A dynamic data structure for flexible molecular maintenance and informatics

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ABSTRACT

Motivation: We present the ‘Dynamic Packing Grid’ (DPG), a neighborhood data structure for maintaining and manipulating flexible molecules and assemblies, for efficient computation of binding affinities in drug design or in molecular dynamics calculations.

Results: DPG can efficiently maintain the molecular surface using only linear space and supports quasi-constant time insertion, deletion and movement (i.e. updates) of atoms or groups of atoms. DPG also supports constant time neighborhood queries from arbitrary points. Our results for maintenance of molecular surface and polarization energy computations using DPG exhibit marked improvement in time and space requirements.

Availability: http://www.cs.utexas.edu/~bajaj/cvc/software/DPG.shtml
Supplementary information: Supplementary data are available at Bioinformatics online.

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1 INTRODUCTION

Many human functional processes are mediated through the interactions among proteins, a major molecular constituent of our anatomical makeup. A computational understanding of these interactions provides important clues for developing therapeutic interventions related to diseases such as cancer and metabolic disorders. Computational methods such as automated docking through shape and energetic complementarity scoring aim to gain insight and predict such molecular interactions. Docking (Bajaj et al., 2009b; Gilson and Zhou, 2007) involves induced complementary fit between flexible protein interfaces. The flexible docking solution space consisting of all relative positions, orientations and conformations of the proteins is searched, and each putative docking is evaluated using combinations of interface complementarity scoring and atomic pairwise charged Coulombic interactions. Also, since proteins function in predominantly watery (solvent) environment, the protein solvation energy also plays an important role in determining intermolecular binding affinities ‘in vivo’ for drug screening, as well as in molecular dynamics simulations and in the study of hydrophobicity and protein folding. When computing the solvation energy for molecules, it is crucial to correctly model and sample the molecular surface.

The most common model for molecules is a collection of atoms represented by spherical balls, with radii equal to their van der Waals radii (Duncan and Olson, 1993; Mezey, 1993). The surface of the union of these spheres is known as the van der Waals surface. Accessibility to the solvent, namely the solvent accessible surface (SAS), can be defined as the locus of the center of a ‘probe’ sphere as it contacts the molecular surface. Usually, the ‘probe’ is a water molecule modeled as a sphere with radius 1.4 Å. Another definition for molecular surface is as a set of contact and reentrant patches (Richards, 1977), commonly known as the solvent contact surface (SCS), or solvent excluded surface (SES) or simply the molecular surface.

While a number of techniques have been devised for the static construction of molecular surfaces (see e.g. Bajaj et al., 2009c for a brief review), not much work has been done on neighborhood data structures for the dynamic maintenance of molecular surfaces under conformational changes and domain movements. Bajaj et al. considered limited dynamic maintenance of molecular surfaces based on Non Uniform Rational BSplines (NURBS) descriptions for the patches (Bajaj et al., 2003). Eyal and Halperin presented an algorithm based on dynamic graph connectivity that updates the union of balls molecular surface after a conformational change in $O(\log^2 n)$ amortized time per affected (by this change) atom (Eyal and Halperin, 2005a, b). In this article, we present the Dynamic Packing Grid (DPG), a space and time efficient neighborhood data structure that maintains a collection of balls (atoms) in 3-space, allowing a range of spherical range queries and updates for rapid scoring of flexible protein–protein interactions (Bajaj et al., 2009a, 2010).

The efficiency of the data structure results from the assumption that the centers of two different balls in the collection cannot come arbitrarily close to each other, which is a natural property of molecules. A consequence of this assumption is that any ball in the collection can intersect at most a constant number of other balls. On a RAM with $w$-bit words, our DPG data structure can report all balls intersecting a given ball or within $O(r_{\text{max}})$ distance from a given point in $O((\log\log w)\cdot t)$ time with high probability (w.h.p.), where $r_{\text{max}}$ is the radius of the largest ball in the collection. It can also answer whether a given ball is exposed (i.e. lies on the union boundary) or buried within the same time bound. At any time, the entire union boundary can be extracted from the data structure in $O(m)$ time in the worst case, where $m$ is the number of atoms on the boundary. There are existing techniques like Weiser et al. (1998, 1999), which can compute/approximate the exposed atoms and the surface area in the same time bound, but do not allow dynamic updates. On the other hand, DPG supports updates (i.e. insertion/deletion/movement of a ball) in $O((\log w)\cdot t)$ time w.h.p.$^1$ The data structure uses linear space.

$^1$For an input of size $n$, an event $E$ occurs w.h.p. (with high probability) if, for any $a \geq 1$ and $c$ independent of $n$, $Pr(E) \leq 1 - \frac{c}{n^a}$.
As we show here, DPGs can be used to maintain both the van der Waals surface and the SCS of a molecule within the performance bounds mentioned above. DPGs can also be used to enable fast energetics calculation by rapidly locating the atoms close to each sampled integration point of the SCS.

Besides protein docking and molecular dynamics, the neighborhood query and surface maintenance of DPG also has potential applications in interactive computer-aided design (CAD) tools developed for de novo drug design, protein folding, n-body simulations, etc. All these applications often need to handle extremely large number of atoms or points.

2 THE DYNAMIC PACKING GRID DATA STRUCTURE

Let $M = \{B_1, \ldots, B_n\}$ be a collection of $n$ balls in 3-space with $c_i$ and $r_i$ being the center and radius, respectively, of $B_i, i \in [1, n]$. Let $r_{\text{max}} = \max_i \{r_i\}$ and let $d_{\text{min}} = \min_{ij} \{d(c_i, c_j)\}$, where $d(c_i, c_j)$ is the Euclidean distance between $c_i$ and $c_j$.

We describe the packing grid data structure for maintaining $M$ efficiently under the following set of queries and updates.

**Queries**

1. **INTERSECT($c, r$):** Returns all balls intersecting $B = (c, r)$.
2. **RANGE(p, δ):** Returns all balls with centers within distance $\delta$ of point $p$. We assume that $\delta = O(r_{\text{max}})$.
3. **EXPOSED(c, r):** Returns true if the ball $B = (c, r) \in M$ contributes to the boundary of the union of the balls in $M$.
4. **SURFACE:** Returns the outer boundary of the union of the balls in $M$. If there are multiple disjoint outer boundaries defined by $M$, the routine returns one of them.

**Updates**

1. **ADD(c, r):** Adds a new ball $B = (c, r)$ to the set $M$.
2. **REMOVE(c, r):** Removes the ball $B = (c, r)$ from $M$.
3. **MOVE(c_1, c_2, r):** Moves the ball with center $c_1$ and radius $r$ to a new center $c_2$.

We assume that the following holds at all times.

**Assumption 2.1**. If $d_{\text{min}}$ is the minimum Euclidean distance between the centers of any two balls in $M$, then $r_{\text{max}} = O(d_{\text{min}})$.

In general, a ball in a collection of $n$ balls in 3-space can intersect $\Theta(n)$ other balls in the worst case, and it has been shown by Clarkson et al. (1990) that the boundary defined by the union of these balls has a worst case combinatorial complexity of $\Theta(n^2)$. However, if $M$ is a ‘union of balls’ representation of the atoms in a molecule, then assumption 2.1 holds naturally (Halperin and Overmars, 1994; Vardney et al., 1994), and as proved by Halperin and Overmars (1994), both complexities improve by a factor of $n$. The following theorem (see Bajaj et al., 2010 for a proof) states the consequences of the assumption.

**Theorem 2.1**. [Theorem 2.1 in Halperin and Overmars, 1994], slightly modified. Each ball in $M$ intersects at most $216 \cdot (r_{\text{max}}/d_{\text{min}})^3 = \Theta(1)$ other balls in $M$ and the combinatorial complexity of the boundary of the union of the balls is $\Theta(h_{\text{max}}/d_{\text{min}})^3 \cdot n = O(n)$.

Therefore, as Theorem 2.1 suggests, one should be able to handle $M$ more efficiently if assumption 2.1 holds. The efficiency of our data structure, listed in Table 1, also depends partly on this assumption.

### Table 1. Time complexities of the operations supported by the packing grid data structure

<table>
<thead>
<tr>
<th>Operations</th>
<th>Time Complexity (w.h.p.)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Assuming</strong></td>
<td><strong>Assuming</strong></td>
</tr>
<tr>
<td>$t_q = O(\log\log w)$</td>
<td>$t_{\nu} = O(\log\log n)$</td>
</tr>
<tr>
<td>$t_{\nu} = O(\log w)$</td>
<td>$t_\nu = O(\log\log\log n)$</td>
</tr>
</tbody>
</table>

**RANGE, INTERSEC, EXPOSED**

| Adding, Remove, Move | $O(\log w)$ | $O(\log\log n)$ |

**Surfaces**

- $O(1)$ (balls on surface) (worst case)

**Assumptions**

(i) RAM with $w$-bit Words.

(ii) Collection of $n$ balls.

(iii) $\delta = O(r_{\text{max}})$ and, (iv) $r_{\text{max}} = O(\text{minimum distance between two balls})$
We are now in a position to present the Theorem follows (further details are available in Bajaj et al., 2010). The description of each level component (i.e. cell, line or plane) is non-empty if it contains the ball data structure of an arbitrary exposed ball in $M$.

We have the following lemma (proved in Bajaj et al., 2010) on the space usage of the data structure.

**Lemma 2.2.** Let Assumption 2.1 hold. Then the packing grid data structure storing $M$ uses $O(n)$ space.

### 2.3 Queries and updates

The queries and updates supported by the data structure are implemented as follows.

**2.3.1 Queries**

1. **Range** $(p, \delta)$: Let $p=(p_x,p_y,p_z)$. First we invoke the function $Q(\mathcal{B}(\delta), h)$ of the range reporting data structure $RR$ under the level 3 grid data structure with $l=(|p_x-\delta|/2r_{\text{max}})$ and $h=(|p_z+\delta|/2r_{\text{max}})$. This query returns a set $S_2$ of non-empty $c$-planes represented as pointers to level 2 grid-plane data structures. Then, for each $c$-plane, we perform similar queries under the corresponding level 2 data structure to obtain the set $X_1$ of non-empty grid-planes. Again, querying under each grid-line data structure produces the set $S_0$ containing non-empty grid-cells. Finally, for each cell in $S_0$, we collect and return each ball whose center lies within distance $\delta$ from $p$.

2. **Correctness**: Under Assumption 2.1, this function runs in $O(t_q)$ time.

**2.3.2 Update**

1. **Insert** $(b, \delta)$: We call $RANGE(c, 0)$ and $RANGE(c, r_{\text{max}})$ and collect the output in set $S$. From $S$ we remove the data structure of each ball that does not intersect $B$, and return the resulting (possibly reduced) set.

The correctness follows from basic geometry and the correctness of RANGE. Under Assumption 2.1, this function runs in $O(t_q)$ time.

**2.3.3 Exposed** $(c, r)$: Let $B=(c,r)$ be the given ball. We locate $B$'s data structure by calling $RANGE(c, 0)$, and return the value stored in its exposed field. Clearly, the function takes $O(t_q+r_{\text{max}}/d_{\text{min}}) \leq r_{\text{max}}$ time (w.h.p.), which reduces to $O(t_q)$ under Assumption 2.1.
2.3 Theorem
Therefore, we have the following theorem.

(4) surface-root pointer under the level 3 ‘grid’ data structure points to the ‘ball’ data structure of a ball \( B \) on the union boundary of \( M \). We scan the set \( F \) of exposed faces of \( B \), and using the pointers to other exposed balls stored in \( F \) we perform a depth-first traversal of all exposed balls in \( M \) and return the exposed faces on each such ball. Let \( m \) be the number of balls contributing to the union boundary of \( M \). Then according to Theorem 2.1, the depth-first search takes \( \mathcal{O}\left(\left(\frac{r_{\text{max}}}{d_{\text{min}}}\right)^{3} m\right) \) time in the worst case, which reduces to \( \mathcal{O}(m) \) under Assumption 2.1.

2.3.2 Updates
(1) \text{Add}( c, r ): Let \( c=(c_x,c_y,c_z) \) and let \( c'_u = \left[ \frac{c_u}{r} \right] \), where \( u \in \{x,y,z\} \). Let \( G \) be the grid data structure. If \( G \) does not exist, then create \( G \). Then, first create and initialize a data structure \( B \) and add to \( M \). Then, we query the range reporting data structure \( G \cdot RR \) to locate the data structure \( P \) for the \( c'_x \)-plane. If \( P \) does not exist, create and initialize \( P \), and insert \( c'_x \) along with a pointer to \( P \) into \( G \cdot RR \). Similar steps are taken for the grid-line and then the grid-cell data structures to identify the \((c'_x,c'_y,c'_z)\)-cell \( C \) and add \( B \) to \( C \). We then use the \text{INTERSECT} query to identify \( \mathcal{N}(B) \), the set of balls intersecting \( B \). Finally we update the arrangement of each ball in \( B_{\cup} \mathcal{N}(B) \), list exposed faces on each ball and update the surface-root pointer if necessary.

Observe that the introduction of a new ball may affect the surface exposure of only the balls it intersects (by burying some/all of them partly or completely), and no other balls. Hence, updating the arrangements of the balls in \( B_{\cup} \mathcal{N}(B) \) (in addition to those in earlier steps) are sufficient to maintain the correctness of the entire data structure. The \text{Add} function terminates in \( \mathcal{O}(t_q) \) assuming \( t_{\text{max}} = \mathcal{O}(d_{\text{min}}) \). Detailed analysis is in (Bajaj et al., 2010).

(2) \text{Remove}( c, r ): This function is symmetric to the \text{Add} function, and has exactly the same asymptotic time complexity. Hence, we do not describe it here.

(3) \text{Move}( c_1, c_2, r_1, r_2 ): This function is implemented in the obvious way by calling \text{Remove}( c_1, r ) \text{ followed by Add}( c_2, r ). It has the same asymptotic time complexity as the two functions above. Therefore, we have the following theorem.

Theorem 2.3. Let \( M \) be a collection of \( n \) balls in 3-space as defined in Theorem 2.1, and let Assumption 2.1 hold. Let \( t_q \) and \( t_u \) be as defined in Theorem 2.2. Then the packing grid data structure storing \( M \) on a word RAM:

(i) uses \( \mathcal{O}(n) \) space;
(ii) supports updates (i.e., insertion/deletion/movement of a ball) in \( \mathcal{O}(t_u) \) time w.h.p.;
(iii) reports all balls intersecting a given ball or within \( \mathcal{O}(t_{\text{max}}) \) distance from a given point in \( \mathcal{O}(t_q) \) time w.h.p., where \( t_{\text{max}} \) is the radius of the largest ball in \( M \); and
(iv) reports whether a given ball is exposed or buried in \( \mathcal{O}(t_u) \) time w.h.p., and returns the entire outer union boundary of \( M \) in \( \mathcal{O}(m) \) worst-case time, where \( m \) is the number of balls on the boundary.

2.4 Molecular surface maintenance using DPG
In this section, we briefly describe applications of the packing grid data structure for efficient maintenance of molecular surfaces.

2.4.1 Maintaining van der Waals surface of molecules
Each atom is simply treated as a ball with a radius equal to the van der Waals radius of the atom see (Batsanov, 2001) for a list of van der Waals radius of different atoms.

2.4.2 Maintaining Lee-Richards (SCS/KES) surface
For the efficient maintenance of the Lee-Richards surface of a molecule within the performance bounds given in Table 1, we maintain two packing grid data structures: DPG and DPG'. The DPG data structure keeps track of the patches on the Lee-Richards surface, and DPG' is used for detecting intersections among concave patches.

Before adding an atom to DPG, we increase its radius by \( r_s \), where \( r_s \) is the radius of the rolling solvent atom. The DPG data structure keeps track of all solvent exposed atoms, i.e. all atoms that contribute to the outer boundary of the union of these enlarged atoms. Theorem 2.1 implies that each atom in DPG contributes \( O(1) \) patches to the Lee-Richards surface, and the insertion/deletion/movement of an atom results in local changes of only \( O(1) \) patches. We can modify DPG to always keep track of where two or three of the solvent exposed atoms intersect, and once we know the atoms contributing to a patch we can easily compute the patch in \( O(1) \) time (Bajaj et al., 2003).

The Lee-Richards surface can self-intersect in two ways: (i) a toroidal patch can intersect itself, and (ii) two different concave patches may intersect (Bajaj et al., 2003). The self-intersections of toroidal patches can be easily detected from DPG. In order to detect the intersections among concave patches, we maintain the centers of all current concave patches in DPG', and use the \text{INTERSECT} query to find the concave patch (if any) that intersects a given concave patch.

2.5 Energetics computation using DPG
Generally, the solvation energy \( G_{\text{sol}} \) of a molecule is decomposed into three components, namely, \( G_{\text{cav}} \) (the energy to form cavity in the solvent), \( G_{\text{vdw}} \) (the solute-solvent van der Waals interaction energy), and \( G_{\text{pol}} \) (the polarization energy or the electrostatic potential energy change due to the solvation). The first two terms \( G_{\text{cav}} \) and \( G_{\text{vdw}} \) are linearly related to the solvent accessible surface area \( S_{\text{acc}} \). The last term, \( G_{\text{pol}} \), can be approximated using the Generalized Born (GB) theory as introduced by Still et al. (1990).

\[
G_{\text{pol}} = \frac{1}{2} \sum_{i,j} \frac{q_i q_j}{\sqrt{r_i^2 + R_i R_j e^{-r_i^2/4d_i R_j}}} \tag{2.1}
\]

where \( \tau = 1 - \frac{1}{\lambda} \), and \( R_i \) is the effective Born radius of atom \( i \) (see Fig. 2a). Either Equations 2.2 or 2.3 can be used as discrete approximation of \( R_i^{-1} \) (Bajaj and Zhao, 2010).

\[
R_i^{-1} = \frac{1}{2\pi} \sum_{k=1}^{N} w_k \frac{(r_k - x_i)^2}{(r_k - x_i)^2 + \tau^2} \tag{2.2}
\]

\[
R_i^{-3} = \frac{1}{4\pi} \sum_{k=1}^{N} w_k \frac{(r_k - x_i)^3}{(r_k - x_i)^3 + \tau^3} \tag{2.3}
\]

where the \( r_k \)'s are \( N \) carefully chosen integration points on the boundary of the molecule, and \( w_k \) is a weight assigned to \( r_k \) to ensure higher order of accuracy for small \( N \) (see Fig. 2b). Other methods have used volume integrals (Tjong and Zhou, 2007) or
integrals over bonded and non-bonded atom pairs (Qui et al., 1997) to approximate Born Radii.

The non-polar terms $G_{pol}$ and $G_{dp}$ can be computed directly from the SAS area $\text{SAS}_i$ of the molecule. The SAS of the molecule can be extracted in $O(\text{ntime})$ and $O(\text{nm})$ time using a DPG data structure, where $\text{nm}$ is the number of atoms in the molecule. The DPG data structure outputs the SAS as a set of spherical and toroidal patches, and we add up the area of each patch in order to calculate $\text{SASA}$.

### 2.5.1 Discrete approximation of Born Radii

In order to approximate the polar term $G_{pol}$, we first need to approximate the Born radius $R_i$ of each atom $i$. We compute the SES as A-spline patches, produce a quality improved meshing of the surface and sample integration points and their weights following (Bajaj and Zhao, 2010) (see Figure 3) and then use Equation (2.2) to approximate $R_i$. But observe that the direct computation of $R_i$ requires $O(n^3)$ time, where $n$ is the number of atoms and assuming that the number of sampled integration points is also $O(n)$. However, since the terms in the summation diminish very fast with the increase of distance, distance cutoffs can be used to approximate it.

Given the set of atoms $\mathcal{A}$, the set of integration points $\mathcal{Q}$ sampled on the surface, and two user-defined parameters $a, b > 0$, for every integration point $q \in \mathcal{Q}$, we place each atom $a \in \mathcal{A}$ in one of the following three categories based on the distance $d$ between $q$ and the center of $a$: (i) near ($d \leq a$), (ii) midway ($a < d < b$) and (iii) far ($a < d$).

Figure 4 shows an example in 2D. For the near categories, the computation is performed exactly. For the midway category, clusters of atoms and integration points are viewed as pseudo-atoms and pseudo-integration points, and hence a coarse computation is performed. For the far category, a single average distance and a single average weighted normal is used for all pairs of clusters.

Separate DPG data structures are used to store the atoms, integration points, pseudo-atoms and pseudo-integration points. DPG is used both for identifying the near, midway and far atoms/pseudoatoms as well as for clustering (see Bajaj et al., 2010 for details).

Assuming that $\tilde{m}_i$ is an upper bound on the number of atoms within distance $\delta$ from any given point in space, the time spent for computing all $R_i$’s is $O(\text{ntime})$, which reduces to $O(\text{ntime})$ since $\tilde{m}_i$ is a constant (though could be quite large) for constant $\delta$. Once all $R_i$’s are computed, $G_{pol}$ can be computed using Equation (2.1) in $O(\text{ntime})$ time in the worst case. The space usage is $O(\text{ntime})$ which is $O(\text{ntime})$ for constant $\delta$.

### 2.6 Maintenance of flexible molecules

Suppose we are given a flexible molecule decomposed into several (mostly) rigid domains which interact either through connected chain segments or large interfaces. We refer to these chain segments and interfaces as connectors. Domains may move with respect to each other through motions applied to the connectors. Two domains connected by at least one connector may undergo bending motion applied to some hinge point around some hinge axis. If they are connected by only one connector, a twisting motion can also be applied to the connector by updating torsion angles along its backbone. If two domains share a large interface area, they may undergo a shearing motion with respect to each other. However, though domains are mostly rigid they may have flexible loops and side chains on their surfaces.

We maintain a separate packing grid data structure $P_j$ for each domain $D_j$. If two domains $D_i$ and $D_j$ are connected and $i < j$, the set $S_{ij}$ of all connectors between these two domains are included in $P_i$, and a transformation matrix $M_{ij}$ is kept with $P_i$ that describes the new relative position and orientation of $P_j$ with respect to that of $P_i$. Whenever some motion is applied to the connectors in $S_{ij}$, we update $P_j$ in order to reflect the changes in the locations of the atoms in these connectors, and also update $M_{ij}$ in order to reflect the new relative position and orientation of $P_j$ with respect to $P_i$.

The complexities of these operations are presented in the following lemma proved in (Bajaj et al., 2010).

**Lemma 2.3.** The surface of a flexible molecule decomposed into (mostly) rigid domains can be maintained using packing grid data structures so that

(i) updating for a bending/shearing/twisting motion applied between two domains takes $O(1+\text{ntime})$ time (w.h.p.), where $\pi$ is the number of atoms in the connectors between the two domains;
To measure the performance of the update and query functions of DPG, we have implemented a much simpler data structure that supports both updates and distance queries in expected $O((\log w)^2)$ time and uses linear space. Since $w$ is usually not more than 64, for most practical purposes a $O((\log w)^2)$ query time should be almost as good as $O((\log(\log w))^2)$ time. This data structure builds on binary search trees, dynamic perfect hashing and $\gamma$-fast trees. However, instead of dynamic perfect hashing we used 'cuckoo hashing' (Rasmus and Flemming, 2004) since it is much simpler, and still supports lookups in $O(1)$ worst case time, and updates in expected $O(1)$ time.

### 3 RESULTS AND DISCUSSIONS

The performance of the basic functions of DPG are reported in Section 3.2. Sections 3.3 and 3.4, respectively, analyzes performance of DPG in molecular surface maintenance and energetics calculation.

#### 3.1 Implementation details

In our current implementation, instead of the 1D integer range-reporting data structure presented in (Mortensen et al., 2005), we have implemented a much simpler data structure that supports both updates and distance queries in expected $O((\log w)^2)$ time and uses linear space. Since $w$ is usually not more than 64, for most practical purposes a $O((\log w)^2)$ query time should be almost as good as $O((\log(\log w))^2)$ time. This data structure builds on binary search trees, dynamic perfect hashing and $\gamma$-fast trees. However, instead of dynamic perfect hashing we used 'cuckoo hashing' (Rasmus and Flemming, 2004) since it is much simpler, and still supports lookups in $O(1)$ worst case time, and updates in expected $O(1)$ time.

#### 3.2 Performance analysis of updates and queries

To measure the performance of the update and query functions of DPG, we use more than 180k quadrature points, generated for energetics computations by sampling uniformly at random on the surface of PSTI (a variant of human pancreatic trypsin inhibitor: 1HPT.pdb) after protonation using PDB2PQR (Dolinsky et al., 2004). Experiments are performed on a 3 GHz 2 x dual core (only one core was used) AMD Opteron 2222 processor with 4 GB RAM. Please refer to (Bajaj et al., 2010) for details of the experiment. Table 2 shows the results of this experiment. The time required is $O((\log w)^2 + K)$ where $K$ is the size of the output or in this case, the number of points returned. The last column of the table shows that as the point set becomes denser, the efficiency of the data structure remains almost the same.

Table 2. Performance of the Query function of packing grid

<table>
<thead>
<tr>
<th>Quadrature Points</th>
<th>Query Distance (Å)</th>
<th>Average Time (ms/Query)</th>
<th>Average number of Points Returned (k/milliseconds)</th>
</tr>
</thead>
<tbody>
<tr>
<td>45654</td>
<td>2</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td>91309</td>
<td>2</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td>136963</td>
<td>2</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td>182618</td>
<td>2</td>
<td>4</td>
<td>8</td>
</tr>
</tbody>
</table>

We randomly assign each of the 182618 points to one of four groups and thus obtain four approximately equal-sized groups. We then run queries from the atom centers (100 queries per atom) on group 1, merge groups 1 and 2 and run queries on this merged group, and so on.

#### 3.3 Performance of molecular surface maintenance

We compared the performance of DPG with the 3D hashing used by (Eyal and Halperin, 2005a, b) in producing and maintaining molecular surfaces. We used the same implementation of 3D arrangement and surface generation (Eyal and Halperin, 2005b), but switched between the two different range query data structures. We measured the space and time requirements for generating the surface of various macromolecules. To verify scalability, multiple chains of the same protein were inserted. For virus capsids, as multiple chains are inserted, not only the number of atoms increases but also the overall structure becomes sparser. The results of this experiment are reported in Table 4. It is clear that the space requirement of the DPG is linear in the number of atoms. The difference in space requirement becomes more pronounced for larger and sparser structures. Also, its running times are comparable with that of 3D hash. Though 3D hash performs insertions and queries in optimal constant time, using too much memory can adversely affect its running time. For example, in the case of RDV P3 with four chains, 3D hash operations run slower than DPG range reporting operations. We believe that this slowdown is due to page faults caused by excessive space requirement of 3D hash.

#### 3.4 Performance of Born Radii and polarization energy calculation

A parallel implementation of the approximation scheme described in Section 2.5.1 was applied to compute the Born Radii, which were used to compute the polarization energy $G_{Pol}$. The experiments were performed on the RANGER cluster, on a single node with 16 cores. First, three different approximations were performed by varying the $\delta$ parameter for the molecules in ZDock Benchmark 2.0 (Mintseris et al., 2005). We shall refer to these as $DPG_{GB_{\delta,x}}$, where $\delta=0.1$, $0.5$, $0.75$, $1.0$ and $D$ is the dimension of a cell in DPG and it means that a $g \times g \times g$ grid was used to generate the surface and integration points on the surface. Both $D$ and $\alpha$ are automatically selected based on the size of the molecules. For each atom $i$ of a molecule, the approximation error is defined as $e_{i} = |\frac{R_{i}^{GR} - R_{i}^{DPG}}{R_{i}^{GR}}| \times 100$, where $R_{i}^{GR}$ and $R_{i}^{DPG}$ are the Born Radii of atom $i$ approximated using DPG-based scheme and by exact (full pairwise) evaluation of Equation (2.2), respectively. The approximation error

Table 3. Insertion and deletion times of our current packing grid implementation

<table>
<thead>
<tr>
<th>Molecule (PDB File)</th>
<th>Number of Atoms</th>
<th>Average Insert Time (µs)</th>
<th>Average Delete Time (µs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GroEL (1GRL)</td>
<td>29274</td>
<td>3.3</td>
<td>4.0</td>
</tr>
<tr>
<td>RDV P8 (1UF2: P)</td>
<td>193620</td>
<td>3.9</td>
<td>4.4</td>
</tr>
<tr>
<td>RDV P8 (1UF2: A)</td>
<td>459180</td>
<td>3.9</td>
<td>4.6</td>
</tr>
<tr>
<td>Dengue (1K4R)</td>
<td>545040</td>
<td>4.0</td>
<td>4.5</td>
</tr>
</tbody>
</table>

The results are averages of four runs. In each run, all atom centers are randomly inserted into the data structure followed by random deletion of all atom centers.
Table 4. Comparison of the performance of the 3D range reporting data structure used by DPG and the 3D hash table used in (Eyal and Halperin, 2005b).

<table>
<thead>
<tr>
<th>Molecule (PDB File)</th>
<th>Number of Chains</th>
<th>Number of Atoms</th>
<th>Number of Cells (k)</th>
<th>Time (s)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>DPG 3D hash</td>
<td>DPG</td>
<td>3D hash</td>
<td></td>
</tr>
<tr>
<td>1H3Q</td>
<td>1</td>
<td>1114</td>
<td>4.68</td>
<td>45.18</td>
</tr>
<tr>
<td>2GLS</td>
<td>1</td>
<td>3636</td>
<td>1.44</td>
<td>9.18</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>18180</td>
<td>7.28</td>
<td>41.40</td>
</tr>
<tr>
<td>2BG9</td>
<td>1</td>
<td>2991</td>
<td>1.20</td>
<td>10.75</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>14955</td>
<td>6.63</td>
<td>31.20</td>
</tr>
<tr>
<td>1UF2: Chain P</td>
<td>1</td>
<td>3227</td>
<td>1.35</td>
<td>9.26</td>
</tr>
<tr>
<td>(RPV P8)</td>
<td>2</td>
<td>6454</td>
<td>2.74</td>
<td>112.04</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>12908</td>
<td>5.47</td>
<td>4426.11</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>25816</td>
<td>10.98</td>
<td>6332.16</td>
</tr>
<tr>
<td>1UF2: Chain A</td>
<td>1</td>
<td>7653</td>
<td>3.23</td>
<td>38.76</td>
</tr>
<tr>
<td>(RPV P3)</td>
<td>2</td>
<td>15306</td>
<td>6.46</td>
<td>927.44</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>22959</td>
<td>9.74</td>
<td>1992.75</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>30612</td>
<td>12.99</td>
<td>3591.70</td>
</tr>
<tr>
<td>1K4R: Chain A and B</td>
<td>1</td>
<td>6056</td>
<td>2.62</td>
<td>20.70</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>12112</td>
<td>5.24</td>
<td>138.60</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>18188</td>
<td>7.85</td>
<td>333.06</td>
</tr>
</tbody>
</table>

for a molecule is the average of the $e_i$'s. Figure 5a reports the approximation errors for each molecule. It is clear that a larger ‘near’ band results in lower error. On the other hand, Figure 5b shows the speedup for each approximation, where speedup is defined as (time taken by exact computation)/(time taken by DPG-based computation). Though there is a clear speed/accuracy trade-off, it only underscores the efficacy and flexibility of the scheme. For example, $DPG_{GB_1, 128}$ is almost 50 times faster than the naive pairwise computation with only 2.41% error.

In Figure 6, we report the errors of $G_{pol}$ computation where, for each molecule, the error is defined as $\frac{G_{pol} - G_{pol}^{validation}}{|G_{pol}^{validation}|} \cdot 100$, where $G_{pol}^{validation}$ and $G_{pol}^{results}$ are, respectively, the $G_{pol}$ computed using $R_{\text{validation}}^i$ and $R_{\text{results}}^i$ for each atom $i$ of the molecule. $G_{pol}$ errors are much lower than the Born Radii errors because the integral of the $G_{pol}$ formulation also falls off with distance and hence accuracy of $G_{pol}$ is more dependent on the accuracy of the Born radii of atoms near the surface. In Table 5, the Born Radii of all atoms of all molecules are grouped into five bins based on $R_{\text{results}}$. It is easy to verify that Born Radii computation errors for the atoms near the surface (having lower values of Born Radii) are indeed much lower. Another notable aspect from the results in Figure 6 is that some of the molecules, especially PPE, have $G_{pol}$ errors that are considerably higher. We found that this trend to happen for molecules which are very small (for example, PPE, which has only 436 atoms) or very flat, in other words does not have much in the ‘far’ band. Our scheme for computing partial sums for ‘far’ bands seem to overestimate in such cases.

We also computed the Born Radii and $G_{pol}$ for the same set of molecules using Amber (Case et al., 2005) and GB6 (Tjong and Zhou, 2007) on the same computing cluster using the same number of nodes and cores. The results in Figure 7a show that DPG-based implementations, are much faster than GB6 and are comparable to Amber. In Figure 7b, we report the ratio of the Born Radii computation time of DPG and Amber, sorted in increasing size of molecules. It is clear that DPG gets better as the size increases and outperforms Amber in a few cases. So, we experimented with Amber, GB6 and DPG for a very large molecule, the Cucumber Mosaic Virus (CMV) capsid, consisting 509K atoms. DPG completed in only 22 s, while Amber needed 172 s and GB6 needed about 3.6 h.

As $G_{pol}$ obtained using different formulations often vary a lot, we decided to compare the consistency instead of the exact values.
Table 5. Distribution of errors for different ranges of Born Radii. Clearly, error is lower for atoms near the surface (smaller Born Radii).

<table>
<thead>
<tr>
<th>Range of Born Radii</th>
<th>Number of atoms in range</th>
<th>Average % error</th>
</tr>
</thead>
<tbody>
<tr>
<td>[0, 2]</td>
<td>17,580</td>
<td>0.83</td>
</tr>
<tr>
<td>(2, 4]</td>
<td>63,101</td>
<td>1.85</td>
</tr>
<tr>
<td>(4, 7]</td>
<td>61,640</td>
<td>3.82</td>
</tr>
<tr>
<td>(7, 10]</td>
<td>38,796</td>
<td>6.74</td>
</tr>
<tr>
<td>(10, ...)</td>
<td>112,765</td>
<td>10.16</td>
</tr>
</tbody>
</table>

Figure 7c displays that DPG consistently produces $G_{pol}$ values similar to Amber’s. In fact, the average deviation of $G_{pol}$ computed by DPG-based scheme from Amber’s is less than 5%.

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Conflict of Interest: none declared.

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Bajaj,C. et al. (2010) A dynamic data structure for flexible molecular maintenance and informatics. Technical Report TR-10-31, ICES, University of Texas at Austin, Austin, TX, USA.


