

Quantum Transport in Nanoporous Graphene

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Abstract: Normally, both your asses would be dead as fucking fried chicken, but you happen to pull this shit while I'm in a transitional period so I don't wanna kill you, I wanna help you. But I can't give you this case, it don't belong to me. Besides, I've already been through too much shit this morning over this case to hand it over to your dumb ass.^a



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🔗 Project Repository: <https://github.com/rwiuff/QuantumTransport>

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I. INTRODUCTION

In recent years so called nano-porous graphene devices (NPGs) has been proposed for various applications. [Insert litt.] These devices are made up of single layered graphene with periodic holes (hence the “porous”). The remaining graphene constitutes ribbons and bridges in the structures. Fig. 1 shows how one such structure can look like. Because of graphenes electrical properties [Insert litt], one should be able to finely control the electron currents in the devices and thus create nanometer circuits for use as e.g. chemical detectors. As a result of its novelty, the fabrication of such devices are limited. Before fabrication one must show promising effects through theoretical simulations. The aim of this project is to develop numerical tight-binding routines in Python using NumPy. Electron transport can then be simulated using Green’s functions as well as clever recursion algorithms. From here we obtain transmission and band structures for simulated devices.

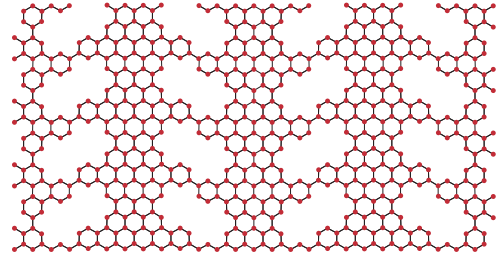


Figure 1: Drawing of a nanoporous graphene device.

Generally speaking the community uses DFT-based simulations through tools like those from the SIESTA project (TBtrans). Results are then analysed using SISL[1]. The DFT results can then be extrapolated to larger scales[2]. However DFT programs might seem as a blackbox. To get a better understanding of electron transport, we avoid DFT and rely solely on tight-binding simulations. We then confirm the validity of the developed products by comparing result to those from SIESTA.

To summarise:

1. Apply quantum mechanics for electron transport in NPGs.
2. Develop numerical methods (using recursion algorithms, linear algebra) with NumPy to implement tight-binding.
3. Calculate band structures and transmission plots for various devices.
4. Gather single-particle Green’s functions and LDOS of said devices.
5. Compare the obtained results and discuss whether or not they sufficiently resemble DFT based simulations.

The report is organised on the following way:

1. Sections II to V deals with the development of the scripts. First by introduction of basic theoretical concepts, followed by how these concepts are implemented practically through programming.
2. Section VI deals with the generated result on various NPGs and the comparison with DFT calculations with similar systems.
3. Section VIII summarises the results and concludes the project.

The code repository (which also includes the L^AT_EX files for this report) can be found on Github: <https://github.com/rwiuff/QuantumTransport>

II. QUANTUM TRANSPORT

In this section, the basics of the tight-binding approximation for electron transport will be explained. This motivates the use of numerical routines using NumPy.

A. Ballistic quantum transport

As graphene is a two dimensional material that consists of carbon atoms arranged in a hexagonal pattern, features in such a material can approach nanometer and sub nanometer scales. Because of the small scale the electrical properties of the material is vastly different from normal materials. Usually when describing the electrical properties of a material, drift-diffusion current models are used. They describe electric charges per area and current per area. This is usually a good description in systems where electron-electron and electron-atom scattering frequently occurs. The distance an electron travels before such a event is called its *mean free path*. However, in small systems as those of NPG-devices, the mean free path is longer than the system itself. Experiments have shown that electrons can move ballistically in graphene and carbon nanotubes[litt], that is, without phonon scattering. Therefore, we model electron transport using the *ballistic model*. In this model the electrons move through the material as waves. The fact that the electrons moves as waves will prove important later on because it gives rise to *Quantum Interference* which can be exploited as a tool when engineering graphene-based devices[3]. Furthermore the model looks at only one electron at a time in the presence of an electron gas. This model has been used with big success for regular graphene and it seems that the ballistic model also gives a good approximation for NPGs.

B. π -orbitals and π -electrons

When modelling the electron transport in graphene one needs to address the orbital structure of carbon lattices. The orbital structure is exactly what motivate the use of tight binding approximation and Green's functions. The two concepts of Tight-binding approximation and Green's functions will be elaborated further in the coming sections. In its basic form graphene can be divided into rings of carbon atoms as shown in Fig. 2a. In the (x,y) -plane the carbon atoms are bound in sp^2 orbitals as shown in Fig. 2b. This

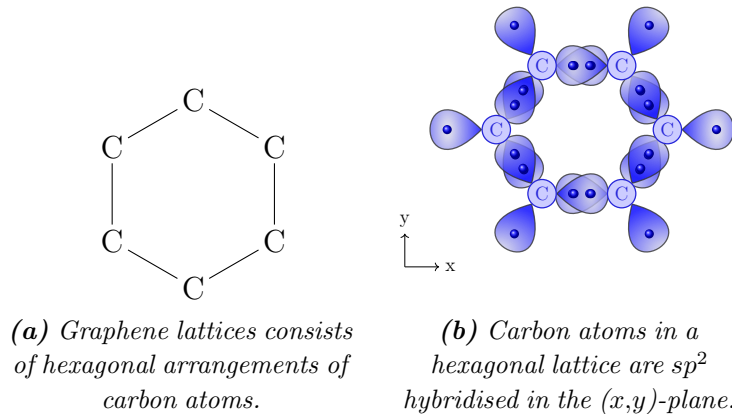


Figure 2: Benzene ring and its sp^2 hybridised orbitals.

hybridisation lock all but one valence electron for the carbon atoms. These electrons exists in a p-orbital in the z -direction. Fig. 3 shows the valence orbitals of carbon.

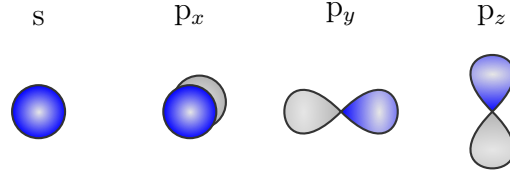


Figure 3: The valence orbitals of carbon.

The last electron in the p_z orbital does not mix with the tightly bound s , p_x and p_y electrons and moves freely. Thus these electrons have higher energies compared to the sp^2 electrons and occupy states at the Fermi level. These electrons dominates transport in the graphene lattice. The p_z orbital is also known as the π -orbital and as such the electron lying there is called a π -electron. Through a carbon lattice the π -electrons will travel through π -orbitals. For a benzene ring the π -electrons at the highest occupied molecular state will travel through the p_π -orbitals switching sign as they travel as shown in Fig. 4.

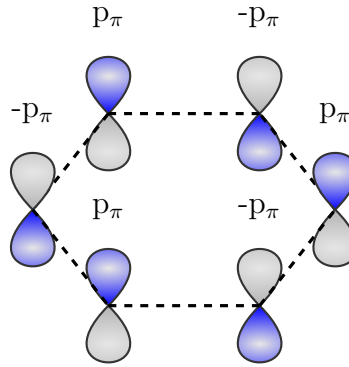


Figure 4: When jumping from one carbon atom to another, the π -electron goes between p_π -orbitals. Such a jump is described by two matrix elements in the system's Hamiltonian.

C. Tight-binding

Now that the transport carrying electrons are defined the next step is describing the transport itself. For this purpose we employ the *tight-binding* approximation. In this approximation the electrons are considered being tightly bound to the atoms. Contrary to a free electron gas approximation, the electrons does not spend time in between orbitals, but jump from orbital in atom a to orbital in atom b . The Hamiltonian is represented as a matrix of hopping elements for a collection of neighbouring atomic orbitals, i.e. molecular orbitals, as well as the energy contained within each orbital (which will be addressed later on). This can be done by describing the orbitals as a Linear Combination of Atomic Orbitals (LCAO). The solution to the Schrödinger equation is then:

$$\Psi_{\text{MO}} = \sum_{\alpha, R} c_{\alpha, R} \phi_{\alpha}(R) \quad (\text{II.1})$$

where $\phi_{\alpha}(R)$ is an atomic orbital at position R , with α denoting the valence of the orbital ($2s, 2p_x, 2p_y, 2p_z$). In electron transport the states close to the Fermi level is of interest. These are namely the highest occupied molecular orbitals (HOMO), or the lowest unoccupied molecular orbitals (LUMO). As stated earlier only the π -electrons is then of interest. The

electrons' motion can be described with the hopping matrix of elements:

$$V_{pp\pi} = \langle \phi_{\pi}(1) | \hat{H} | \phi_{\pi}(2) \rangle \quad (\text{II.2})$$

Physically this means that there is a potential between the π orbitals of neighbouring atoms 1 and 2. In our tight-binding approximation we consider only hop between nearest neighbours. The element

$$\epsilon_0 = \langle \phi_{\pi}(1) | \hat{H} | \phi_{\pi}(1) \rangle \quad (\text{II.3})$$

is the average energy of the electron on atom 1 and, it is common to define the hopping energy relative to this, i.e. $\epsilon_0 = 0$. If the atoms or their environment differs, so does the on-site potential.

Appendix A contains an illuminating example of how the tight-binding approximation can be used to describe simple carbon systems.

III. HAMILTONIAN FOR PERIODIC SYSTEMS

In the following sections, the focus will be to present and explain how to calculate band structures, local density of states and transmission, through *python*-programming, using Tight Binding approximation for any periodic structure. For simplicity, all initial examples and calculations will be done on a simple system, to make sure the different steps are easy to follow. The system can be seen in Fig. 5a.

A. Creating the on-site Hamiltonian and hopping matrices

The first and most essential parts needed for calculations is the *on-site* Hamiltonian \mathbf{h}_0 and the *hopping* matrices \mathbf{V} , \mathbf{V}^\dagger . The starting point is a matrix, containing set of coordinates x_0, y_0, z_0 , representing atom positions and a set of unit vectors \mathbf{u}_x , \mathbf{u}_y , \mathbf{u}_z . The unit vectors will be the basis of the unit cell containing all atom coordinates. From now on, only the x and y coordinates will be considered as graphene is considered purely a 2D material. The on-site Hamiltonian represents the interaction of atoms within the unit cell and the hopping matrices represents the interaction of atoms between periodically repeated unit cells. In Fig. 8 a visual representation of NPG with periodically repeated unit cells can be seen. For the rest of the report, the on-site Hamiltonian will all ways be the centre cell while the hopping matrices will be the cells surrounding the on-site Hamiltonian (See Fig. 6 for a generalised visual representation of the concept).

In practice, the scenario is that only a data set of coordinates given from scratch. The first step is to get the on-site Hamiltonian. As mentioned the on-site Hamiltonian represents the interaction of atoms within the unit cell. The approach is then to find the atoms which interact. The interaction is based on the inter-atomic distance between atoms, so naturally one wants to find the distance between all atoms in the unit cell. To do this a subtraction of all possible combinations of two sets of atom coordinates must be done. Then taking the norm of all individual results to get the distance. A function called *Onsite* have been developed to do just this. In Listing 1 the function can be seen.

```

31
32 def Onsite(xyz, Vppi, f):
33     h = np.zeros((xyz.shape[0], xyz.shape[0]))
34     for i in range(xyz.shape[0]):

```

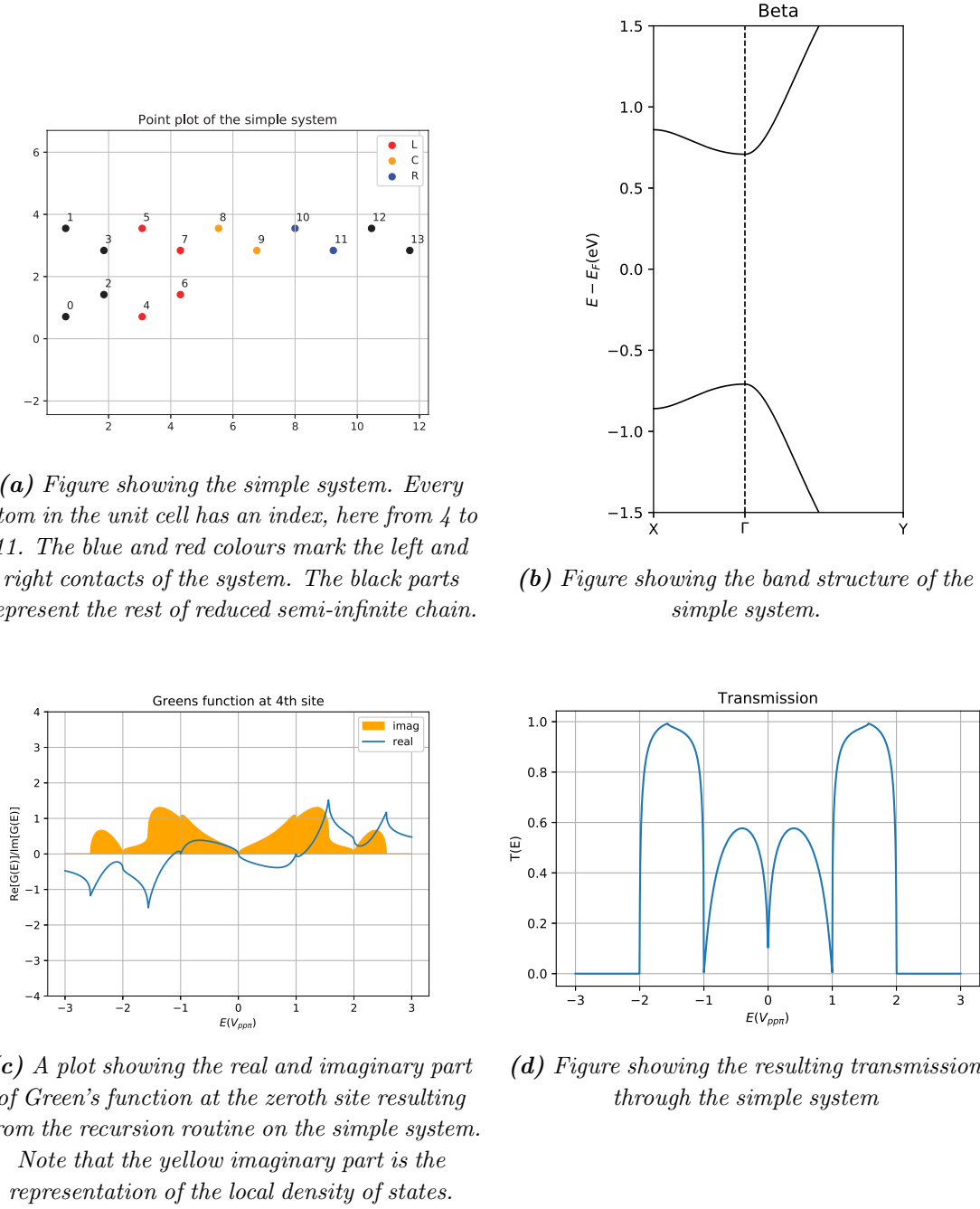


Figure 5: Figure of the different calculations executed on the simple system, using the developed scripts.

```

35     for j in range(xyz.shape[0]):
36         h[i, j] = LA.norm(np.subtract(xyz[i], xyz[j]))
37     h = np.where(h < 1.6, Vppi, 0)
38     h = np.subtract(h, Vppi * np.identity(xyz.shape[0]))

```

Listing 1: The outer operator in numpy is manifested as two nested loops. On lines xx-xx each atomic distance is calculated. Line xx replaces all nearest neighbour distances with an input potential, leaving the rest as zero. Lastly the diagonal is subtracted from the matrix.

The function produces a matrix which contain all distances between all atoms in the unit cell. The Tight Binding model dictates that only atoms with a specific inter-atomic distance

interact. Therefore the function has implemented a threshold (Listing 1 line xx) to determine whether a given distance is too great for interaction or small enough for interaction. All distances above the threshold will be changed to a 0-element in the on-site Hamiltonian matrix, representing zero interaction and all distances below the threshold will be changed to 1 to represent interaction between atoms. Finally The on-site Hamiltonian is multiplied with a on-site potential (scalar). The on-site potential $V_{pp\pi}$ differs depending on the system. Now the on-site Hamiltonian is complete and the product is a matrix containing 0's and 1's to represent interaction between atoms in a unit cell.

Moving on to the hopping matrices one first has to realise that the interactions are happening in a 2D plane. This has to be kept in mind when describing interaction between unit cells repeated in all directions in the plane. Effectively this means that six hopping matrices should be created. One in the x-direction, one in the y-direction, one in the xy-direction and their hermitian conjugates. Graphically this corresponds to a structure of this kind:

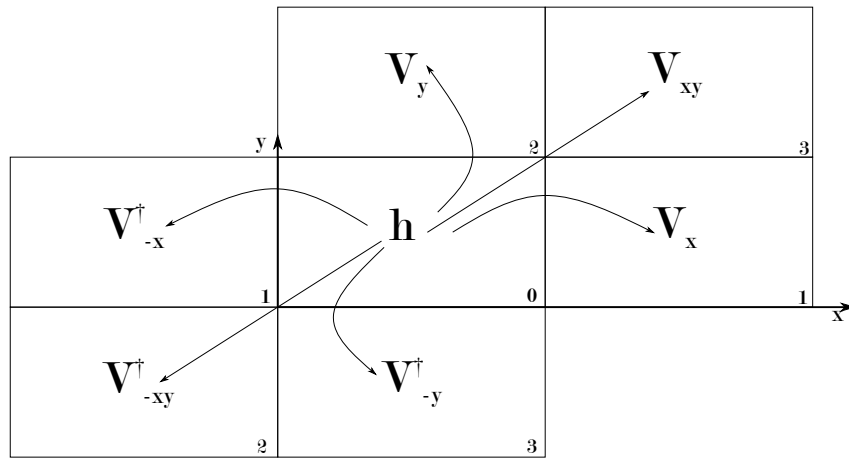


Figure 6: Representative figure of how the on-site Hamiltonian along with its hopping matrices are structured

In practice this is done by shifting the original x_0, y_0 coordinates by the given unit vectors $\mathbf{u}_x, \mathbf{u}_y$. By addition of the unit vectors to the original coordinate matrix one can get three new coordinate matrices $\mathbf{xy}_{shift-x} = x_0, y_0 + \mathbf{u}_x$, $\mathbf{xy}_{shift-y} = x_0, y_0 + \mathbf{u}_y$ and $\mathbf{xy}_{shift-xy} = x_0, y_0 + \mathbf{u}_x + \mathbf{u}_y$. With these three matrices what follows is basically the same method used to get the on-site Hamiltonian. The only difference being that it will be distances between atoms in the on-site Hamiltonian and the shifted matrices respectively. That way it is the distance, and thus the interaction, between the on-site Hamiltonian and the repeated unit cells that is calculated. The three resulting hopping matrices are denoted V_{1x} , V_{2y} and V_{3xy} . They represent interaction (hopping) in the "forward" direction (left-to-right) (See Fig. 6). To create the hopping matrices hopping in the "backwards" (right-to-left) direction (See Fig. 6) one simply has to transpose the hopping matrices. These matrices are denoted with a dagger: V_{1x}^\dagger , V_{2y}^\dagger and V_{3xy}^\dagger . To show how the on-site Hamiltonian and the hopping matrices look, see Fig. 7 for a figure of the resulting matrix-maps from calculation on the small simple system. It has been stitched together like in Fig. 6.

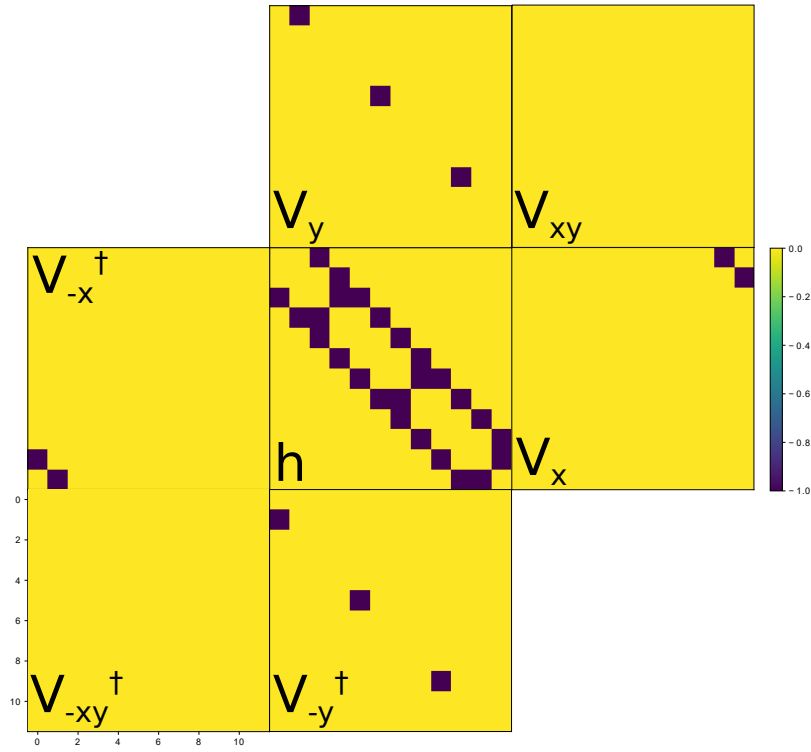


Figure 7: Matrix maps from calculation on an arbitrary graphene system with a unit cell of 12 atoms. The on-site Hamiltonian along with all its hopping matrices are stitched together like in figure Fig. 6. All the dark spots represent a hopping of an electron to its nearest neighbour i.e. a 1 element and yellow represents a 0 element

B. Defining the full Hamiltonian and solving the Schrödinger equation

Now that the on-site Hamiltonian along with its hopping matrices have been created, the next step is to create the full Hamiltonian in order to solve the Schrödinger equation for the system as a whole. This is an eigen-value/vector problem. The Schrödinger equation needs to be solved to get the eigen energies for the system as they will be used to produce band structure plots later on. In essence the full Hamiltonian denoted \mathbf{H} is a sum of the on-site Hamiltonian and its corresponding hopping matrices multiplied by a complex exponential function that has the appropriate phase relative to the hopping matrix:

$$\begin{aligned} \mathbf{H}(k_x, k_y) = & \mathbf{h}_0 + (\mathbf{V}_{1x} e^{-ik_x} + \mathbf{V}_{1x}^\dagger e^{ik_x} \\ & + \mathbf{V}_{2y} e^{-ik_y} + \mathbf{V}_{2y}^\dagger e^{ik_y} \\ & + \mathbf{V}_{3xy} e^{-ik_x} e^{-ik_y} + \mathbf{V}_{3xy}^\dagger e^{ik_x} e^{ik_y}) \end{aligned} \quad (\text{III.1})$$

Here k represents a continuous variable between 0 and π along the $\frac{1}{x}$ - and $\frac{1}{y}$ -axis in reciprocal space. Using the full Hamiltonian, the Schrodinger equation can be solved

$$\mathbf{H}(k_x, k_y) \phi_k = \epsilon_n(k_x, k_y) \phi_k \quad (\text{III.2})$$

Where ϕ_k is the and $\epsilon(k_x, k_y)$ is the eigen energies.

In practice this is done by defining a function, here called *Hkay*, that takes the on-site

Hamiltonian, the hopping matrices, and $k_{x/y}$ as inputs and outputs the eigenvalues, using numpy's `numpy.linalg.eigh`. The number of eigenvalues in the output corresponds to the dimension of the full Hamiltonian. In Listing 2 the code for the function is shown.

```

50     if struct >= 3:
51         p = float(input('Potential: '))
52         h[-1, -1] = p
53         h[-2, -2] = p
54     if struct <= 2:
55         p = float(input('Potential: '))
56         h[-1, -1] = p
57         h[-2, -2] = p
58         h[-3, -3] = p
59         h[-4, -4] = p

```

Listing 2: Function producing the full hamiltonian, corresponding to Eq. (III.1) the inputs x and y corresponds to the k_x, k_y .

C. Producing band structures

In order to calculate and visualise the band structure of the simple system, one need to define the full Hamiltonian \mathbf{H} in two directions. When working with band structures and periodic systems it is common to note points in space with respect to the *Brillouin Zone* which is a primitive cell in reciprocal space. Therefor a continuous variable k is introduced. it extends in two directions in $(-k_x)$ and (k_y) , which correspond to lengths between the symmetry points X, Γ and Y in the Brillouin zone. Here Γ is the origin $(0,0)$. Practically this corresponds to making two plots, one for each pair of symmetry points. The y-values in each plot correspond to the eigenvalues obtained by the *Hkay* function described in Section III B. The number of eigen energies, and effectively the number of bands in the plot is dictated by the dimension of the Hamiltonian. $n \times n$ -matrix $\rightarrow n$ eigen energies (bands). However plots produced in this report will only show a few of these bands in a small energy range. In the case of the simple system, the full Hamiltonian for obtaining the eigen energies that corresponds to directions X and Y are:

$$X: \mathbf{H}_X = \mathbf{h}_0 + (\mathbf{V}_{1x}e^{ik_x} + \mathbf{V}_{1x}^\dagger e^{-ik_x} + \mathbf{V}_{2y} + \mathbf{V}_{2y}^\dagger + \mathbf{V}_{3xy}e^{ik_x} + \mathbf{V}_{3xy}^\dagger e^{-ik_x}) \quad (\text{III.3})$$

$$Y: \mathbf{H}_Y = \mathbf{h}_0 + (\mathbf{V}_{1x} + \mathbf{V}_{1x}^\dagger + \mathbf{V}_{2y}e^{-ik_y} + \mathbf{V}_{2y}^\dagger e^{ik_y} + \mathbf{V}_{3xy}e^{-ik_y} + \mathbf{V}_{3xy}^\dagger e^{ik_y}) \quad (\text{III.4})$$

Using the eigenvalues as y-values in the two plots, putting the two plots together will yield a final plot of the band structure shown in Fig. 5b.

IV. GREENS FUNCTIONS, SELF ENERGY AND THE RECURSION ROUTINE

The Green's function and self energies play the central role when it comes to obtaining the LDOS as well as electron transport in a system. In fact, the imaginary part of the Green's function is the LDOS for a specific site in a system. What the Green's function and self energy actually is and how they come about will here be explained formally, to motivate the practical use in the following sections.

A. Green's functions and self-energy

Firstly one should note that some of the concepts in this section will be explained using a figure of NPG as an example (Fig. 8). However, in the following section (Section IV B) the focus will revert back to the simple system from Fig. 5a.

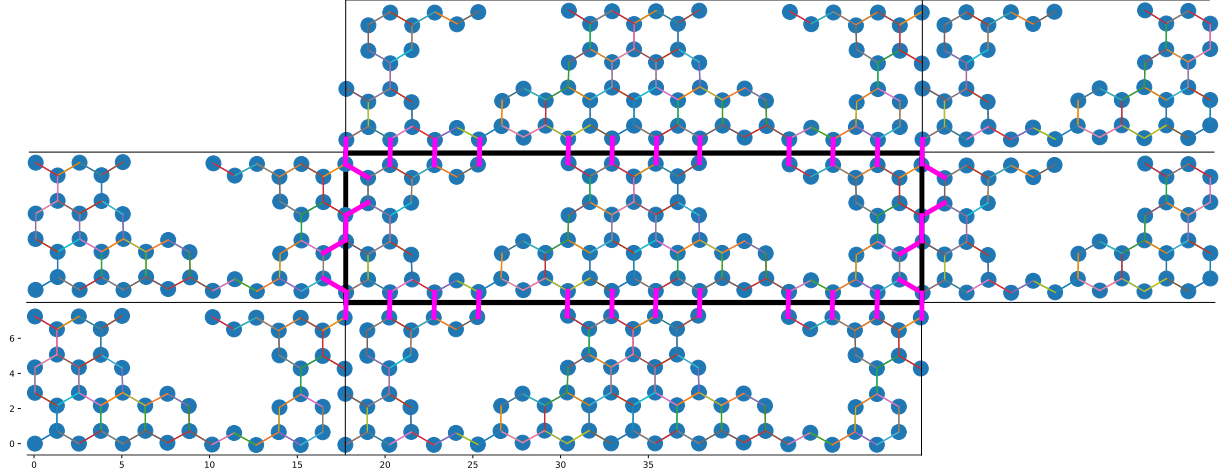


Figure 8: Visual representation of the periodic NPG-structure. The atoms surrounded by the black box in the centre represents the unit cell. The neighbouring boxes are unit cells repeated periodically. Note that the two cells left and right with respect to the centre cell has been cut in half for figure space. The pink lines crossing the black box represents the link between the nearest neighbours in the adjacent cell.

Imagine a system like the one in Fig. 8. It contains a unit cell in the centre, marked by a black border, surrounded by repeated unit cells in all directions. The aim is to explain how electrons move through this region. Suppose all cells surrounding the centre cell are considered "contacts" in the sense that they represent a semi-infinite chain of molecules and that they are the source of electrons (or states) that is injected in to the centre cell. What the Green's function is doing is that it "takes the states through" the centre region. It propagates the states in this particular area. In other words, the Green's function is the solution to the Schrödinger Equation in this area and the equation has the form

$$[(E+i\eta)\mathbf{1}-\mathbf{H}]\mathbf{G}(E)=\mathbf{1} \quad (\text{IV.1})$$

From this equation one can also get the Green's function as

$$\mathbf{G}(E)=\mathbf{1}([(E+i\eta)\mathbf{1}-\mathbf{H}])^{-1} \quad (\text{IV.2})$$

$$=[(E+i\eta)\mathbf{1}-\mathbf{H}]^{-1} \quad (\text{IV.3})$$

The Green's functions in these equations are represented as matrices that contain all the individual Green's functions for the unit cell as well as the Green's functions for the rest of the chain. As seen in the equations, all that is needed to get the Green's function for a unit cell, in theory, is an energy and the Hamiltonian of the unit cell. Note that the solution to the Green's function matrix is a diagonal matrix with the two first off diagonals because of rules for nearest neighbour interaction dictated by the Tight Binding approximation. As the Green's functions for all unit cells in a potentially semi-infinite system are needed, in practice, one has to turn to more sophisticated methods to obtain all the Green's functions, namely recursion. More on that shortly. For now this is the introduction to the Green's function. How it relates to a unit cell in a system and that it is the source of the LDOS in a

unit cell.

As described one can use the Green's functions to get the propagation of states through a specific on-site Hamiltonian. However, if the system contains a range of cells, possibly infinitely many, the Hamiltonian would be of infinite size and the inversion in Eq. (IV.2) would be impossible to do practically. The solution to this, is to model a semi-infinite tight binding chain of atom/molecules and then use *recursion* on this chain. The way the recursion is done is to remove every second cell in the chain. Because the chain is semi-infinite, the yield would just be a new semi-infinite chain. Continuing this way the system can be reduced to a finite size which can actually be worked on. Say one continues to remove every second element in the chain, then in the end, the cells would be too far apart to interact and no hopping between cells would occur. At this point the recursion should stop. More on how this is done practically later. For now one just have to keep in mind that the removing cells in the chain effectively changes to coupling between them and this is where *self energy* comes in. The self energy is what describes the effective coupling between a cell and the rest of the semi-infinite chain. And it can be derived by looking at a cell at the very end of the semi-infinite chain and see how it couples to the rest. First one needs the Green's functions. The Green's matrix for this single cell would be given by the equation in Eq. (IV.2). This is before when only one cell and thus one matrix had to be considered. But now, there is an semi-infinite amount of cells and an semi-infinite amount of matrices to consider. However, the cell in the end of the chain only interacts with the cell next to it and so on. Considering this one can write up an equation equivalent to that of Eq. (IV.1) but as system of matrix equations for the chain.

$$\begin{pmatrix} z\mathbf{1} - \mathbf{H}_c & -\mathbf{V}^\dagger \\ -\mathbf{V} & (z - \varepsilon')\mathbf{1} \end{pmatrix} \begin{pmatrix} \mathbf{X} & \mathbf{G}_{0c} \\ \mathbf{G}_{c0} & \mathbf{G}_{00} \end{pmatrix} = \begin{pmatrix} \mathbf{1} & \mathbf{0} \\ \mathbf{0} & \mathbf{1} \end{pmatrix} \quad (\text{IV.4})$$

where ε' is the on-site Hamiltonian of the first cell, z is $E + i\eta$, $\mathbf{G}_{0c/c0}$ is the Green's matrices coupling the cell to the rest of the chain and \mathbf{X} is the Green's matrices for the rest of the chain. This is also assuming one knows the Green's function within the chain \mathbf{G}_c and that the chain has constant hopping and on-site elements $\mathbf{H}_c, \mathbf{V}, \mathbf{V}^\dagger$. Solving this system for \mathbf{G}_{00} and eliminating \mathbf{G}_{0c} , which is unknown, one gets

$$\mathbf{G}_{00}(z) = (z - \varepsilon' - \Sigma(z))^{-1} \quad (\text{IV.5})$$

where $\Sigma(z)$ is the self-energy. One can isolate the self energy from the equations above to

$$\Sigma(z) = \mathbf{V}[z\mathbf{1} - \mathbf{H}_c]^{-1}\mathbf{V}^\dagger \quad (\text{IV.6})$$

And this concludes the formal introduction to Green's functions and self energy.

B. Obtaining first cell self-energy and Green's matrix through programming

For simplicity and in order to check whether the routine would yield the expected results, the system in Fig. 5a is use as an example. The goal is to get the Green's functions for the centre unit cell in the semi-infinite chain and the self energies coupling to rest of the chain right and left. Specifically for the simple system one should imagine first having one centre unit cell like Fig. 5a and then repeating it infinitely in the left and right direction. The fact that there is a left *and* right self energy is that the unit cell lies within the semi-infinite chain and not at the very end as described in Section IV A. To be assured, this does not conflict with any of the preciously mentioned formalism and the left and right self energies

are quite easily obtained as one shall see shortly. As mentioned the goal is to get the Green's functions of a specific unit cell and the self energies related to it. If the Green's matrix \mathbf{G} represents the whole chain, then the equation of the whole system would be equivalent to that of Eq. (IV.1). Considering the Green's functions for specific unit cell in question, it would correspond to one column in the system of equations, say the first. One can define the on-site Hamiltonian \mathbf{h}_0 for the specific unit cell and its hopping matrices $\mathbf{V}, \mathbf{V}^\dagger$. The two hopping matrices correspond to hopping left or right in the chain respectively. These can be obtained using the functions already developed in Section III. Throughout this section they will be named $a_0 = \mathbf{V}^\dagger$, $b_0 = \mathbf{V}$, $e_{s0} = \mathbf{h}_s$. The recursion is an iterative process and so the zero index indicates the starting point of the iterations and the s index indicates that it is the Hamiltonian of the specific wanted cell. One can also define a Green's function for a single unit cell as $g_0 = (z - e_0)^{-1}$ just like Eq. (IV.1) where $e_0 = \mathbf{h}$ which is the on-site Hamiltonian of the other cells. With these elements a system of equations, similar to Eq. (IV.1) can be setup. The first difference being that the identity matrix is replaced by its first column, because the solution of interest is that one first column in the Green's matrix. The second is that the first element in the Hamiltonian matrix \mathbf{H} is related to the specific single unit cell \mathbf{h}_s . Next a range of multiplications of the different elements stated so far will be shown, and afterwards it will be explained how these affect the system of equations to give recursion. The multiplications are:

$$\begin{aligned} a_1 &= a_0 \times g_0 \times a_0 \\ b_1 &= b_0 \times g_0 \times b_0 \\ e_1 &= e_0 + a_0 \times g_0 \times b_0 + b_0 \times g_0 \times a_0 \\ e_{1s} &= e_{10s} + a_0 \times g_0 \times b_0 \\ g_1 &= (z - e_1)^{-1} \end{aligned} \tag{IV.7}$$

These equations constitutes the first iteration in the recursion and they can be repeated indefinitely. In the matrix system of equations these multiplications effectively shifts all elements in the matrix by one column and because the matrix is diagonal, it will leave the first column of the matrix empty. The column can then be removed and this is exactly what corresponds to removing a cell in the semi-infinite chain. Keeping on doing these multiplications, raising the index by +1 every time, one can move through reduce the system as a whole removing of columns (cells) in the system of equations. In the end one will obtain re-normalised Hamiltonians and hopping matrices which is then used to get the Green's functions and self energies through these simple equations:

$$\begin{aligned} \Sigma_R &= e_s - h \\ \Sigma_L &= e - h - \Sigma_R \\ \mathbf{G}00 &= (z - e_s)^{-1} \end{aligned} \tag{IV.8}$$

Programming this recursion is fairly simple as all which is needed is a while loop which iterates over the equations in Eq. (IV.7) until a threshold has been reached. The threshold is determined by the value of the hopping matrix a_0 . As it reaches a value close to zero, there is no longer any effective interacting (hopping) between the cells because of removal of cells and the recursion should stop. In Listing 3 the code for the routine is shown. Line xx-xx is the listing of elements before iteration, xx-xx is the while loop with the equations from Eq. (IV.7). Note that some intermediate multiplications are made f.ex. $ag = a0 @ b0$. This is for run-time optimisation only. In line xx-xx the iteration indexed 0 gets redefined so that it corresponds to the most recent iteration. Finally in xx-xx the definition of the outputs as

per Eq. (IV.8) is stated.

```
62
63 def Hop(xyz, xyz1, Vppi):
64     hop = np.zeros((xyz1.shape[0], xyz.shape[0]))
65     for i in range(xyz1.shape[0]):
66         for j in range(xyz.shape[0]):
67             hop[i, j] = LA.norm(np.subtract(xyz1[i], xyz[j]))
68     hop = np.where(hop < 1.6, Vppi, 0)
69     return hop
70
71
72 def Hkay(Ham, V1, V2, V3, x, y):
73     Ham = Ham + (V1 * np.exp(-1.0j * x)
74                 + np.transpose(V1) * np.exp(1.0j * x)
75                 + V2 * np.exp(-1.0j * y)
76                 + np.transpose(V2) * np.exp(1.0j * y)
77                 + V3 * np.exp(-1.0j * x) * np.exp(-1.0j * y)
78                 + np.transpose(V3) * np.exp(1.0j * x) * np.exp(1.0j * y))
79     e = LA.eigh(Ham)[0]
80     v = LA.eigh(Ham)[1]
81     return e, v
82
83
84 def RecursionRoutine(En, h, V, eta):
85     z = np.identity(h.shape[0]) * (En - eta)
86     a0 = V.conj().transpose()
87     b0 = V
88     es0 = h
89     e0 = h
```

Listing 3: The while loop in the recursion routine. The matrix elements are overwritten with the new variables until the resulting matrix is small enough to diagonalise

This concludes how recursion works and how the first cell Green's function as well as the self-energies is obtained.

C. Plotting the real and imaginary part of the first cell Green's function

One of the results possible to obtain via the recursion routine is the Green's function of the centre unit cell in relation to the rest of the chain. As mentioned the imaginary part of the elements Green's matrix is the LDOS of the different sites in the unit cell. With a relatively simple approach, the Green's matrix elements can be obtained as a function of energy, using a *for loop*, looping over a range of energies which is then used as input in the *RecursionRoutine* function (Listing 3), see Listing 4:

```
64 G00 = np.zeros((En.shape[0]), dtype=complex)
65 for i in range(En.shape[0]):
66     G, SelfER, SelfEL = RecursionRoutine(En[i], h, V, eta)
67     G = np.diag(G)
68     G00[i] = G[0]
```

Listing 4: Code showing the loop which produces the complex Green's function (or y) values for a range of energies used in the plot.

This gives information about the LDOS at a specific energy and place in space, namely a specific atom in the unit cell. The resulting plot for the simple system (atom index 4) can be seen in Fig. 5c. As seen in the plot... Note that the plot only represents the LDOS for a specific site on the molecule and that they may change radically from site to site (see Appendix B, Fig. 21 for an example using the same system as Fig. 5a). The site can be changed by choosing another index in Listing 4 line 68, which corresponds to the atom indices in Fig. 5a.

V. TRANSMISSION ROUTINE

This section will mark the conclusion of the preliminary work done in Sections II to IV. All the functions producing on-site Hamiltonians, hopping matrices, full Hamiltonians, band structures as well as self energy and Green's functions by recursion, will be used to get the transmission through the material.

First of all a sentence as to what transmission is: Transmission is the probability of an electron being transported through a specific region for a specific range of energies and thus how the region affects the overall current flow of electrons through the system as a whole. Below is an equation stating it formally

$$P(t)_{mn} = \left| \langle m | e^{i\mathbf{H}t/\hbar} | n \rangle \right|^2 \quad (\text{V.1})$$

where m, n is the density of states in each side of the region of interest (states going in/out) and $e^{i\mathbf{H}t/\hbar}$ is the solution to the Green's function.

To give an overview and explain the different concepts of transmission this section will rely heavily on Fig. 9 where all the different parts of the system have been translated from the actual material into mathematical formalism in the shape of matrices. The first and central piece is the so-called "Device Region" with the on-site Hamiltonian \mathbf{H}_D (Green area in Fig. 9). The device region contains at least one central unit cell as well as a "left" and "right" unit cell (Red and blue area in Fig. 9). The left and right unit cells represent the contact region of the device i.e. the two parts that connects to the rest of the system/molecule. They have on-site Hamiltonians $\mathbf{H}_L, \mathbf{H}_R$ and they interact with rest of the system via hopping matrices $\mathbf{V}_{L/R}, \mathbf{V}_{L/R}^\dagger$. As \mathbf{H}_D contains $\mathbf{H}_L, \mathbf{H}_R$ they can be picked out of \mathbf{H}_D , without further calculation (See Fig. 9) once the \mathbf{H}_D has been calculated. The cells next to the contact region can be reduced into a single Hamiltonian by recursion to have same dimension as $\mathbf{H}_L, \mathbf{H}_R$. Note that $\mathbf{H}_L, \mathbf{H}_R$ need not be the same dimensions. Related to $\mathbf{H}_L, \mathbf{H}_R$ is the left and right self energies $\Sigma_{L/R}$ and on-site Green's matrices $\mathbf{g}_L, \mathbf{g}_R$. These can be obtained using the theory and developed methods from Section IV. However the aim is to obtain the Green's matrix for the device region, \mathbf{G}_D , as it is the one needed to fully describe the transmission in the region of interest. In other words, propagation of the states in the green area in Fig. 9. To obtain it, one simply has to keep in mind that the effective coupling of the device region to the rest of the system is determined by the two contact regions ($\mathbf{H}_L, \mathbf{H}_R$) and thus the correction to the device Green's functions will be determined by the self energy of those contact regions. So the Green's matrix will be given by the same equation as Eq. (IV.2) but

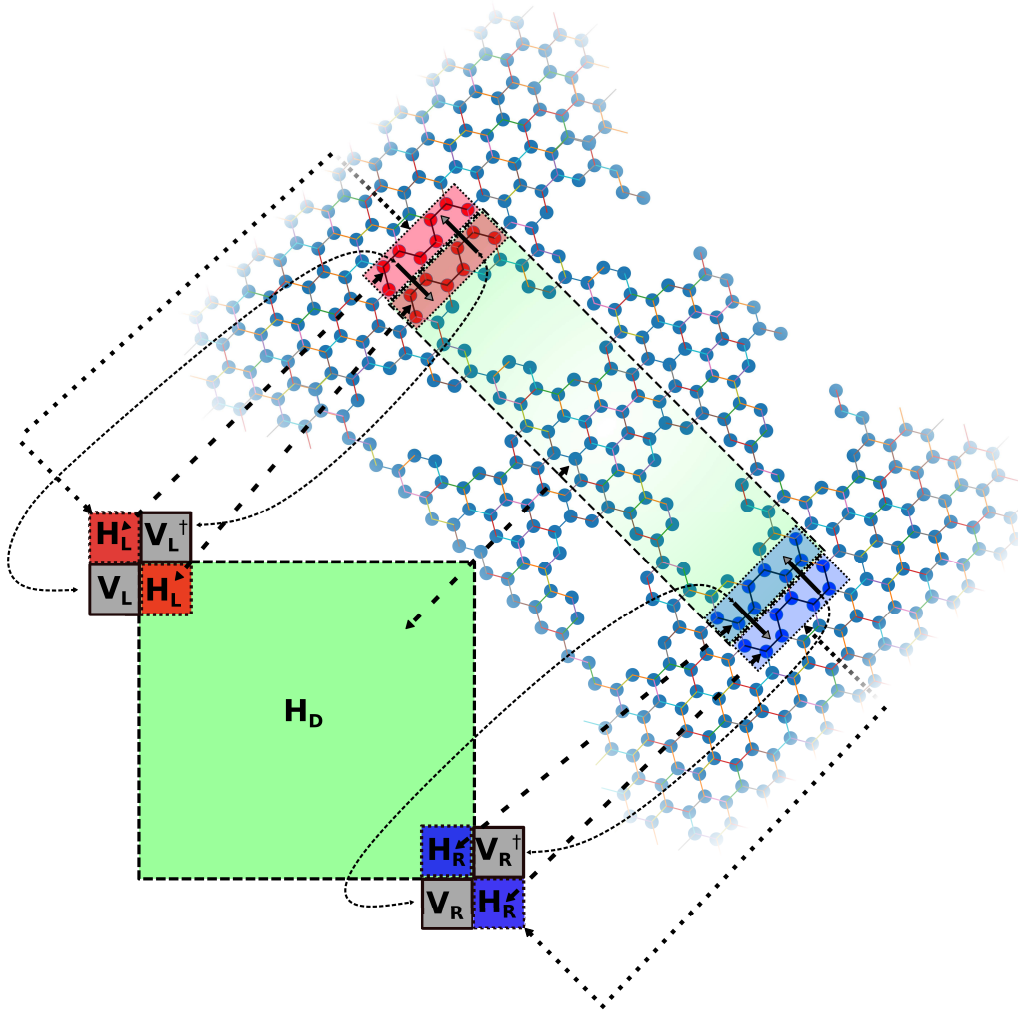


Figure 9: Illustration showing how the different parts of the system are translated into matrix blocks in NPG. The green box is the unit cell of the device with the Hamiltonian \mathbf{H}_D . It includes one red and blue box which themselves are unit cells of the left and right contacts and have the Hamiltonians \mathbf{H}_L , \mathbf{H}_R . The two other unit cells lying outside the device region represents what could be an infinite contact region reducible by recursion. Finally the two fat black arrows (not dotted) on each side of the device represents the hopping between the device- and contact region. Note that the direction of hopping corresponds to a specific hopping matrix. F.ex. left-to-right is the ordinary hopping matrix (\mathbf{V}) while right-to-left is its conjugate (\mathbf{V}^\dagger) (for both left and right side of the device).

with a self energy correction:

$$\mathbf{G}_D = [\mathbf{1}(E + i\eta) - \mathbf{H}_D - \Sigma_L(E) - \Sigma_R(E)]^{-1} \quad (\text{V.2})$$

Looking back at Eq. (V.1) the Green's function needed has been obtained, but what about the states going in and out of the device region $\langle m|$ and $|n\rangle$? As states travel, their corresponding self-energies change in time. Rate operators Γ are defined as the change in imaginary self-energy. They describe the 'rate' by which the self-energies of the states moving in and out, change in time. The rate matrices are given by

$$\Gamma_{L/R} = i(\Sigma_{L/R} - \Sigma_{L/R}^\dagger) \quad (\text{V.3})$$

Similarly the change in the imaginary Green's matrix is defined as

$$\mathbf{A} = i(\mathbf{G} - \mathbf{G}^\dagger) \quad (\text{V.4})$$

$$\begin{aligned} &= i(\mathbf{G}^\dagger [\mathbf{G}^\dagger - \mathbf{G}] \mathbf{G}) \\ &= i(\mathbf{G}^\dagger [E - \mathbf{H}^\dagger - \Sigma^\dagger - (E - \mathbf{H} - \Sigma)] \mathbf{G}) \\ &= i(\mathbf{G}^\dagger [-\Sigma^\dagger + \Sigma]) \mathbf{G} \\ &= i(\mathbf{G}^\dagger \mathbf{\Gamma} \mathbf{G}) \end{aligned} \quad (\text{V.5})$$

Here it have been utilised that the Green's matrix is symmetric in time ($\mathbf{G} = \mathbf{G}^T$, $\mathbf{G}^T \mathbf{G} = \mathbf{I}$, $\mathbf{G}^T = \mathbf{G}^{-1}$) as well as the fact that $\mathbf{G} = z\mathbf{1} - \mathbf{H} - \Sigma$. Additionally the Hamiltonians cancel out as they are unitary. The definition of \mathbf{A} is that it is a *spectral function*. It is the change of the imaginary Green's functions. As seen in the equations above it can be described by the Green's matrix and the rate matrix. From the previous sections it is know that the imaginary part of the Green's functions represent the LDOS. The spectral function is thus describing the density of states, changing by the rate $\mathbf{\Gamma}$. The spectral function can also be described in 'left/right' terminology as

$$\mathbf{A}_{L/R} = \mathbf{G}_D^\dagger \mathbf{\Gamma}_{L/R} \mathbf{G}_D \quad (\text{V.6})$$

Taking the left spectral function as an example, it represents the density of states of a wave coming from the left entering the device. To describe how the density of states pass through the device region one just have to multiply the spectral function by the rate matrix. Again using the left spectral function as an example

$$\text{Tr}[\mathbf{A}_L \mathbf{\Gamma}_R] = \text{Tr}[\mathbf{G}_D^\dagger \mathbf{\Gamma}_L \mathbf{G}_D \mathbf{\Gamma}_R] \quad (\text{V.7})$$

Here the trace of the product is taken as all states besides the one in the left contact region are zero. This corresponds to the density of states coming from the left, which then pass on through the right electrode by the rate $\mathbf{\Gamma}_R(E)$. Additionally the trace is cyclic so

$$\text{Tr}[\mathbf{A}_L \mathbf{\Gamma}_R] = \text{Tr}[\mathbf{A}_R \mathbf{\Gamma}_L] \quad (\text{V.8})$$

This ultimately leads to transmission because transmission is in essence an expression of how much of the density of states passes trough the device and as explained Eq. (V.8) is exactly the density of states, coming from the left (or right) and then passes through the right (left) by rate $\mathbf{\Gamma}_{L/R}(E)$. So using the Green's function, left/right self energies as well as the left/right rate matrices, the transmission, as a function of energy, can be obtained via the following equation:

$$T(E) = \text{Tr}[\mathbf{\Gamma}_R \mathbf{G}_D \mathbf{\Gamma}_L \mathbf{G}_D^\dagger](E) \quad (\text{V.9})$$

A. Transmission in 1D

Again the developed routine in this section will be used on the simple system (Fig. 5a) as an example and in order to make sure that the obtained results are as expected. Thereafter it will be generalised to suit all kinds and sizes of system. First thing is to define the device in the same manner as Fig. 9 so that the device Hamiltonian \mathbf{H}_D can be obtained through the already defined function *Onsite*. The left and right Hamiltonian $\mathbf{H}_{L/R}$ are thus picked out as described earlier. An implementation has been made to the script to allow the user to see the

left and right contact cells graphically as red and blue marked atom indices in the plot of the unit cell (See Fig. 5a). This allows the user to get an overview of dimensions of $\mathbf{H}_L, \mathbf{H}_R$ so they can be picked out of the device Hamiltonian correctly. From $\mathbf{H}_L, \mathbf{H}_R$ the corresponding hopping matrices are defined using the *Hop* function. Then the developed *EnergyRecursion* function is used to obtain the device Green's matrix. This function is a more elaborate version of the earlier mentioned *RecursionRoutine* and it takes $\mathbf{H}_D, \mathbf{H}_L, \mathbf{H}_R, \mathbf{V}_L, \mathbf{V}_R$, a range of energies and η as inputs. It uses the old recursion routine to calculate the self energies for the left and right cells ($\Sigma_{L/R}$) (see line xxx-xxx Listing 5) and then uses those to calculate the device Green's function \mathbf{G}_D as well as the left and right rate matrices $\Gamma_{L/R}$, using equations Eq. (V.2), Eq. (V.3) (see Listing 5 line xxx-xxx).

```
156
157 def DefineDevice(xyz):
158     L = np.fromstring(
159         input('Left contact atomic indices (#-#): '), dtype=int, sep='-')
160     R = np.fromstring(
161         input('Right contact atomic indices (#-#): '), dtype=int, sep='-')
162     L = np.arange(L[0], L[1] + 1, 1, dtype=int)
163     R = np.arange(R[0], R[1] + 1, 1, dtype=int)
164     C = np.arange(L[1] + 3, R[0], 1, dtype=int)
165     RestL = np.arange(0, L[0], dtype=int)
166     RestR = np.arange(R[1] + 3, xyz.shape[0], 1, dtype=int)
167     print(RestL)
168     print(L)
169     print(C)
170     print(R)
171     print(RestR)
172
173     Lxyz = xyz[L]
174     Rxyz = xyz[R]
175     Cxyz = xyz[C]
176     RmArray = np.append(L, C).astype(int)
177     RmArray = np.append(RmArray, R).astype(int)
178     Restxyz = np.delete(xyz, RmArray, 0)
179
180     plt.scatter(Lxyz[:, 0], Lxyz[:, 1], c='red', label='L')
181     plt.scatter(Cxyz[:, 0], Cxyz[:, 1], c='orange', label='C')
182     plt.scatter(Rxyz[:, 0], Rxyz[:, 1], c='blue', label='R')
183     plt.scatter(Restxyz[:, 0], Restxyz[:, 1], c='k')
184     plt.legend()
185     plt.title('Point plot of the simple system')
```

Listing 5: Code showing how the device Green's functions as well as the left and right rate matrices are computed. First defining the different parts as described in the text above (line xx-xx), then looping over a range of energies (line xx-xx), using the old Recursion Routine and then inputting the self-energies in the equations from Eq. (V.2) and Eq. (V.3) (line xx-xx).

The output of the *EnergyRecursion* function is the two rate matrices $\Gamma_{L/R}$ as well as the device Green's function \mathbf{G}_D and as per Eq. (V.9) the matrices needed for transmission have been obtained. As seen in Listing 6 the function *Transmission* simply carries out the matrix product and subsequent trace of the matrices resulting from *EnergyRecursion* and outputs

a range of transmission probabilities which is then plotted against an energy range. Do mind that this is still just 1D in the sense that the transmission only moves in one direction. A plot of the transmission for the simple 1D system (the one in Fig. 5a) can be seen in Fig. 5d.

```

188     s = i
189     xy = (xyz[i, 0], xyz[i, 1])
190     plt.annotate(s, xy)
191     plt.grid(b=True, which='both', axis='both')
192     # savename = 'pointplot.eps'
193     # plt.savefig(savename, bbox_inches='tight')
194     plt.show()
195     return RestL, RestR, L, R, C

```

Listing 6: Code showing how the transmission probabilities are created. Taking in the rate matrices, device Green's function and a range of energies it takes the trace of the matrix product of for a range of energies as in Eq. (V.9) (line xx-xx).

B. Development of transmission to 2D

Lastly the transmission routine needs to be generalised so it can handle transport in two directions. The most convenient approach is to work with five real space unit cells as a starting point. One centre cell, a right and a left cell representing the contacts and then two additional cells on the left and right, representing the rest of the contact region. This would be the minimum amount of cells needed to generalise the transmission. One might have more center cells if the structure changes from one of those cells to the other. First these five unit cells will be defined using already developed tools. Then a big Hamiltonian, including all coordinates from the five cells representing real space are created, again using existing functions. One could call this big Hamiltonian $\mathbf{H}_{\text{Bigreal}}(x_0 y_0 z_0, x_0 y_0 z_0)$. It is a function of two sets of identical coordinates, namely the ones used to create the Hamiltonian itself. This has also been the case for all previous calculations, but the following steps will make it clear why it is explicitly stated for this Hamiltonian. The left/right on-site Hamiltonians and hopping matrices can thus be picked out of $\mathbf{H}_{\text{Bigreal}}(x_0 y_0 z_0, x_0 y_0 z_0)$ as before to get the Green's functions, self energies for transmission in real space, just as in the previous section. However, before the Green's function, self energies and transmission are calculated, the full left/right on-site Hamiltonian as well as their hopping matrices are defined as functions of a variable k which is added as a phase to the hopping matrices. As an example the following is the equation for the full right side Hamiltonian using the right on-side Hamiltonian with its hopping matrices: $\mathbf{H}_R(k) = \mathbf{V}_R e^{ik} + \mathbf{V}_R^\dagger e^{-ik} + \mathbf{h}_R$. This added k -variable phase corresponds to transmission in the direction transverse to that in real space and it has 2π periodic boundary conditions. This means that transport of electrons in the transverse direction is only dependent on a phase. However, one still needs the interaction between the centre on-site Hamiltonian (or device Hamiltonian) and the cells repeated in the transverse direction. Firstly the hopping between $\mathbf{H}_{\text{Bigreal}}(x_0 y_0 z_0, x_0 y_0 z_0)$ and a transversely shifted Hamiltonian is defined as $\mathbf{W} = \mathbf{H}_{\text{Bigtrans}}(x_0 y_0 z_0, x_1 y_1 z_1)$ (Here using \mathbf{W} as not to confuse it with \mathbf{V} which is hopping between cells in real space). The index of 1 in the second set of coordinates in \mathbf{W} is to mark that the original coordinates have been shifted in the transverse direction. With the hopping matrices \mathbf{W} for the transverse direction defined a

Hamiltonian dependent on k -point values can be defined as:

$$\mathbf{H}(k) = \mathbf{h} + \mathbf{W}e^{ik} + \mathbf{W}^\dagger e^{-ik} \quad (\text{V.10})$$

$$= \mathbf{H}_{\text{Bigreal}}(x_0 y_0 z_0, x_0 y_0 z_0) + \mathbf{H}_{\text{Bigtrans}}(x_0 y_0 z_0, x_1 y_1 z_1) e^{ik} + \mathbf{H}_{\text{Bigtrans}}^\dagger(x_0 y_0 z_0, x_1 y_1 z_1) e^{-ik}$$

Now that a Hamiltonian, dependent of a variable k has been defined, it is now possible to get self energies, Green's functions that is k -dependent as well. This means that the transmission will also k -dependent. Thus transmission in 2D is essentially defined by a continuous variable in a range energies in real space and a continuous variable between $-\pi, \pi$ in inverse space (transverse direction). This hereby concludes the all the initial effort to explain the formalism needed to get transmission in a two dimensional material such as NPG. Following is a walk through as to how this last step has been implemented through code programming.

To get the transmission in 2D the function *PeriodicHamiltonian* is nested in a for loop, looping over transverse k-points (See Listing 7 line xx-xx). The function *PeriodicHamiltonian* basically translates the device Hamiltonian in the transverse direction (See Appendix B, Listing 8 for the code piece). Picked out from the resulting Hamiltonian is the left/right device Hamiltonian and left/right hopping matrix (See Listing 7 line xx-xx). Still within the loop the *EnergyRecursion* is used to get the device Greens function, and left/right rate matrices and lastly the transmission is done with the *NPGTransmission* script (Listing 7 line xx). The function *Transmission* basically computes Eq. (V.9) as it stands, it can be seen in Appendix B, Listing 9. All these functions are used per k-point which effectively gives transmission in two dimensions.

```

34 GG = np.zeros((kP.shape[0], En.shape[0]), dtype=complex)
35 q = 0
36 for i in kP:
37     print('-----')
38     print('Calculating for k-point:  {}'.format(i))
39     Ham = PeriodicHamiltonian(xyz, UY, i)
40     HL = Ham[L]
41     HL = HL[:, L]
42     HR = Ham[R]
43     HR = HR[:, R]
44     VL = Ham[L]
45     VL = VL[:, RestL]
46     VR = Ham[RestR]
47     VR = VR[:, R]
48     # gs = GridSpec(2, 2, width_ratios=[1, 2])
49     # a = plt.figure(figsize=(7, 4))
50     # ax1 = plt.subplot(gs[:, 1])
51     # plt.imshow(Ham.real)
52     # ax2 = plt.subplot(gs[0, 0])
53     # plt.imshow(HL.real)
54     # ax3 = plt.subplot(gs[1, 0])
55     # plt.imshow(HR.real)
56     # a.show()
57     # b = plt.figure(figsize=(7, 4))
58     # plt.subplot(121)
59     # plt.imshow(VL.real)

```

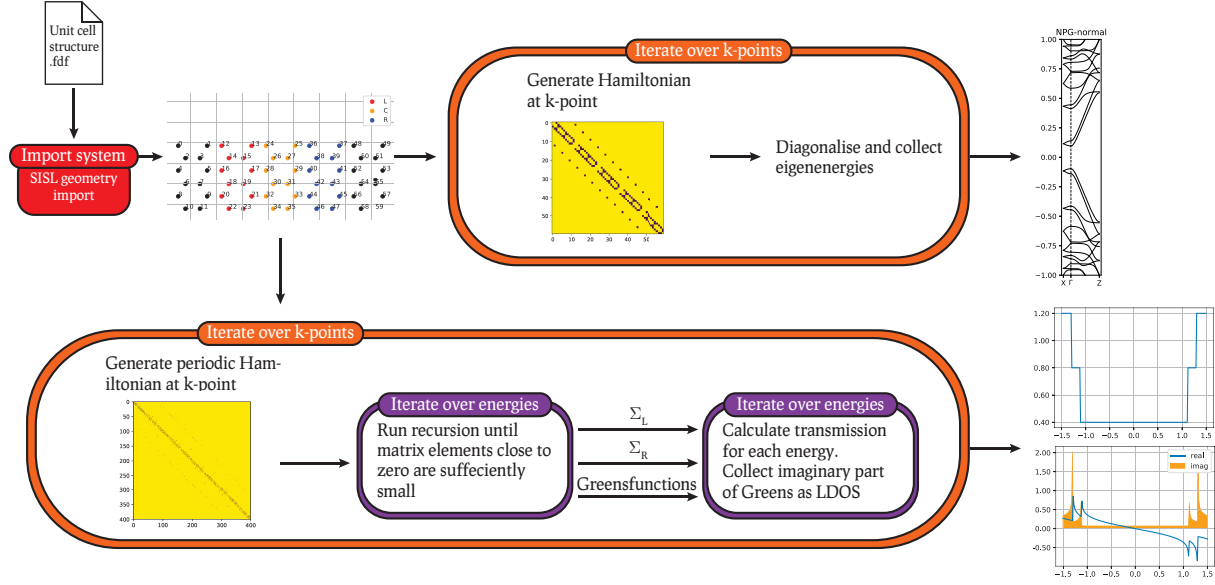


Figure 10: Flowchart depicting the routines run in python. SISL is used to import the geometry. Afterwards the coordinates are either used for band structure plots or for transmission plots. For the band structures, a Hamiltonian at each desired k-point is generated and diagonalised in order to get the eigenenergies. These energies are then plotted. With transmission, a periodic Hamiltonian at various transverse k-points are generated and reduced to self energies in the transport direction (using the recursion algorithm). The self energies and the Green's functions retrieved here are then multiplied as to get the transmission.

```

60  # plt.subplot(122)
61  # plt.imshow(VR.real)
62  # b.show()
63  # input('Press any key to continue')
64
65  GD, GammaL, GammaR = EnergyRecursion(Ham, HL, HR, VL, VR, En, eta)
66
67  G = np.zeros((En.shape[0]), dtype=complex)
68  bar = Bar('Retrieving Greens function ', max=En.shape[0])
69  for i in range(En.shape[0]):
70      G[i] = GD["GD{:d}".format(i)].diagonal()[0]
71      bar.next()
72  bar.finish()

```

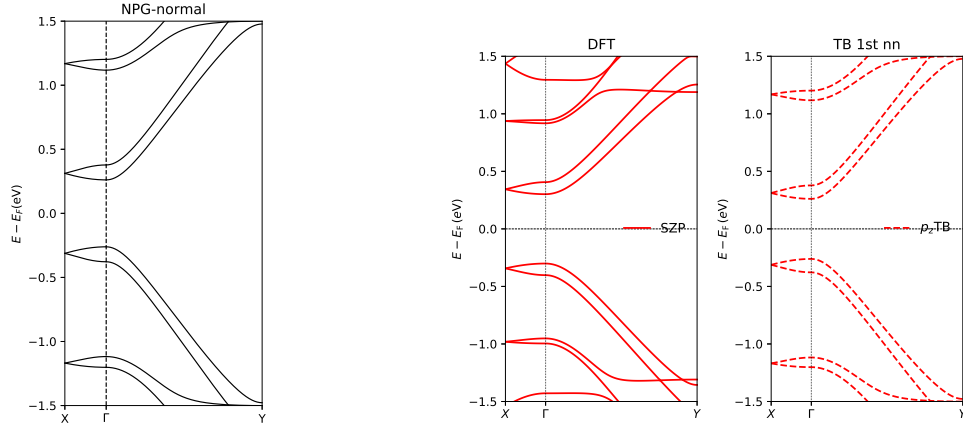
Listing 7: Code piece showing the transmission routine.

Plots for transmission per k-point will be shown for NPG in Section [V D](#).

C. Summary of Methodology

D. Comparing Tight Binding with DFT and TBtrans for transmission and band structure calculations in NPG

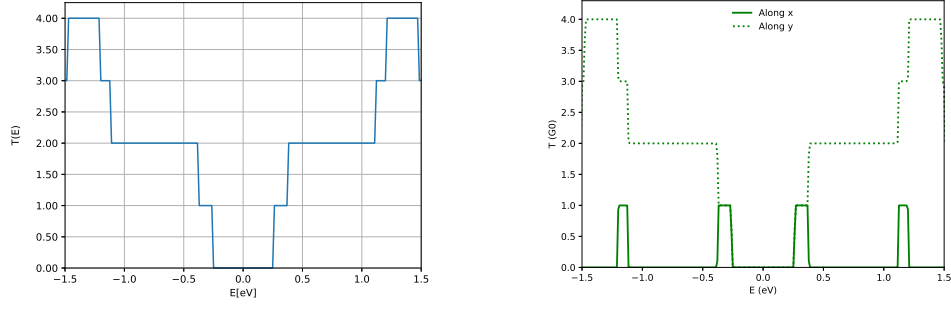
All the scripts necessary for calculation have been developed and they can now be used on a system of NPG. The following results are based on this structure similar to that of Fig. 8. Firstly the band structure obtained using the script described in Section [III B](#) is shown together with band plots obtained from DTF₁ and TBtrans calculations.



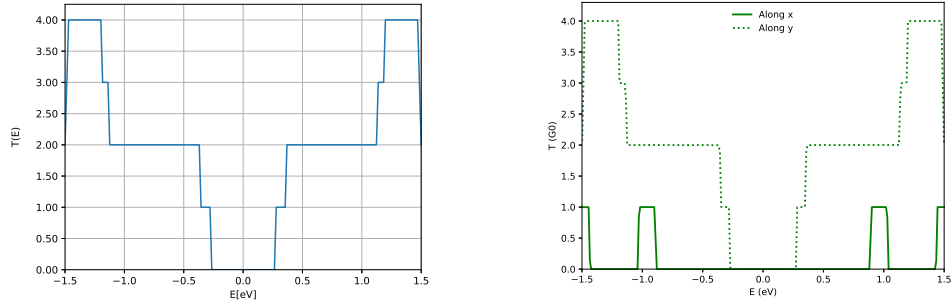
(a) Figure showing the band structure for NPG (b) Figure showing the bands structures obtained with normal bridges obtained with the script described in Section III B from DFT and TBtrans calculations.

Figure 11: Figure showing how the band plots compare for DFT, TBtrans and the developed script.

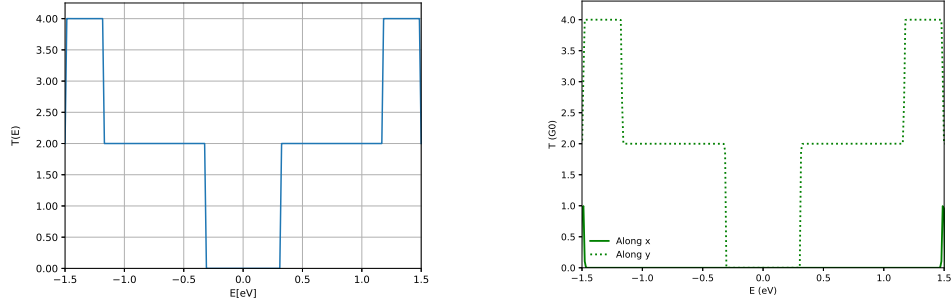
The band plot obtained in Fig. 11a shows almost 1-to-1 correspondence with the plot obtained using TBtrans Fig. 11b (right) and is also very similar to the plot obtained from DFT Fig. 11b (left), proving that the script is capable of creating band structures for NPG-systems. Next is a comparison of the transmission in NPG for different k-points in reciprocal space. The plots are made for transmission through NPG in real space (x-direction) for each three different k-points in the reciprocal space ($\frac{1}{y}$ -direction). The three k-points are $0, \frac{\pi}{2}, \pi$. Additionally an average over these k-points is plotted as well. In Fig. 12 transmission plots obtained with the script described in Section VB is compared with transmission plot obtained through DTF, using the same k-points.



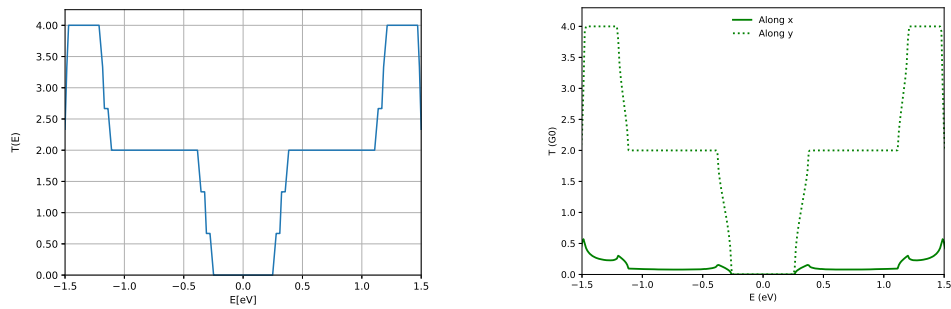
(a) Transverse k -point 0



(b) Transverse k -point $\frac{\pi}{2}$



(c) Transverse k -point π



(d) Average over k -points 0, $\frac{\pi}{2}$, π

Figure 12: Figure showing the comparison between plots of transmission through NPG obtained using the developed scripts (left/blue) and obtained using DFT (right/green).

As one can see in Fig. 12 The plots show very good correspondence with the DFT calculation. Again proving that the scripts developed on the basis of the Tight Binding approximation

can produce valid results, when it comes to band structure and transmission through NPG. This concludes the preliminary work. The tools for calculation of band structures, LDOS and transmission has been successfully developed, using *python*-programming and the Tight Binding approximation. Following will be a range of tests on different NPG systems, using the developed tools.

VI. EXPLORING FUNCTIONALITY OF GNR BRIDGES

In this section a range of tests will be conducted on different NPG structures in order to uncover the effect of chemical modification of the bridges between the Graphene Nano Ribbons (GNR's) in the NPG. From an applied perspective, one of the main motivations is to find out how these bridges can be chemically modified in order to control the current through the material. A recent study[4], submitted for publication in JACS[5], has shown how one could possibly confine current flow to a single GNR channel by modification of bridges between GNR's in NPG utilising *Quantum Interference* (QI) effects (See Fig. 13). This provides a solution to an important requirement in carbon-based nanocircuitry design, namely nano confinement of electron flow. The study was focused on the difference in effect of having *meta* and *para* bridges between GNR's. Meta and para bridges are essentially benzene rings connected in two different ways (See Fig. 14). The meta and para bridges are 'static' cases in the sense that once made through organic synthesis, they are not interchangeable. However, if the bridges are functionalised with oxygen they become sensitive to f.ex. hydrogenation in basic/acidic environments, which tends to affect QI. Thus by hydrogenation it will be possible to tune the electrical properties of the material and make it sensitive to external environments. Studies[6] show that hydrogenation of specific sites on nano meter scale is possible experimentally. By the use of the functions developed in previous sections, this section will try to uncover what happens when oxygen is added to the benzene rings in the meta and para bridges. Subsequently hydrogenation of the oxygen will be tested. Following is a section introducing para and meta NPG in detail.

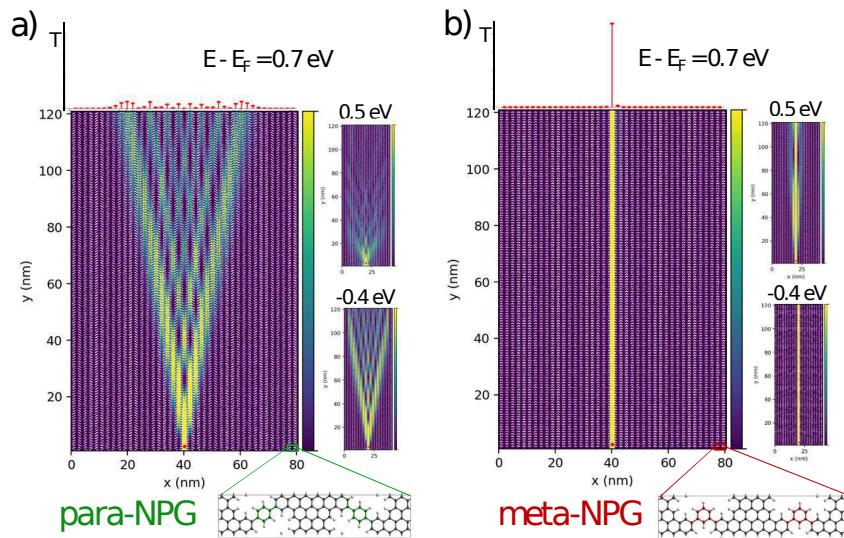


Figure 13: Figure showing the currents through the GNR's in a large piece of NPG. Note how the current is spread across GNR's with the para bridge (a) and confined to a single GNR with meta bridge (b). Used with permission of ISAAC

A. Differences in para and meta bridges

In broad terms the difference in the *meta* and *para* structures lies in the path an electron will travel through the benzene ring to get across the bridge between GNR's in NPG. In the para bridge, the path across the aromatic ring is symmetric and so the electron will pass above or below with equal probability. Since the para bridge has three bonds in each direction across the ring, the path length in the para bridge is the same on each side (See Fig. 14 a)). This will cause constructive QI of the states once the waves meet on the other side of the ring. Which for para NPG causes electronic coupling between the GNR channels. For the meta bridge the way across the aromatic ring is not symmetric in the sense that there is two bonds across the path below and four bonds across on the path above (See Fig. 14 b)). This will cause a shift by half a wavelength between the two paths and thus create destructive QI between waves meeting on the other side of the ring. In the meta NPG, this causes electronic decoupling between GNR channels, allowing for confinement of injected currents in a single GNR channel[4]. In Fig. 15 band plots as well as transmission plots are shown for para and meta NPG. In the band plots the two sets of valence/conduction bands around the fermi level shows separation for para and interference for meta NPG. Looking at the transmission plots directly below one can see there is transmission and thus coupling of the states between the GNR's for para. The area between the two peaks at 0.500 eV and 1.20 eV show transport between the GNR's. In the transmission plot for meta the transmission is confined. In the transmission plot the area between the two peaks is now pretty much 0. This means that states occurs between GNR's are decoupled in meta system. To summarise these results qualitatively: Separations of the bands in the band plots, corresponds to effective coupling of the states between the GNR's. Bands on top of each other, showing QI, corresponds decoupling of the states to a single GNR thus decoupling states between GNR's. In the following sections, band plots will mainly be used to show results. Therefore one should keep in mind how the band structures, qualitatively, relate to transmission. In Appendix B, Fig. 22 a figure obtained from the developed functions with band plots of normal, para and meta NPG can be seen.

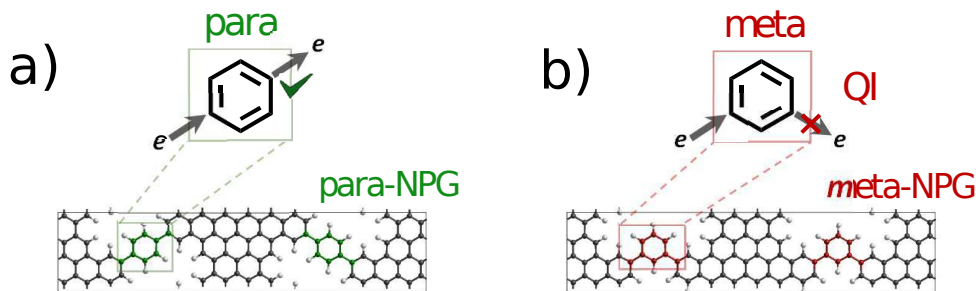


Figure 14: a) showing the para NPG, b) showing the meta NPG. Used with permission from **Isaac**

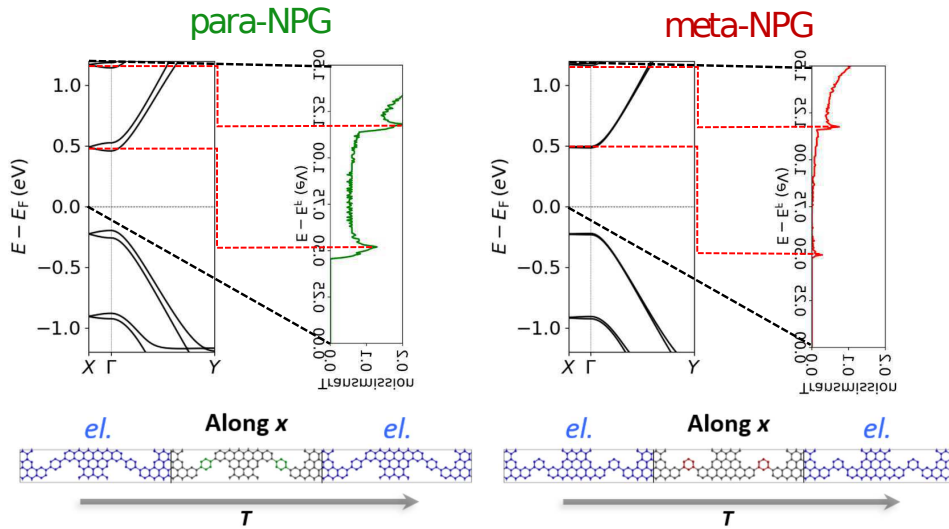


Figure 15: Figure showing band plots and transmission plots for para and meta NPG. In the bottom of each plot is a schematic showing which way the transmission occurs in relation to the NPG. *Used with permission of ISAAC*

B. Tests with modified meta and para NPG

The tests consist of two kinds of chemical modification. Firstly it will be adding oxygen sites to the meta and para NPG (Addition of Oxygen will be simulated by addition of another carbon site to the structure, effectively adding another pi-electron). Secondly simulations of hydrogenation will be done by having added hydroxide groups. By removing hydroxide sites entirely, the aim is to simulate the removal of the extra pi-electron which the oxygen originally provided, but now lost by hydrogenation. These modifications will be carried out separately. The aim is then to show that using the methods developed, based on Tight Binding models, it is possible to reproduce bands structures calculated from DFT. If successful, it will provide a much easier way to understand the effect of the implemented chemical modification compared to the DFT approach. Band plots, as well as some on-site potential maps, calculated with DFT has been provided by *Isaac* for comparison. The geometries, on which the calculations are used, are optimized by DFT. They will also be provided by *ISAAC*.

C. Test 1: Para-O₄-NPG

In the first test is considering the Para-O₄-NPG. The basis structure is para-NPG where 4 oxygen sites are bonded, two on each benzene ring (See Fig. 16a). The first thing to notice is that in Fig. 16b the valence band show QI and thus decouples the GNR's. So in spite having a para bridge, decoupling occurs when oxygen is bonded to the ring. To simulate this practically, the developed method considers the bonded oxygen as carbon atoms. It does not differentiate between the type of atoms only the distance between them. As a baseline the potential of these atoms are thus the same. Moreover, the hydrogen, included in the provided optimised geometries, will be removed before any calculations take place. In Fig. 16c one can see the resulting band structure plot, where calculations have been carried out, using only the provided geometry. No modifications were made. The band plot does not show much resemblance with the one obtained, using DFT. It is pretty much symmetric around the Fermi level and it is hard to make out whether there is coupling or decoupling

between GNR's. This is expected. As seen in the potential map of Fig. 16e, the sites where the oxygen is bonded, have a potential much different from that of the rest of the system (the four dark blue spots). As mentioned, the baseline of the method does not take into account differentiating on-site potentials within a cell. So to compensate for this, the on-site potential of the four bonded oxygen is changed. In Fig. 16d one can see the resulting band plot after the on-site potential of the bonded oxygen has been change to -0.500 eV. The resulting band plot resembles the DFT calculations much more. There is now QI in the valence bands which means decoupling of the GNR's.

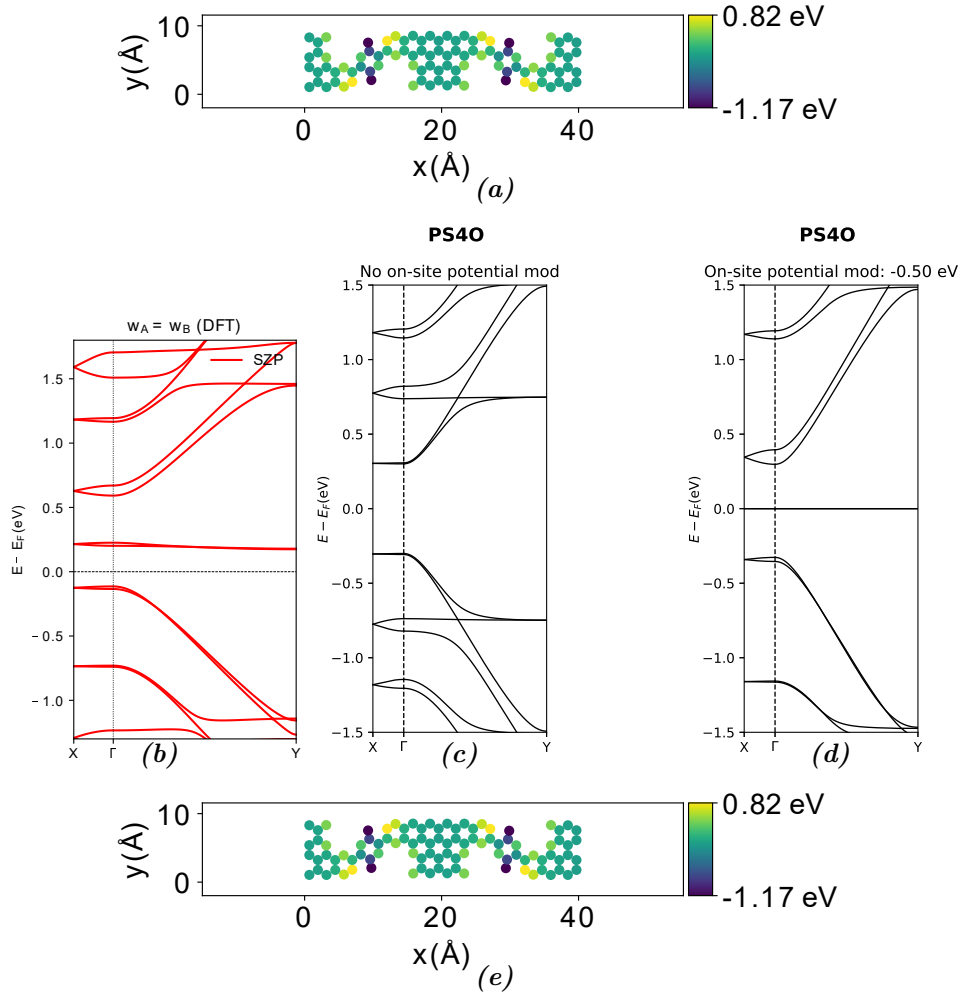


Figure 16: Figure showing the band structure obtained using DFT a), band structures obtained using developed program with no on-site potential mods b) and with the on-site potential changed to -0.500 eV c). Lastly a potential map of the system d)

D. Test 2: P-(OH)₄-NPG

Next test will be with the P-(OH)₄-NPG system. Again the basis structure is para-NPG with added oxygen, but here the aim is to simulate hydrogenation, so therefore the oxygen atoms added will become hydroxide groups (See Appendix B, ??, no. 4). Here the test is to show the difference between removing a OH site entirely (effectively the hydrogen in hydroxide removes the extra pi-electron in oxygen from the system, which can be simulated by removing the atoms entirely) and lowering the on-site potential of the oxygen in the

OH group significantly in relation to the rest of the system. Again the results from DTF is shown in Fig. 17b and following the band plots from the developed scripts (Figs. 17c and 17d and ??). Multiple on-site potentials as well as removal of the specific atomic sites were tested

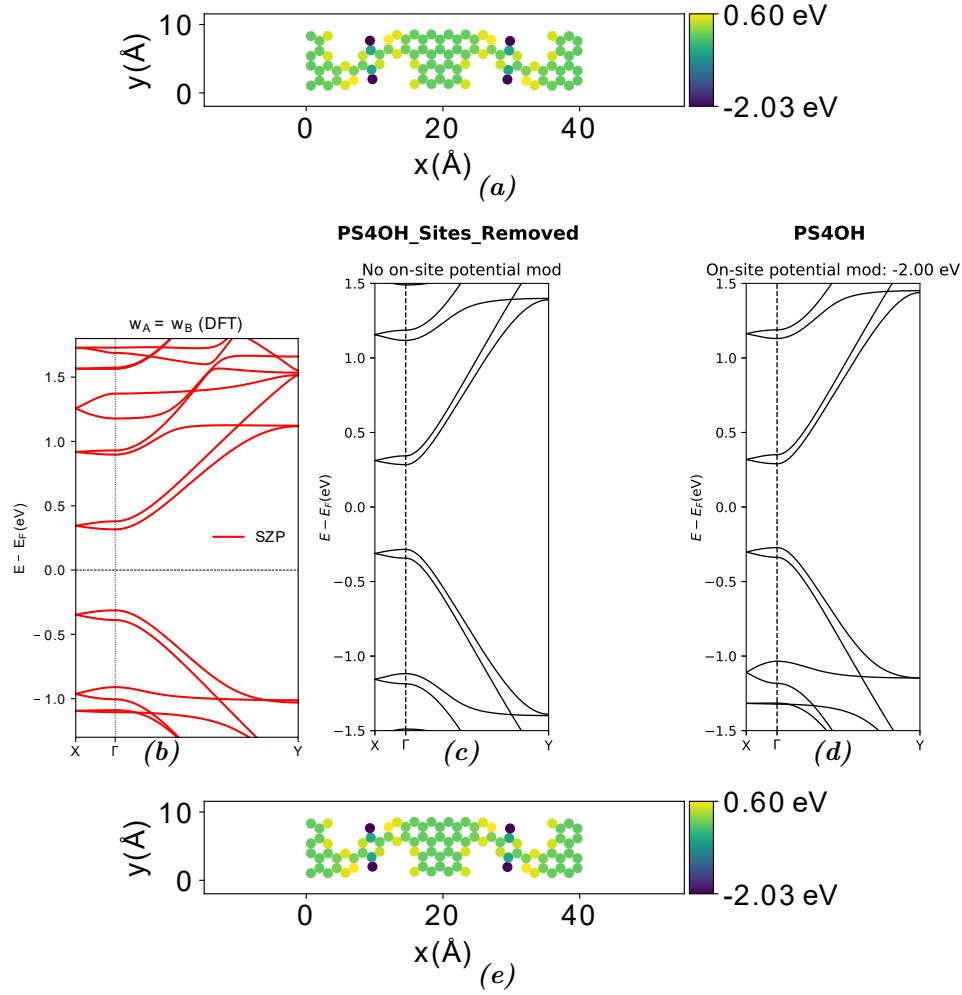


Figure 17: Figure showing the band structures obtained using DFT a), band plot where the added sites have been removed b), a potential map of the system c), band plot where the on-site potential has been changed by -2.50 eV d), and band plot where the on-site potential has been changed by -2.00 eV e).

to see which one came closest to that of the band structures in Fig. 17b. The removal was done by removing specific coordinates in the given files before it was run through the script. As seen in Fig. 17c the effect of removing the sites gives a plot, somewhat in agreement with Fig. 17b. However the lowest and highest bands does not show. The two other plots in ?? and Fig. 17d show how gradually changing the on-site potential gets better and better agreement with DFT. A on-site potential of -2.50 eV proved to be a bit too high, though still showing good agreement. Lowering the potential to -2.00 eV which is the value similar to that given by the lowest potential in the potential map Fig. 17e, yielded a result that is pretty much spot on, considering the valence bands, when compared with DFT.

E. Test 3: Meta-NPG with oxygen added symmetrically

This test is done in the same manner as Section VI B. The only difference being that the system is different. Here the basic system is the meta-NPG and two oxygen have been

added symmetrically with respect to the periodically repeating GNR's (See Appendix B, ??, no. 1). As seen in Fig. 18 three band plots have been produced to compare with the fourth which is from DFT calculations. In general it spreading of the bands is observed even though the basic structure is meta. Meta should according to the results mentioned in Section VI A confine the transmission but this is not what is seen in these results. The explanation is that the added oxygen provides an extra pi-electron to the system, thus allowing for some transmission between GNR's. In Fig. 18c the bands at the fermi level

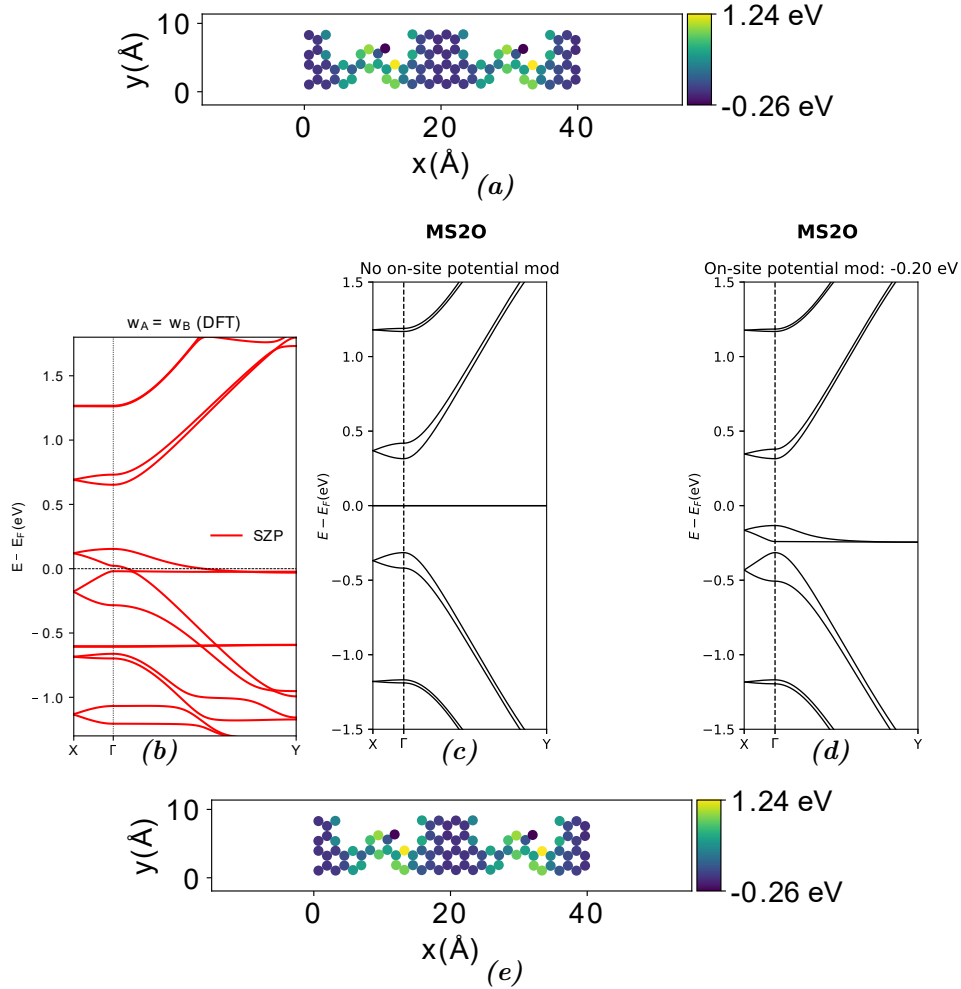


Figure 18: Figure showing the band structure obtained using DFT a), band structures obtained using developed program with no on-site potential mods b) and with the on-site potential changed to -0.200 eV c). Lastly a potential map of the system d)

show QI in all directions. This is not in good agreement with the DFT plot. The DFT plot seem to have this straight band located further down around -0.580 eV. However, is the on-site potential of the oxygen is changed, the match with DFT is much better. In Fig. 18d there is spreading of the bands in the centre like the DFT plot. The spreading of the next set of bands is also larger, showing good agreement with DFT.

F. Test 4: Simulating hydrogenation of meta-NPG with symmetrically added oxygen

The fourth and final test will be with the same approach as Section VID only here the hydrogenation is of the meta-NPG with oxygen added symmetrically (See Appendix B, ??, no. 2). In Fig. 19 the result of the test are shown. Now that the oxygens have hydrogenated the extra pi-electron provided is taken by hydrogen. This means that the system is similar to the regular meta system discussed in Section VIA. One can see QI in all three plots in Fig. 19

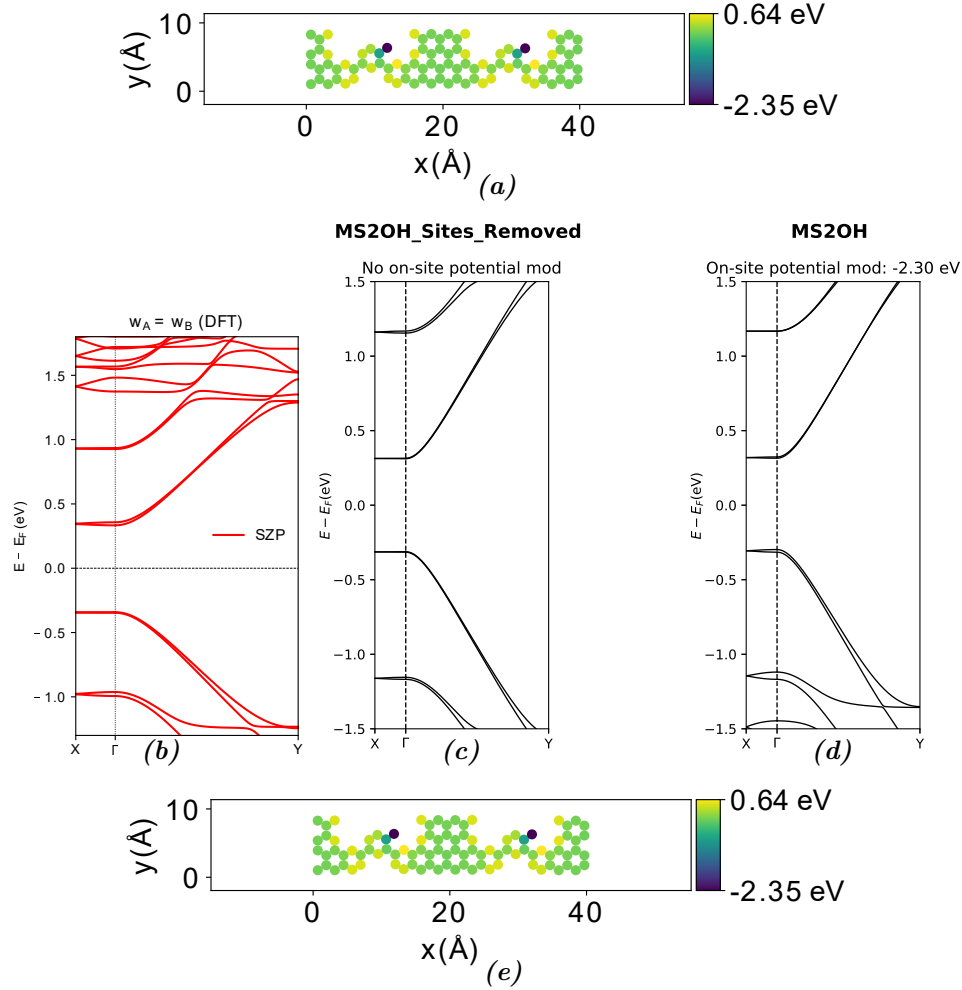


Figure 19: Figure showing the band structures obtained using DFT a), band plot where the added sites have been removed b), a potential map of the system c), band plot where the on-site potential has been changed by -1.50 eV d), and band plot where the on-site potential has been changed by -2.30 eV e).

obtained from the developed scripts. And the all show relatively good agreement with the DFT plot. However, the best result came from tweaking the on-site potential to -2.30 eV as seen in Fig. 19d. Comparing the plots with the regular meta system from Section VIA indeed show good agreement as well.

G. Test summary

For the para systems, the added oxygen introduced some QI to the system. It was possible to show that the developed program could reproduce the results obtained from DFT. This

did require some adjustment to the on-site potential of the added oxygen. By hydrogenation of the oxygen it was shown that the system again returned to spreading of the bands. Again by adjusting the on-site potential it was possible to obtain results very close to the DFT calculation. The results are also comparable with the ones mentioned in Section [VIA](#). This shows that hydrogenation of oxygen can change the system to resemble regular para-NPG, even if it has oxygens added. For the meta systems it was shown the it is possible to manipulate the system. First by having some transmission between GNR's by adding in oxygen as in Section [VIE](#). Then by hydrogenating the system inSection [VIF](#), getting QI and thus confinement. This turned out to be similar to un-modified meta NPG. All in all these results give a better, intuitive understanding of what happens with the electron transport in NPG. This is because all manipulations can be followed with ease and the results are easy to interpret.

VII. DISCUSSION

VIII. CONCLUSION

ACKNOWLEDGMENTS

The authors would like to thank...

-
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Appendices

A. THE BENZENE MOLECULE

As an example the Hamiltonian of benzene is considered. In Fig. 20 one can see the indices of a benzene molecule. Remember that $\langle \phi_\pi(1) | \hat{H} | \phi_\pi(1) \rangle = 0$ and Eq. (II.2), the Hamiltonian reads:

$$\mathbf{H} = V_{pp\pi} \begin{matrix} & 1 & 2 & 3 & 4 & 5 & 6 \\ \begin{matrix} 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \end{matrix} & \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 0 & 1 \\ 1 & 0 & 0 & 0 & 1 & 0 \end{pmatrix} \end{matrix} \quad (\text{A.1})$$

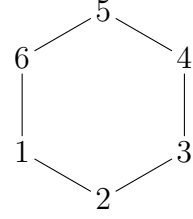


Figure 20: Indices of a benzene molecule

As a helping aid, Eq. (A.1) shows the atomic indices of the atom on the top and to the left of the matrix. This will give an understanding of how to work with such matrices. The structure of the benzene molecule is rotationally symmetric and rotating the indices one sixth must yield the same Hamiltonian. Consider the energy eigenvector:

$$\phi = (c_1 \ c_2 \ c_3 \ c_4 \ c_5 \ c_6) \quad (\text{A.2})$$

There must exist an operator that rotates the indices as such:

$$C_6 \phi = (c_2 \ c_3 \ c_4 \ c_5 \ c_6 \ c_1) \quad (\text{A.3})$$

The rotated Hamiltonian is the same, and thus C_6 and \mathbf{H} commute. The rotated vector must be an eigenvector with the same energy and it should be possible to find simultaneous eigenvectors to C_6 and \mathbf{H} .

$$C_6 \phi = (c_2 \ c_3 \ c_4 \ c_5 \ c_6 \ c_1) = \lambda (c_1 \ c_2 \ c_3 \ c_4 \ c_5 \ c_6) \quad (\text{A.4})$$

This operator C_6 is represented with the matrix:

$$\mathbf{C}_6 = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad (\text{A.5})$$

It can quickly be shown that the normalised eigenvectors to C_6 are

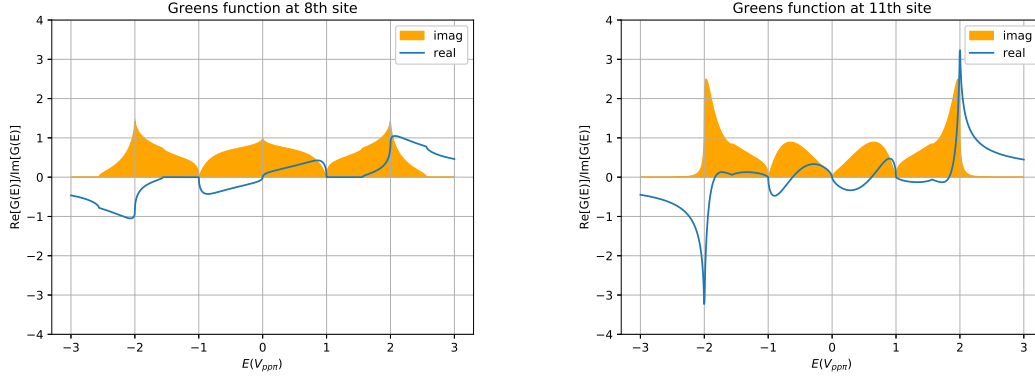
$$\phi_n = \frac{1}{\sqrt{6}} (\lambda_n^0 \ \lambda_n^1 \ \lambda_n^2 \ \lambda_n^3 \ \lambda_n^4 \ \lambda_n^5), \quad \lambda_n = \exp\{-i2\pi n/6\}, \quad n=0,1,2,3,4,5 \quad (\text{A.6})$$

These eigenvectors are also eigenvectors for \mathbf{H} with the eigenvalues:

$$\varepsilon_n = \lambda_n + \lambda_{n-1} = 2\cos n\pi/3 \quad (\text{A.7})$$

Thus thanks to the rotational symmetry it was possible to find the eigenvectors and eigenenergies for the Hamiltonian.

B. ADDITIONAL FIGURES



(a) Figure showing a plot of the Green's function at the 8th site (b) Figure showing a plot of the Green's function at the 11th site

Figure 21: Two plots showing how the Green's function changes as the site is changed. The 8th and 11th sites are corresponding to atoms of those indices (8, 11) in Fig. 5a. Note how the LDOS changes (imaginary part) for the different sites.

```

245     return T
246
247
248 def PeriodicHamiltonian(xyz, UY, i):
249     h, p = Onsite(xyz=xyz, Vppi=-1, f=1)
250     V = Hop(xyz=xyz, xyz1=xyz + np.array([0, UY, 0]), Vppi=-1)
251     # plt.imshow(V.real)
252     # plt.show()

```

Listing 8: Code piece showing how the periodic Hamiltonian, shifted in the transverse direction i created using the given unit vector in the y direction.

```

234     return GD, GammaL, GammaR
235
236
237 def Transmission(GammaL, GammaR, GD, En):
238     T = np.zeros(En.shape[0], dtype=complex)
239     bar = Bar('Calculating Transmission ', max=En.shape[0])
240     for i in range(En.shape[0]):
241         T[i] = np.trace((GammaR["GammaR{:d}"].format(i)] @ GD["GD{:d}"].format(
242             i)] @ GammaL["GammaL{:d}"].format(i)] @ GD["GD{:d}"].format(i)].conj().transpose()).tod

```

Listing 9: Code piece showing how the transmission per energy point, using equation Eq. (V.9)

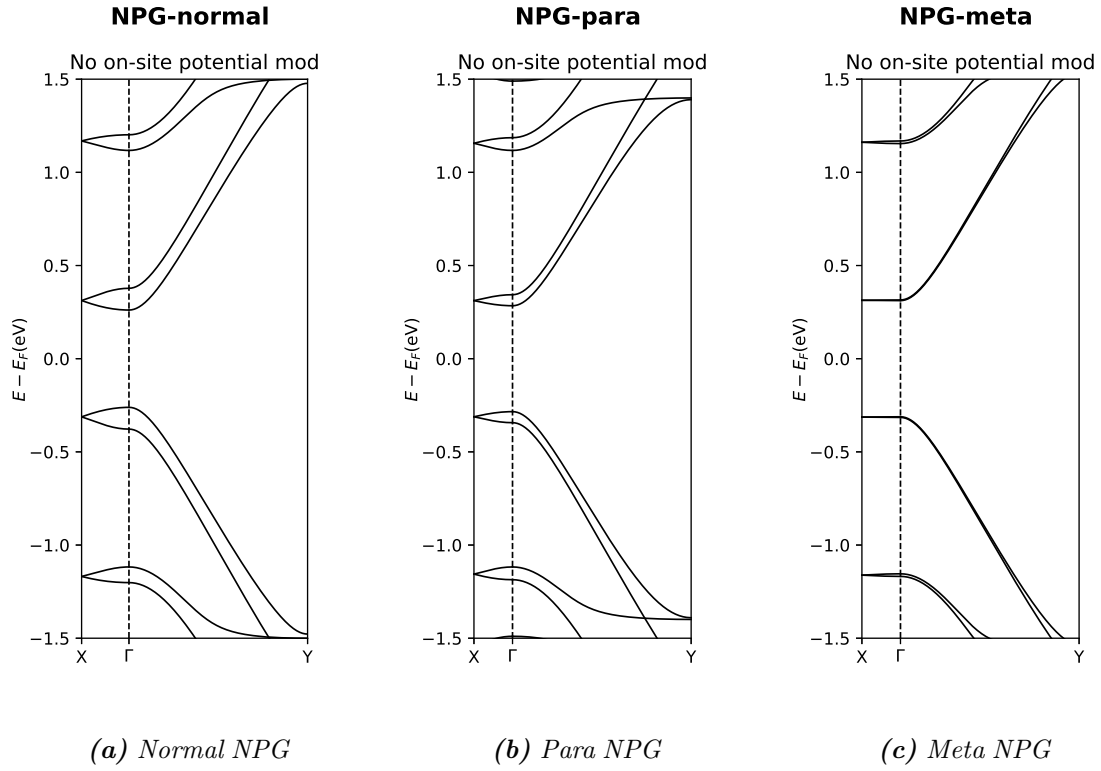


Figure 22: Plot showing band structures in the energy range -1.50 eV to 1.50 eV for normal, para and meta NPG. The are plotted between symmetry points X and Y with respect to the origin Γ