

# **ASSIGNMENT 13: SOLUTION**

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Written in X<sub>E</sub>L<sup>A</sup>T<sub>E</sub>X

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# POTENTIAL ENERGY SURFACES

## THEORETICAL BACKGROUND

### Corrugation Function as a Fourier Series

In previous tutorials, we have demonstrated that a hard-wall corrugation function can be constructed for a close-packed plane. This is achieved by expanding the surface potential as a two-dimensional Fourier series, which can be fitted to the lattice; the properties of the fitted series must match the real lattice, and so we must specify several conditions: the corrugation function must match the periodicity of the underlying lattice, and thus must take the form:

$$\zeta(\mathbf{R}) = \sum_{\mathbf{G}} A(\mathbf{G}) e^{i\mathbf{G}\cdot\mathbf{R}},$$

where  $\mathbf{G}$  is any reciprocal lattice vector, and  $A(\mathbf{G})$  is its corresponding Fourier coefficient.

The hard-wall potentials tutorial gives the following strategy for constructing a corrugation function:

1. Determine the Bravais lattice of the surface.
2. Find the set of basis lattice vectors for the aforementioned lattice, denoted  $\mathbf{a}_1$  and  $\mathbf{a}_2$ .
3. Find the corresponding basis reciprocal lattice vectors, denoted  $\mathbf{b}_1$  and  $\mathbf{b}_2$ .
4. Use the basis vectors of the reciprocal lattice to find as many reciprocal lattice vectors as necessary of the form:

$$\mathbf{G} = h\mathbf{b}_1 + k\mathbf{b}_2,$$

where  $h$  and  $k$  are integers.

5. Use the reciprocal lattice vectors to construct a truncated Fourier series for the corrugation function. The coefficients for the terms should be chosen such that the corrugation has local maxima at the positions of the atoms composing the surface.

## Number of Fourier Components

Different numbers of Fourier components are required, dependent on circumstance, to construct the desired features of a lattice. In this assignment, we consider the example of a close-packed plane. This is because it has remarkable symmetry properties.

In the previous tutorial it was shown that two reciprocal lattice vectors were insufficient to represent the rotational symmetry of a close-packed plane. Three vectors successfully represented the symmetry, but failed to distinguish between the three types of bridge site, and the two types of hollow site. A labelled corrugation function for a close-packed plane is given in the margin to act as a memory aid.

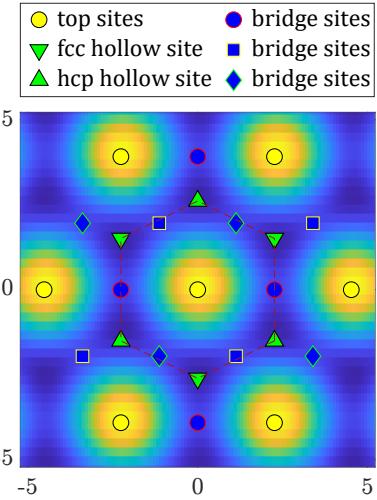
## The Wigner-Seitz Unit cell

The dashed line in the figure denotes the *Wigner-Seitz* unit cell of the lattice. The Wigner-Seitz cell around a lattice point is defined as the locus of points that are closer to that lattice point than any others. This cell is primitive, and tessellates all of real space. This concept is used in the discussion of generating advanced potential energy surfaces.

## Computing Higher Fourier Components

In principle, it is possible to compute the corrugation function exactly for each point in the Wigner-Seitz (WS) unit cell of the lattice; and then this function can then be tessellated over all of real space, giving the complete corrugation function. This method is impractical: it would require sampling an infinite number of points in space, which cannot be done. How do we avoid this problem? A common approach is to discretise the WS unit cell. The number of samples required can be further reduced by exploiting the symmetry of the lattice; thus we only sample a portion of the WS cell, at the expense of losing the distinction between some sites on the potential surface.

A common approach is to calculate the corrugation across a grid of points in the so-called *irreducible triangle*. This is defined to be the smallest triangle on which the FCC and HCP hollow sites differ. Seen in the figure 2 in the margin, the large circles are sufficient to differentiate between hollow sites. However, these large circles form a hexagonal grid rotated at 30° to the cartesian basis vectors. This makes operations such as the Fourier transform more problematic; extra points are included to avoid a rotated grid, and to improve the resolution of the simulated functions. The figure contains 31 discrete points, which form a hexagonal grid; this grid has the same orientation as the lattice, but a different spacing. The lattice defined by this grid of points is known as the “grid lattice”. The number 31 is not arbitrary.



**Figure 1** | A labelled plot of the corrugation as computed in the hard-wall corrugation assignment.

Whilst a 31 point grid cannot distinguish between bridge sites, it is the minimum number of points required to represent the bridge sites as local minima (as they should be).

Once the potential has been calculated across the grid, the triangle can be tessellated across real space using symmetry operations. This produces a corrugation function. However, since our irreducible triangle as appearing in the figure only contains one bridge site, tessellating in the manner described below will produce a corrugation function that does not distinguish between bridge sites (according to whether they represent FCC or HCP structures). For all sites to be distinguished, three irreducible triangles would be required. Fortunately the distinction between bridge sites is not important for most adsorbates; but the distinction between hollow sites is of interest in the study of adsorption and adsorbate motion on the surface, because adsorbate positions at hollow sites are usually more stable.

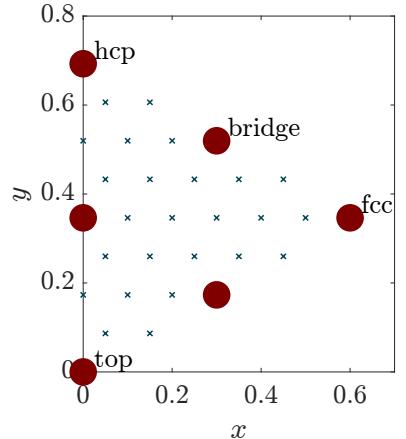
The process of tiling the surface exploits the hexagonal symmetry of the lattice, and in our case is:

1. Reflect the irreducible triangle across one face.
2. Rotate the diamond formed about one of the points common to both the original and reflected triangle to tile a hexagonal unit cell. Points on opposite sides of the hexagon are equivalent since they are one lattice vector apart.
3. The unit cell produced by this process is a WS cell in the basic lattice, and can be used to tessellate all of real space by translating the hexagonal grid by basic lattice vectors.

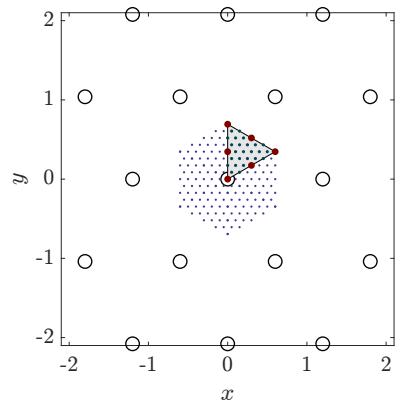
In this construction the top-hcp distance is  $1/3$  of the basic lattice nearest-neighbour distance in the same direction, and the top-bridge distance is  $1/2$  the basic lattice separation. Thus the separation of the grid lattice is  $1/12$ th that of the basic lattice. The reciprocal grid lattice is therefore 12 times the spacing of the reciprocal basic lattice, and the WS cell of the reciprocal basic space (the 1st BZ) is correspondingly 12 times the size of the WS cell of the reciprocal grid lattice.

The 1st BZ contains all information required to describe every reciprocal lattice vector corresponding to the grid in real space. To describe points outside the WS cell we can add an integer multiple of a unique reciprocal lattice vector in the 1st BZ (we denote such reciprocal lattice vector by  $\mathbf{G}_1$ ) to get back to the first BZ. Thanks to the properties of complex exponentiation, when such a sum has its inner product taken with any of the real space vectors in the expression for the corrugation, the corrective  $\mathbf{G}_1$  component reduces to a factor  $\exp(2\pi i) = 1$ . The Fourier coefficients of the reciprocal lattice vectors that lie outside the 1st BZ will also be equivalent to those inside.

Considering only the unique reciprocal vectors within the 1st BZ,



**Figure 2 |** The large red circles are the only points required to differentiate between hollow sites. However, additional points have been included to provide a more general procedure, giving a total of 31 points.



**Figure 3 |** Depiction of the real space lattice along with the irreducible triangle (shaded) and the set of points encompassed by the WS cell.

the corrugation at the grid point  $\mathbf{R}_j$  (for  $j \in \{1, 2, \dots, n_R\}$ ) is given by:

$$\zeta(\mathbf{R}_j) = \sum_{\mathbf{G}_1} A(\mathbf{G}_1) e^{i\mathbf{G}_1 \cdot \mathbf{R}_j}.$$

In general, the process for computation is as follows:

1. Take a grid of points in real space which have the same hexagonal structure as the basic lattice but shrunk by an integer factor  $N$  (31 in the previous example).
2. Compute the unique reciprocal lattice vectors,  $\mathbf{G}_1$ , inside the 1st Brillouin zone as determined by a reciprocal space lattice that has  $N$  times the dimensions of the basic reciprocal lattice.
3. Calculate the corrugation at each point in the real space WS cell, where the coefficients  $A(\mathbf{G}_1)$  are free variables in the model. It is necessary to give a fractional ‘weight’ to each point so that the potential at edges/corners is not double/triple counted respectively during tessellation.

### **Anthraquinone**

The task below uses the motivating example of the potential energy surface for an Anthraquinone (AQ) molecule adsorbed on the Cu(111) plane, so it would be prudent to establish a good phenomenological understanding of this system.

Anthraquinone is composed of three benzene rings fused in a linear arrangement with oxygens bonded at its midpoint, often called the ‘linkers’ of the AQ molecule. The molecule has two-fold rotational symmetry about any axis through its centre-of-mass and perpendicular to its main surface.

Since AQ is a large rod-like molecule it can’t be modelled as occupying a single site on the substrate lattice. On the Cu(111) surface, both of the oxygen linkers interact strongly with the substrate whereas the central body of the molecule remains somewhat raised above the surface (in fact, the ends of the rod bend away from the surface whilst the centre remains close to it [1]). As such, in constructing a potential energy surface for the molecule we must consider not only the position of its centre-of-mass, but also its polar angle with respect to the basis of the substrate lattice.

Modelling using Density Functional Theory shows that AQ molecules preferentially adsorb on hcp hollow sites, which are the global minima of the surface. There are local maxima at fcc sites and local minima at bridge sites. The molecules adsorb on top sites.

This unusual mode of adsorption lends itself to some unusual properties. Anthraquinone can diffuse uniaxially along the close-packed directions of the surface [2,3]. Additionally, AQ molecules may ‘pick up’ light adsorbates (e.g. CO<sub>2</sub>) that pass close to its oxygen

linkers, carrying them along the surface and thereby acting as a cargo-carrying agent. The unusual adsorption also causes AQ adsorbates to form honeycomb structures at high coverages, but that is beyond the scope of this assignment.

However, the AQ molecule does not move in a straight line as one might expect. Instead, it performs four rotations of  $\pm 15^\circ$  about one of its linkers to move one substrate lattice spacing, producing a characteristic ‘walking’ motion.

Note that each stage is named after the type of site above which the centre-of-mass of the molecule lies. In modelling the potential surface it is possible to consider only the position of the molecule’s centre-of-mass, as well as its orientation. Its orientation is given by the angle  $\theta$ , defined as the anticlockwise angle of its length from the [1 0] azimuth (positive  $x$ -direction).

Rotations of greater than  $\pm 15^\circ$  are possible but have a much higher energetic barrier so are less common. Thus, AQ motion the Cu(111) surface is characterised by long periods of linear walking motion interspersed with rotations through larger angles.

## TASK

1. The first task is to investigate the existing code for producing the potential energy surface. To represent all bridge sites as local minima, which is required in modelling the motion of AQ on Cu(111), 31 points are required in the irreducible triangle. However, since AQ is a rod-shaped molecule it is not rotationally-symmetric, and as such one must compute the potential for each allowed orientation of the AQ molecule.
  - (a) To start, run `file1.m`. This file constructs an initial estimate of the potential based on experimentally-determined values. It generates a file `Potential_AQ_base_file.mat`, which stores the following values:
    - `x ypos`, a  $157 \times 2$  vector of all the  $(x, y)$ -positions of grid points in the WS cell. 157 points is the regular number of points obtained from tiling a 31-point irreducible triangle across the WS cell.
    - `thetapos`, a  $1 \times 24$  vector of all the allowed orientations of the AQ molecule with respect to the surface lattice. Note that  $\theta$  is the angle of the main body of the AQ molecule, measured anticlockwise from the [1 0] azimuth on the surface.
    - `weight`, a  $1 \times 157$  vector of weights for each  $x, y$ -position to prevent double/treble counting for edges/corners of the WS cell respectively.
    - `V3Dinterp_AQ`, a  $157 \times 24$  vector of potential values for each

- point (rows) with given AQ orientation (columns). Since the values in this file are purely experimental it is simply given in the appendix.
- (b) Note that in neither `file1.m` nor in `file2.m` is there any mention of flipping or rotation of an irreducible triangle - the entire WS cell (in fact, a rectangle encompassing said cell) is constructed and then different values set for the Fourier components at each angle. Why was the irreducible triangle method **not** used here? (Note you do not have to fully understand the code in each file - use the comments to get a general understanding).
2. (a) Second, run `file2.m`. This should produce:
    - A plot of all the points in the WS cell. Note the first 31 points are in the irreducible triangle.
    - A plot of all the points in the WS cell after interpolation. This plot is performed within the `halvespacing.m` function, given in the appendices.
    - 13 plots of the corrugation function for varying angles of the AQ molecule in the range  $0^\circ$  to  $360^\circ$ .
  - (b) Having produced the above plots of the potential, note that the shape of the potential changes for each orientation of the rod-like molecule. Why is the change in potential periodic, with a period of  $180^\circ$ ?
  3. With reference to the discussion of AQ motion in the theoretical background, explain the shape of the potential energy surface at each orientation.
  4. (a) Take the generated file, `loadPES.mat`, and run it in PIGLE to simulate a trajectory of a single AQ molecule on the Cu(111) surface using MD methods. The motion should match that described in the theoretical background.

The required code for the PIGLE UI files is given below:

The first file, `pigle_ui.m`, sets up the preferences for several options, as well as the scattering parameters and the length of the simulation.

```

1 % parameters for config_model.m
2
3 z_enabled = 0; % Enable/Disable (1/0) motion
    perpendicular to the surface
4 dKz_include_in_isf = 0; % Enable/Disable (1/0)
    calculation of the ISF for perpendicular momentum
    transfer
5 theta_enabled = 1; % Enable/Disable (1/0) rotation of
    rigid body (rotation axis perpendicular to the
    surface)
6 zero_p_init = 0; % set initial momentum be set to zero?
    if set to 0, p_init will correspond to thermal
    distribution)
7 interactions_active = 0; % Enable/Disable (1/0)
```

```

    interadsorbate interactions
8 N_runs = 1; % Number of runs
9 run_parallel = 1; % Enable/Disable (1/0) of parallel
    computing. If parallel computing toolbox is not
    installed – set this option to zero.
10
11 % Specify dK as a 2D vector, 3rd dim is azimuths.
12 dK = [0.05 0.1 0.15 0.2:0.1:5];
13 azim_1 = [0 1];
14 azim_2 = [1 1];
15
16 % specify beam parameters and geometrical parameters for
    scattering calculations
17 theta_tot = 44.4; % Degrees
18 beam_ki = 3.3977; % Angstrom ^{-1}
19
20 % Specify simulation time parameters
21 % (those will be adjusted by the program, see below if
    interested)
22 sample_time = 2e-3;
23 sample_time_clist = 1e-2;
24 isf_sample_time = 5e-2; % time step for which the
    position will be recorded, for later use in the ISF
    calculations
25 thermalizing_time = 20; % during this initial period, the
    trajectory won't be recorded.
26 stop_time = 1024*10;% Total simulation time.
27
28 % N_steps and N_ISF_steps are calculated after PIGLE
    adjusts the requested time parameters
29 max_N_steps = 1e10; % The simulation won't start if the
    calculated number of steps is greater than
    max_N_steps. Prevents too-long runs.
30 max_N_ISF_steps = 6e5; % The simulation won't start if
    the calculated number of steps is greater than
    max_N_ISF_steps. Prevents insensible memory
    exploitation

```

The next file, `pigle_ui_surface_params.m`, sets up the parameters of the surface as well as the adsorbates on it. It also sets up the potential by calling `@loadPES`

```

1 %% params for surface_params.m
2 T=200; % Temperature in Kelvin
3 Nprtcl_total = 1; % will be rounded to justify the number
    density
4 mass_list = [208]; % vector of masses for all species (
    one mass per species ...)
5 radius = 6; % for calculating angular mass, however, one
    can define angular mass directly (see below)
6 number_density = [0.05]; % relative number density for
    each mass.
7 eta = 2; % helps to define variables down below, but the
    user can define it directly or using any other method
8 eta_theta = 100; %
9 tau = [1]; %
10
11 a1=2.5560; % Copper 111
    lattice constant in Angstrom
12 x0 = 0; nx = 120; xdim = a1; % x dimension
    params of the unitcell/PES

```

```

13 y0 = 0; ny = 200; ydim = a1*sqrt(3.0);      % y dimention
   params of the unitcell/PES
14 z0 = 0; nz = 20; zdim = 10;                  % z dimention
   params of the unitcell/PES
15 theta0 = 0; ntheta = 24; thetadim = 2*pi; % theta
   dimention params of the unitcell/PES
16 numOfPrmtvCells = [1 1]; % How many primitive cells exist
   in the XY potential (with periodic boundary
   conditions)
17
18 unitcell = prepFuncs.make_unitcell([nx xdim x0],[ny ydim
   y0],[nz zdim z0 z_enabled],'theta',[ntheta
   thetadim theta0 theta_enabled],'numOfPrmtvCells',
   numOfPrmtvCells);
19
20 angular_mass_list = mass_list.*radius.^2;
21
22 Nmass = length(mass_list);
23
24 %%%%%%%%%%%%%%
25 % Adsorbate configuration %
26 %%%%%%%%%%%%%%
27 % See prepare_configuration.m.
28 % If new adsorbate_conf_case_num (in addition to '1') are
   implemented in
29 % prepare_configuration.m, surface_params.m needs to be
   updated.
30 % Case '1' is for top symmetric molecule
31 % Each parameter needs to be stored either as a single
   cell (which will be distributed to all
32 % populations), or as a cell-array (with the i'th element
   distributed to the i'th
33 % population)
34 %
35 r_conf_case_num = {1};
36 r_conf_radius = {0};
37 r_conf_Natoms = {1};
38 CoM_form_factor_case_num = {1}; % The configuration case
   refer to form_factor.m.
39 CoM_form_factor_hemisphere_radius = {0.5};
40 form_factor_case_num = {repmat(1,r_conf_Natoms{1},1)}; %
   The configuration case refer to form_factor.m.
41 form_factor_hemisphere_radius = {repmat(0.5,r_conf_Natoms
   {1},1)};
42
43 %%%%%%%%%%%%%%
44 % Translational Friction %
45 %%%%%%%%%%%%%%
46 % Depending on the case (see calc_A function in
   calculate_sim_params.m),
47 % different fields of the structure A_struct are expected
   . For new cases in
48 % calculate_sim_params, ammend also surface_params.m
49 % Each parameter needs to be stored either as a single
   cell (which will be distributed to all
50 % populations), or as a cell-array (with the i'th element
   distributed to the i'th
51 % population)
52 %
53 A_case = {1};
54 A_w0 = {eta};

```

```

55 A_dw    = {1./tau};
56 A_eta   = {eta};
57 A_tau   = {tau};
58 A_spatial_dependend_friction = {0};
59
60 %%%%%%%%%
61 % Angular Friction %
62 %%%%%%%%%
63 % Depending on the case (see calc_A function in
       calculate_sim_params.m),
64 % different fields of the structure A_struct are expected
       .
65 % Each parameter needs to be stored either as a single
       cell (which will be distributed to all
66 % populations), or as a cell-array (with the i'th element
       distributed to the i'th
67 % population)
68 %
69 A_theta_case = {1};
70 A_theta_w0   = {eta_theta};
71 A_theta_dw   = {1};
72 A_theta_eta  = {eta_theta};
73 A_theta_tau  = {1};
74 A_spatial_dependend_theta_friction = {0};
75
76 %%%%%%%%%
77 % Surface-Adsorbate Potential %
78 %%%%%%%%%
79
80 % For each population, PIGLE generate a potential of up
       to 4D (which will be called here PES, for potential
       energy surface).
81 % PIGLE will generate the potential using a function
       which is defined by
82 % the user, with parameters to that function defined by
       the user as well.
83
84 % Pointers to the population specific functions for
       generating the PES
85 PES_func_list = {@loadPES};
86
87 % Define variables to hold the arguments which are stored
       in PES_arg_list (see below)
88 params_for_function_prepare_potential
89
90 % Define the arguments for PES generation, i.e. arguments
       to @loadPES
91 PES_arg_list = {'loadPES.mat', 'PES4D_AQ'};
92
93 %% Parameters for Interactions
94
95 prepare_params_for_interactions
96
97 % assign functions to species:
98 % For each pair in f_perm, a function case is defined in
       f_func. This
99 % function case is taken from f_interaction.m - and
       f_func_params contain
100 % the arguments for each function.
101 f_perm = [1 1; 1 2; 2 2];
102 f_func = [repmat(1,1,3)];

```

```

103 f_func_params = {[fparam1 4],[fparam2 4],[fparam3 4]};
104 % Define the boundaries for interactions:
105 % out_cutoff_r - The supercell must be larger than that
106 % number (see calculate_sim_params.m).
107 % TODO: include in connection lists, once
108 % implemented
109 % in_cutoff_r - the force between particles will be
110 % calculated for r >= r_in
111 out_cutoff_r = norm(unitcell.celldim)*10*0+49;
110 in_cutoff_r = 0.1;
111
112 % x_interactions - the points in which the force is to be
113 % calculated
113 x_min = in_cutoff_r/10; % in Angstrom
114 x_max = out_cutoff_r + 1; % in Angstrom
115 numOfPoints_interactions = 500;
116 x_interactions = linspace(x_min, x_max,
    numOfPoints_interactions); %x_min/max in Angstrom

```

The file pigle\_wrapper\_params.m deals with the main options that determine what the program should output.

```

1 %% Wrapper parameters
2
3 isISF      = 1; % 0 - just run the simulation (single
4 % run), 1 - calculate an averaged ISF
5 isSave      = 0; % save results (on/off)
6 ISF2save    = [1 2]; % which ISF to save? 1-Incoherent,
7 % 2-Coherent (needs isSave to be turned-on)
8 toPlot      = 0; %
9 reduceData   = 2; % 0 - don't reduce. 1 - remove p and
10 % r_supercell. 2 - Leave only one trajectory for each
11 % population. 3 - Remove all trajectories from all
12 % populations
13 clearParams = 1; % Clear the structure containing all
14 % the model-configuration parameters from previous runs

```

For simulating only one particle one must also change the following file by commenting out the second entry:

```

1 % define a structure to be passed as argument to the
2 % function which creates the potential
3
4 %% POT 1
5 pot_strct(1).ref_De = [1600 1600 1600 1600 1600 1600]*0;
6
7 %pot_strct(1).V = [192 168 ; 0.5 0.5; 0.5 0.5; 18 62 ;
8 %    112 104 ; 156 118 ]*1; % top, slope1,slop2,bridge,hcp
9 %,fcc
8 %pot_strct(1).V = [0 0 ; 0.5 0.5; 0.5 0.5; 80 80 ; 80 80
10 % ; 80 80 ]*1; % top, slope1,slop2,bridge,hcp,fcc
9 pot_strct(1).V = [250 ; 0.5 ; 0.5 ; 110 ; 22 ; 0]; % top,
10 % slope1,slop2,bridge,hcp,fcc
10
11 pot_strct(1).is_potval = [1 0 0 1 1 1];
12 pot_strct(1).a = [1 NaN NaN 1 1 1]*1;
13 pot_strct(1).r_e = [2 NaN NaN 2 2 2];
14 pot_strct(1).f_2D = @hexagonal6interp;
15
16

```

```

17
18 %% POT 2
19
20 %pot_strct(2) = pot_strct(1);
21 %pot_strct(2).V = [exp(15*number_density(2))-1 ; 0.5 ;
22    0.5 ; 240 ; 270 ; 280]; % top, slope1,slop2,bridge,
23   hcp,fcc

```

With these files edited, one can place the file `loadPES.mat` in the root directory of the PIGLE folder and run `run_pigle.m`. This will run the simulation with the above parameters. To view the motion, one may either run the command `make_movie(params, data)` to produce an animation of the motion or run the following code to plot the full trajectory of the molecule over the simulation:

```

1 % extract positional and orientational data from pigle
2 r = data.prtcl.r;
3
4 % reshape positional data into rows
5 rx = reshape(r(1,:,:), [1 length(r)]);
6 ry = reshape(r(2,:,:), [1 length(r)]);
7 rz = zeros(size(rx));
8
9 % reshape orientational data into a row
10 rtheta = reshape(r(3,:,:), [1 length(r)]) .* 180/pi;
11
12 % plot figure
13 figure();
14
15 % label axes
16 xlabel('$x$ /Å'); ylabel('$y$ /Å');
17
18 % use trick with surface() to plot a continuous gradient
19 % on the trajectory where the colours correspond to
20 % angles theta
21 surface([rx;rx], [ry;ry], [rz;rz], [rtheta;rtheta], '
22   FaceColor', 'none', 'EdgeColor', 'interp');
23
24 % default 2-D view
25 view(2);
26
27 % add colourbar for theta
28 c = colorbar;
29
30 % format colourbar
31 c.Title.String = '$\theta$ /$^\circ$'; c.Title.
32   Interpreter = 'latex';
33 c.TickLabelInterpreter = 'latex';

```

- (b) Having produced this visualisation, do the trajectories fit with the qualitative predictions in the theoretical background? Are the angles at each point along the trajectory as you would expect?
- (c) Try varying the following parameters and observe how the trajectory is affected:
  - mass, the molecular mass

- radius, the approximate molecular radius
  - eta, the translational frictional coupling constant
  - eta\_theta, the rotational frictional coupling constant
- (d) Try disabling rotations and observe how this affects the motion. This can be done by setting theta\_enabled=0; on line 5 of `pigle_ui.m`.

## EXTENSION

1. Try plotting the ISF and fitting it to an exponential decay.
2. Plot the dephasing rate of the fit against momentum transfer for both azimuths  $\langle 0\ 1 \rangle$  and  $\langle 1\ 1 \rangle$

## REFERENCES

1. J. Chem. Phys. 142, 101907 (2015); <https://doi.org/10.1063/1.4906048>
2. Science 315 (5817), 1391-1393; 10.1126/science.1135302
3. Phys. Rev. Lett. 95, 166101; 10.1103/PhysRevLett.95.166101

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# APPENDIX

## HALVESPACE.M

The function `halvespace()` is given below. It takes as arguments:

- `V3D`, the computed potential values across the grid defined by `x ypos`,
- `x ypos`, a grid of positions for an entire WS cell,
- `weight`, the weights of each position in `x ypos`,
- `np`, the number of grid points in `x ypos`,
- `nscale`, the integer factor  $N$  in the theoretical background which determines the grid lattice spacing,
- `a`, the basic lattice spacing,
- `nneb`, the number of neighbours to use in the interpolation.

The function then uses a cubic interpolation scheme to calculate the potential across a grid of half the spacing than the input. This gives us twice the resolution at a much cheaper cost. Given this context the outputs are relatively self-explanatory.

```
1 function [ V3Dnew, x yposnew, weightnew, npnew, nscalenew ] =
2     halvespace( V3D, x ypos, weight, np, nscale, a, nneb )
3 % For a hexagonal cell it makes sense to sample it with a grid
4 % of points
5 % of the same symmetry as the basic lattice - and this will be
6 % computed
7 % originally on a lattice with spacing a/nscale if the original
8 % lattice
9 % constant is a. This routine interpolates between this original
10 % grid,
11 % doubling the point spacing, using a cubic interpolation scheme
12 % nneb is the number of neighbours to use in the interpolation
13 % find list of new points needed
14 %clear x yposreq weightreq
15 dum10=a;
16 dumvec0=size(V3D);
17 nz=dumvec0(2);
18 del=0.0001*a*a;
19 a2=a*a/nscale/nscale;
20 annn2=a2*3;
21 npnew=0;
22 radius=a*(1/sqrt(3.0)+2/nscale);
23 V3Dnew=V3D;
24 V3Dextra=V3D;
25 for ip1=1:np-1
26     for ip2=ip1+1:np
27         dum=(x ypos(ip1,1)-x ypos(ip2,1))^2+(x ypos(ip1,2)-x ypos(
```

```

    ip2,2))^2;
23 if( abs(dum-a2)<del)
24     npnew=npnew+1;
25     x yposreq(npnew,1)=0.5*(x ypos(ip1,1)+x ypos(ip2,1));
26     x yposreq(npnew,2)=0.5*(x ypos(ip1,2)+x ypos(ip2,2));
27     weightreq(npnew)=1;
28 end
29 if(abs(dum-annn2)<del) && (weight(ip1)+weight(ip2)<1.1)
30     % we have a new edge point
31     npnew=npnew+1;
32     x yposreq(npnew,1)=0.5*(x ypos(ip1,1)+x ypos(ip2,1));
33     x yposreq(npnew,2)=0.5*(x ypos(ip1,2)+x ypos(ip2,2));
34     weightreq(npnew)=0.5;
35 end
36 end
37 end
38 x yposnew=x ypos;
39 weightnew=weight;
40 x yposnew(np+1:np+npnew,:)=x yposreq(:,,:);
41 weightnew(np+1:np+npnew)=weightreq(:,,:);
42 nscalenew=n scale*2;
43 figure(2000)
44 clf
45 hold on
46 plot(x ypos(:,1),x ypos(:,2),'rx')
47 plot(x yposreq(:,1),x yposreq(:,2),'go')
48 sumofrealspaceweightinhalfspacingcell=sum(weight)+sum(weightreq)
49 title(['orig. pts redx. new pts green o, interpolation grid
        blue square'])
50 % this total should be equal to nscalenew^2
51 %
52 % we need points outside the original unit cell - so need to add
      points
53 % from copies of that cell along the 6 sides of the original
      ones
54 %
55 % first translate to left and right - one needs all the points
      except the
56 % corner points along y=0
57 x poseextra=x ypos;
58 np extra=np;
59 del=a/n scale*0.01;
60 for ip=1:np
61     if(abs(x ypos(ip,1)+a/2)>del)
62         % the point is not on the left row of the original cell
            so copy
63         % right
64         np extra=np extra+1;
65         x poseextra(np extra,1)=x ypos(ip,1)+a;
66         x poseextra(np extra,2)=x ypos(ip,2);
67         if(x poseextra(np extra,1)^2+x poseextra(np extra,2)^2 >
            radius^2)
68             np extra=np extra-1;
69         else
70             V3Dextra(np extra,:)=V3D(ip,:);
71         end
72     end
73 end
74 if(abs(x ypos(ip,1)-a/2)>del)
75     % the point is not on the right row of the original cell
            so copy

```

```

76      % left
77      npextra=npextra+1;
78      xyposextra(npextra,1)=xypos(ip,1)-a;
79      xyposextra(npextra,2)=xypos(ip,2);
80      if(xyposextra(npextra,1)^2+xyposextra(npextra,2)^2 >
81          radius^2)
82          npextra=npextra-1;
83      else
84          V3Dextra(npextra,:)=V3D(ip,:);
85      end
86  end
87  if(weight(ip)==1)
88      % the point is not on an edge or corner, so copy other 4
89      npextra=npextra+1;
90      xyposextra(npextra,1)=xypos(ip,1)+a/2;
91      xyposextra(npextra,2)=xypos(ip,2)+a*sqrt(3)/2;
92      if(xyposextra(npextra,1)^2+xyposextra(npextra,2)^2 > radius^2)
93          npextra=npextra-1;
94      else
95          V3Dextra(npextra,:)=V3D(ip,:);
96      end
97
98      npextra=npextra+1;
99      xyposextra(npextra,1)=xypos(ip,1)+a/2;
100     xyposextra(npextra,2)=xypos(ip,2)-a*sqrt(3)/2;
101     if(xyposextra(npextra,1)^2+xyposextra(npextra,2)^2 > radius^2)
102         npextra=npextra-1;
103     else
104         V3Dextra(npextra,:)=V3D(ip,:);
105     end
106
107     npextra=npextra+1;
108     xyposextra(npextra,1)=xypos(ip,1)-a/2;
109     xyposextra(npextra,2)=xypos(ip,2)+a*sqrt(3)/2;
110     if(xyposextra(npextra,1)^2+xyposextra(npextra,2)^2 > radius^2)
111         npextra=npextra-1;
112     else
113         V3Dextra(npextra,:)=V3D(ip,:);
114     end
115
116     npextra=npextra+1;
117     xyposextra(npextra,1)=xypos(ip,1)-a/2;
118     xyposextra(npextra,2)=xypos(ip,2)-a*sqrt(3)/2;
119     if(xyposextra(npextra,1)^2+xyposextra(npextra,2)^2 > radius^2)
120         npextra=npextra-1;
121     else
122         V3Dextra(npextra,:)=V3D(ip,:);
123     end
124
125 end
126 if((abs(xypos(ip,1)-a/2)<del) && weight(ip)>0.4)
127     % the point is on the right row of the original cell so
128     % copy
129     % and is not in a corner - so copy up and down
130     % diagonally
131     npextra=npextra+1;

```

```

130      xyposextra(npextra,1)=x ypos(ip,1)-a/2;
131      xyposextra(npextra,2)=x ypos(ip,2)+a*sqrt(3)/2;
132          if(xyposextra(npextra,1)^2+xyposextra(npextra,2)
133              ^2 >radius^2)
134          npextra=npextra-1;
135      else
136          V3Dextra(npextra,:)=V3D(ip,:);
137      end
138
139      npextra=npextra+1;
140      xyposextra(npextra,1)=x ypos(ip,1)-a/2;
141      xyposextra(npextra,2)=x ypos(ip,2)-a*sqrt(3)/2;
142          if(xyposextra(npextra,1)^2+xyposextra(npextra,2)
143              ^2 >radius^2)
144          npextra=npextra-1;
145      else
146          V3Dextra(npextra,:)=V3D(ip,:);
147      end
148  end
149 xyposextrasize=size(xyposextra);
150 V3Dextrasize=size(V3Dextra);
151 plot(xyposextra(:,1),xyposextra(:,2),'bs')
152 % we now have a candidate neighbours - npextra of them,
153 % xyposextra in
154 % position with values of potential stored in V3Dextra and we
155 % are looking
156 % to find potential values at the npnew points listed in
157 % xyposreq. V3Dnew
158 % already has the existing np points loaded into it.
159 %
160 % now find nearest neighbours of all required points
161 distance2=zeros(npnew,npextra);
162 distance=zeros(npnew,npextra,2);
163 dumvec=linspace(0,0,npextra);
164 ipextraindex=linspace(0,0,npextra);
165 distance0=linspace(0,0,nneb);
166 distancetemp=linspace(0,0,nneb);
167 D=linspace(0,0,nneb);
168 sigma=linspace(1,1,nneb);
169 sigma(5:nneb)=100;
170 tol=a/nscale*0.01;
171 iflag=0;
172 ni=10;
173 f=zeros(ni,nneb);
174 for ipnew=1:npnew
175     for ipextra=1:npextra
176         distance(ipnew,ipextra,:)=xyposextra(ipextra,:)-xyposreq
177             (ipnew,:);
178         distance2(ipnew,ipextra)=distance(ipnew,ipextra,1)^2+
179             distance(ipnew,ipextra,2)^2;
180     end
181     [dumvec,ipextraindex]=sort(squeeze(distance2(ipnew,:)));
182     distance2(ipnew,:)=dumvec;
183     distance(ipnew,:,:1)=squeeze(distance(ipnew,ipextraindex,1));
184     distance(ipnew,:,:2)=squeeze(distance(ipnew,ipextraindex,2));
185     % so now have points in order - ipextraindex has indices of
186     % the
187     % ipextras
188     % now calculate

```

```

183     distancetemp=sqrt(squeeze(distance2(ipnew,1:nneb)));
184     if(iflag==0)
185         iflag=1;
186         distance0=distancetemp;
187     else
188         if (sum(abs(distancetemp-distance0))>tol)
189             xohhelp=1
190         end
191     end
192 % pause on
193 % figure(2000)
194 % clf
195 % hold on
196 % plot(xposextra(:,1),xposextra(:,2),'rx')
197 % plot(xposreq(:,1),xposreq(:,2),'go')
198 % plot(xposreq(ipnew,1),xposreq(ipnew,2),'ro')
199 % for ij=1:nneb
200 %     plot(xposextra(ipextraindex(ij),1),xposextra(
201     ipextraindex(ij),2),'bs')
202 % end
203 % pause;
204 % pause off
205     for ij=1:nneb
206         dx=distance(ipnew,ij,1);
207         dy=distance(ipnew,ij,2);
208         % index of neighbour
209         f(1,ij)=1;
210         f(2,ij)=dx;
211         f(3,ij)=dy;
212         f(4,ij)=dx*dx;
213         f(5,ij)=dx*dy;
214         f(6,ij)=dy*dy;
215         f(7,ij)=dx*dx*dx;
216         f(8,ij)=dx*dx*dy;
217         f(9,ij)=dx*dy*dy;
218         f(10,ij)=dy*dy*dy;
219     end
220     M=zeros(ni,ni);
221     for ik=1:ni
222         for ii=1:ni
223             for ij=1:nneb
224                 M(ik,ii)=M(ik,ii)+f(ik,ij)*f(ii,ij)/sigma(ij)
225                     ^2;
226             end
227         end
228         pause on
229         for iz=1:nz
230 % figure(2001)
231 % clf
232 % hold on
233 % % xlim([xposreq(ipnew,1)-2*a/nscale,xposreq(ipnew,1)+2*a/
234 % nscale])
235 % % ylim([xposreq(ipnew,2)-2*a/nscale,xposreq(ipnew,2)+2*a/
236 % nscale])
237 % plot3(xposextra(:,1),xposextra(:,2),V3Dextra(:,iz),'rx')
238 % plot(xposreq(ipnew,1),xposreq(ipnew,2),'go')
239 % for ij=1:nneb
240 % plot3(xposreq(ipnew,1)+distance(ipnew,ij,1),xposreq(

```

```

    ipnew,2)+distance(ipnew,ij,2),V3Dextra(ipextraindex(ij),iz)
    , 'bs')
240 % end
241 % pause
242     for ij=1:nneb
243         D(ij)=V3Dextra(ipextraindex(ij),iz);
244     end
245     B=linspace(0,0,ni);
246     for ik=1:ni
247         for ij=1:nneb
248             B(ik)=B(ik)+D(ij)*f(ik,ij)/sigma(ij)^2;
249         end
250     end
251     AVec=B/M;
252     V3Dnew(np+ipnew,iz)=AVec(1);
253 end
254 pause off
255 end
256 npnew=npnew+np;
257
258
259 end

```

## INHEXRECIP.M

The function InHexRecip() is given below. It takes as arguments:

- $\mathbf{G}$ , any given reciprocal lattice vector,
- $G_1$ , the spacing of the reciprocal lattice,
- $n$ , the integer factor  $N$  in the theoretical background which determines the grid lattice spacing.

It then assigns a weight to the reciprocal lattice vector  $\mathbf{G}$  based on its position in the WS cell. Bulk points are assigned a weight of 1, edge points are assigned 1/2 and corner points 1/3.

```

1 function weight=InHexRecip(G,G1,n)
2 x=G(1);
3 y=G(2);
4 del=G1/1e4;
5 r3=sqrt(3);
6 weight=0;
7 if ( (y+del>-n*G1/2) && (y-del<n*G1/2) && (y-del< n*G1-r3*x) &&
     (y+del>r3*x-n*G1) && (y+del>-r3*x-n*G1) && (y-del<r3*x+n*G1))
8 % we have a point inside the Wigner-Seitz cell
9     weight=1;
10 % now need to check if its on an edge or corner
11
12     dum=0;
13     if( abs(y+n*G1/2)<del)
14         dum=dum+1;
15     end
16
17     if( abs(y-n*G1/2)<del)
18         dum=dum+1;
19     end
20
21     if( abs(y-n*G1+r3*x)<del)
22         dum=dum+1;

```

```

23      end
24
25      if( abs(y-r3*x+n*G1)<del)
26          dum=dum+1;
27      end
28
29      if( abs(y+r3*x+n*G1)<del)
30          dum=dum+1;
31      end
32
33      if( abs(y-r3*x-n*G1)<del)
34          dum=dum+1;
35      end
36      if(dum==1)
37          % its on an edge
38          weight=1/2;
39      end
40      if(dum==2)
41          % its at a corner
42          weight=1/3;
43      end
44
45 end

```

## FILE1.M

```

1 % Potential for 157 pt. script
2 %% parameters
3
4 num_ang=24; % number of angles
5 num_pos=157; % number of potential positions
6 potential_mat=zeros(num_pos,num_ang);
7 new_file='Potential.mat';
8
9 %% position values
10
11 % top1=600;
12 % top2=470;
13 % top3=370;
14 % top4=270;
15
16 top1new=1000;
17 top2new=900;
18 top3new=800;
19 top4new=700;
20 top5new=600;
21 top6new=550;
22 top7new=500;
23 top8new=450;
24 top9new=400;
25 % top10new=600;
26 % top11new=600;
27 % top12new=600;
28
29 nearfccmin=85;
30 nearfccmax=250;
31
32 nearhcpmin=5;
33 nearhcpmax=65;

```

```

34 nearhcphighmax=100;
35
36 hcpmin=0;
37 hcpmax=60;
38 hcphighmax=80;
39
40 fccmin=75;
41 fccmax=210;
42
43 bridgemin=35;
44 bridgemax=300;
45
46 bridgebarmin=90;
47 bridgebarmax=340;
48
49 nearbridgebarmin=65; % positions near bridge sites
50 nearbridgebarmax=360; % positions near bridge sites
51
52 otherpoints=190;
53
54 %% positions
55
56 % top1pos=[1];
57 % top2pos=[2,6,136,114,91,84,62,32];
58 % top3pos=[3,7,10,13,140,110,118,124,100,95,88,58,66,39,36,33];
59 % top4pos
60 % [4,8,11,14,17,146,143,137,115,121,127,131,106,103,98,92,85,63,69,72,43,40,37,34];
61 % topnewpos=[1, 6,136,114,84,62,32, 2,13,110,91,58,39,
62 % 10,140,118,88,66,36,
63 % 7,17,146,137,115,124,95,85,63,72,43,33,
64 % 3,14,22,143,111,121,100,92,59,69,48,40,
65 % 11,20,149,141,119,127,98,89,67,75,46,37,
66 % 8,18,25,153,147,138,116,125,131,103,96,86,64,73,79,51,44,34,
67 % 4,15,23,28,151,144,112,122,129,106,101,93,60,70,77,54,49,41,
68 % 12,21,27,155,150,142,120,128,133,105,99,90,68,76,81,53,47,38,
69 % 9,19,26,30,157,154,148,139,117,126,132,135,108,104,97,87,65,74,80,83,56,52,45,35,
70 % 5,16,24,29,31,42,50,55,57,61,71,78,82,94,102,107,109,113,123,130,134,145,152,156];
71 topnewpos1=[1];
72 topnewpos2=[6,136,114,84,62,32];
73 topnewpos3=[2,13,110,91,58,39];
74 topnewpos4=[10,140,118,88,66,36];
75 topnewpos5=[7,17,146,137,115,124,95,85,63,72,43,33];
76 topnewpos6=[3,14,22,143,111,121,100,92,59,69,48,40];
77 topnewpos7=[11,20,149,141,119,127,98,89,67,75,46,37];
78 topnewpos8
79 =[8,18,25,153,147,138,116,125,131,103,96,86,64,73,79,51,44,34];
80
81 topnewpos9
82 =[4,15,23,28,151,144,112,122,129,106,101,93,60,70,77,54,49,41];
83
84 % topnewpos10
85 =[12,21,27,155,150,142,120,128,133,105,99,90,68,76,81,53,47,38];

```

```
73 % topnewpos11
    =[9,19,26,30,157,154,148,139,117,126,132,135,108,104,97,87,65,74,80,83,56,52,45,35];

74 % topnewpos12
    =[5,16,24,29,31,42,50,55,57,61,71,78,82,94,102,107,109,113,123,130,134,145,152,156];

75
76 nearhcpo=[35,9,65,87,117,139];
77 nearfccpo=[30,157,83,56,108,135];
78
79 hcpo=[5,61,113];
80 fccpo=[31,57,109];
81
82 bridge1po=[50,130];
83 bridge2po=[24,102];
84 bridge3po=[78,152];
85
86 bridge1barpo=[42,55,123,134];
87 bridge2barpo=[16,29,94,107];
88 bridge3barpo=[71,82,145,156];
89
90 nearbridge1po=[45,47,52,126,128,132];
91 nearbridge2po=[19,21,26,97,99,104];
92 nearbridge3po=[74,76,80,148,150,154];
93
94 for i=1:num_ang/2
95     for j=1:size(topnewpos1,2)
96         pos_temp=topnewpos1(j);
97         potential_mat(pos_temp,i)=top1new;
98     end
99     for j=1:size(topnewpos2,2)
100        pos_temp=topnewpos2(j);
101        potential_mat(pos_temp,i)=top2new;
102    end
103    for j=1:size(topnewpos3,2)
104        pos_temp=topnewpos3(j);
105        potential_mat(pos_temp,i)=top3new;
106    end
107    for j=1:size(topnewpos4,2)
108        pos_temp=topnewpos4(j);
109        potential_mat(pos_temp,i)=top4new;
110    end
111    for j=1:size(topnewpos5,2)
112        pos_temp=topnewpos5(j);
113        potential_mat(pos_temp,i)=top5new;
114    end
115    for j=1:size(topnewpos6,2)
116        pos_temp=topnewpos6(j);
117        potential_mat(pos_temp,i)=top6new;
118    end
119    for j=1:size(topnewpos7,2)
120        pos_temp=topnewpos7(j);
121        potential_mat(pos_temp,i)=top7new;
122    end
123    for j=1:size(topnewpos8,2)
124        pos_temp=topnewpos8(j);
125        potential_mat(pos_temp,i)=top8new;
126    end
127    for j=1:size(topnewpos9,2)
128        pos_temp=topnewpos9(j);
129        potential_mat(pos_temp,i)=top9new;
```

```

130      end
131  %     for j=1:size(topnewpos10,2)
132  %       pos_temp=topnewpos10(j);
133  %       potential_mat(pos_temp,i)=top10new;
134  %     end
135  %     for j=1:size(topnewpos11,2)
136  %       pos_temp=topnewpos11(j);
137  %       potential_mat(pos_temp,i)=top11new;
138  %     end
139  %     for j=1:size(topnewpos12,2)
140  %       pos_temp=topnewpos12(j);
141  %       potential_mat(pos_temp,i)=top12new;
142  %     end
143 end
144
145 % topnewpos=[1,    6,136,114,84,62,32,    2,13,110,91,58,39,
146   10,140,118,88,66,36,
147   3,14,22,143,111,121,100,92,59,69,48,40,
148   11,20,149,141,119,127,98,89,67,75,46,37,
149   8,18,25,153,147,138,116,125,131,103,96,86,64,73,79,51,44,34,
150   4,15,23,28,151,144,112,122,129,106,101,93,60,70,77,54,49,41,
151   12,21,27,155,150,142,120,128,133,105,99,90,68,76,81,53,47,38,
152   9,19,26,30,157,154,148,139,117,126,132,135,108,104,97,87,65,74,80,83,56,52,45,35];
153 otherpoints=[];
154 % for i=1:157
155 %   if sum(ismember([i],topnewpos))==1;
156 %     continue
157 %   else
158 %     sizeotherpoints=size(otherpoints,2);
159 %     otherpoints(sizeotherpoints+1)=i;
160 %   end
161 % end
162 %% angles
163
164 % all angles - top sites same for all angles
165
166 % for i=1:num_ang/2
167 %   for j=1:size(top1pos,2)
168 %     pos_temp=top1pos(j);
169 %     potential_mat(pos_temp,i)=top1;
170 %   end
171 %   for j=1:size(top2pos,2)
172 %     pos_temp=top2pos(j);
173 %     potential_mat(pos_temp,i)=top2;
174 %   end
175 %   for j=1:size(top3pos,2)
176 %     pos_temp=top3pos(j);
177 %     potential_mat(pos_temp,i)=top3;
178 %   end
179 %   for j=1:size(top4pos,2)
180 %     pos_temp=top4pos(j);
181 %     potential_mat(pos_temp,i)=top4;
182 %   end
183 %%%% 0, 60, 120 degrees (first inputting 0 degrees values)
184

```

```
180 %% hcp, fcc
181 for i=1:size(hcppos,2)
182     potential_mat(hcppos(i),1)=hcpmin;
183 end
184
185
186 for i=1:size(fccpos,2)
187     potential_mat(fccpos(i),1)=fccmin;
188 end
189
190 %% near hcp, fcc
191
192 for i=1:size(nearhcppos,2)
193     potential_mat(nearhcppos(i),1)=nearhcpmin;
194 end
195
196 for i=1:size(nearfccpos,2)
197     potential_mat(nearfccpos(i),1)=nearfccmin;
198 end
199
200 %% bridge sites, barriers, near bridge sites
201
202 % bridge 1
203
204 for i=1:size(bridge1pos,2)
205     potential_mat(bridge1pos(i),1)=bridgemax;
206 end
207
208 for i=1:size(bridge1barpos,2)
209     potential_mat(bridge1barpos(i),1)=bridgebarmax;
210 end
211
212 for i=1:size(nearbridge1pos,2)
213     potential_mat(nearbridge1pos(i),1)=nearbridgebarmax;
214 end
215
216 % bridge 2
217
218 for i=1:size(bridge2pos,2)
219     potential_mat(bridge2pos(i),1)=bridgemax;
220 end
221
222 for i=1:size(bridge2barpos,2)
223     potential_mat(bridge2barpos(i),1)=bridgebarmax;
224 end
225
226 for i=1:size(nearbridge2pos,2)
227     potential_mat(nearbridge2pos(i),1)=nearbridgebarmax;
228 end
229
230 % bridge 3
231
232 for i=1:size(bridge3pos,2)
233     potential_mat(bridge3pos(i),1)=bridgemax;
234 end
235
236 for i=1:size(bridge3barpos,2)
237     potential_mat(bridge3barpos(i),1)=bridgebarmax;
238 end
239
240 for i=1:size(nearbridge3pos,2)
```

```
241     potential_mat(nearbridge3pos(i),1)=nearbridgebarmax;
242 end
243
244 %% Same values for 60, 120 degrees
245
246 potential_mat(:,5)=potential_mat(:,1);
247 potential_mat(:,9)=potential_mat(:,1);
248
249 %%%% 30, 90, 150 degrees (first inputting 30 degrees values)
250
251 %% hcp, fcc
252
253 for i=1:size(hcppos,2)
254     potential_mat(hcppos(i),3)=hcphighmax;
255 end
256
257 for i=1:size(fccpos,2)
258     potential_mat(fccpos(i),3)=fccmax;
259 end
260
261 %% near hcp, fcc
262
263 for i=1:size(nearhcppos,2)
264     potential_mat(nearhcppos(i),3)=nearhcphighmax;
265 end
266
267 for i=1:size(nearfccpos,2)
268     potential_mat(nearfccpos(i),3)=nearfccmax;
269 end
270
271 %% bridge sites, barriers, near bridge sites
272
273 % bridge 1
274
275 for i=1:size(bridge1pos,2)
276     potential_mat(bridge1pos(i),3)=bridgemax;
277 end
278
279 for i=1:size(bridge1barpos,2)
280     potential_mat(bridge1barpos(i),3)=bridgebarmax;
281 end
282
283 for i=1:size(nearbridge1pos,2)
284     potential_mat(nearbridge1pos(i),3)=nearbridgebarmax;
285 end
286
287 % bridge 2
288
289 for i=1:size(bridge2pos,2)
290     potential_mat(bridge2pos(i),3)=bridgemax;
291 end
292
293 for i=1:size(bridge2barpos,2)
294     potential_mat(bridge2barpos(i),3)=bridgebarmax;
295 end
296
297 for i=1:size(nearbridge2pos,2)
298     potential_mat(nearbridge2pos(i),3)=nearbridgebarmax;
299 end
300
301 % bridge 3
```

```
302 for i=1:size(bridge3pos,2)
303     potential_mat(bridge3pos(i),3)=bridgemax;
304 end
305
306
307 for i=1:size(bridge3barpos,2)
308     potential_mat(bridge3barpos(i),3)=bridgebarmax;
309 end
310
311 for i=1:size(nearbridge3pos,2)
312     potential_mat(nearbridge3pos(i),3)=nearbridgebarmax;
313 end
314
315 %% Same values for 90, 150 degrees
316
317 potential_mat(:,7)=potential_mat(:,3);
318 potential_mat(:,11)=potential_mat(:,3);
319
320 %%%% 15, 45 degrees (first inputting 15 degrees values)
321
322 %% hcp, fcc
323
324 for i=1:size(hcppos,2)
325     potential_mat(hcppos(i),2)=hcpmax;
326 end
327
328 for i=1:size(fccpos,2)
329     potential_mat(fccpos(i),2)=fccmax;
330 end
331
332 %% near hcp, fcc
333
334 for i=1:size(nearhcppos,2)
335     potential_mat(nearhcppos(i),2)=nearhcpmax;
336 end
337
338 for i=1:size(nearfccpos,2)
339     potential_mat(nearfccpos(i),2)=nearfccmax;
340 end
341
342 %% bridge sites, barriers, near bridge sites
343
344 % bridge 1
345
346 for i=1:size(bridge1pos,2)
347     potential_mat(bridge1pos(i),2)=bridgemin;
348 end
349
350 for i=1:size(bridge1barpos,2)
351     potential_mat(bridge1barpos(i),2)=bridgebarmin;
352 end
353
354 for i=1:size(nearbridge1pos,2)
355     potential_mat(nearbridge1pos(i),2)=nearbridgebarmin;
356 end
357
358 % bridge 2
359
360 for i=1:size(bridge2pos,2)
361     potential_mat(bridge2pos(i),2)=bridgemax;
362 end
```

```

363
364 for i=1:size(bridge2barpos,2)
365     potential_mat(bridge2barpos(i),2)=bridgebarmax;
366 end
367
368 for i=1:size(nearbridge2pos,2)
369     potential_mat(nearbridge2pos(i),2)=nearbridgebarmax;
370 end
371
372 % bridge 3
373
374 for i=1:size(bridge3pos,2)
375     potential_mat(bridge3pos(i),2)=bridgemax;
376 end
377
378 for i=1:size(bridge3barpos,2)
379     potential_mat(bridge3barpos(i),2)=bridgebarmax;
380 end
381
382 for i=1:size(nearbridge3pos,2)
383     potential_mat(nearbridge3pos(i),2)=nearbridgebarmax;
384 end
385
386 %% Same values for 45 degrees
387
388 potential_mat(:,4)=potential_mat(:,2);
389
390 %%%% 135, 165 degrees (first inputting 135 degrees values)
391
392 %% hcp, fcc
393
394 for i=1:size(hcppos,2)
395     potential_mat(hcppos(i),10)=hcpmax;
396 end
397
398 for i=1:size(fccpos,2)
399     potential_mat(fccpos(i),10)=fccmax;
400 end
401
402 %% near hcp, fcc
403
404 for i=1:size(nearhcppos,2)
405     potential_mat(nearhcppos(i),10)=nearhcpmax;
406 end
407
408 for i=1:size(nearfccpos,2)
409     potential_mat(nearfccpos(i),10)=nearfccmax;
410 end
411
412 %% bridge sites, barriers, near bridge sites
413
414 % bridge 1
415
416 for i=1:size(bridge1pos,2)
417     potential_mat(bridge1pos(i),10)=bridgemax;
418 end
419
420 for i=1:size(bridge1barpos,2)
421     potential_mat(bridge1barpos(i),10)=bridgebarmax;
422 end
423

```

```

424 for i=1:size(nearbridge1pos,2)
425     potential_mat(nearbridge1pos(i),10)=nearbridgebarmax;
426 end
427
428 % bridge 2
429
430 for i=1:size(bridge2pos,2)
431     potential_mat(bridge2pos(i),10)=bridgemin;
432 end
433
434 for i=1:size(bridge2barpos,2)
435     potential_mat(bridge2barpos(i),10)=bridgebarmin;
436 end
437
438 for i=1:size(nearbridge2pos,2)
439     potential_mat(nearbridge2pos(i),10)=nearbridgebarmin;
440 end
441
442 % bridge 3
443
444 for i=1:size(bridge3pos,2)
445     potential_mat(bridge3pos(i),10)=bridgemax;
446 end
447
448 for i=1:size(bridge3barpos,2)
449     potential_mat(bridge3barpos(i),10)=bridgebarmax;
450 end
451
452 for i=1:size(nearbridge3pos,2)
453     potential_mat(nearbridge3pos(i),10)=nearbridgebarmax;
454 end
455
456 %% Same values for 165 degrees
457
458 potential_mat(:,12)=potential_mat(:,10);
459
460 %%% 75, 105 degrees (first inputting 75 degrees values)
461
462 %% hcp, fcc
463
464 for i=1:size(hcppos,2)
465     potential_mat(hcppos(i),6)=hcpmax;
466 end
467
468 for i=1:size(fccpos,2)
469     potential_mat(fccpos(i),6)=fccmax;
470 end
471
472 %% near hcp, fcc
473
474 for i=1:size(nearhcppos,2)
475     potential_mat(nearhcppos(i),6)=nearhcpmax;
476 end
477
478 for i=1:size(nearfccpos,2)
479     potential_mat(nearfccpos(i),6)=nearfccmax;
480 end
481
482 %% bridge sites, barriers, near bridge sites
483
484 % bridge 1

```

```
485 for i=1:size(bridge1pos,2)
486     potential_mat(bridge1pos(i),6)=bridgemax;
487 end
488
489 for i=1:size(bridge1barpos,2)
490     potential_mat(bridge1barpos(i),6)=bridgebarmax;
491 end
492
493 for i=1:size(nearbridge1pos,2)
494     potential_mat(nearbridge1pos(i),6)=nearbridgebarmax;
495 end
496
497 % bridge 2
498
499 for i=1:size(bridge2pos,2)
500     potential_mat(bridge2pos(i),6)=bridgemax;
501 end
502
503 for i=1:size(bridge2barpos,2)
504     potential_mat(bridge2barpos(i),6)=bridgebarmax;
505 end
506
507 for i=1:size(nearbridge2pos,2)
508     potential_mat(nearbridge2pos(i),6)=nearbridgebarmax;
509 end
510
511 % bridge 3
512
513 for i=1:size(bridge3pos,2)
514     potential_mat(bridge3pos(i),6)=bridgemin;
515 end
516
517 for i=1:size(bridge3barpos,2)
518     potential_mat(bridge3barpos(i),6)=bridgebarmin;
519 end
520
521 for i=1:size(nearbridge3pos,2)
522     potential_mat(nearbridge3pos(i),6)=nearbridgebarmin;
523 end
524
525 %%% Same values for 105 degrees
526
527 potential_mat(:,8)=potential_mat(:,6);
528
529
530 %%%% All other points on matrix
531
532 for i=1:num_pos
533     for j=1:num_ang
534         if potential_mat(i,j)==0
535             potential_mat(i,j)=otherpoints;
536         end
537     end
538 end
539
540 potential_mat(:,((num_ang/2)+1):num_ang)=potential_mat(:,1:(num_ang/2));
541
542 %%%% Create new file
543
544
```

```
545 V3Dinterp_AQ=potential_mat;
546 general_file='Potential_AQ_base_file.mat';
547 copyfile(general_file, new_file);
548 save(new_file, 'V3Dinterp_AQ', '-append');
549 clear;
```

## FILE2.M

```
1 clear;
2 %

3 % load in Potential.mat
4 %

5
6 load('Potential.mat');
7 % contains: - matrix of grid point (x,y)-positions
8 %           - vector of AQ angles
9 %           - vector of weights for each point
10 %          - matrix of sampled potentials (i.e. Fourier
11 %            components at each point and each angle)
12 %

13 % plot the locations of the 157 grid points
14 %

15
16 % Plotting of 157 pts.
17 figure; hold on; axis equal;
18 x_157=x ypos(:,1); y_157=x ypos(:,2);
19 for i=1:size(x ypos,1)
20     plot (x_157(i),y_157(i),'.')
21     text(x_157(i),y_157(i),num2str(i));
22 end
23
24
25
26 % Number of Interpolation Points for rectangular grid & angle
27 % interpolation
27 nx=120;
28 ny=200;
29 ntheta=25; % to request 30 theta vals., starting at 0, e.g., set
29 ntheta=31
30
31 % define range over which potential will be calculated
32 % potential is calculated across region (x,y) \in ([0,ax],[0,ay]
32 ])
33
34 % the maximum x-displacement of the WS cell is half the basic
34 % horizontal lattice spacing
35 ax=2*max(x ypos(:,1));
36
37 % the maximum y-displacement of the WS cell is half the basic
37 % vertical lattice spacing
38 ay=3*max(x ypos(:,2));
```

```
39 % axes are typically chosen such that dir(x) || dir(a1)
40 a=ax;
41
42 % number of points in non-interpolated WS cell
43 np=157;
44
45 V3Dinterp=V3Dinterp_AQ;
46
47 %%
48 %%  
-----  
49 % interpolating in theta
50 %  
-----  
51 % intitial number of angles
52 ntheta0=length(theta);
53
54 % generate new linearly-spaced vector from [0,2*pi) with ntheta
      -1 entries
55 thetavec=linspace(0,2*pi,ntheta); thetavec=thetavec(1:(ntheta-1));
56
57 ntheta=ntheta-1;
58
59 % use cubic interpolation with spline() function to interpolate
      in theta dimension for each position (x,y)
60 for ixy=1:(size(xpos,1))
61   V3Dinterp_temp(ixy,:)=spline(theta,V3Dinterp(ixy,:),
      thetavec); % spline() uses cubic interpolation
62 end
63 V3Dinterp=V3Dinterp_temp;
64
65 %%
66 %%  
-----  
67 % interpolating in x and y
68 %  
-----  
69 % original integer factor N as defined in the theoretical bckgd
70 nscale=12;
71
72 % use halvespacing() method to double the resolution of
    V3Dinterp
73 [V3Dnew, xposnew, weightnew, npnew, nscalenew] = halvespacing(
    V3Dinterp, xpos, weight, np,nscale,a,14);
74
75 %%
76 %%  
-----  
77 % interpolating in x and y
78 %  
-----  
79 % basic vertical reciprocal lattice spacing
80 G1=4*pi/sqrt(3)/a;
81
82 % basic vertical reciprocal lattice spacing
```

```

84 Gx0=2*pi/ax;
85
86 % basic vertical reciprocal lattice spacing
87 Gy0=2*pi/ay;
88
89 %this gives twice the point spacing in the original grid
90
91 % iGp is the number of mesh cells in real space to lattice cell
92 % along one direction
92 iGp=0;
93
94 % iterate through desired no of points
95 for ix=1:nx
96   for iy=1:ny
97     if(mod(ix+iy,2)==0)
98
99       % place origin at centre of grid by limiting range
100      % to +/- nx or ny:
100
101      % limit x
102      ixind=ix-1;
103      if(ixind>nx/2)
104        ixind=ixind-nx;
105      end
106
107      % limit y
108      iyind=iy-1;
109      if(iyind>ny/2)
110        iyind=iyind-ny;
111      end
112
113      % find corresponding reciprocal vector for given
114      % posn, Gtemp
114      Gtemp(1)=ixind*Gx0; Gtemp(2)=iyind*Gy0;
115
116      % weight that position based on its position within
117      % the range
117      weighttemp=InHexRecip(Gtemp,G1,nscalenew);
118
119      % if the point is within the basic reciprocal WS
120      % cell... (weight=1,1/2,1/3)
120      if(weighttemp~=0)
121
122        % add the point to the set of considered
123        % reciprocal vectors
122        iGp=iGp+1;
123
124        Gxp(iGp)=ixind*Gx0; Gyp(iGp)=iyind*Gy0;
125
126        weightp(iGp)=weighttemp;
127      end
128    end
129  end
130 end
131
132 % total no of reciprocal grid vectors in basic reciprocal WS
132 % cell
133 nGp=iGp;
134
135 % set of moduli of reciprocal grid lattice vectors
136 Gmag=(Gxp.*Gxp+Gyp.*Gyp);
137

```

```

138 % sort Gmag and store the permutation of the old order to the
139 % new order in IX
140 [Gmag, IX]=sort(Gmag);
141 % we can now use IX to reorder the points (Gxp,Gyp) by their
142 % modulus (reorder all their properties)
143 Gdum=Gxp(IX); Gxp=Gdum;
144 Gdum=Gyp(IX); Gyp=Gdum;
145 Gdum=weightp(IX); weightp=Gdum;
146
147 % Normalise the (ixGp,iyGp) to integers defining the reciprocal
148 % vectors
149 ixGp=round(Gxp./Gx0);
150 iyGp=round(Gyp./Gy0);
151
152 % Switch to 1-indexing for use in the Fourier transform
153 ix0Gp=ixGp+1;
154 iy0Gp=iyGp+1;
155
156 % add multiples of nx,ny to map all points (ix0Gp,iy0Gp)<1, i.e.
157 % points outside the range [1,nx] & [1,ny] to 1,2,...
158 for iGp=1:nGp
159     if(ix0Gp(iGp)<1)
160         ix0Gp(iGp)=ix0Gp(iGp)+nx;
161     end
162     if(iy0Gp(iGp)<1)
163         iy0Gp(iGp)=iy0Gp(iGp)+ny;
164     end
165 end
166
167 % Gxp,Gyp are the x and y components of the nGp reciprocal
168 % vectors used to describe the potential.
169
170 % ixGp and iyGp give these vectors as integer multiples of Gx0
171 % and Gy0 which are the basic G vectors of the rectangular
172 % unit cell
173
174 % ix0Gp and iy0Gp are these integers, but mapped on to the range
175 % 1 to nx and 1 to ny where (1,1) is the (Gx,Gy)=(0,0) - i.e.
176 % these are the integers to use in the fourier transforms
177
178 % so now ix0Gp and iy0Gp have the integers that will locate each
179 % G vector in the matrix for a ifft2'ed potential
180
181 %%
```

---

```

174 % calculate potential Fourier components for interpolated
175 % potential
```

---

```

176 %VG(iGp,iz)
177 VGnew=zeros(nGp,ntheta);
178 for iGp=1:nGp
179     for itheta=1:ntheta
180         dum=0.0;
181         for ip=1:npnew % sum weighted contributions of each
182             % Fourier component
183             dum=dum+V3Dnew(ip,itheta)*exp(-1i*(Gxp(iGp)*xyposnew(ip,1)+
```

```

183     Gyp(iGp)*x yposnew(ip,2)))*weightnew(ip);
184     end
185     VGnew(iGp,itheta)=dum/nscalenew/nscalenew;
186   end
187
188 %%
```

---

```

189 % weight the potential
190 %
```

---

```

191
192 pe3D=zeros(nx,ny,ntheta);
193
194 for itheta=1:ntheta
195
196 clear A
197 A=zeros(nx,ny);
198 for iGp=1:nGp
199   % weight the potential at each point to account for
      double/treble-counting
200   A(ix0Gp(iGp),iy0Gp(iGp))=VGnew(iGp,itheta)*weightp(iGp);
201 end
202 % take the real (cosine) part so that there is a top site at
      the origin
203 B=real(fft2(A));
204 pe3D(:,:,:,itheta)=B(:,:,:);
205 end
206
207 %%
```

---

```

208 % produce grid of positions we wish to sample in our plot, as
      defined by nx and ny
209 %
```

---

```

210
211 % Note we calculate it across a rectangle cell rather than a WS
      cell for ease of use
212 X=zeros(nx,ny);
213 Y=X;
214 for ix=1:nx
215   for iy=1:ny
216     X(ix,iy)=ax*(ix-1)/nx;
217     Y(ix,iy)=ay*(iy-1)/ny;
218   end
219 end
220
221 %%
```

---

```

222 % plot potentials for each calculated theta in [0,180] degrees
223 %
```

---

```

224
225 % define plot parameters
226 color_scale_min=0; color_scale_max=1050;
```

```

227 asp = [1 1 1/color_scale_max];
228 Lx = [0 max(X,[],'all')]; Ly = [0 max(Y,[],'all')];
229
230 % plot surface/contour map for each calculated angle theta in
    [0,180] degrees
231 for i = 1:24
232     figure(100+i);
233     xlim(Lx); ylim(Ly);
234
235     % surf plot
236     % stest = surf(X,Y,pe3D(:,:,i*3-2)); set(stest,'LineStyle',
        'none'); daspect(asp); caxis([color_scale_min
        color_scale_max]); view([0 90]);
237
238     % contour plot
239     stest = contourf(X,Y,pe3D(:,:,i*3-2)); axis equal;
240
241     % export graphics to png files
242     exportgraphics(gcf,sprintf('deg%d.png',round(theta(i)
        *3*(180/pi))), 'Resolution', '300');
243 end
244
245 %%
```

---

```

246 % prepare potential object for implementation in MD simulation
247 %
```

---

```

248
249 % Including 3rd z dimension BUT only with length 1 because we
    defined a single corrugation surface z(x,y)
250 PES4D_AQ(:,:,1,:)=pe3D;
251
252 %permute axes t: y,x,z,theta
253 PES4D_AQ=permute(PES4D_AQ,[2 1 3 4]);
254
255 % save potential in file 'loadPES.mat'
256 save('loadPES', 'PES4D_AQ');
```

---

# SOLUTIONS

## POTENTIAL ENERGY SURFACES: MAIN TASK

### Task 1: Questions

- (a) To start, run the file called `file1.m`. This file constructs an initial estimate of the potential based on experimentally-determined values. It generates a file named `Potential_AQ_base_file.mat`, which stores the following values:
- `x ypos`, a  $157 \times 2$  vector of all the  $(x, y)$ -positions of grid points in the WS cell. 157 points is the regular number of points obtained from tiling a 31-point irreducible triangle across the WS cell.
  - `thetapos`, a  $1 \times 24$  vector of all the allowed orientations of the AQ molecule with respect to the surface lattice. Note that  $\theta$  is the angle of the main body of the AQ molecule, measured anticlockwise from the  $[1\ 0]$  azimuth on the surface.
  - `weight`, a  $1 \times 157$  vector of weights for each  $x, y$ -position to prevent double/treble counting for edges/corners of the WS cell respectively.
  - `V3Dinterp_AQ`, a  $157 \times 24$  vector of potential values for each point (rows) with given AQ orientation (columns).
- Given the values in this file are experimental, the file is given in the appendix.
- (b) You may have noticed that there is no explicit mention of an irreducible triangle in either `file1.m` or in `file2.m`. The entire WS cell (a rectangle encompassing the cell, for ease of use) is constructed, and then different values set for the Fourier components at each angle. To what extent was the irreducible triangle method used here, and why?

### Task 1: Solution

The AQ molecule cannot be modelled as a single particle since it has an extended, rodlike shape. In general this shape breaks the hexagonal symmetry of the interaction between the molecule and the surface;

therefore tiling the irreducible triangle across the WS cell in the manner described in the theoretical background is no longer reasonable for certain angles.

For angles of  $0^\circ, 30^\circ, 60^\circ, 90^\circ, \text{etc.}$  the rod lies along the close-packed directions; the irreducible triangle method can be used to find the corrugation function. You can see this in the code where Fourier components of the PES are copied onto multiple points at these angles.

## Task 2: Questions

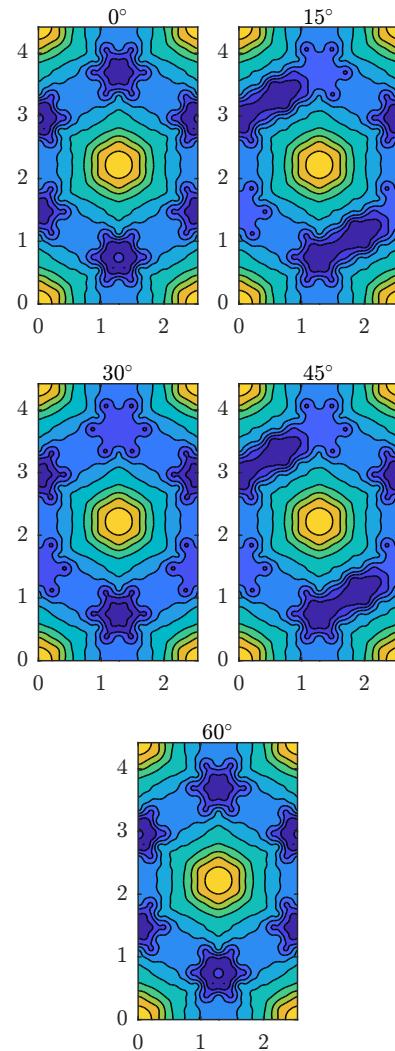
- (a) Second, run `file2.m`. This should produce:
  - A plot of all the points in the WS cell. Note the first 31 points are in the irreducible triangle.
  - A plot of all the points in the WS cell after interpolation. This plot is performed within the `halvespacing.m` function, given in the appendices.
  - 13 plots of the corrugation function for varying angles of the AQ molecule in the range  $0^\circ$  to  $360^\circ$ .
- (b) Having produced the above plots of the potential, explain the shapes of the potential seen for each orientation of the rod-like molecule. Why is the change in potential periodic, with a period of  $180^\circ$ ?

## Task 2: Solutions

When plotting the figures for the corrugation, you may find it more instructive to plot the surface using the `surf()` function and choose `view([0 90])` to see more detail in the corrugation (especially around the local minima).

We should first consider the static potential at  $0^\circ$ . There are local minima at both the fcc and bcc sites; however the deeper hcp sites have small local maxima at their centres. This demonstrates the fact that these sites can behave very differently; and as such it is often useful to distinguish between them in models. While the hcp sites are always minima, the fcc sites are only local minima for certain orientations. Therefore adsorption to the surface occurs preferentially at hcp sites.

We expect the change in potential to be periodic with period  $180^\circ$ . This is because anthraquinone is a rod-shaped molecule with 2-fold rotational symmetry about any axis parallel or perpendicular to its surface and through its centre (called a diad), and as so the interaction between the surface and either end of the molecule is equivalent. For a spherically-symmetric adsorbate we expect a period of  $360^\circ$ .



**Figure 4 |** Contours of the AQ/surface corrugation function

### Task 3: Question

With reference to the discussion of AQ motion in the theoretical background, explain the shape of the potential energy surface at each orientation.

### Task 3: Solution

The simplest motion to consider is that along the [1 0] azimuth on the surface, for which the crucial angles of interest are  $\theta = 0^\circ$  and  $\pm 15^\circ$ .

Considering the position and orientation of the molecule at each step in the walking process should give a clear picture of how the potential guides the observed motion; each rotation of  $\pm 15^\circ$  changes the shape of the potential such that the next site in the walking process becomes the nearest local minimum.

Note that the corrugation only shows the potential of the centre-of-mass at each position - do not be fooled into thinking that the linkers occupy wells on this plot. The potential plotted here is what is 'seen' by the centre of mass due to the positioning of its linkers on the 'real' potential surface.

You may find it instructive to calculate the potential over a higher resolution in theta (by increasing `ntheta` in `file2.m`) and observe the gradual shift in potential that allows each transition to the next step in the walking motion.

### Task 4: Question

- Take the generated file, `loadPES.mat`, and run it in PIGLE to simulate a trajectory of a single AQ molecule on the Cu(111) surface using MD methods. The motion should match that described in the theoretical background.

The required code for the PIGLE UI files is given in the original question.

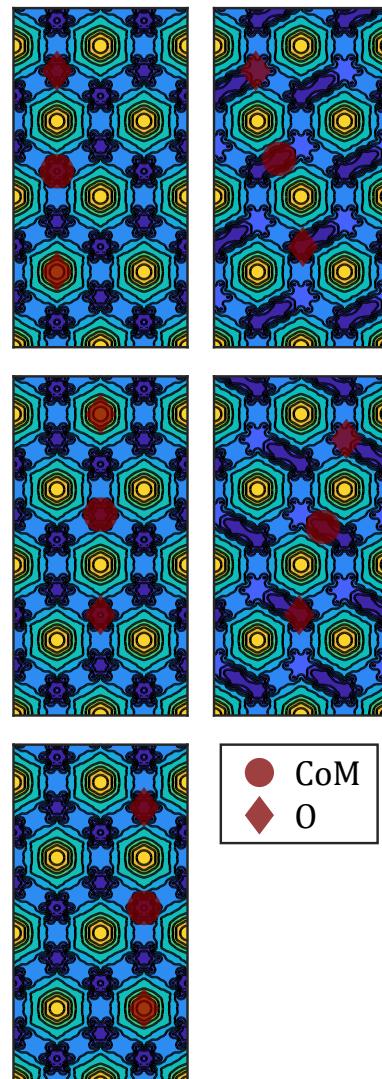
With the pigle setup files edited, one can place the file `loadPES.mat` in the root directory of the PIGLE folder and run `run_pigle.m`.

This will run the simulation with the above parameters. To view the motion, one may either run the command `make_movie(params, data)` to produce an animation of the motion or run the following code to plot the full trajectory of the molecule over the simulation:

```

30 % extract positional and orientational data from pigle
31 r = data.prtcl.r;
32
33 % reshape positional data into rows
34 rx = reshape(r(1,:,:), [1 length(r)]);
35 ry = reshape(r(2,:,:), [1 length(r)]);
36 rz = zeros(size(rx));
37

```



**Figure 5** | The AQ/Cu(111) potential energy surface at each stage of the walking motion.

```

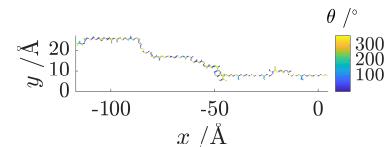
38 % reshape orientational data into a row
39 rtheta = reshape(r(3,:,:), [1 length(r)]) .* 180/pi;
40
41 % plot figure
42 figure();
43
44 % label axes
45 xlabel('$x$ /Å'); ylabel('$y$ /Å');
46
47 % use trick with surface() to plot a continuous gradient on
    % the trajectory where the colours correspond to angles
    % theta
48 surface([rx;rx], [ry;ry], [rz;rz], [rtheta;rtheta], '
    FaceColor', 'none', 'EdgeColor', 'interp');
49
50 % default 2-D view
51 view(2);
52
53 % add colourbar for theta
54 c = colorbar;
55
56 % format colourbar
57 c.Title.String = '$\theta^\circ$'; c.Title.Interpreter =
    'latex';
58 c.TickLabelInterpreter = 'latex';

```

- (b) Having produced this visualisation, do the trajectories fit with the qualitative predictions in the theoretical background? Are the angles at each point along the trajectory as you would expect?
- (c) Try varying the following parameters and observe how the trajectory is affected:
  - mass, the molecular mass
  - radius, the approximate molecular radius
  - eta, the translational frictional coupling constant
  - eta\_theta, the rotational frictional coupling constant
- (d) Try disabling rotations and observe how this affects the motion. This can be done by setting theta\_enabled=0; on line 5 of `pigle_ui.m`.

#### Task 4: Solution

- (a) The given ui files along with the existing pigle code of the correct version (v1.1.0-alpha1) should produce a figure similar to the following when the above code is run after pigle:
- (b) The trajectory does fit with the predictions of theory since it shows predominantly linear motion along the close-packed directions. In addition, the angle of the molecule at each point further supports theory, as it switches between blue (between 0° and 15°) and yellow (between 0° and -15 degree) with each step. At each hollow site the colour is either blue, green or yellow, corresponding to angles of 0°, 180° or 360° respectively.
- (c) This is largely intended to be an exploratory exercise so no com-

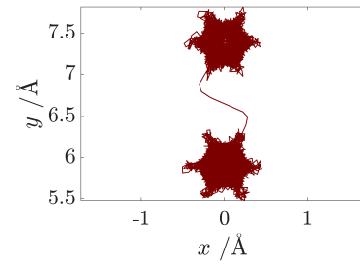


**Figure 6** | Trajectory of an AQ molecule on the Cu(111) surface over 50 ps. The colours give the angle  $\theta$  of the molecule at each position (in degrees).

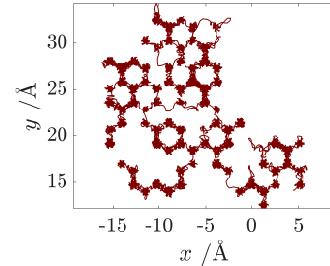
plete solution is given, however there are some general trends one should note:

- For smaller masses, the linear inertia is reduced so large changes in motion due to random lattice impulses becomes more likely. This causes the motion to become less linear since the molecule is more free to move to higher-energy sites. In the low-mass limit the motion is Brownian
  - For smaller radii, the moment of interia is reduced so large changes in angular motion due to random lattice impulses become more likely. This causes the motion to be less linear since the molecule is more free to change its walking direction. In the low-radius limit the particle can gain very large rotational kinetic energies and the model breaks down. This in turn makes it less likely for the molecule to perform walking motion since the time-scale of rotation is too fast compared to the time-scale for translation.
- (d) With rotations disabled the motion is as would generally be expected for a pointlike particle, since at an angle of  $0^\circ$  the potential has local minima at both hollow sites. In fact, since the mass of the molecule is very large, without rotations the average time between jumps is very large, giving the following trajectory: which depicts only a single jump between an hcp (top) and fcc (bottom) site.

With a smaller mass of 75 u we get the more characteristic trajectory for jump diffusion between sites



**Figure 7** | Trajectory of an AQ molecule (of mass 208 u) on the Cu(111) surface with no rotations permitted. The trajectory is calculated over 50 ps.



**Figure 8** | Trajectory of a molecule of mass 75 u on the Cu(111) surface with no rotations permitted. The trajectory is calculated over 50 ps.