, HVpm, HVpmQ1, HVpmQ2, HVpmQ3, HVpmQ4, HIE, HIEQ1,
HIEQ2, HIEQ3, HIEQ4, HEAi, HEAiQ1, HEAiQ2, HEAiQ3, HEAiQ4, HFpp,
HFppQ1, HFppQ2, HFppQ3, HFppQ4, HFmm, HFmmQ1, HFmmQ2, HFmmQ3,
HFmmQ4, HFpm, HFpmQ1, HFpmQ2, HFpmQ3, HFpmQ4, HFSpp, HFSppQ1,
HFSppQ2, HFSppQ3, HFSppQ4, HFSmm, HFSmmQ1, HFSmmQ2, HFSmmQ3,
HFSmmQ4, HFSpm, HFSpmQ1, HFSpmQ2, HFSpmQ3, HFSpmQ4, Rr, Rpp, Rmm,
Ri, Re, RFpp, RFmm, RFpm, RFSpp, RFSmm, RFSpm
```



The MolID column contains the name of the molecule as given in its SDF-file and similarities for each type of autocorrelation as follows:

Table 12: Definitions of the elements of the autocorrelation similarity block in the output SDF file.

Autocorrelation	Similarity				Entropy				Correl. Coeff.		
	Total	Quartal			Total	Quartal					
		1	2	3		4	1	2		3	4
Shape	shape	shapeQ1	shapeQ2	shapeQ3	shapeQ4	Hshape	HshapeQ1	HshapeQ2	HshapeQ3	HshapeQ4	Rr
MEP +/+	Vpp	VppQ1	VppQ2	VppQ3	VppQ4	HVpp	HVppQ1	HVppQ2	HVppQ3	HVppQ4	Rpp
MEP -/-	Vpm	VpmQ1	VpmQ2	VpmQ3	VpmQ4	HVpm	HVpmQ1	HVpmQ2	HVpmQ3	HVpmQ4	Rpm
MEP +/-	Vmm	VmmQ1	VmmQ2	VmmQ3	VmmQ4	HVmm	HVmmQ1	HVmmQ2	HVmmQ3	HVmmQ4	Rmm
IE _L	IE	IEQ1	IEQ2	IEQ3	IEQ4	HIE	HIEQ1	HIEQ2	HIEQ3	HIEQ4	Ri
EA _L	EA	EAQ1	EAQ2	EAQ3	EAQ4	HEA	HEAQ1	HEAQ2	HEAQ3	HEAQ4	Re
F _N +/+	Fpp	FppQ1	FppQ2	FppQ3	FppQ4	HFpp	HFppQ1	HFppQ2	HFppQ3	HFppQ4	RFpp
F _N -/-	Fpm	FpmQ1	FpmQ2	FpmQ3	FpmQ4	HFpm	HFpmQ1	HFpmQ2	HFpmQ3	HFpmQ4	RFpm
F _N +/-	Fmm	FmmQ1	FmmQ2	FmmQ3	FmmQ4	HFmm	HFmmQ1	HFmmQ2	HFmmQ3	HFmmQ4	RFmm
F _N +/+ (scaled)	FSpp	FSppQ1	FSppQ2	FSppQ3	FSppQ4	HFSp	HFSpQ1	HFSpQ2	HFSpQ3	HFSpQ4	RFSpp
F _N -/- (scaled)	FSpm	FSpmQ1	FSpmQ2	FSpmQ3	FSpmQ4	HFSp	HFSpQ1	HFSpQ2	HFSpQ3	HFSpQ4	RFSpm
F _N +/- (scaled)	FSmm	FSmmQ1	FSmmQ2	FSmmQ3	FSmmQ4	HFSp	HFSpQ1	HFSpQ2	HFSpQ3	HFSpQ4	RFSmm

The last five entries are the correlation coefficients for the eleven autocorrelations.



3.13 Shared files

The Vhamil.par and SIM files are accessed in shared, read-only mode so that multiple ParaSurf™ jobs can access the same files.



4 TIPS FOR USING PARASURF'10™

4.1 Choice of surface

ParaSurf™ was originally written to use isodensity surfaces. However, calculations that use a solvent-excluded surface are very much faster than their equivalents with isodensity surfaces and will usually give comparable results. Surface-integral models may benefit from using a solvent-excluded surface with a solvent radius of 0.5-1.0 Å as this appears to be the most relevant surface for many physical properties. Surfaces fitted to spherical-harmonic expansions require more CPU-time than marching-cube surfaces but are essential for fast numerical applications such as ParaFit™. Again, solvent-excluded shrink-wrap surfaces are faster to calculate than their isodensity equivalents.

4.2 ParaSurf™ and ParaFit™

ParaFit™ is Cepos InSilico's very fast shape-matching program that is based on spherical-harmonic expansions generated by ParaSurf™. ParaFit™ can be used to overlay molecules with a common scaffold by defining the centre to be used for generating the spherical-harmonic fit in ParaSurf™ in the input SDF-file (see [1.1.4](#) and [2.2](#))

4.3 QSAR using grids

As outlined in [3.8.2](#), ParaSurf™ can generate a grid for the lead molecule automatically that can then be used for a set of aligned (e.g. with ParaFit™) molecules for grid-based QSAR. This procedure has proven to be especially effective for test datasets, especially if the molecules are aligned to a common scaffold, as outlined in [4.2](#).

5 SUPPORT

5.1 Contact

Questions regarding ParaSurf™ should be sent directly to:

support@ceposinsilico.com

5.2 Error reporting

Some of the routines in ParaSurf™ may detect error conditions that have not yet been encountered in our tests. In this case, an error message will be printed requesting that the input and output files be sent to the programming team at the above e-mail address. We realize that this will not always be possible for confidentiality reasons, but if the details can be sent, we will be able to treat the exception and improve the program.

5.3 CEPOS InSilico Ltd.

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