# Supporting Information for Nonpolar Solvation Free Energy from Proximal Distribution Functions

Shu-Ching Ou, Justin A. Drake, and B. Montgomery Pettitt<sup>\*</sup>

Sealy Center for Structural Biology and Molecular Biophysics, University of Texas Medical Branch, 301 University Blvd, Galveston, TX 77555-0304, United States

> E-mail: mpettitt@utmb.edu Phone: (409)772-0723

### Illustration of Voronoi Polyhedra

In the manuscript, we use

$$
g_{\perp}^{k}(r) = \sum_{t=0}^{T} \sum_{j=1}^{n} \frac{\delta(Inf[|\vec{r_{ij}}(t)|]_{i=1,m} - r)}{\delta \tau(\vec{r_{j}}(t),k)}
$$
(S1)

to define the proximal distribution function  $g_{\perp}(r)$ . We use Figure S1 to illustrate this process. Assume the solute has four atoms  $(i = 1 \sim 4)$ . The rest of the space can be divided into Voronoi polyhedra ( $k = I \sim IV$ ) depending on the closest solute atom. If the  $j_{th}$  solvent molecule locates in  $k_{th}$  polyhedron, the distance between  $i_{th}$  solute atom and the  $j_{th}$  solvent molecule (marked as  $r_{ij}$ ) is then recorded for  $g_{\perp}(r)$  pair correlation calculation. In other words, the polyhedra define the sampling volume for the corresponding solute atoms. The solvent distribution is considered isotropic within each sampling space.



Figure S1: Illustration of Equation 1 in the manuscript.  $i = 1 \sim 4$  represents the solute atoms, with  $k = I \sim IV$  the corresponding Voronoi polyhedra sampling volume. The case of an atom enveloped within another is demonstrated with atom "H". The exclusion factors are discussed below in this context.

#### Cavity & Exclusion Factors

During the pDF-reconstructions, we used two factors  $\delta_{\text{cav}}$  and  $\delta_{\text{excl}}$  in order to remove the grid points that overlap with solute atoms. The total van der Waals solute-solvent interaction can be written as

$$
U^{\text{vdW}} = \sum_{j}^{n} \sum_{i}^{m} U_{ij}^{\text{vdW}} \tag{S2}
$$

where i loops over solute atoms and j loops over the solvent molecules.  $m$  is the number of atoms in the solute and  $n$  is the number of solvent molecules. Thus,

$$
\frac{\partial U^{\text{vdW}}}{\partial \lambda} = \frac{\partial \left( \sum_{j}^{n} \sum_{i}^{m} U_{ij}^{\text{vdW}} \right)}{\partial \lambda} \tag{S3}
$$

We can take a representative term from the above equation

$$
\frac{\partial U_i^{\text{vdW}}}{\partial \lambda} = \frac{\partial \left( \sum_j^n U_{ij}^{\text{vdW}} \right)}{\partial \lambda} \tag{S4}
$$

For this value, we define a variable  $\Delta_i$  as the difference between simulated and pDFreconstructed of  $i_{th}$  solute atom,

$$
\Delta_i = \left(\frac{\partial U_i^{\text{vdW}}}{\partial \lambda}\right)_{\text{Reconstructed}} - \left(\frac{\partial U_i^{\text{vdW}}}{\partial \lambda}\right)_{\text{Simulated}}
$$
\n(S5)

We can then compare  $\Delta_i$  for each solute atom with both factors applied and only one of the factors applied during the pDF-reconstructions. We choose the reconstruction of ala<sub>1</sub> as the example. The results are presented in Figure S2.

When  $\lambda = 0.1, \Delta_i$  are within 0.5 kcal/mol, and the results using both factors are well reproduced. The exclusion factor  $\delta_{\text{excl}}$  does not seem to be crucial when the cavity volume is already well-defined by the cavity factor  $\delta_{\text{cav}}$ . Without  $\delta_{\text{cav}}$ , it is possible to reconstruct solvent densities for grid points laid between two different solute atoms since all  $g_{\perp}(r)$  become non-zero at small r when  $\lambda$  is small. On the other hand, when  $\lambda = 1$ , both  $\delta_{\rm cav}$  or  $\delta_{\rm excl}$ 

itself are required to reproduce the simulated  $\langle \partial U_i^{\text{vdW}}/\partial \lambda \rangle$ . Therefore, we keep both factors during our reported pDF-reconstructions.



Figure S2: Comparison of  $\Delta_i$  using both factors or only one factor during the pDFreconstruction, for  $\lambda = 0.1$  and 1.

# Solute Configurations



Figure S3: Solute configurations used in fixed simulations. For  $ala_{10}$ , peptide backbones are represented with red ribbons. For convenience, we designate d, d1, d2 and d3 for the configuration of deca-alanines respectively. Configurations are visualized using VMD.<sup>1</sup>





Figure S4: pDF of butane/propanol atoms to water hydrogen atoms at different  $\lambda$ . Numbers above each pDF indicate the corresponding  $\lambda$  of this atom type.



Figure S5: pDF of alanine/glycine atoms to water hydrogen atoms at different  $\lambda$ . Numbers above each pDF indicate the corresponding  $\lambda$  of this atom type.



Figure S6: pDF of HB2 atoms to water oxygen/hydrogen atoms at different  $\lambda$ . Numbers above each pDF indicate the corresponding  $\lambda$  of this atom type.

# Convergence:  $\langle \partial U^{\rm vdW}/\partial \lambda \rangle$  and  $\lambda$  Spacing

In this section we address the convergence issues. Figure S7 shows the  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  as a function of sampling time at different  $\lambda$  windows, for the case of ala<sub>10</sub> (configuration d), since the deca-alanine is the largest solute throughout this study. In all cases,  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$ is certainly converged within 2 ns. One might argue that the uncertainties for small  $\lambda$  cases  $(∼ 1)$  are still large relative the uncertainties for larger  $\lambda$  ( $∼ 0.2$ ), but we should realize that these uncertainties are already within 1% of the reported  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$ .



Figure S7:  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  as a function of sampling time. The values with uncertainties indicate the simulated  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  reported in the main text.

Due to the nature of simulating the soft-core potential at  $\lambda = 0$  we simply zero the value of the correlation for our reported studies. Here we present the results of simulated  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  and  $\Delta G_{\text{vdW}}$  using different  $\Delta \lambda$  in Figure S8. We use error propagation to estimate the uncertainties of  $\Delta G_{\text{vdW}}$ , thus the uncertainty reduces as the number of  $\lambda$  decreases. Compared with the  $\Delta\lambda = 0.05$  case,  $\Delta G_{\text{vdW}}$  becomes more than doubled when  $\Delta\lambda$ = 0.2. When  $\Delta\lambda$  = 0.1, the  $\Delta G_{\text{vdW}}$  is overestimated with 1.82 kcal/mol, which is already within the uncertainty of  $\Delta G_{\text{vdW}}$  obtained from  $\Delta \lambda = 0.05$  case. Therefore, to simplify the illustration of our results and focus on the method itself, we chose the case of  $\Delta\lambda = 0.1$  in our main text.



Figure S8: Simulated  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  using the  $\lambda$  spacings of 0.05, 0.10, and 0.20. The inset shows the corresponding cumulative  $\Delta G_{\text{vdW}}$ . Uncertainties are estimated using the propagation of block standard errors at the  $\lambda$  windows.

## pDF-Reconstructions for  $\text{Ala}_{10}$

Simulated and pDF-reconstructed  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  at each  $\lambda$  window for different configuration of  $ala_{10}$ .



Figure S9: Simulated and pDF-reconstructed  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$  at each  $\lambda$  window for different configuration of  $ala_{10}$ . The inset of each panel shows the difference between the simulated and pDF-reconstructed  $\langle \partial U^{\text{vdW}}/\partial \lambda \rangle$ .

### References

(1) Humphrey, W.; Dalke, A.; Schulten, K. VMD: Visual Molecular Dynamics. J. Mol. Graph. 1996, 14, 33–38.