It was once purported that biological systems were far too ‘warm and wet’ to support quantum phenomena mainly owing to thermal effects disrupting quantum coherence. However, recent experimental results and theoretical analyses have shown that thermal energy may assist, rather than disrupt, quantum coherent transport, especially in the ‘dry’ hydrophobic interiors of biomolecules. Specifically, evidence has been accumulating for the necessary involvement of quantum coherent energy transfer between uniquely arranged chromophores in light harvesting photosynthetic complexes. The ‘tubulin’ subunit proteins, which comprise microtubules, also possess a distinct architecture of chromophores, namely aromatic amino acids, including tryptophan. The geometry and dipolar properties of these aromatics are similar to those found in photosynthetic units indicating that tubulin may support coherent energy transfer. Tubulin aggregated into microtubule geometric lattices may support such energy transfer, which could be important for biological signalling and communication essential to living processes. Here, we perform a computational investigation of energy transfer between chromophoric amino acids in tubulin via dipole excitations coupled to the surrounding thermal environment. We present the spatial structure and energetic properties of the tryptophan residues in the microtubule constituent protein tubulin. Plausibility arguments for the conditions favouring a quantum mechanism of signal propagation along a microtubule are provided. Overall, we find that coherent energy transfer in tubulin and microtubules is biologically feasible.

1. Introduction

Since Schrödinger asked ‘what is life?’ [1], a possible link between the ‘weird’ world of quantum phenomena and biology has been hypothesized. It has often been argued that living systems are too ‘warm and wet’ to support quantum effects; however, recent research suggests this is not necessarily always the case. From quantum coherent transport in photosynthesis and magnetoreception in birds to quantum olfaction [2] and single-photon effects in vision [3], the field of quantum biology is leaping into the mainstream. This leads us to inquire, where else might the effects of quantum biology be found?

Without a doubt, the standard bearer for the emergence of quantum biology has been the long-lived electronic quantum coherence found in the light harvesting antennae used in photosynthesis. In 2007, Engel et al. [4] directly observed quantum oscillations caused by electronic coherence at 77 K in the Fenna–Matthews–Olsen (FMO) photosynthetic light-harvesting complex (LHC), a temperature pushing the ‘warm’ limit for quantum processes, catapulting this field into the spotlight [4]. This limit was further pushed to 277 K, nearing physiological temperature, and effectively ruling out the ‘warm and wet’ limit for quantum phenomena in biology [5]. Furthermore, these coherent...
effects do not seem to be restricted to the FMO complex alone, and have been shown for LHCs in plants (LHCl) [6–8], bacteria (LH2) [9,10] and phycobiliproteins [11,12]. The theoretical basis of this coherent energy transfer is the photo-induced interaction of transition dipoles in chlorophyll molecules. The unique chromophoric nature of chlorophyll and the elegant geometrical arrangement of these pigments in the LHCs of plants and bacteria allow for photon energy to be efficiently captured and funnelled from the environment to reaction centres. This biological light harvesting critically depends on the quantum mechanism through which photon-induced excitations hop between chromophores [13]. An initially excited donor chromophore can convey its electronic energy to an acceptor chromophore via electrodynamic coupling of their transition electric dipole moments owing to the close correspondence, or ‘resonance’, between their energy levels. This resonance energy transfer (RET), which was originally pioneered by Förster [14] and is more specifically termed FRET, remains the dominant theory applied in electronic energy transport [15,16]. However, this process is not unique to photosynthesis. J-aggregates (aka Scheibe aggregates), collections of dyes, are an artificial form of LHC capable of capturing and manipulating photon energy [17,18]. At the root, this phenomenon is attributable to the optimal packing of chromophores with a significant transition dipole.

Interestingly, tubulin, the microtubule constituent protein, possesses a network of chromophoric tryptophan (Trp) amino acids (figure 1). The fluorescence quantum yield for pure Trp is 0.14, and the experimentally observed yield for wild-type tubulin is 0.06 at room temperature [19]. These are comparable to the room temperature fluorescence quantum yields of bacteriochlorophyll of 0.18, and the yield for LH1 of 0.08 and LH2 of 0.10 [20], respectively. The ‘red edge effect’ has also been observed in tubulin [21] indicating Trp to Trp energy transfer [22]. Thus, these may serve as potential conduction pathways in tubulin and microtubules [23]. Could these aromatic chromophores support coherent quantum effects within tubulin? As persistent electronic coherences may be a general property of any system of compact nearly static chromophores coupled to the environment [24], we investigate the biological feasibility of coherent energy transfer in the tubulin dimer. Via a combination of homology modelling, molecular dynamics (MD) simulations, quantum chemistry and optical biophysics, we apply structure-based simulations similar to current studies of the FMO complex [25,26], and larger LHCs [27] to probe potential energy transfer mechanisms in tubulin, and by extension microtubules.

2. Results and discussion

The dominant spatial distribution and orientation of the Trp residues in tubulin after 8 ns of molecular dynamics simulation are shown in figure 1a. Between nearest-neighbours, spacing ranges between 11.4 and 41.6 Å (figure 1b). Importantly, this range is comparable to the distances between the bilin chromophores in cryptophyte marine algae, which has been shown to support quantum-coherent transfer of electronic excitation [11].

This spatial range, i.e. the average separation between neighbouring dipoles, is considered larger than the extension of the Trp transition densities and, so the point-dipole (PD) approximation was used to determine the inter-Trp excitonic couplings. In calculating the excitonic interaction coefficients, the choice of the dielectric constant value, and the method chosen for screening and local field effects is no trivial matter [28]. Typically, effective protein dielectric constant values are chosen between 2 and 4; however, experimental measures of the dielectric coefficients in protein hydrophobic pockets indicate this value is well above this range, arguing against this practice [29]. The experimentally measured tubulin optical dielectric value of 8.41 falls well outside this range [30], and is expected to have a significant impact on coupling strengths.

In the Förster approximation, accounting only for electrostatic screening effects owing to the polarizable medium being present between the dipoles, the dipolar couplings are small indicating little to no interaction between Trps, regardless of the dielectric value chosen. This is consistent with previous estimates of Förster dipole–dipole energy transfer between Trps in tubulin [19]. This study also calculates negligible intramolecular Trp–Trp energy transfer efficiencies in tubulin, however these are based on an estimated dielectric constant of 2 and an assumed spectral overlap integral for
N-acetyl-L-tryptophanamide in tris-(hydroxymethyl)amino-
methane buffer at pH 7.8. As Trp is highly sensitive to its
local environment [31], these results are seemingly inaccurate
as the calculation does not accurately reflect the protein environ-
ment. However, accounting for electrostatic screening effects of
local environment [31], these results are seemingly inaccurate
and Trps 2 and 3, owing to the close site energies between
these pigments and their relatively large couplings.

While the coupling strengths become increasingly non-
egligible as the dielectric constant value increases above 2, the
general line shape of the simulated spectra does not align well
with experiment for values between 2 and 4. This is most promi-
nently seen in the circular dichroism (CD) spectra, and is not
accounted for by simple shifts in \( E_0 \) alone (figure 2). However,
when the experimentally measured optical dielectric value of
tubulin is used the simulated spectra align well with experi-
mental values (figure 2). This supports the use of the experimentally
measured dielectric value over values between 2 and 4.

Population dynamics calculations from the Haken &
Strobl [33] method were applied to the Hamiltonian in
table 1 for initial excitations occurring on each of the eight
Trp residues (figure 3). It was determined that coherent beat-
ing last for approximately 600 fs with a pure dephasing rate
of 50 cm\(^{-1}\), when the excitation starts at Trps 2, 3, 4 or 7, and
for less than 300 fs when starting at Trp 6 or 8. Excitations
starting at Trp 1 or 5 did not produce any beating effects.
When starting at Trp 2 or 3, the excitation can be seen to
spread to Trp 4 and 7 reaching close to the equal population
distribution of 0.125 within approximately 2 ps. Negligible
exciton populations in the remaining Trps are observed in
this time frame. When starting at Trp 4 or 7, the same effect
is observed for Trps 2 and 3 with additional increases in exciton

delocalization of excited state energies is relatively small.
Only for the exciton states at 36 054, 36 176 and 36 300 cm\(^{-1}\)
is there a significant delocalization over more than one pig-
ment, with meaningful contributions between Trps 4 and 7,
and Trps 2 and 3, owing to the close site energies between
these pigments and their relatively large couplings.

Table 1. Site energies (diagonal, shown in italics are with respect to 35 888 cm\(^{-1}\)) and interaction energies in units of cm\(^{-1}\).

<table>
<thead>
<tr>
<th>Trp</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
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<td>-13</td>
<td>0</td>
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<td>-1</td>
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<td>2</td>
<td>0</td>
<td>388</td>
<td>-41</td>
<td>4</td>
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<td>1</td>
<td>-4</td>
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<td>-13</td>
<td>-41</td>
<td>342</td>
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<td>4</td>
<td>2</td>
<td>207</td>
<td>-4</td>
<td>6</td>
<td>-59</td>
<td>-1</td>
</tr>
<tr>
<td>5</td>
<td>-2</td>
<td>1</td>
<td>0</td>
<td>-4</td>
<td>57</td>
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<td>11</td>
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<td>1</td>
<td>0</td>
<td>6</td>
<td>21</td>
<td>102</td>
<td>5</td>
</tr>
<tr>
<td>7</td>
<td>5</td>
<td>-4</td>
<td>-6</td>
<td>-59</td>
<td>2</td>
<td>5</td>
<td>248</td>
<td>3</td>
</tr>
<tr>
<td>8</td>
<td>-1</td>
<td>1</td>
<td>1</td>
<td>-1</td>
<td>11</td>
<td>-51</td>
<td>3</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 2. Excited state energies (cm\(^{-1}\)), and coefficients of the eigenvectors resulting from diagonalization of the Hamiltonian in table 1. Coefficients larger than 50% are shown in italics.

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>35 863</td>
<td>0.04</td>
<td>0.00</td>
<td>0.00</td>
<td>-0.02</td>
<td>-0.22</td>
<td>0.40</td>
<td>-0.02</td>
<td>0.89</td>
</tr>
<tr>
<td>35 888</td>
<td>-1.00</td>
<td>0.00</td>
<td>-0.04</td>
<td>0.01</td>
<td>0.05</td>
<td>0.01</td>
<td>0.02</td>
<td>0.02</td>
</tr>
<tr>
<td>35 946</td>
<td>-0.04</td>
<td>0.00</td>
<td>0.00</td>
<td>0.03</td>
<td>0.95</td>
<td>0.12</td>
<td>0.00</td>
<td>0.28</td>
</tr>
<tr>
<td>36 014</td>
<td>0.01</td>
<td>0.00</td>
<td>0.00</td>
<td>0.12</td>
<td>-0.22</td>
<td>-0.90</td>
<td>0.09</td>
<td>0.35</td>
</tr>
<tr>
<td>36 054</td>
<td>0.02</td>
<td>0.00</td>
<td>0.01</td>
<td>0.81</td>
<td>0.01</td>
<td>0.15</td>
<td>0.57</td>
<td>0.04</td>
</tr>
<tr>
<td>36 176</td>
<td>0.00</td>
<td>-0.14</td>
<td>0.21</td>
<td>0.56</td>
<td>0.02</td>
<td>0.00</td>
<td>0.79</td>
<td>-0.01</td>
</tr>
<tr>
<td>36 208</td>
<td>0.04</td>
<td>-0.48</td>
<td>-0.84</td>
<td>-0.14</td>
<td>0.00</td>
<td>0.00</td>
<td>0.21</td>
<td>0.00</td>
</tr>
<tr>
<td>36 300</td>
<td>-0.02</td>
<td>-0.86</td>
<td>0.50</td>
<td>-0.01</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
</tbody>
</table>
Additionally, the unique cylindrical lattice symmetries found coherent tunnelling and incoherent relaxation/excitation of energy along the protofilament length via a combination of the interdimer spacing of Trps is uninterrupted (figure 4), it most likely alters this energy landscape. However, tubulin dimer. Stacking tubulin dimers end to end in a microtubule would most likely alter this energy landscape. Generalized Förster effects [36], induced by geometrical symmetries, can enhance the exciton diffusion length along cylindrically symmetric structures [37], similar to the helical arrangement of tubulin, and its chromophores, in microtubules.

Is this effect unique to tubulin and microtubules? Trp is a ubiquitous amino acid found in almost all proteins in low abundance, and FRET between Trp residues and other fluorophores is a technique commonly used to probe protein structure and dynamics. In most cases, this RET is restricted to a single isolated protein, or between two adjacent interacting proteins or molecules. Crystalized globular proteins have the potential to efficiently transfer energy between Trp residues [38], yet these are rarely, if ever, found in biology. Protein polymers, such as the cell cytoskeleton, on the other hand, are pervasive in biology, offering candidate structures for this type of energy transmission. While crystal structures for the majority of cytoskeletal components do not currently exist, comparison of their amino acid sequences reveals that the majority of intermediate filaments have a Trp abundance less than a third of that found in tubulin (table 3) suggesting unfavourable conditions for RET. Only actin and synemin possess comparable densities, suggesting that polymers of these molecules could support RET similar to that in tubulin and microtubules. Although the crystal structure of actin is available and reveals 4 Trp per subunit with intramolecular separations ranging between 10 and 23 Å, the intermolecular distances between these Trp clusters is more than 40 Å (figure 4) suggesting unfavourable conditions for RET within a microfilament.

Whether coherent energy transfer in tubulin and microtubules has a biological role remains open. Such rapid signalling through Trp conduction pathways may coordinate the complex organization of the microtubule cytoskeleton required for the tasks of cell division, motor protein trafficking and motility. Microtubules have been shown to reorganize in a dose-dependent manner after exposure to UV light [39–42], with the greatest effect being observed around 280 nm [42]. Feasible mechanisms for these changes include the reduction of disulfide or peptide bonds induced by photoexcitation of Trp groups [43–46], or subtle protein structural changes owing to photo-induced alterations in Trp flexibility [46]. Such a signalling mechanism may explain the observed apparent UV mediated cell-to-cell influence on cell division [47]. Only further investigation, both theoretically and experimentally, will tell.

Thus, we conclude that, based on this initial analysis, the unique Trp network within an individual tubulin dimer can possess significant dipolar couplings capable of supporting quantum coherent beating effects similar to those observed in the FMO photosynthetic complex [4,5], LHCI [7,8], LH2 [9,10] and phycobiliprotein LHCs [11,12]. Furthermore, our results suggest that this network may support coherent energy transfer at physiological temperature between clusters of Trps in tubulin, and microtubule structures. One of the main objectives of this paper is to stimulate future experimental work in this area. While this is purely a computational prediction it supports the continued investigation of coherent energy transfer mechanisms in tubulin and microtubule lattices. Our predictions are experimentally feasible to verify employing the same methods as those used in the case of photosynthetic complexes.
3. Methods

Here, we give a brief summary of the computational procedures yielding site energies, excitonic couplings, optical spectra and time evolution of exciton populations. All data will be made available on request.

3.1. Molecular dynamics simulation/dominant tryptophan confirmation

MD simulations were performed based on previous methods [48,49], using NAMD [50]. Coordinates for the αβ-tubulin dimer at 3.5 Å, GDP, GTP and magnesium ion are from the Brookhaven National Laboratory Protein Data Bank [51] entry 1JFF [52] and PDB2PQR 1.7 [53] was used to generate per-atom charge and radius, at pH 7.0 using PROPKA [54,55], and the AMBER [56] force field. Swiss-PdbViewer v. 4.0 [57] was used to model the missing residues in the crystal structure (α-tubulin: 1, 35–60, 440–451, β-tubulin: 1, 438–455). GDP and GTP were modelled for use by the AMBER 94/99 force field by Meagher et al. [58]. PTRAJ, using the AMBER99SB force field [59] from AMBER 10 [56], was used to neutralize the system, add counterions to reproduce physiological ionic concentrations, and add a TIP3P water cube buffer of 25 Å (63 283 molecules of water). After minimization and heating to 310 K, equilibration occurred for 519 ps while gradually releasing constraints on backbone atoms. Then, using periodic boundary conditions, a 17 ns simulation occurred where atomic coordinates were saved from the trajectory every 2 ps.

Figure 3. Time evolution of the exciton population of each tryptophan in tubulin via the Haken–Strobl model. Initial pure states are set as (a) Trp1: αW21, (b) Trp2: αW346, (c) Trp3: αW388, (d) Trp4: αW407, (e) Trp5: βW21, (f) Trp6: βW101, (g) Trp7: βW344 and (h) Trp8: βW397. (Online version in colour.)
PTRAJ was used to analyse the 17 ns trajectory for root mean square deviation (RMSD) of the backbone of non-C-terminus residues of both alpha- and beta-tubulin, as well as the beta-factor of all residues. The RMSD was found to stabilize after approximately 8 ns. The final 8 ns of the total trajectory was chosen for further analysis. The GROMACS program g_cluster [60] was used to cluster the Trp atom positions of all frames via single linkage with a cut-off of 0.5 Å. The middle structure of the largest cluster was taken as the dominant conformation for the Trp residues.

### 3.2. Vertical excitation energies for tryptophan/site energy calculations

Site energies were derived from structure-based calculations of the free energy change of the protein–pigment complex (PPC) that occurs when the ground state charge density of Trp is shifted to the first excited state, analogous to methods used for the FMO complex [26,61,62].

Quantum chemical calculations of the pigments in vacuo yield the charge distributions of the S0 and 1La state transition energies differing the orientations of the Trps. Trp side chains were each isolated from the dominant conformation (described above) and capped with a hydrogen atom to complete the valence. *Ab initio* geometry optimizations at the ground state were performed using density functional theory at the B3LYP/6-311G(d,p) [63] level. Quantum chemical calculations of the eight lowest singly excited vertical transition energies of Trp were done using time-dependent density functional theory [64,65] at the B3LYP/6-311+G(d,p) [63] level. All calculations were performed using ORCA v. 2.8 (http://www.mpq.de/forum/).

The vertical transition energies for the 1La state of the Trp side chains were found to be comparable to previous work using similar methods [66], however, such as these results our values were found to be lower than experimentally determined values [66,67]. To align with experiment (38 473 cm⁻¹), a scaling factor of 1.02 was applied to the calculated values. The relative quantum correction, ΔE_{opt}, to the site energy was taken as the difference between the scaled and the experimental values.

The second part of the site energy calculation results in a contribution ΔE_{coul} owing to classical electrostatic interaction between the charge distributions of the S0 and 1La states with the protein environment. Using the charge density coupling [61,62] method, the site energy shift of the nth Trp is calculated from the Coulomb interaction of the difference of the S0 and 1La state partial charges ΔQ_{S0}^{(m)} and ΔQ_{1La}^{(m)}, obtained from the Löwdin atomic point charges in the above quantum chemical calculations, with the remaining background charges of the protein q_{bg}.

$$\Delta E_{coul} = \frac{1}{\epsilon_{opt}} \sum_{j \neq m} \sum_{i} \left( \frac{\Delta Q_{j}^{(m)} \cdot \Delta Q_{i}^{(m)}}{\epsilon_{m} \epsilon_{j}} - \frac{\Delta Q_{j}^{(m)} \cdot q_{i}^{(bg)}}{\epsilon_{m}} \right)$$

where N is the number of partial charges of the nth Trp side chain, K is the total number of background partial charges (including other Trp residues), and |p_{i}^{(m)} - r_{j}^{(bg)}| is the distance between the ith difference partial charge of the nth pigment and the jth partial charge of the background. Background charges were taken from the AMBER99SB force field [59]. Here, we use the measured high-frequency dielectric constant ε = 8.41 [30].

The site energy for the nth Trp is thus given as

$$E_{n} = E_{0} + \Delta E_{coul} + \Delta E_{opt}$$

where $E_{0}$ is taken as 35 000 cm⁻¹ (285 nm) to align with experimental spectra (described below).

### 3.3. Excitonic coupling interactions

Excitonic couplings are calculated using the PD approximation, valid as the distance between pigments is large compared with the extension of their transition densities. The PD excitonic coupling is given as

$$V_{nm} = \frac{\mu_{nm}^2}{R_{nm}} |e_{nm} \cdot e_{m} - 3(e_{nm} \cdot e_{m})(e_{nm} \cdot e_{m})|$$

where $e_{nm}$ is a unit vector along the transition dipole moment of the nth Trp, the unit vector $e_{nm}$ is oriented along the line connecting the centres of Trps $m$ and $n$, $\mu_{nm}$ is the transition dipole moment of the 1La transition of Trp in vacuum, and the factor $f$ effectively takes into account local field and screening effects in an effective way. In the simplest approximation, owing to Förster, $f = 1/\epsilon_{opt}$, accounting only for screening effects. However, when screening effects of the medium as well as local field effects are included, this becomes $f = e_{opt}^{-3/2} (\epsilon_{opt} + 2)/3$.

### Table 3. Tryptophan abundance in cytoskeletal constituent molecules.

<table>
<thead>
<tr>
<th>Cytoskeletal Molecule</th>
<th>Total Residues</th>
<th>Trp Residues</th>
<th>Trp Abundance (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tubulin</td>
<td>~450</td>
<td>4</td>
<td>0.9</td>
</tr>
<tr>
<td>Actin</td>
<td>375</td>
<td>4</td>
<td>1.1</td>
</tr>
<tr>
<td>α-internexin</td>
<td>499</td>
<td>1</td>
<td>0.2</td>
</tr>
<tr>
<td>Desmin</td>
<td>470</td>
<td>1</td>
<td>0.2</td>
</tr>
<tr>
<td>GFAP</td>
<td>432</td>
<td>1</td>
<td>0.2</td>
</tr>
<tr>
<td>Keratin</td>
<td>564</td>
<td>2</td>
<td>0.3</td>
</tr>
<tr>
<td>Neurofilament</td>
<td>916</td>
<td>3</td>
<td>0.3</td>
</tr>
<tr>
<td>Peripherin</td>
<td>470</td>
<td>1</td>
<td>0.2</td>
</tr>
<tr>
<td>Syncoilin</td>
<td>482</td>
<td>0</td>
<td>0.0</td>
</tr>
<tr>
<td>Synemin</td>
<td>1565</td>
<td>15</td>
<td>1.0</td>
</tr>
<tr>
<td>Vimentin</td>
<td>466</td>
<td>1</td>
<td>0.2</td>
</tr>
</tbody>
</table>
[68–71]. Here, we consider both these cases. The optical dielectric constant for a typical protein environment is given in the range of 2–4; however, tubulin’s high-frequency dielectric coefficient has been measured as 8.41 [30]. For comparison, we consider the two extremes of 2 and 8.41.

3.4. Alignment with experimental spectra

The tight-binding Hamiltonian for an interacting N-body system in the presence of a single excitation is given by [72]

\[ H_S = \sum_{m=1}^{N} e_m |m\rangle\langle m| + \sum_{m>n} V_{mn} |m\rangle\langle n| + |n\rangle\langle m|, \]

where the states \(|m\rangle\) denote the excitation being at site \(m\). The site energies and coupling terms are given by \(e_m\) and \(V_{mn}\), respectively, and are calculated as described above. Exciton stick spectra for absorption, CD and linear dichroism (LD) were calculated by applying a Gaussian function to each exciton transition and the diagonalized Hamiltonian matrix using the formula described by Pearlstein [73]. Experimental spectra were calculated by applying a Gaussian function to each exciton transition using an assumed full-width half maximum value of 3500 cm\(^{-1}\) as commonly observed for Trp [74,75]. These were then compared with experimental absorption, CD and LD spectra adapted from Mozo-Villarias et al. [76], Clark et al. [77] and Marrington et al. [78], respectively.

3.5. Exciton population dynamics

Time evolution of the exciton population in the Trp network in the presence of thermal fluctuations of the environment is modelled using the Haken & Strobl model [33]. Here, it is assumed that thermal fluctuations of the environment couple to the Trips by an electron–phonon interaction, acting only on the diagonal elements of the Hamiltonian system \(H_S\), with the fluctuations being unbiased, uncorrelated and Gaussian in nature. Under these assumptions, the Haken–Strobl equation for the density operator \(\rho\) in the Schrödinger picture is given as

\[ \dot{\rho}(t) = -\frac{i}{\hbar} [H_S, \rho(t)] + L_d(\rho(t)), \]

where the pure-dephasing Lindblad operator is given by

\[ L_d(\rho) = \sum_{m=1}^{N} \gamma_m \left( A_m \rho(t) A_m^\dagger - \frac{1}{2} A_m^\dagger A_m \rho(t) - \frac{1}{2} \rho(t) A_m A_m^\dagger \right), \]

with \(A_m\) and \(A_m^\dagger\) being the creation and annihilation operators, and \(\gamma_m\) the pure dephasing rates for the \(m\)th Trp. As a reasonable assumption, here we take \(\gamma_m\) to be 50 cm\(^{-1}\) for all sites. All population dynamics were computed using QuTip 2 [79].

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