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SISTEMA DE ESTUDIOS DE POSGRADO

ESTUDIO DE COHERENCIA Y TRANSPORTE
CUÁNTICOS EN LAS DINÁMICAS ENERGÉTICAS
DURANTE LA CAPTACIÓN DE ENERGÍA LUMÍNICA EN
SISTEMAS FOTOSINTÉTICOS

Tesis sometida a la consideración de la Comisión del Programa de
Estudios de Posgrado en Química para optar al grado y título de
Maestría Académica en Química

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Dedicatoria

A mi madre Marjorie, y a mi padre Roberto: que sin su apoyo incondicional
no habría llegado hasta donde estoy.

A mis hermanos, Kari y Fer, por su compañía, por su confianza, y por siempre
demostrarme cada día que hay que luchar por lo que se quiere.

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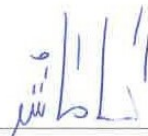
Gran parte de esta investigación involucró gran cantidad de conocimientos previos que fueron no obtenidos durante mi bachillerato, por lo que gran parte del tiempo de realización consistió en el aprendizaje de estos contenidos y técnicas. En estos esfuerzos, mi pasantía a la Universidad de Ulm fue fundamental. Agradezco al Sistema de Estudios de Posgrado por el financiamiento otorgado para esta pasantía, sobretodo considerando la situación extraordinaria causada por la pandemia de COVID19. Deseo agradecer profundamente a los profesores Martin Plenio y Susana Huelga, quienes me acogieron en el grupo de Control de Dinámicas Cuánticas, al profesor Felipe Caycedo por guiarme al navegar en este fascinante mundo de la Biología Cuántica. Además, quiero agradecer a la Dra. Gerlinde Walliser, secretaria del Centro de Biociencias Cuánticas, cuya colaboración fue indispensable en mi estancia en Ulm.

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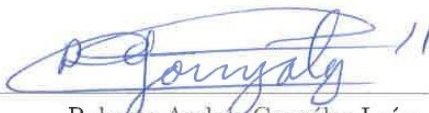
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Resumen

La fotosíntesis es uno de los procesos biológicos más ampliamente estudiados en la historia. Su capacidad para fijar carbono en moléculas nutritivas es la base de toda cadena trófica, y su eficiente explotación de la energía solar inspira aplicaciones como las celdas solares o la síntesis de compuestos de importancia biológica.

Durante los primeros milisegundos de la fotosíntesis, la luz solar se absorbe y transfiere a un centro de reacción, donde provee de energía a la conversión de dióxido de carbono en carbohidratos y otras moléculas combustibles. La comprensión de las dinámicas energéticas en este procesos es esencial para el diseño de sistemas similares. En las últimas décadas, técnicas de espectroscopía electrónica ultrarápida y multidimensional han revelado la presencia de fenómenos cuánticos, como el transporte y la coherencia cuántica, durante el transporte de energía en la fotosíntesis; estos se sugieren que contribuyen a su eficiencia inusualmente alta. A pesar de que la presencia de fenómenos en complejos fotosintéticos puede ser investigada empíricamente, su aplicación es limitada debido a la dificultad de la técnica, alto precio de los equipos, análisis de datos complejo y poca aplicabilidad en muestras *in vivo*. En consecuencia, las técnicas *in silico* proveen una plataforma para el estudio de estos fenómeno sin estas limitaciones experimentales.

En este trabajo, se presenta el estudio de la presencia de coherencia y transporte cuánticos en un complejo proteína-pigmento a través de métodos completamente computacionales. Primeramente, se desarrolla y valida una metodología para el cálculo de parámetros espectroscópicos con alta exactitud. A partir de estos, se utilizan ecuaciones cuánticas maestras para obtener las dinámicas de transporte energético, para analizar fenómenos cuánticos y su prevalencia en aras de dilucidar mecanismos y factores que puedan extender su vida media.

Summary

The photosynthesis is one of the most studied biological processes through history. Its capacity to fix carbon into nutritional molecules is the base of all food chains. Its efficient exploitation of the solar energy inspires application such as solar cells, or synthesis of biologically important compounds.

During the first milliseconds of the photosynthesis, sunlight is harvested and transferred to a reaction center, where it powers the conversion of carbon dioxide into carbohydrates and other fuel molecules. The understanding of the dynamics in this process is essential for the design of similar systems. In the last decades, ultrafast multidimensional electronic spectroscopy techniques have revealed the presence of quantum phenomena, such as quantum coherence and transport, during the energy transport in the photosynthesis, which are suggested to contribute to its unusually large efficiency.

Although the presence of quantum phenomena in photosynthetic complexes can be probed empirically, its application is limited by the technique difficulty, highly expensive equipment, complex data analysis and its low transferability to *in vivo* samples. As such, *in silico* techniques provide a platform to study these phenomena without this experimental limitations.

In this work, the study of the presence of quantum coherence and quantum transport in a protein-pigment complex is presented through fully computational methods. First, a methodology is developed and validated for the calculation of highly accurate spectroscopical parameters of the complex. From these, quantum master equations are used to obtain the dynamics of the excitation energy transport, and probe for the quantum effects and its prevalence, in order to elucidate mechanisms and factors that may extend their lifetime.

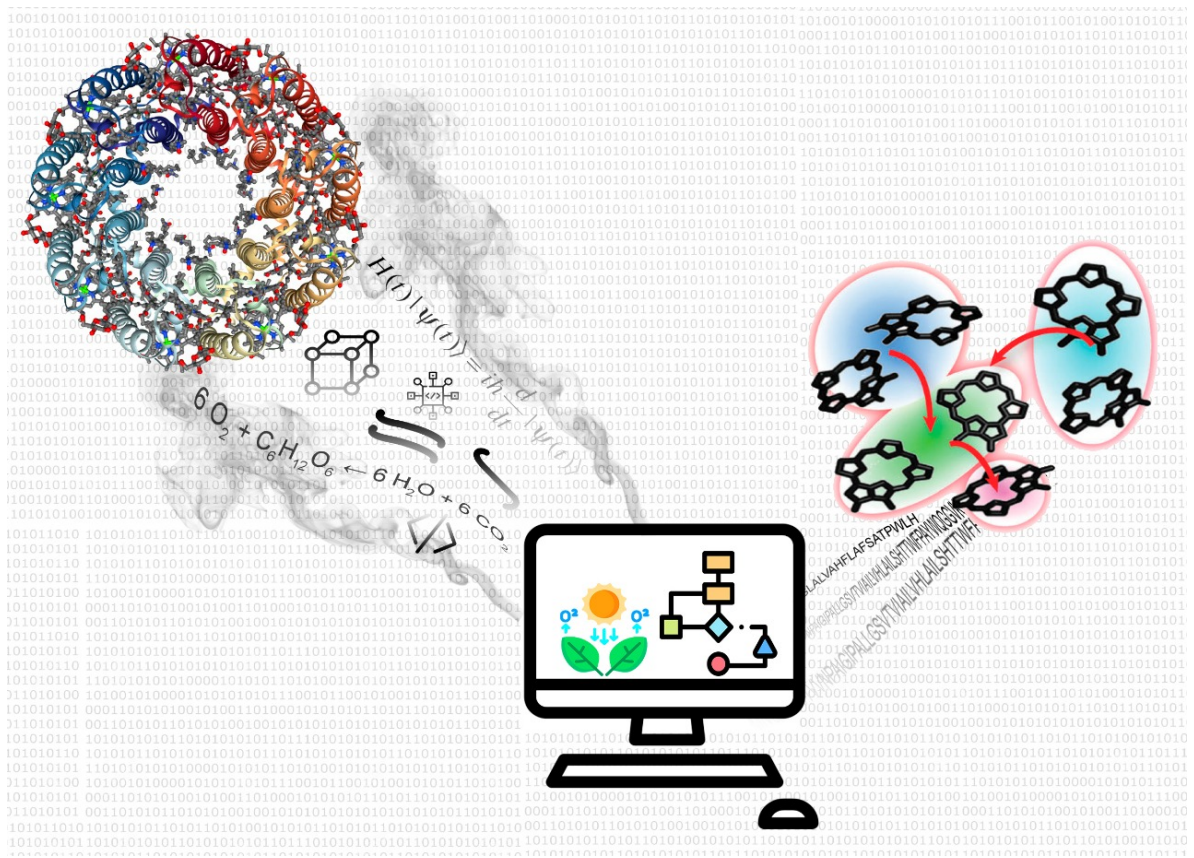


Figure 1: Graphical abstract of the thesis project.

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List of Abbreviations

2DES	Two-dimensional Electronic Spectroscopy
AO	Atomic Orbitals
BChl a/b/c/d/e	Bacteriochlorophyll a/b/c/d/e
bil	Bilin
car	Carotenoid
<i>c.c.</i>	Complex Conjugate
CC	Coupled-Cluster
CCSD	Coupled-Cluster Singles and Doubles
CHELP-BOW	Boltzmann-weighted Charges from Electrostatic Potential
Chl a/b/c1/c2/d/e	Chlorophyll a/b/c1/c2/d/e
Chl a – OH	13'2-hydroxyl-chlorophyll a
CT	Charge Transfer
Δ -FLN	Difference Fluorescence Line-Narrowing Spectroscopy
D3BJ	DFTD3 dispersion correction with Becke-Johnson Damping
DFT	Density Functional Theory
DFTB	Density Functional Theory Tight Binding
DLPNO	Domain-based Local Pair Natural Orbital
DMRG	Density Matrix Renormalization Group
EET	Excitation Energy Transfer

EOM	Equation of Motion
FCP	Fucoxanthin and Chlorophyll a/c Polypeptide
FFT	Fast Fourier Transform
FMO	Fenna-Matthews-Olson complex
FTD	Fragment Transition Density
FWMH	Full Width Mid-Height
GGA	Generalized Gradient Approximation
<i>h.c.</i>	Hermitian conjugate
HEOM	Hierarchical Equations of Motion
HF	Hartree-Fock
HRF	Huang-Rhys Factor
ISC	Intersystem crossing
KS	Kohn-Sham
LH1/2	Light-harvesting Complex 1/2 of Purple Bacteria
LHC	Light-harvesting Complex
LHCSR	Stress Related Light-harvesting Complex
LHS	Left Hand Side
MD	Molecular Dynamics
MM	Molecular Mechanics
MMpol	Polarizable Molecular Mechanics
MO	Molecular Orbital
NRMSE	Normalized Root-Mean Squared Error
ODE	Ordinary Differential Equation
PBP	Phycobiliprotein
PBS	Phycobilisome

PCP	Peridinin-chlorophyll Protein
PDA	Point-Dipole Approximation
PDB	Protein Data Bank
PDB ID	Identification Code in the Protein Data Bank
PDE	Partial Differential Equation
PPC	Pigment-Protein Complex
PPP	Pariser-Parr-Pople method
PSI	Photosystem I
PSII	Photosystem II
QC	Quantum Chemical
QM	Quantum Mechanical
QME	Quantum Master Equation
RDM	Reduced Density Matrix
RHS	Right Hand Side
RMSD	Root-Mean Squared Distance
RMSE	Root-Mean Squared Error
RS	Range Separated
RSD	Relative Standard Deviation
SCF	Self Consistent Field
SEET	Singlet Excitation Energy Transfer
STEOM	Second similarity Transformation Equation of Motion
T-TEDOPA	Finite Temperature Time-Evolving Density Operator with Orthogonal Polynomials
TD-DFT	Time-dependent Density Functional Theory
TD-DFTB	Time-dependent Density Functional Theory Tight Binding
TD-DMRG	Time-dependent Density Matrix Renormalization Group

TDA	Tamm-Dancoff Approximation
TDFI	Transition Density Fragment Interaction
TEDOPA	Time-Evolving Density Operator with Orthogonal Polynomials
TEET	Triplet Excitation Energy Transfer
TLS	Two-level System
TMA	Transition Monopole Approximation
TrEsp	Transition Charges from Electrostatic Potential
UV	Ultraviolet
VCP	Violaxanthin-chlorophyll Protein
WSCP	Water Soluble Chlorophyll-Binding Protein
XLH	<i>Xanthonema</i> Light-harvesting Complex
ZDO	Zero Differential Overlap
ZINDO	Zerner's Intermediate Neglect of Differential Overlap



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Chapter 1

Introduction

From the birth of Quantum Mechanics (QM) and its experimental studies, one of the premises is that quantum phenomena such as coherence and entanglement cannot have any big relevance in biological processes, owed to their complexity and sources of decoherence, which often escape rigorous mathematical description (Lambert et al., 2013). However, with the development of more powerful tools, modeling constantly bigger biological systems from a physical perspective have been successful. One of the more famous examples is the prediction of DNA properties from purely physical principles by Erwin Schrödinger (1992).

Moreover, the question of the existence of organisms that incorporate quantum phenomena in its functional mechanism, to provide to competitive advantage or process control, remains open and evasive. Quantum Biology emerges from this question, and from its postulation, there have been proposals and tests for different quantum mechanisms to explain the dynamics of several biological process such as photosynthesis, olfaction, vision, proton transfer, enzyme activity and biogeomagnetism (Mohseni et al., 2014; Lambert et al., 2012; Fleming et al., 2011).

Studying the biological process from this perspective can give better insight on previously unknown or unexplained mechanisms, limited by only considering classical analysis. It can also give information of how QM states and dynamics interplay to result in macroscopical highly complex systems.

1.1 Light-Harvesting in Photosynthesis

Photosynthesis is one of most studied biological processes. Using this process, organisms like bacteria, algae and plants, convert solar energy into chemical energy, producing approximately 105 billion tons of biomass annually in the whole planet (B. Green & Parson, 2003). This biomass is the base of all food chains, therefore, the photosynthesis is considered as the base of all life.

The diversity of photoautotrophic organisms is very wide: around 350 000 species of photosynthetic organisms have been described (Sage & Stata, 2015) distributed along Bacteria and Eukarya dominions; the Archaea dominion is excluded, because there are

no known species of archaeas that fix carbon using photosynthetic mechanisms (Bryant & Frigaard, 2006). This diversity is illustrated in Fig. 1.1. Every species present different machinery to exploit sunlight, because each has evolved to incorporate certain characteristics and tune their mechanisms to account for the effects of temperature, humidity, precipitation, insolation and even topography (Blankenship, 2010).

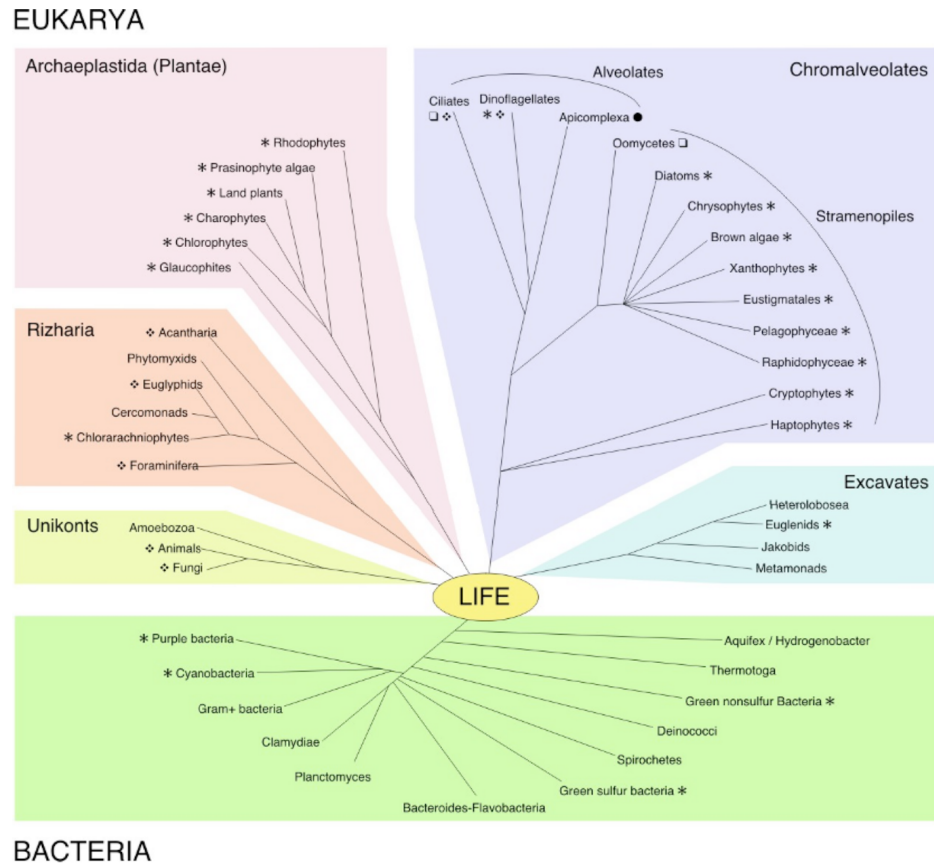
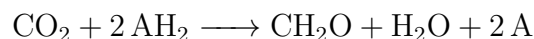


Figure 1.1: Evolutionary tree at class and clade level for the Eukarya and Bacteria dominions. Taken from Collini et al. (2009). The tree annotations indicate the photosynthetic function distributions along groups: * represents organisms with known photosynthetic functions, ● organisms with apicoplasts but without photosynthesis-related genes, □ algae species with photosynthetic symbionts or sequestered plastids, ◇ organisms that do not present any plastid but with genes that potentially codify for the photosynthetic proteins.

Photosynthesis convert solar energy and stores it into organic molecules that fuel other metabolic functions, such as cellular respiration. The photosynthesis reaction is, in its most general form (Niel, 1932):



where AH_2 represents an electron donor in its reduced form, and A its oxidated form. The electron donor varies depending on the photosynthetic species in question, corresponding to water in the oxygenic mechanisms, and other substances such as hydrogen sulfide, sulfite, succinate, lactate, iron(II) (Bryant & Frigaard, 2006) or arsenite (Kulp et al., 2008) in anoxygenic mechanisms.

The photosynthesis process can be summarized into 2 steps: the light-dependent reactions and the light-independent reactions. During the light-dependent phase, initially the light is absorbed by a protein complex incrustrated in the photosynthetic membrane of a plastid. This complex includes pigments: chromophoric molecules that have an electronic structure in some region that allows it to absorb light and store it momentarily in a quasiparticle called exciton. The exciton is transported quickly through an efficient excitonic transport (EET) chain to the reaction center (RC). In the RC, the excitonic energy is used to produce a charge separation reaction between two neighbouring pigments or a pigment and a nearby residue, this captures the light energy from the exciton in a pair of two stable total charges. Both charges are transported by the photosynthetic membrane by following electron transport reactions to produce adenosine triphosphate (ATP) and a reductor, which then enter the light-independent reactions to fix the carbon from CO_2 into fuel molecules (Cogdell et al., 2008; van Amerongen et al., 2000).

The first step of the light-dependent reactions is of interest here, since the EET chains to RC can have quantum efficiencies particularly high, of 95% to even almost 100% (van Amerongen et al., 2000). Compared to other light transmission devices, such as fiber optics, the maximum efficiency of visible light transmission is 92% for coherent and polarized sources and transparent media (Mollers et al., 2009).

To explain this extremely high efficiency of harvest and light transport in natural (wet, complex and non-ideal) conditions, mechanisms including quantum coherence and entanglement have been proposed, in which the energy levels of the chromophores superpose, and efficient transport routes are built in a quantum walk mechanism (Hildner et al., 2013). In contrast, classical theories propose incoherent energy jumps, which would imply energy loss with each jump.

The presence of quantum coherence in photosynthetic complexes was demonstrated for the first time by Engel et al. (2007) using two-dimensional electronic spectroscopy (2DES) at 77 K in the bacteriochlorophyll Fenna-Matthews-Olson complex (FMO) isolated from *Chlorobaculum tepidum*. This new perspective has led to multiple studies focusing on getting insight on the importance of quantum coherence in improving photosynthetic efficiencies (H. Lee et al., 2009), their prevalence in physiological conditions (Panitchayangkoon et al., 2010) and across the tree of life (Collini, 2012).

1.1.1 Light-Harvesting Complexes

In the first part of the photosynthesis, the energy from sunlight is captured by the photosynthetic membrane, then, this energy is transported to the RC. This job is done by protein complexes called light-harvesting complexes (LHCs). An array of LHCs is an antenna complex, which are synthesized to improve the light-harvesting in the available power spectrum, while also increasing the harvesting sites, and the probability of light absorption and transport without heat relaxation, even in a diffuse source such as sunlight. The diversity of these designs are shown in Fig. 1.2.

The LHCs are made of proteins and pigment molecules that absorb sunlight through excitations of their chromophoric groups. These pigments are called “photosynthetic pigments” or “accessory pigments”, however, the latter can be misinterpreted, as the role of harvesting or photoprotection of these pigments are vital for the EET (Collini, 2019). In general, they are also called “chromophores” of the LHC. The diversity of LHCs in Nature is vast, considering type, organization and amount of chromophores. Also, LHCs can assemble in complex quaternary structures, denominated “photosynthetic supercomplexes”; they can include different types of LHCs, RCs, and other subunits for photoprotection, electronic transport, among others. Also, in some species, the subunits can form a LHC by themselves (Collini et al., 2009).

Comparing the macrostructures of the protein complexes, almost no similar characteristics are conserved across different types (Cogdell et al., 2008), for example, the LH2 complex present in purple bacteria, is a modular nonamer of apoproteins organized in a ring structure; carotenoids and bacteriochlorophylls function as chromophores and

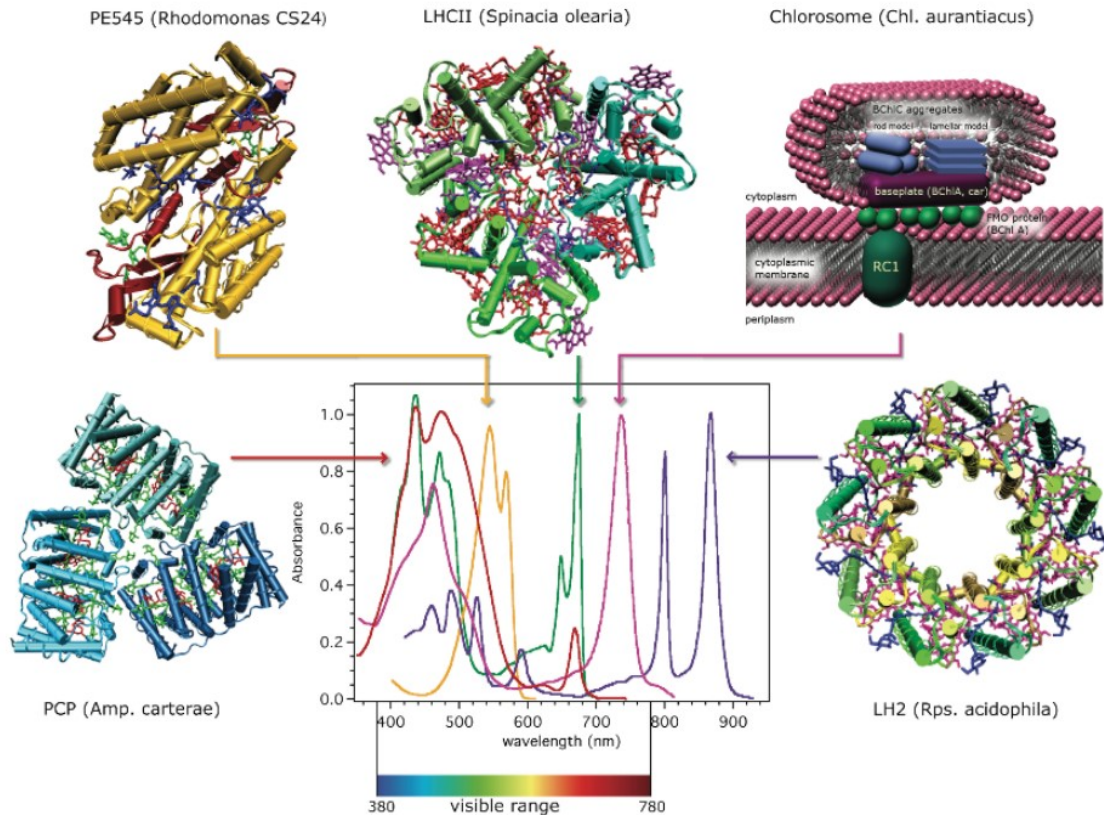


Figure 1.2: Absorption spectra and structure of some representative LHCs at 77 K. Taken from Collini et al. (2009). In parenthesis, the name of the species from which the corresponding structure shown.

are organized by non-covalent interactions inside the monomers (Prince et al., 1997). However, the photosystem II (PSII) of higher plants has a very complex structure, composed by an heterodimer with multiple LHC subunits with different structures, and also electron transport units, RCs, photoprotective units, and others, which can also shift slightly in position depending on the stage (Kern et al., 2018). This diversity is summarized in table 1.1.

Table 1.1: Types of light-harvesting complexes and supercomplexes and their pigments.

LHC Type	Pigments	Reference
B808-865 Complex	BChl a/c + car	Olson et al. (2007) Klappenbach & Pierson (2004)

Table 1.1: Types of light-harvesting complexes and supercomplexes and their pigments. Continued.

LHC Type	Pigments	Reference
Chromophyte chlorophyll a/c-binding LHC (Chl a/c-LHC)	Chl a/c2 + car + bil	Graham & Wilcox (2000) B. R. Green & Durnford (1996)
Chlorosome	BChl a/c/d/e + car	Orf & Blankenship (2013)
Photosystem I (PSI)	Chl a + car	Jordan et al. (2001)
Photosystem II (PSII)	Chl a/b + car	Loll et al. (2005)
Chlorophyll-binding LHC I of higher plants (LHCI)	Chl a/b/d + car + bil	Liu et al. (2004)
Chlorophyll-binding LHC II of higher plants (LHCII)	Chl a/b + car	Drop et al. (2014)
Subunits of the PSII-LHCII (CP24, CP26, CP29, CP43, CP47)	Chl a/b + car	Barera et al. (2012) Bassi et al. (1997)
Fucoxanthin and chlorophyll a/c polypeptide (FCP)	Chl a/c/c1,c2 + car	Graham & Wilcox (2000) Passaquet et al. (1991)
Fenna-Mathews-Olson (FMO) Complex	BChl a/d/e + car	Camara-Artigas et al. (2003)
RC-binding LHC1 of purple bacteria (LH1-RC)	BChl a/b + car	Roszak (2003) Hoogewerf et al. (2003)
LHC2 of purple bacteria (LH2)	BChl a/b + car	Papiz et al. (2003) Cogdell et al. (1996)
Stress Related LHC (LHCSR)	Car	Bailleul et al. (2010) Peers et al. (2009)
Phycobiliprotein (PBP)	Chl a/c2 + car + bil	Kieselbach et al. (2018) Kannaujiya et al. (2017)

Table 1.1: Types of light-harvesting complexes and supercomplexes and their pigments. Continued.

LHC Type	Pigments	Reference
Phycobilisome (PBS)	Chl a/b/c/d + car + bil	Marx & Adir (2013) Gantt (1996)
Peridinin-chlorophyll Protein (PCP)	Chl a/c2 + car	Hiller et al. (1993)
Violaxanthin-chlorophyll Protein (VCP)	Chl a + car	Bína et al. (2014) Wolf et al. (2018)
<i>Xanthonema</i> LHC (XLH)	Chl a + car	Streckaite et al. (2018) Durchan et al. (2012)

Notation: *Chl* = chlorophyll, *BChl* = bacteriochlorophyll, *car* = carotenoid, *bil* = bilin.

During light-harvesting, there exists a competition between several possible destinies of the energy (Fassioli et al., 2013):

1. It can be relaxed through internal conversions and disperse as heat
2. It can be relaxed by photon emission
3. It can be transmitted to another molecule and continue the EET

The competition between these processes occurs in the femtosecond scale, completing the EET process in scales of 0.1 – 10 ns (Mullineaux et al., 1993; Geacintov et al., 1986) with reported quantum efficiencies for the PSII LHCs of higher plants between 84 and 90%, from light-harvesting to the charge separation in the RC (Wientjes et al., 2013).

The photosynthetic pigments are embedded in a protein scaffold, in which the pigments and cofactors are arranged in precised positions to optimize the EET. Pigments like chlorophyll show almost total self-quenching at concentrations greater than 0.1 mol L⁻¹ in solution; however, in LHCs like PSI and PSII, the concentrations are as a high as 0.5 mol L⁻¹, and almost no self-quenching is observed (Beddard & Porter,

1976). Also, the energy transfer is extremely dependent on the distance and interaction between chromophores (Scholes & Ghiggino, 1994). In some cases, the chromophore-protein interaction causes shifting in the absorption spectra of the chromophore, important in the optimization of the absorption probability of the photon, as is the case for BChl a of *Rhodobacter sphaeroides* (Fowler et al., 1992).

Thus, the arrangement of the chromophores inside the LHC is dense, which leads to strong Coulombic interactions (between 10 and 300 cm^{-1} for the LHCII according to Fröhlich & Walla (2006)) that result in an ultrafast EET, and the emergence of quantum phenomena such as quantum coherence and quantum entanglement (Schlaich-Cohen et al., 2012).

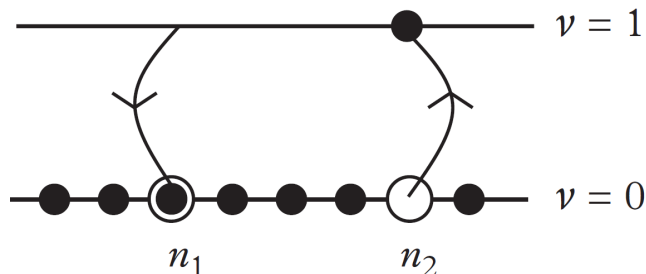


Figure 1.3: Schematic diagram of a Frenkel exciton transport between different sites through a crystal. Each site is shown with its ground ($\nu = 0$) and first excited ($\nu = 1$) states. Taken from Combescot & Shiau (2016).

Because its high density packing inside the LHCs, a solid-state approach is valid, in particular, the excitations in the LHC can be modelled as excitations in a solid crystal. Considering this, the excitation of an electron leaves a positive hole in the ground state, and a bound state between the excited electron and the hole is formed, this is called an exciton, and can even be seen as a quasiparticle. If the exciton is highly localized to a chromophore, the Frenkel exciton model is valid (Frenkel, 1931). Frenkel excitons appear when the spatial extension of the molecular orbitals (MOs) is small compared to the unit cell size, as in organic crystals. In this limit, the crystal can be seen as a set of individual atoms positioned at the crystal lattice nodes, and, therefore, suffer atomic excitations localized around their equilibrium position. Excitons come from the promotion of an electron to an excited state with different position than the ground

state, leaving a hole in their original position; the hole and the electron are bound together by their Coulombic interaction. As Frenkel excitons are highly localized around their origin, they can rapidly recombine by thermal or radiative decay; however, they can jump to other sites if there exist additional Coulombic interaction with them, effectively delocalizing. Following the diagram in Fig. 1.3, the simplest mechanism for exciton transport is the relaxation of the excited electron in the $1 \rightarrow 0$ direction at site n_1 , while simultaneously another electron excites at site n_2 in the $0 \rightarrow 1$ (Combescot & Shiau, 2016). In general, these excitations and relaxations can happen at any site and to any excited state, therefore, their complete description is complex.

In LHCs, the pigments are tightly embedded on the protein scaffold, thus, the “organic crystal approach” is valid. However, deviations from this model have to be evaluated, for example, chromophores in LHCs are multiatomic molecules (around 150 atoms per pigment) with complex structures themselves. Also, by considering each pigment a site, the “lattice” is also not symmetrical, and the relative orientation of pigments have to be evaluated. These deviations make the description of the LHC chromophoric aggregate complicated, and robust, high level Quantum Chemical methods are needed to accurately describe their behaviour and the EET phenomena.

1.2 Optical Spectroscopy of PPCs

The optical spectroscopy of PPCs results from the interaction of light with a chromophoric aggregate. Given the rigidity of the protein scaffold, this considers a solid matrix with embedded pigments which interacts with a light beam. The excitation generates an exciton: a bosonic quasiparticle formed between an electron and a hole bound by electrostatic and exchange interactions. Excitons can transfer energy without transporting electric charge; and can be classified given their spatial extent compared to the lattice.

1.2.1 The Frenkel Exciton Model

A chromophoric aggregate consists of a set of N molecules bound by non-covalent interactions in such a spatial array that their electronic states interact with each other. The chromophores can, in general, be any type of molecule, however, to be considered “pigments” they should be susceptible to electronic optical absorption by UV/Vis light; thus, the probability of absorption should be high in those regions. For solar cell applications, the optical absorption spectrum of the pigment should be similar to the one of the Sun at Earth’s surface. In photosynthetic complexes, their pigments and their spatial distributions have evolved to harvest the available light in their corresponding habitat.

The excitons in a chromophoric aggregate are bound to a PPC unit, therefore their spatial extent is much smaller than the lattice parameter; these are called Frenkel excitons, and are localized to one or a few pigments at any given time (Frenkel, 1931).

The total aggregate hamiltonian can be written in terms of the molecular hamiltonians \hat{H}_n and the intermolecular Coulombic interactions \hat{V}_{mn} , this takes the form (May & Kühn, 2011),

$$\hat{H}_{\text{agg}} = \sum_n \hat{H}_n + \frac{1}{2} \sum_{m,n} \hat{V}_{mn} \quad (1.2.1)$$

Introducing the interacting electronic states of the molecule n , $|\phi_{na}\rangle$ y $|\phi_{nb}\rangle$, then the hamiltonian matrix elements $H_n(ab)$ and the Coulomb matrix elements $J_{mn}(ab, cd)$ are given by,

$$H_n(ab) = \langle \phi_{na} | \hat{H}_n | \phi_{nb} \rangle \quad (1.2.2)$$

$$J_{mn}(ab, cd) = \langle \phi_{ma}\phi_{nb} | \hat{V}_{mn} | \phi_{nc}\phi_{md} \rangle \quad (1.2.3)$$

sustituting in (1.2.1),

$$\hat{H}_{\text{agg}} = \sum_n \sum_{a,b} H_n(ab) |\phi_{na}\rangle \langle \phi_{nb}| + \frac{1}{2} \sum_{m,n} \sum_{a,b,c,d} J_{mn}(ab, cd) |\phi_{ma}\phi_{nb}\rangle \langle \phi_{nc}\phi_{md}| \quad (1.2.4)$$

In natural environments, specially for photosynthetic microorganisms in low insolation habitats, many photosynthetic complexes only sustain one excitation at a time (Blankenship, 2014). Thus, each molecule can be treated as a two-level system (Fig. 1.4) and the Hilbert space of the aggregate quantum states \mathcal{H} is restricted to the subspaces of zero excitations (\mathcal{H}_0) and one excitation (\mathcal{H}_1), so that $\mathcal{H} = \mathcal{H}_0 \otimes \mathcal{H}_1$.

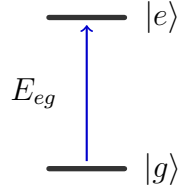


Figure 1.4: Energy levels of a two-level system. The system excitation energy is shown as E_{eg} .

In this approximation, the states are $a = g, e$, where g refers to a ground state and e refers to a first excited state. Substituting,

$$\hat{H}_{\text{agg}} = \sum_n \sum_{a=g,e} H_{na} |\phi_{na}\rangle \langle \phi_{na}| + \sum_{m,n} J_{mn} |\phi_{me}\phi_{ng}\rangle \langle \phi_{ne}\phi_{mg}| \quad (1.2.5)$$

in the Born–Oppenheimer approximation, the nuclear coordinates are fixed at their equilibrium position, thus, the equilibrium potential energy E_{na} and the electronic part of the aggregate hamiltonian is given by,

$$\hat{H}_{\text{agg}}^{(\text{el})} = \sum_n \sum_{a=g,e} E_{na} |\phi_{na}\rangle \langle \phi_{na}| + \sum_{m,n} J_{mn} |\phi_{me}\phi_{ng}\rangle \langle \phi_{ne}\phi_{mg}| \quad (1.2.6)$$

Rearranging the electronic states, the site basis is introduced. In this base, $|n\rangle$ denotes the state where only the chromophore n is excited. Hence,

$$|n\rangle = |\phi_{ne}\rangle \prod_{n \neq m} |\phi_{mg}\rangle \quad (1.2.7)$$

also, the collective ground state of the aggregate is expressed as

$$|0\rangle = \prod_n |\phi_{ng}\rangle \quad (1.2.8)$$

In the site basis, equation (1.2.6) is written as,

$$\hat{H}_{\text{agg}} \approx \hat{H}_{\text{agg}}^{(0)} + \hat{H}_{\text{agg}}^{(1)} = E_0 |0\rangle \langle 0| + \sum_{m,n} H_{mn} |m\rangle \langle n| \quad (1.2.9)$$

the aggregate ground state energy is introduced as,

$$E_0 = \sum_n E_{ng} \quad (1.2.10)$$

The aggregate first excitation hamiltonian $\hat{H}_{\text{agg}}^{(1)}$ is expanded as,

$$\begin{aligned} \hat{H}_{\text{agg}}^{(1)} &= \sum_{m,n} (\delta_{mn} E_0 + E_{mn}) |m\rangle \langle n| \\ &= \sum_{m,n} [\delta_{mn} E_0 + (\delta_{mn} E_n + (1 - \delta_{mn}) J_{mn})] |m\rangle \langle n| \\ \hat{H}_{\text{agg}}^{(1)} &= \sum_n (E_0 + E_n) |n\rangle \langle n| + \sum_{m \neq n} J_{mn} |m\rangle \langle n| \end{aligned} \quad (1.2.11)$$

thus, the site energy $E_n = E_{ne} - E_{ng}$ corresponds to the vertical excitation energy of first excited state of each chromophore; also called Franck–Condon transition energies. Finally, taking $E_0 = 0$, the aggregate hamiltonian is given by,

$$\hat{H}_{\text{agg}} \approx \hat{H}_{\text{agg}}^{(1)} = \sum_n E_n |n\rangle \langle n| + \sum_{m \neq n} J_{mn} |m\rangle \langle n| \quad (1.2.12)$$

notice that the hamiltonian on (1.2.12) is completely analogous to the Frenkel hamiltonian for excitations on atomic crystals (Combescot & Shiau, 2016).

The electronic states of the chromophores are combined to give new states, which represent the energy levels of the system that the excitations occupy. These excitations generate a bosonic quasiparticle, via the interaction between the excited electron and the hole it leaves on the ground state: this is called an exciton. The Frenkel excitons are created by interactions between the electronic states localized in the involved chromophores, and the delocalized by Coulombic and Dexter interactions (You & Hsu, 2014). The diagonalization of \hat{H}_{agg} in (1.2.12) gives the excitonic energy levels depicted

in Fig. 1.5.

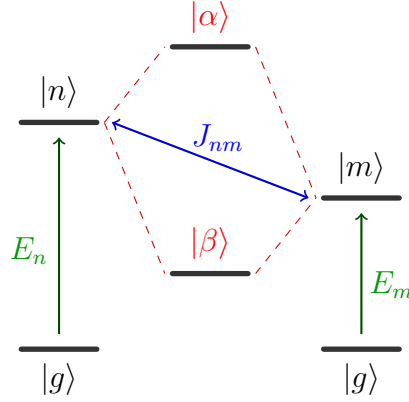


Figure 1.5: Excitonic levels for a two-level dimer. The spectroscopic parameters shown in the Frenkel hamiltonian model are: site energies E_n and E_m , and excitonic coupling J_{nm} .

The excitonic states $|\alpha\rangle$ are given by,

$$\hat{H}_{\text{ex}} |\alpha\rangle = E_\alpha |\alpha\rangle \quad (1.2.13)$$

where E_α are their corresponding energies. The states $|\alpha\rangle$ are expanded in the site basis as,

$$|\alpha\rangle = \sum_n c_\alpha^{(n)} |n\rangle \quad (1.2.14)$$

As $|\alpha\rangle$ are orthogonal, the excitonic hamiltonian satisfies that

$$\hat{H}_{\text{ex}} = \sum_\alpha E_\alpha |\alpha\rangle \langle\alpha| \quad (1.2.15)$$

and the exciton transition dipole moments $\vec{\mu}_\alpha$,

$$\vec{\mu}_\alpha = \sum_n c_\alpha^{(n)} \vec{\mu}_n \quad (1.2.16)$$

where $\vec{\mu}_n$ are the transition dipoles of the $S_0 \rightarrow S_1$ transitions of each chromophore.

1.2.2 Excitonic Couplings

The interexcitonic transfer coupling J_{ij} (also called simply “excitonic coupling”) between two pigments (i, j) establishes the magnitude of interaction between the excitons E_i and E_j , fully localized at their respective sites. The excitonic coupling allows for the transfer of populations and energy between sites.

When a pigment-protein complex (PPC) interacts with light an excitation energy transfer (EET) process starts. This is a photophysical process in which the electronic excitation energy is transferred from a donor to an acceptor chromophore. This process usually starts with a chromophore being optically excited, then the exciton is subsequently transferred to a nearby site that has a non-null excitonic coupling. This process can happen between singlet or triplet states, which are dubbed SEET and TEET processes respectively (You & Hsu, 2014). SEET is the process involved in the light-harvesting and energy transport in photosynthetic chromophoric aggregates (Peterman et al., 1997). TEET is present in systems where relaxation via intersystem crossing (ISC) stabilizes a triplet state much faster than SEET transfer; this is present in the transfer between triplet oxygen and photoprotective pigments such as carotenoids (Cogdell & Frank, 1987).

Considering the Frenkel hamiltonian, the excitonic coupling is given by,

$$J_{ij} = \langle i | \hat{H}_{agg} | j \rangle \quad (1.2.17)$$

Using first-order perturbation theory in the SEET regimen, the contributions to the excitonic couplings are given by (You & Hsu, 2014),

$$J_{ij} = J_{ij}^{\text{Coul}} + J_{ij}^{\text{exch}} + J_{ij}^{\text{ovlp}} \quad (1.2.18)$$

where J_{ij}^{Coul} is the contribution of Coulombic interactions between electronic transitions; J_{ij}^{exch} is the exchange contribution, also called Dexter coupling, that accounts for the indistinguishability of electrons in the wavefunctions; and J_{ij}^{ovlp} comes from the orbital overlap between the donor and acceptor electron densities.

For an excitation from the ground state $|\Psi_g\rangle$ to the excited state $|\Psi_e\rangle$, the one-particle transition density matrix γ_{eg}^T can be expressed as (Curutchet & Mennucci, 2017),

$$\gamma_{eg}^T(\mathbf{r}, \mathbf{r}') = N \int \cdots \int \Psi_e^*(\mathbf{r}, \mathbf{r}_2 \dots \mathbf{r}_N) \Psi_g(\mathbf{r}', \mathbf{r}_2 \dots \mathbf{r}_N) d\mathbf{r}_2 d\mathbf{r}_3 \dots d\mathbf{r}_N \quad (1.2.19)$$

the electron density associated with the electronic transition on a fixed site (transition density) ρ^T is given by the diagonal elements of γ_{eg}^T ,

$$\rho^T(\mathbf{r}) = \gamma_{eg}^T(\mathbf{r}, \mathbf{r}) \quad (1.2.20)$$

The contributions in (1.2.18) can then be expressed in terms of γ_{eg}^T and ρ^T (You & Hsu, 2014):

$$J_{ij}^{\text{Coul}} = \int d\mathbf{r} \int d\mathbf{r}' \rho_i^{\text{T}*}(\mathbf{r}) \frac{1}{|\mathbf{r} - \mathbf{r}'|} \rho_j^T(\mathbf{r}') \quad (1.2.21)$$

$$J_{ij}^{\text{exch}} = - \int d\mathbf{r} \int d\mathbf{r}' \gamma_i^{\text{T}*}(\mathbf{r}, \mathbf{r}') \frac{1}{|\mathbf{r} - \mathbf{r}'|} \gamma_j^T(\mathbf{r}, \mathbf{r}') \quad (1.2.22)$$

and J_{ij}^{ovlp} can be estimated from the overlap integrals, $S_{AB} = \langle \Psi_A | \Psi_B \rangle$.

1.2.2.1 Coulombic Contributions

It can be considered that in SEET processes generally the Coulombic contribution is much more important than the others, thus,

$$J_{ij} \approx J_{ij}^{\text{Coul}} \quad (1.2.23)$$

In principle, any computational method that allows the calculation of the transition density can be used to directly evaluate the integrals in (1.2.21). However, their direct calculation is often very computationally expensive, therefore other methods are used to approximate them.

In the limit of weak coupling, and when the distance between sites is much bigger than the size of the chromophores, the coupling can be calculated from the interac-

tion between two electric point–dipoles. This is called the point–dipole approximation (PDA), and was proposed by Förster (1948) as part of his theory of EET to explain fluorescence phenomena, based on Fermi’s golden rule.

Under PDA, the excitonic coupling is calculated as the energy between the transition dipole $\vec{\mu}_i$ in the electric field produced by another transition dipole $\vec{\mu}_j$, localized at their respective “chromophoric centers”. The final expression reads,

$$J_{ij}^{\text{PDA}} = \frac{|\vec{\mu}_i||\vec{\mu}_j|}{4\pi\epsilon_0} \frac{\kappa}{R_{ij}^3} \quad (1.2.24)$$

where $|\vec{\mu}_i|$ and $|\vec{\mu}_j|$ are their respective dipole lengths, R_{ij} is the distance between chromophoric centers and κ is a purely geometric factor, which considers the relative orientation of the dipoles, and is given by,

$$\kappa = \hat{\mu}_i \cdot \hat{\mu}_j - 3 \left(\hat{\mu}_i \cdot \hat{R}_{ij} \right) \left(\hat{\mu}_j \cdot \hat{R}_{ij} \right) \quad (1.2.25)$$

therefore, the quality of the calculated couplings by the PDA method depend on the geometric description of the spatial position on the point dipoles, and also their magnitudes. Besides, this method considers that the dipole lengths are not affected by the presence of another dipole.

A correction for the environment screening can be introduced changing ϵ_0 to the electrical permittivity of the medium ϵ_r . However, its most important limitation is that, at short distances, the coupling is greatly overestimated, and when the relative orientation of the dipole is almost perpendicular, the coupling tends to zero, which does not happen in the interaction between transition densities (Curutchet & Menucci, 2017). Because of the PDA limitations, other methods are proposed to consider the full geometry of the chromophores, and not only their relative orientation along an axis.

Another low cost method to model the excitonic coupling is to decompose the transition density into point–charges localized at the equilibrium positions of the atoms of each chromophore, called transition charges. The excitonic coupling is then the Coulombic energy of interaction between the two sets of transition charges.

There are several protocols to determine the transition charges. One of them is the Transition Monopole Approximation (TMA), proposed by Chang (1977), in which each charge is built from the atomic orbitals (AOs) that contribute to the MOs of the ground and excited states.

Let ϕ_μ be an MO of certain molecule (i or j). Each MO is expressed as a linear combination of AOs χ_i , then,

$$\phi_{\mu,i} = \sum_{I=1}^{N_i} C_{I,\mu} \chi_I \quad (1.2.26)$$

assuming zero differential overlap (ZDO), $\chi_I(\mathbf{r}) \chi_J(\mathbf{r}) = \chi_I \chi_J \delta_{IJ}$ and the form of the Coulombic energy between two charges, the excitonic coupling is given by,

$$J_{ij}^{\text{TMA}} = \frac{1}{4\pi\epsilon_0} \sum_{I=1}^{N_i} \sum_{J=1}^{N_j} 2C_{I,\nu}^i C_{I,\lambda}^i C_{J,\nu}^j C_{J,\lambda}^j \frac{e^2}{|\mathbf{R}_I - \mathbf{R}_J|} \quad (1.2.27)$$

where $C_{I,\lambda}^i$ represents the AO coefficient of the atom I of molecule i in the state λ ; hence, λ, ν are the ground and excited states in some given order. From equation (1.2.27), the populations of the AOs can be identified, and the effective transition charges $q_{i,I}(\nu, \lambda)$ are defined as,

$$q_{i,I}(\nu, \lambda) = \sqrt{2} e C_{I,\nu}^i C_{I,\lambda}^i \quad (1.2.28)$$

Substituting (1.2.28) in (1.2.27), the excitonic coupling can be written as,

$$J_{ij}^{\text{TMA}} = \frac{1}{4\pi\epsilon_0} \sum_{I=1}^{N_i} \sum_{J=1}^{N_j} \frac{q_{i,I}(\nu, \lambda) q_{j,J}(\nu, \lambda)}{|\mathbf{R}_I - \mathbf{R}_J|} \quad (1.2.29)$$

In this method, it is necessary to calculate the MOs and their decomposition in terms of the AOs, therefore the decomposition method plays a key role in the procedure. Originally, Chang (1977) used a semiempirical approach, in this case, the Pariser–Parr–Pople method (SCF–MO–PPP). Other decomposition schemes can be considered.

In the TrEsp method, the transition density (calculated on the electrostatic potential of the molecule) of each pigment for the states ν, λ is broken down into a set of transition charges $q(\nu, \lambda)$, first by calculating an electric potential field associated with the transition density and then using the CHELP-BOW method (Sigfridsson & Ryde,

1998) to express the electric field as sourced by point charges at the equilibrium position of the atomic centers. These transition charges are then used as atomic point charges centered at the atomic positions of the pigment, and are rescaled by a constant K so that the transition dipole moment,

$$\vec{\mu}^{\text{TrEsp}} = \sum_I q_I(\nu, \lambda) \mathbf{R}_I \quad (1.2.30)$$

gives the same magnitude than some experimental dipole value μ^{exp} , where \mathbf{R}_I is the position vector of atom I . Hence,

$$K = \frac{\mu^{\text{exp}}}{\mu^{\text{TrEsp}}}. \quad (1.2.31)$$

Finally, the excitonic coupling is given by the transfer coupling of the two excitons, given by the electric potential energy stored in the set of transition charges of the two pigments at the geometries of the complex. That is,

$$V_{ij}^{\text{TrEsp}} = \frac{K_i K_j}{4\pi\epsilon_0} \sum_{I,J} \frac{q_{i,I}(\nu, \lambda) q_{j,J}(\nu, \lambda)}{|\mathbf{R}_I - \mathbf{R}_J|} \quad (1.2.32)$$

Notice that the expression (1.2.32) and (1.2.29) are very similar. However, they differ in two fundamental things:

1. The expression for TrEsp includes correction factors for the calculated transition charges, based on the experimental transition dipoles. In the TMA this correction factor can be introduced as an effective dielectric constant of the environment. Also, one can define the same correction factor K in an analogous way as in equation (1.2.31) using the transition charges of TMA.
2. The way the transition charges are built. In the case of TMA, the transition charges are built directly from atomic orbitals, in contrast with TrEsp, that considers the breaking down of the electric potential surface associated with the calculated transition density into charges at atomic positions. This means that TMA uses a more quantum mechanical argument, and TrEsp a more electrostatic

argument, to calculate the transition charges.

For both the TMA and TrEsp method, the quality of the coupling depends on the quality of the transition charges (thus, the *ab initio* calculations behind them and the localization method), the geometry of coupled pigments and the experimental transition dipole used for rescaling. This kind of discretization suffers from accuracy losses because of the cumulative losses on these factors (Curutchet & Mennucci, 2017). In fact, it was shown that the TrEsp method can underestimate drastically the excitonic couplings, specially at short distances (Olbrich & Kleinekathöfer, 2010). Table 1.2 summarizes the methods and previous estimations of excitonic couplings for type II WSCP pigment dimers.

Table 1.2: Exciton coupling and transition dipoles for type II WSCP pigment dimers reported on the literature.

Reference	Organism	Pigment	J_{14} (cm^{-1})	$ \vec{\mu}_{0\rightarrow 1} $ (D)	Method
Hughes et al. (2006)	<i>B. oleracea</i> var. <i>botrytis</i>	Chl a	90 ± 20	4.36 ± 0.03	PDA
		Chl d	130 ± 25	5.00 ± 0.06	
Renger et al. (2007)	<i>B. oleracea</i> var. <i>botrytis</i>	Chl a	84	4.0	TrEsp
		Chl b	72	3.6	
Renger et al. (2009)	<i>L. virginicum</i>	Chl a	77	4.0	
		Chl b	69	3.6	
Dinh & Renger (2015)	<i>B. oleracea</i> var. <i>botrytis</i>	Chl a	77	4.0	
		Chl b	69	3.6	

1.2.2.2 Short-range contributions: Diabatization approaches

The methods previously discussed only deal with Coulombic long-range interactions. As the distance between chromophores becomes smaller, other interactions can become important; thus, the short-range interactions have to be added to the total excitonic coupling. In general, there are three pathways in which the exciton can be transferred from a donor site to an acceptor site (Wehner & Baumeier, 2017), illustrated in Fig. 1.6:

- a) Förster-like mechanism: Coulombic interactions between the donor and the acceptor lead to an energy transfer via a virtual photon.

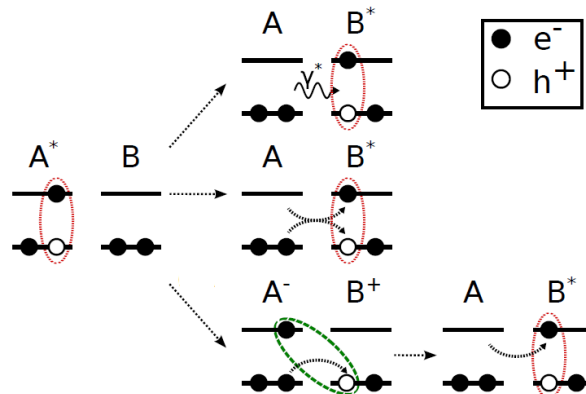


Figure 1.6: Different mechanisms for the excitonic transfer from donor site A to acceptor site B . *Upper:* Förster-like Coulombic excitonic transfer. *Middle:* Dexter-like exchange excitonic transfer. *Lower:* Dexter-like excitonic transfer *via* charge-transfer state. Taken from Wehner & Baumeier (2017).

- b) Dexter-like exchange mechanism: exciton transfer through the simultaneous exchange of the electron and the hole from the donor to the acceptor.
- c) Dexter-like charge-transfer mediated mechanism: exciton transfer through the exchange of electron and hole in two steps; the first of them leads to an intermediate charge-transfer state.

The PDA, TMA and TrEsp methods only consider Förster-like mechanisms, leading to a general underestimation of the excitonic couplings, specially at short distances (Kitoh-Nishioka et al., 2020; Liess et al., 2017; Błasiak et al., 2015).

The contributions of each term are difficult to calculate explicitly, as they require very expensive integrals, involving the ground and excited state wavefunctions of each chromophore. Other methods have been proposed to overcome this limitations, mainly taking advantage of the integrals that are already efficiently calculated in *ab initio* methods.

One of such alternative approaches is based on the full quantum chemical (QC) calculation at a given level of theory of the whole chromophoric network. This is known as the supermolecule approach (S. J. Jang & Mennucci, 2018). These schemes use the fact that the full QC calculation considers the adiabatic transitions of the whole chromophoric system, whose electronic Hamiltonian eigenvalues yield (in principle) to the exact energies of the excitonic states involved in the excitation dynamics. By

projecting this excitonic Hamiltonian onto the sites basis, one can reach to expressions for the excitonic couplings in terms of the adiabatic states and the site energies of the corresponding diabatic states. As this method does not assume an explicit form for the excitonic couplings, this includes the exchange and overlap interactions along with the Coulombic interactions. The quality of these “exact” total excitonic couplings depends on the accuracy of the level of theory used for the calculation in the “supermolecule” and the individual sites, and also, in the validity of the model Hamiltonian used to describe the electronic Hamiltonian of the whole system.

Consider a molecular system of a two-level dimer, in the Frenkel exciton formulation, the Hamiltonian in the site and excitonic basis is given by,

$$\begin{bmatrix} E_1 & J_{12} \\ J_{12} & E_2 \end{bmatrix}_{\text{site}} \Leftrightarrow \begin{bmatrix} E_+ & 0 \\ 0 & E_- \end{bmatrix}_{\text{exc}} \quad (1.2.33)$$

An electronic structure calculation on the whole system necessarily yields the adiabatic states $\{E_-, E_+\}$, which are the eigenstates of the electronic Hamiltonian in the site basis at the equilibrium geometry. In this framework, the adiabatic excited states of the aggregate are expressed via diabatic excited states. These diabatic states are not necessarily unique in the general multisite, multilevel system, and have to be chosen carefully, considering wavefunction arguments or chemical arguments. For complex multilevel, multiconfigurational systems, extensive localization schemes have to be used to determine the matrix transformation between diabatic and adiabatic states, such as the fragment transition density (FTD) method (Voityuk, 2014b).

In particular, for a two-state dimer model, the diabatic states $\{\phi_i, \phi_j\}$ can be selected to be fully localized in the monomers (Voityuk, 2014a). A unitary transformation connects them to the adiabatic states $\{\psi_i, \psi_j\}$,

$$\begin{bmatrix} \phi_i \\ \phi_j \end{bmatrix} = \begin{bmatrix} \cos \omega & \sin \omega \\ -\sin \omega & \cos \omega \end{bmatrix} \begin{bmatrix} \psi_i \\ \psi_j \end{bmatrix} \Rightarrow \Phi = \Omega \Psi \quad (1.2.34)$$

Then, the excitonic coupling is given by,

$$J_{ij}^{Diabat} = \langle \phi_i | \hat{H} | \phi_j \rangle = \frac{E_+ - E_-}{2} \sin 2\omega \quad (1.2.35)$$

where E_+, E_- are the excitonic energies. Ω transforms also the transition dipoles of the diabatic ($\{\vec{\mu}_i, \vec{\mu}_j\}$) and adiabatic ($\{\vec{M}_i, \vec{M}_j\}$) states, then, the coupling is given by

$$J_{ij}^{Diabat} = (E_+ - E_-) \frac{(\vec{M}_i \cdot \vec{M}_j) (\mu_i^2 - \mu_j^2) - (\vec{\mu}_i \cdot \vec{\mu}_j) (M_i^2 - M_j^2)}{(M_i^2 - M_j^2)^2 + 4 (\vec{M}_i \cdot \vec{M}_j)^2} \quad (1.2.36)$$

In completely symmetrical complexes in an isotropic immediate environment, a particular resonance case in which $\varepsilon_1 = \varepsilon_2$ case is achieved. In the resonance condition, $\mu_i^2 = \mu_j^2$ and the coupling can be determined through the oscillator strengths of the excitonic transitions $\{f_+, f_-\}$ and the angle between the dipoles θ , giving that,

$$J_{ij}^{Diabat} = (E_+ - E_-) \frac{E_+ f_- - E_- f_+}{E_+ f_- + E_- f_+} \frac{1}{2 \cos \theta} \quad (1.2.37)$$

Also, the resonance condition assures that the system is at the avoided crossing point, therefore, the direct diagonalization of the Frenkel hamiltonian in the site basis (eq. (1.2.34)) yields the pure adiabatic states. Thus, one can obtain the excitonic coupling from the excitonic splitting as (You & Hsu, 2014),

$$J_{12}^{Diag} = \frac{|E_+ - E_-|}{2} \quad (1.2.38)$$

Notice that these diabaticization approaches depend from electronic structure calculation, therefore, several different methods can be selected to calculate them; from completely wavefunction methods to time-dependent density functional methods.

1.2.3 Linear Optical Absorption

Several spectroscopical techniques can be used to characterize PPCs, however, the most common and least expensive is the linear optical absorption spectroscopy.

In linear absorption spectroscopy, the lineshape of the spectrum represents the interaction between external electromagnetic radiation and the chromophoric aggregate expressed as a linear response of the electric field. Experimentally, the sample is irradiated with a monochromatic light with an initial intensity of I_0 , that, after interacting with the sample, is reduced to $I(z)$. According to Beer's law (May & Kühn, 2011),

$$I(z) = I_0 e^{-\alpha z} \quad (1.2.39)$$

where the linear absorption coefficient $\alpha(\omega)$ depends only on the wavelength of the incident light and the refractive index of the system. Assuming randomly oriented aggregates with density n_{agg} , in a media with refractive index n_r ,

$$\alpha(\omega) = \frac{4\pi\omega n_{\text{agg}}}{3\hbar n_r c} \text{Re} \left[\int_0^\infty dt e^{i\omega t} C_{\text{d-d}}(t) \right] \quad (1.2.40)$$

where $C_{\text{d-d}}(t)$ is the electric transition dipole-dipole correlation function, which depends on the electric transition dipole moment $\vec{\mu}$ as,

$$C_{\text{d-d}}(t) = \langle \vec{\mu}(t) \cdot \vec{\mu}(0) \rangle_{th} \quad (1.2.41)$$

where $\langle \cdot \rangle_{th}$ corresponds to the thermal distribution average operator. Considering the statistical equilibrium operator in the absence of an external field, $\hat{W}_{\text{eq}} = \frac{e^{-\frac{\hat{H}_{\text{ex}}}{k_B T}}}{\mathcal{Z}}$, with partition function $\mathcal{Z} = \text{Tr} \left[e^{-\frac{\hat{H}_{\text{ex}}}{k_B T}} \right]$, the dipole-dipole correlation function, is expressed using the electric transition moment operator $\hat{\mu}$ as (Dinh & Renger, 2015),

$$C_{\text{d-d}}(t) = \text{Tr} \left[\hat{\mu}(t) \cdot \hat{\mu}(0) \hat{W}_{\text{eq}} \right] = \text{Tr} [\hat{\mu} \rho(t)] \quad (1.2.42)$$

For a vibronic system, the electronic behavior is given by the projection of the total aggregate state into the ground-state $|0\rangle$, then, the correlation function is written as (May & Kühn, 2011),

$$C_{\text{d-d}}(t) = \text{Tr}_{vib} \left[\text{Tr}_g \left[\hat{W}_{\text{eq}} U_{\text{agg}}^\dagger(t) \hat{\mu} U_{\text{agg}}(t) \hat{\mu} \right] \right] \quad (1.2.43)$$

where $\hat{W}_{eq} = \hat{R}_0 |0\rangle \langle 0|$ operates over the ground-state, moreover, \hat{R}_0 describes the vibrational equilibrium state of the aggregate, hence,

$$C_{d-d}(t) = \text{Tr}_{vib} \left[\hat{R}_0 \langle 0| U_{agg}^\dagger(t) \hat{\mu} U_{agg}(t) \hat{\mu} |0\rangle \right] \quad (1.2.44)$$

in this representation, the transition dipole operator is given by,

$$\hat{\mu} = \sum_n \hat{\mu}_n \equiv \sum_n \vec{\mu}_n |n\rangle \langle 0| + h.c. \quad (1.2.45)$$

substituting in (1.2.44),

$$C_{d-d}(t) = \sum_{n,m} \text{Tr}_{vib} \left[\hat{R}_0 \hat{\mu}_n^\dagger \langle n| e^{-i\hat{H}_{ext}t} |m\rangle \hat{\mu}_m \right] \quad (1.2.46)$$

Changing to the excitonic basis (eq. (1.2.14)) to diagonalize \hat{H}_{ex} ,

$$C_{d-d}(t) = \sum_{\alpha,\beta} \text{Tr}_{vib} \left[\hat{R}_0 \hat{\mu}_\alpha^\dagger \langle \alpha| e^{-i\hat{H}_{ext}t} |\beta\rangle \hat{\mu}_\beta \right] \quad (1.2.47)$$

Taking the Condon approximation, the transition dipole moment does not depend on the vibrational modes, thus,

$$C_{d-d}(t) = \sum_{\alpha,\beta} \vec{\mu}_\alpha^\dagger \vec{\mu}_\beta \text{Tr}_{vib} \left[\hat{R}_0 \langle \alpha| e^{-i\hat{H}_{ext}t} |\beta\rangle \right] \quad (1.2.48)$$

Equation (1.2.48) is general, and can be used for explicit expression of \hat{R}_0 in the excitonic basis.

If vibronic coupling is neglected, the excitonic states do not mix, then,

$$\begin{aligned} C_{d-d}(t) &= \sum_{\alpha,\beta} \delta_{\alpha\beta} \vec{\mu}_\alpha^\dagger \vec{\mu}_\beta \text{Tr}_{vib} \left[\hat{R}_0 \langle \alpha| e^{-i\hat{H}_{ext}t} |\beta\rangle \right] \\ &= \sum_{\alpha} |\vec{\mu}_\alpha|^2 \text{Tr}_{vib} \left[\hat{R}_0 e^{-iE_\alpha t} \right] \\ C_{d-d}(t) &= \sum_{\alpha} \mu_\alpha^2 e^{-iE_\alpha t} \end{aligned} \quad (1.2.49)$$

substituting (1.2.49) in (1.2.40),

$$\alpha(\omega) \propto \omega \sum_{\alpha} \mu_{\alpha}^2 \delta(\hbar\omega - E_{\alpha}) \quad (1.2.50)$$

This gives a distribution of sharp peaks, called a Dirac comb; to get a proper spectrum lineshape, the Dirac delta function is exchanged by a broadening profile function, which considers the effect of the static disorder. To do this, the statistical distribution $\mathcal{F}(E, \sigma)$ is introduced in substitution of $\delta(E, \sigma)$, and its centered at the excitonic levels E_{α} with a standard deviation σ . Thus, the linear absorption optical spectrum, neglecting vibronic coupling, has the form

$$\alpha(\omega) \propto \omega \sum_{\alpha} \mu_{\alpha}^2 \mathcal{F}(\hbar\omega - E_{\alpha}, \sigma) \quad (1.2.51)$$

for a given distribution $\mathcal{F}(E, \sigma)$.

For the vibronic case, the general time evolution of the transition dipoles has to be considered in equation (1.2.48) via open-quantum system approaches. To consider the continuous lineshape, optical response functions dependent on the wavelength of the incident radiation are used. Description of the interaction between the chromophoric system and the electromagnetic radiation follows from the density matrix formalism and its equations of motion (Gelzinis et al., 2015; Schröter et al., 2015; Jing et al., 2013; Polyutov et al., 2012; Chen et al., 2009; Schröder et al., 2007; Lukeš et al., 2006; Schröder et al., 2006; Yang, 2006; Kleinekathöfer et al., 2005; Yang, 2005; Evers et al., 2001; Renger & May, 2000). Other formulations include the path integral formalism (Moix et al., 2015), and perturbative methods that expand the equations of motion like the cumulants method (S. J. Jang, 2019; Ke & Zhao, 2017; Dinh & Renger, 2015; Gelzinis et al., 2015; J. Ma & Cao, 2015; Banchi et al., 2013; S. Jang & Silbey, 2003). Recently, the tensor product formalism has been extended to the prediction of optical spectra through the TD-DMRG method (Jiang et al., 2020; H. Ma et al., 2018; Yao et al., 2018), giving excellent results, but limited to dimers (Xie et al., 2019; Ren et al., 2018).

1.2.4 *In silico* Determination of Frenkel Parameters

The parameters of the hamiltonian in the Frenkel exciton model describe the relevant electronic structure features of the pigments. An excellent estimation of them is essential to predict the optical properties and dynamics of PPCs.

Their determination is usually performed by fitting experimental spectra to a line-shape model using optimization algorithms as the simplex method (Khmelnitskiy et al., 2019) or genetic algorithms (Renger et al., 2007; Adolphs & Renger, 2006; Raszewski et al., 2005). To predict their values from a theoretical paradigm, TD-DFT methods have been used (Schwinn et al., 2020; Khan et al., 2020; Zanetti-Polzi et al., 2017; Plötz et al., 2016; Wang et al., 2007), perturbative methods (Rocca et al., 2010) or vibronic as TDFI (Fujimoto & Balashov, 2017). Other protocols use multireference techniques to describe excitations in highly symmetric pigments (Anda et al., 2016; Kleinschmidt et al., 2009). More expensive methods use the temporal evolution of the transition density, and then the spectrum is obtained through their Fourier transform (Tussupbayev et al., 2015; Peng et al., 2015; Morzan et al., 2014).

With the improvement of the computational capacity, previously prohibitedly expensive methods are now available, for example, the coupled-cluster method (CC) (Caricato et al., 2015; Höfener & Visscher, 2016). However, this methods still demand a lot of computational resources, therefore, TD-DFT is still the most popular method, as it provides good accuracy at a reasonable amount of computational expense (Curutchet & Mennucci, 2017). Nonetheless, TD-DFT results are heavily dependent on the choice of the associated functional (Bokareva et al., 2015; Jacquemin et al., 2014; Okuno et al., 2012).

The effect of the chosen technique is often evaluated on only one of the spectroscopic parameters, with scarce cases of the evaluation of the joint effect on the spectrum (Kocherzhenko et al., 2017).

1.2.5 Time-Dependent Density Functional Theory (TD-DFT)

In the Density Functional Theory (DFT) formalism, the properties of the ground-state of the molecule are uniquely determined by the tridimensional electron density, which is calculated solving the variational problem of minimizing the energy functional. To consider the system response to an external electromagnetic field, the formalism is extended to the time domain. As the system is conservative, this is given by the one-particle Liouville equation,

$$i\frac{\partial}{\partial t}\gamma(t, \mathbf{r}, \mathbf{r}') = \left[\hat{H}_s, \gamma(t, \mathbf{r}, \mathbf{r}') \right] \quad (1.2.52)$$

where $\gamma(t, \mathbf{r}, \mathbf{r}')$ is the one-particle density matrix constructed from Kohn-Sham orbitals $\phi_i(t, \mathbf{r})$,

$$\gamma(t, \mathbf{r}, \mathbf{r}') = \sum_i \phi_i(t, \mathbf{r}) \phi_i^*(t, \mathbf{r}') \quad (1.2.53)$$

and the diagonal elements of $\gamma(t, \mathbf{r}, \mathbf{r}')$ yield to the time-dependent electron density of the system $\rho(t, \mathbf{r})$.

Eq. (1.2.52) provides a general framework for the response of the electron density to an external potential, however, for vertical transitions, is sufficient to expand $\gamma(t, \mathbf{r}, \mathbf{r}')$ to first-order in the frequency domain, resulting in the linear response equations,

$$\gamma(t) \approx \gamma^{(0)} + \lambda \left(\gamma^{(1)}(\omega) e^{i\omega t} + \gamma^{(1)}(-\omega) e^{-i\omega t} \right) \quad (1.2.54)$$

$$\Rightarrow \left[\hat{H}_s^{(1)}, \gamma^{(0)} \right] + \left[\hat{H}_s^{(0)}, \gamma^{(1)} \right] = \omega \gamma^{(1)} \quad (1.2.55)$$

expanding the linear response density matrix $\gamma^{(1)}$ in Kohn-Sham static orbitals,

$$\gamma^{(1)} = \sum_{ia} [X_{ia}^\omega \phi_a(\mathbf{r}) \phi_i(\mathbf{r}') + Y_{ia}^\omega \phi_i(\mathbf{r}) \phi_a(\mathbf{r}')] \quad (1.2.56)$$

where i runs over the occupied orbitals and a over the virtual orbitals. Using the formalism derived by Casida, the transition energies are computed by solving the eigenvalue

problem:

$$\begin{bmatrix} \mathbf{A} & \mathbf{B} \\ \mathbf{B}^* & \mathbf{A}^* \end{bmatrix} \begin{bmatrix} \mathbf{X} \\ \mathbf{Y} \end{bmatrix} = \omega \begin{bmatrix} 1 & 0 \\ 0 & -1 \end{bmatrix} \begin{bmatrix} \mathbf{X} \\ \mathbf{Y} \end{bmatrix} \quad (1.2.57)$$

the matrices \mathbf{A} y \mathbf{B} are given by,

$$A_{ia,jb} = \delta_{ij}\delta_{ab}(\varepsilon_a - \varepsilon_i) + (ia|jb) + (ia|f_{xc}|jb) \quad (1.2.58)$$

$$B_{ia,jb} = (ia|bj) + (ia|f_{xc}|bj) \quad (1.2.59)$$

this calculation can be computationally expensive, therefore a common approximation implemented is the Tamm-Dancoff approximation (TDA), in which the matrix \mathbf{B} in eq. (1.2.57) is neglected, thus the eigenvalue problem becomes hermitic and is reduced to,

$$\mathbf{A}\mathbf{X} = \omega\mathbf{X} \quad (1.2.60)$$

Usually, TDA calculations are much faster and give similar results than the full TD-DFT calculation (Curutchet & Mennucci, 2017).

The last term in the \mathbf{A} and \mathbf{B} matrices is dependent of the f_{xc} function, which corresponds to the exchange-correlation kernel in the adiabatic approximation,

$$f_{xc} = \frac{\partial^2 E_{xc}}{\partial \rho(\mathbf{r}) \partial \rho(\mathbf{r}')} \quad (1.2.61)$$

this term depends on the exchange-correlation energy E_{xc} , hence the expression is dependent on the selection of the functional $E_{xc}[\rho(\mathbf{r})]$, thus, the excitation energies and the involved orbitals also depend on the functional selection.

1.3 Quantum Effects in the EET

The chromophoric system usually is nowhere near isolated, thus, it is imperative to include couplings between electronic and vibrational states (vibronic coupling). To describe these effects, the density matrix formalism is used.

1.3.1 Density Matrix Formalism

For a system with wavefunction $|\Psi(t)\rangle$, the density matrix $\rho(t)$ is defined as,

$$\rho(t) \equiv |\Psi(t)\rangle \langle \Psi(t)| \quad (1.3.1)$$

Then, for an operator \hat{O} , its expected value is given by,

$$\langle \hat{O} \rangle = \langle \Psi | \hat{O} | \Psi \rangle = \langle \Psi | \hat{O} | \Psi \rangle \langle \Psi | \Psi \rangle = \text{Tr} [\hat{O} \rho] \quad (1.3.2)$$

In the site basis $\{|n\rangle\}$, the wavefunction is expanded as $|\Psi(t)\rangle = \sum_n c_n(t) |n\rangle$, then,

$$\rho(t) = \sum_{nm} c_n(t) c_m^*(t) |n\rangle \langle m| \quad (1.3.3)$$

$$\Rightarrow \langle \hat{O}(t) \rangle = \sum_{nm} c_n(t) c_m^*(t) \langle m | \hat{O} | n \rangle \quad (1.3.4)$$

However, for statistical ensembles of pure states $|\psi_k\rangle = \sum_n c_n^{(k)} |n\rangle$ each with an occupation probability p_k , then, the density matrix is given by (Breuer & Petruccione, 2002),

$$\rho(t) \equiv \sum_k p_k |\psi_k(t)\rangle \langle \psi_k(t)| \quad (1.3.5)$$

As the ensemble is statistical, the occupation probability of each state is given by a thermal distribution,

$$p_n = \frac{e^{-\beta E_n}}{\mathcal{Z}} \quad (1.3.6)$$

where E_n are the eigenvalues of the system hamiltonian, $\hat{H} |n\rangle = E_n |n\rangle$. The statistical equilibrium density matrix is then,

$$\rho_{\text{eq}} = \frac{e^{-\beta\hat{H}}}{\mathcal{Z}} \quad (1.3.7)$$

where the partition function is $\mathcal{Z} = \text{Tr} [e^{-\beta\hat{H}}]$. The matrix elements of ρ_{eq} are then,

$$\langle n | \rho_{\text{eq}} | m \rangle = \langle n | \frac{e^{-\beta\hat{H}}}{\mathcal{Z}} | m \rangle = \frac{1}{\mathcal{Z}} \langle n | e^{-\beta\hat{H}} | m \rangle = \frac{e^{-\beta E_n}}{\mathcal{Z}} \delta_{nm} = p_n \delta_{nm} \quad (1.3.8)$$

Thus, the thermally averaged expected value of \hat{O} is,

$$\langle \hat{O} \rangle_{th} = \frac{1}{\mathcal{Z}} \sum_n e^{-\beta E_n} \langle n | \hat{O} | n \rangle = \text{Tr} [\hat{O} \rho_{\text{eq}}] \quad (1.3.9)$$

Notice that ρ_{eq} is the matrix representation of \hat{W}_{eq} , thus \hat{W}_{eq} is the thermal equilibrium density operator (May & Kühn, 2011).

Also, the correlation function C_{OO} is defined as the thermally averaged expected value of the fluctuation of \hat{O} over a time period,

$$C_{OO}(t) = \langle \hat{O}(t) \hat{O}(0) \rangle_{th} = \sum_n p_n \langle n | \hat{O}(t) \hat{O}(0) | n \rangle \quad (1.3.10)$$

from (1.3.8), $p_n = \langle n | \rho_{\text{eq}} | n \rangle$, then,

$$C_{OO}(t) = \text{Tr} [\rho_{\text{eq}} \hat{O}(t) \hat{O}(0)] = \text{Tr} [\hat{O}(t) \hat{O}(0) \rho_{\text{eq}}] \quad (1.3.11)$$

Then, the dipole–dipole correlation function is expressed as (Dinh & Renger, 2015),

$$C_{\text{d-d}}(t) = \text{Tr} [\hat{\mu}(t) \cdot \hat{\mu}(0) \rho_{\text{eq}}] \quad (1.3.12)$$

and therefore, the absorption spectra can be determined from the density matrix dynamics.

1.3.2 Time evolution of the density matrix

The time evolution of a closed quantum system with wavefunction $|\Psi(t)\rangle$ is expressed by time-dependent Schrödinger equation. If the system is a pure state in a Hilbert space \mathcal{H} , then (Rivas & Huelga, 2012),

$$\frac{\partial}{\partial t} |\Psi(t)\rangle = -\frac{i}{\hbar} \hat{H}(t) |\Psi(t)\rangle \quad (1.3.13)$$

In terms of the density matrix,

$$\begin{aligned} \frac{\partial \rho(t)}{\partial t} &= \frac{\partial}{\partial t} [|\Psi(t)\rangle \langle \Psi(t)|] \\ &= \left[\frac{\partial}{\partial t} |\Psi(t)\rangle \right] \langle \Psi(t)| + |\Psi(t)\rangle \left[\frac{\partial}{\partial t} \langle \Psi(t)| \right] \\ &= -\frac{i}{\hbar} \hat{H}(t) |\Psi(t)\rangle \langle \Psi(t)| + \frac{i}{\hbar} |\Psi(t)\rangle \langle \Psi(t)| \hat{H}(t) \end{aligned} \quad (1.3.14)$$

using (1.3.1), the Liouville–von Neumann equation is obtained,

$$\frac{d}{dt} \rho(t) = -\frac{i}{\hbar} [\hat{H}, \rho(t)] \quad (1.3.15)$$

As the hamiltonian is hermitian, the solution of eq. (1.3.13) is given in terms of the time evolution operator $U(t, t_0)$, a unitary operator so that,

$$|\Psi(t)\rangle = U(t, t_0) |\Psi(t_0)\rangle \quad (1.3.16)$$

Substituting the eq. (1.3.1),

$$\rho(t) = U(t, t_0) \rho(t_0) U(t, t_0)^\dagger \quad (1.3.17)$$

In the case of a time-independent hamiltonian, the system is conservative and the solution is direct,

$$U(t, t_0) = \exp \left[-\frac{i(t-t_0) \hat{H}}{\hbar} \right] \quad (1.3.18)$$

However, when the hamiltonian is time-dependent, the system is not conservative and the time evolution operator is formally expressed as a Dyson expansion (Rivas & Huelga, 2012),

$$U(t, t_0) = \mathcal{T} \exp \left[-\frac{i}{\hbar} \int_{t_0}^t \hat{H}(t') dt' \right] \quad (1.3.19)$$

where \mathcal{T} is the time-ordering operator. For closed non-conservative quantum systems, analytical solutions of eq. (1.3.19) are limited. Instead, perturbative and series expansion techniques are used to correctly describe the time evolution.

To evaluate the expected value of an operator, from eq. (1.3.2), and substituting eq. (1.3.17),

$$\langle \hat{O}(t) \rangle = \text{Tr} [\hat{O}\rho(t)] = \text{Tr} [\hat{O}U\rho(t_0)U^\dagger] = \text{Tr} [U\hat{O}U^\dagger\rho(t_0)] \quad (1.3.20)$$

where $\hat{O}(t) = U^\dagger\hat{O}U$.

1.3.3 Open Quantum System Dynamics

An open quantum system is one that can exchange matter and energy with other quantum system. Usually, the second quantum system corresponds to an ideal quantum model of the environment in which the first system is embedded. Then, the first system is the one of interest is referred simply as “system” and the second one as the “bath” (Rivas & Huelga, 2012).

In general, for an open system, the time evolution operator is not necessarily unitary. To describe correctly its dynamics, the equation of motion (EOM) of the system density matrix: this is called a quantum master equation (Breuer & Petruccione, 2002).

The formulation in terms of the density matrix starts by considering a quantum system S coupled to another quantum system B that corresponds to the bath, the interaction results in a total system $S + B$ (fig. 1.7). The total system is assumed to be closed, and follows the non-dissipative dynamics.

The state of the system S then changes because of its internal dynamics and its interaction with the environment. This coupling leads to system-bath correlations, that cannot be expressed in general as unitary operators. The dynamics of the subsystem S

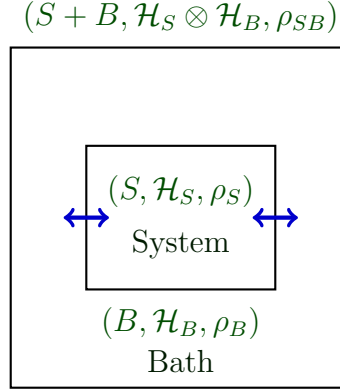


Figure 1.7: Diagram of an open quantum system and its description.

induced by the time evolution of $S + B$ are called reduced system dynamics, therefore, S is often referred as the reduced system.

The Hilbert space of $S + B$ is the tensor product of each subsystem's Hilbert space, that is, $\mathcal{H}_{SB} = \mathcal{H}_S \otimes \mathcal{H}_B$. Then, the total system hamiltonian can be written as,

$$\hat{H}(t) = \hat{H}_S \otimes \mathbb{I}_B + \mathbb{I}_S \otimes \hat{H}_B + \hat{H}_{SB}(t) \quad (1.3.21)$$

where \hat{H}_S is the reduced system hamiltonian, \hat{H}_B is the bath hamiltonian, and \hat{H}_{SB} is the hamiltonian that describes the system–bath interaction.

In terms of the density matrix, the dynamics of S are contained in the reduced density matrix ρ_S , that relates to the total system density matrix, ρ_{SB} , through the partial trace over the bath. Thus,

$$\rho_S = \text{Tr}_B [\rho_{SB}] \quad (1.3.22)$$

Then, the observables of S are expressed as operators of the form $\hat{O} \otimes \mathbb{I}_B$, in eq. (1.3.2),

$$\langle \hat{O} \rangle = \text{Tr}_S [\hat{O} \text{Tr}_B [\rho_{SB}]] = \text{Tr}_S [\hat{O} \rho_S] \quad (1.3.23)$$

The time evolution of the reduced density matrix is obtained by tracing out the bath from the unitary time evolution of the total system density matrix,

$$\rho_S(t) = \text{Tr}_B [U(t, t_0) \rho_{SB}(t_0) U^\dagger(t, t_0)] \quad (1.3.24)$$

substituting in (1.3.15),

$$\frac{d}{dt}\rho_S(t) = -\frac{i}{\hbar}\text{Tr}_B \left[\left[\hat{H}(t), \rho_{SB}(t) \right] \right] \quad (1.3.25)$$

The solution of eq. (1.3.25) can be very difficult, if not impossible, due to the large and complicated structure of the environment and the complex relations to the system. Therefore, several assumptions and approximations about the reduced dynamics are used to simplify and solve the QME.

For instance, one of such assumptions is that the system state only depends on the previous state, therefore, it has no memory of its history. This condition defines a Markovian process, and in this approximation the initial state is a non-correlated product state $\rho_{SB}(t_0) = \rho_S(0) \otimes \rho_B$. Markovian QMEs can be derive from this, like Gornik–Kossakowski–Sudashan–Lindblad (commonly just called simply the Lindblad equation) and the Redfield equation. For non-Markovian process, numerically exact approaches are needed, such as the density matrix renormalization group (DMRG) and hierarchical equations of motion (HEOM) (Ishizaki & Fleming, 2009; Tanimura, 2006; Breuer & Petruccione, 2002; Tanimura & Kubo, 1989).

1.3.4 Quantification of Quantum Phenomena

The presence of quantum phenomena; such as superposition, coherence, interference or entanglement; in macroscopic processes is difficult to probe, as the access to the system is limited by the delicate dynamics of quantum systems and the projective nature of the measurements; as the wavefunction collapses upon measurement.

For the photosynthetic PPC, once the dynamics of the system is modelled, the question to answer is: “the characteristics of this EET can only be explained by the presence of quantum phenomena?”. This is specially difficult to demonstrate for biological systems, as the environment is usually very complex, constantly changing and at high temperatures.

To evaluate this question, multiple protocols have been proposed, and can be classified into two categories (C.-M. Li et al., 2012). The first one is the imposition of a

classical restriction: *if the behaviour of the system can be totally explained by classical theories, then it must meet this condition.* For these protocols, conditions proper of classical systems are assumed and then tested in terms of the system. Two of them stand out: if macrorealism and the ability to make non-invasive measurements are imposed, then the system must follow the Leggett-Garg inequality for the system to be considered “classical” (Leggett & Garg, 1985); however, if realism and locality are imposed instead, then the system must follow the Bell inequality to be classical (Bell, 1964). Nevertheless, this type of test present multiple experimental challenges, as the design of non-invasive experiments with very high resolution observables (Wilde et al., 2010) or the simultaneous measurement of different observables in isolation and spatial separation condition (Żukowski & Brukner, 2002).

The second group of protocols are based on deductive logic: *if the dynamics observed correspond sufficiently well with the ones predicted by quantum theory, then the system must be quantum;* similarly for classical systems. Quantum witnesses are found in this second category: functions that are defined from quantum theory and are parametrized in terms of the system observables or states, so that their numerical value serves as a metric that gives direct information about the presence or absence of a particular quantum effect in the system. This allows for the direct evaluation of the quantum characteristics from experimental data, with a quick and effective method, without experimental procedure modifications that increases the overhead in the methodology.

The witnesses have been used to quantify multiple quantum phenomena, for example, they have been used to demonstrate the existence of quantum coherence (Monras et al., 2014), quantum entanglement (Hansen et al., 2015), non-locality (Horodecki et al., 1995), quantum discord (Rulli & Sarandy, 2011; Ollivier & Zurek, 2002), quantum teleportation (Salikhov et al., 2007), and even the *quantumness* itself of the system (C.-M. Li et al., 2012).

For PPCs, the presence of quantum coherence has been experimentally observed (Collini et al., 2010), and since then, theoretical examinations have been used to probe for other quantum features in the EET. For example, quantum coherence has been examined through the concurrence witness (Hill & Wootters, 1997) in multiple theoretical

examinations as a basic characterization (Saber et al., 2016; Bengtson et al., 2016; Oka, 2016; Sarovar et al., 2010). Moreover, other studies have used quantum discord to demonstrate the presence of unequivocally quantum correlations in LHCs (Brádler et al., 2010), or the von Neumann entropy to demonstrate the existence of quantum entanglement between the excitonic levels of the chromophoric aggregate (Sarovar et al., 2010), or to demonstrate the teleportation of quantum information across the biological membranes through charge separation in transmembrane RCs (Salikhov et al., 2007). The selection of adequate quantum witnesses and their evaluation allows to analyze the influence of quantum phenomena on the EET dynamics of photosynthetic systems.

1.3.5 Quantum Coherence

Two waves are coherent when their frequency and waveform coincide (Griffiths & Schroeter, 2018). As both waves interfere with each other, the coherence implies the correlation between both signals, which show a constant relative phase between them (Glauber, 1963). Coherence is an essential feature of quantum systems, as its in the center of the superposition of quantum states (Huelga & Plenio, 2013).

Several witnesses can be proposed to probe for quantum systems, usually based on functions of the off-diagonal entries of the density matrix, following the physical intuition from the statistical definition of correlation (Baumgratz et al., 2014). For multichromophoric PPCs, the distribution of coherence can be tested usgin the concurrence witness (Sarovar et al., 2010; Hill & Wootters, 1997). In this case, the premise of superposition between the excited states of two chromophores can be interpreted as the 2-qubit entanglement, leading to a global mixed state; thus, the off-diagonal elements of the density matrix should be non-zero. Hence, the concurrence witness for each pair of chromophores (i, j) is given by,

$$C_{ij} = 2 |\rho_{ij}| \quad ; \quad i \neq j \quad (1.3.26)$$

and proper measures of total coherence are the ones which are monotonically decreasing upon the decrease of coherence, which lead to several measures (Baumgratz et al., 2014).

Two of them are: the L^1 -norm of coherence,

$$\mathcal{C}_{L^1} = \sum_{i,j:i \neq j} |\rho_{ij}| \quad (1.3.27)$$

and the relative entropy of coherence,

$$\mathcal{C}_S(\rho) = S(\rho_{diag}) - S(\rho) \quad (1.3.28)$$

where S is the von Neumann entropy and ρ_{diag} denotes the matrix built by only taking the diagonal elements of ρ and setting the rest off-diagonal elements to zero.

The prevalence of quantum coherence has been studied on several PPCs through ultrafast spectroscopic techniques (Schlau-Cohen et al., 2012; Engel et al., 2007). Multiple experimental studies have explored the quantum coherence on cryogenic temperatures (Meneghin et al., 2019, 2018; Dostál et al., 2012), at physiological temperatures (Panitchayangkoon et al., 2010), their dependence on pH (Turner et al., 2012), robustness (Hayes et al., 2011), among other effects. Its functional relevance and potential as a light-harvesting resource is still an active area of research, as no consensus has been reached on the scientific community (Romero et al., 2014; Ai et al., 2013; Calhoun & Fleming, 2011; Hoyer et al., 2010; Sarovar et al., 2010; H. Lee et al., 2009).

1.3.6 Quantum Transport

The term “quantum transport” has been referred to the regimen where the effects of quantum coherence alters the energy transfer dynamics. This means that not only the quantum coherence is present, but also it modulates the excitonic populations on each site. In this sense, the necessary and sufficient condition to sustain quantum transport is the coupling between the quantum coherence and site excitonic occupations in their time evolution (Panitchayangkoon et al., 2011).

The dynamics of quantum transport in a PPC can be observed through the coupling of the coherence and occupations witnesses of the reduced density matrix. In this framework, the transfer of populations of entries in the $\rho_{kl} \rightarrow \rho_{ii}$ direction, with $k \neq l$,

indicates quantum transport. This implies that excitonic site occupations are transferred through the zones where quantum coherence is present, impulsing an specific route and quantum coherence drives the dynamics. This reduces the incoherent jumps and intersystem crossings that lead to thermal relaxation. This mechanism is the one suggested to explain the abnormally high efficiencies observed in EET in photosynthetic LHCs (Chin et al., 2013; Hayes et al., 2010; Ishizaki et al., 2010; Caruso et al., 2009; Mohseni et al., 2008; Plenio & Huelga, 2008).

To witness quantum transport, the interplay between the excitonic coherence $\rho_{\alpha\beta}(t)$ between the two excitons $|\alpha\rangle$ and $|\beta\rangle$, and the site populations ρ_{ii} must show the same oscillation frequency, which implies that both phenomena are synchronized (Panitchayangkoon et al., 2011; Hayes et al., 2010).

Chapter 2

Computational Methods

2.1 WSCP Structure Preparation

The studied PPC corresponds to the chlorophyll *b* chromophoric aggregate of the WSCP type II recombinant from cauliflower (*Brassica oleracea* var. *Botrytis*), shown on figure 2.1.

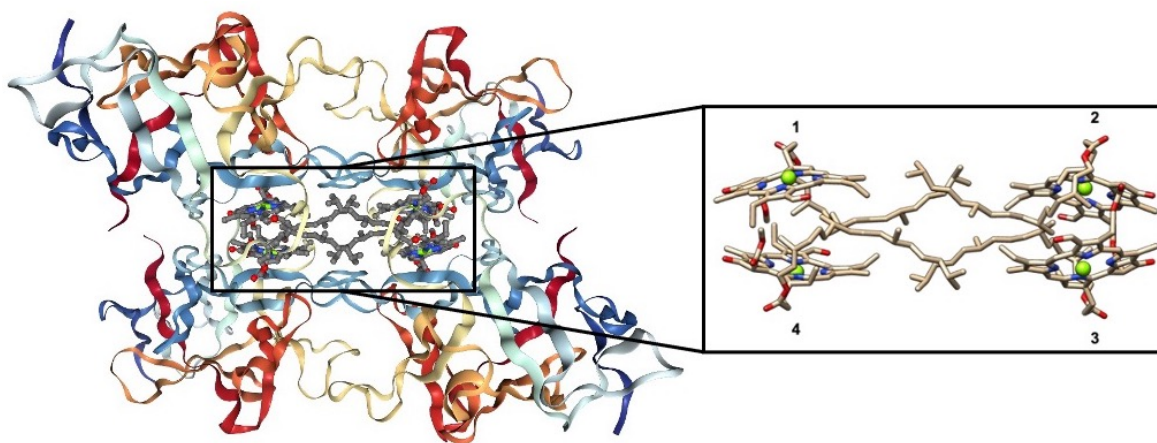


Figure 2.1: Crystal structure of the Class II WSCP-Chl *b* from cauliflower studied (PDB ID: 6S2Z), and detailed view of the geometry of the chromophoric network.

The most recent XRD crystal structure was used for the Chl *b* WSCP (Agostini et al., 2019), deposited on the Protein Data Bank (Burley et al., 2021) with code 6S2Z. The experimental coordinates were obtained directly from the PDB website (<https://www.rcsb.org/>) and cleaned using the `pdb4amber` functionality of AmberTools2022 (Case et al., 2022). All hydrogens were added using the MolProbity web service (Williams et al., 2018).

The biological assembly shows that the protein chains self-assemble into a tetramer quaternary structure, however the XRD structure resolves only the monomer. The other subunits are built using C_2 symmetry operations, therefore, the coordinates of each chromophore are equivalent in their own frame of reference with the origin at their center-of-mass. The dimer is built from the coordinates of the two chromophores facing each other (chains A and D of the biological assembly for 6S2Z), including all hydrogens, the chlorin macrocycle, the magnesium center and the phytol tail. The PDB file was converted to XYZ format using the OpenBabel software (O’Boyle et al., 2011). No geometry optimization was performed, the structure is analyzed as is. The

coordinates used in the calculations are given in the Appendix A.

2.2 TD-DFT Calculations

To determine the Frenkel parameters of the studied PPCs by computational *ab initio* methods, the TD-DFT paradigm was used. The calculation was performed using the all electron def2-TZVP basis sets in every atom. To account for the variety of definitions and parametrizations of functionals, 21 different functionals were considered, divided in 5 categories:

- GGA: BLYP (Becke, 1988; C. Lee et al., 1988), BP86 (Becke, 1988; Perdew, 1986), PBE (Perdew, Burke, & Ernzerhof, 1996; Perdew, Ernzerhof, & Burke, 1996).
- meta-GGA: B97M-V (Mardirossian & Head-Gordon, 2015), B97M-D3BJ (Najibi & Goerigk, 2018), M06-L (Zhao & Truhlar, 2008, 2006), TPSS (Perdew et al., 2004; Tao et al., 2003).
- General Hybrids: BHHLYP (Becke, 1993b), B3LYP (Becke, 1993a), X3LYP (Xu & Goddard, 2004), O3LYP (Hoe et al., 2001; Cohen & Handy, 2001), PBE0 (Adamo & Barone, 1999).
- meta-GGA Hybrids: M06 (Zhao & Truhlar, 2008), M06-2X (Zhao & Truhlar, 2008), TPSSh (Staroverov et al., 2003).
- Range-Separated Hybrids: LC-BLYP (Iikura et al., 2001), ω B97X-V (Mardirossian & Head-Gordon, 2014), ω B97X-D3BJ (Najibi & Goerigk, 2018), CAM-B3LYP (Yanai et al., 2004), CAMh-B3LYP (Shao et al., 2020), Tuned-CAM-B3LYP (Okuno et al., 2012).

Two variations of the calculations were considered: the full TD-DFT calculation and employing the Tamm-Dancoff approximation (TDA). For all available cases, dispersion correction was taken into account by means of the DFTD3 with Becke-Johnson damping (D3BJ): for the functionals O3LYP, X3LYP, M06, M06-L, M06-2X and LC-BLYP, D3BJ corrections are not available. For B97M and ω B97X, the dispersion corrections

are included in the functionals B97M-D3BJ and ω B97X-D3BJ respectively; the functionals B97M-V and ω B97X-V use the VV10 scheme for the dispersion corrections. All calculations were performed with the ORCA 4.2.1 quantum chemical package (Neese, 2018, 2012).

For comparison, the monomer spectra was determined using TD-DFTB, an approximate semiempirical method based on TD-DFT theory. This calculation was performed using the Casida formalism, and the 3ob-3-1 Slater-Koster files, using the D3BJ dispersion. These calculations were performed using the DFTB+ 19.1 suite (Hourahine et al., 2020).

To compare TD-DFT and TD-DFTB results, the transitions obtained were broadened using a Gaussian distribution each peak i centered around $\tilde{\nu}_i$, given by

$$\varepsilon_i(\tilde{\nu}) = \varepsilon_i^{max} \exp \left[- \left(\frac{\tilde{\nu} - \tilde{\nu}_i}{\sigma} \right)^2 \right] \quad (2.2.1)$$

where $\varepsilon_i(\tilde{\nu})$ is the molar absorptivity at a wavenumber $\tilde{\nu}$ and σ is the full-width mid-height (FWMH). The values of $\varepsilon_i(\tilde{\nu})$ were determined from the oscillator strengths f_i using the relation,

$$\varepsilon_i^{max} = \frac{\sqrt{\pi} e^2 N_A}{1000 \ln 10 c^2 m_e \sigma} f_i \quad (2.2.2)$$

$$= (1.3062974 \times 10^8 \text{ L mol}^{-1} \text{ cm}^{-2}) \frac{f_i}{\sigma} \quad (2.2.3)$$

Both the TD-DFT and TD-DFTB calculated transitions were broadened using the same procedure with the same FWHM ($\sigma = 282 \text{ cm}^{-1}$).

2.3 Frenkel Model Parametrization

Model hamiltonians were obtained, according to the Frenkel exciton approach in eq. (1.2.12). Therefore, the hamiltonian takes only the site energy and the excitonic coupling. By symmetry, the structure is bidimeric, with $J_{14} = J_{23} \gg J_{12}, J_{13}, J_{34}$, therefore, the modeling can be simplified to the dimer case with a 2×2 matrix hamiltonian, by neglecting

all couplings except for J_{14} remaining (Renger et al., 2009).

For the experimental parameters, the site energies are taken from spectroscopical data (Dinh & Renger, 2015), the excitonic couplings were calculated using the TrEsp method employing the previously reported transition charges (Renger et al., 2009, 2007; Madjet et al., 2006), for the rescaling constants, a transition dipole intensity of 3.6 D was used, based on experimental data from Chl b linear absorption spectroscopy (Renger et al., 2007; Knox & Spring, 2003). The TrEsp coupling found in the literature is 72 cm^{-1} , however, this was calculated using the Chl a WSCP structure from *Lepidinium virginicum*, reconstituted with Chl b (PDB ID: 2DRE); in this work, this value was corrected using the coordinates from Chl b WSCP from *Brassica oleracea* var. *botrytis*, which results in a corrected value of 75.3 cm^{-1} .

For the calculated site energies, the transition energy of the vertical $S_0 \rightarrow S_1$ transition of the monomer is taken directly as the site energy. The transition is considered valid only if it is pure and is distinctly higher in intensity and well separated from other transitions, therefore, the highest of the first 10 calculated transitions was selected as the site energy. For the Chl b monomer studied, this criteria is sufficient to ensure the quality of the site energies, however, it should be noted that this is not a general method, and for other systems the transitions have to be carefully analyzed, as dark transitions can play a fundamental role in the EET. In addition to this, very diffuse transitions can be calculated, which render the Frenkel approximation invalid in the selected Hilbert space.

In the case of the excitonic couplings, both Coulombic and diabatic methods were evaluated. For the Coulombic methods, the point-dipole approximation (PDA), the transition monopole approximation (TMA) with the transition charges previously reported (Chang, 1977), and the TrEsp method were used. For the PDA, the transition dipole vectors were centered on each magnesium atom of the chlorin macrocycle, and are oriented in the $N_A - N_C$ directions. For both TMA and TrEsp, both methods were rescaled using the 3.6 D experimental dipole.

The diabatic method employed corresponds to the Fragmented Transition Density (FTD) method (Voityuk, 2014b), for the two-level dimer particular case (Voityuk,

2014a). This method is based on the calculation of the diabatic and adiabatic states, therefore TD-DFT calculations were performed on the monomers and dimers. From the monomers calculations, the diabatic states are obtained, selecting them with the same criteria as the site energies. From the dimer calculation, the adiabatic states are selected as the two most intense transitions from the first 15 excited states calculated, such that the splitting between their transition energies was at least in the order of 10^2 cm^{-1} . As the coupling relies on the full *ab initio* calculation of the supermolecule, one coupling is obtained for each functional. For all selected excited states, their characteristics (transition electric dipole, transition energy, oscillator strength) were used as is, no further rescaling was applied.

2.4 Optimization of Linear Absorption Spectra

For the modeling of the optical spectra, the parametrization takes the hamiltonian and the electric transition dipole of the monomers, according to eq. (1.2.40). The hamiltonian was parametrized using the Frenkel model, as previously specified, making use of experimental and *ab initio* parameters. For the transition dipoles, also both versions were considered, and matched correspondingly for the modelling.

The experimental electric transition dipole strength of 3.6 D was considered in the direction between the nitrogen atoms from the A and C pyrrol rings (N_A-N_C) of each chromophore (Renger et al., 2007), with the Mg at the chromophoric center of the pigment. Also, a variation of the transition dipole vector was considered, using the best fitting angle of $\theta \approx 39^\circ$ determined from the experimental absorption spectra by Dinh & Renger (2015). These vectors coordinates were calculated assuming that:

- The dipole strength is kept at 3.6 D
- The center of each chromophore is kept at the Mg atom
- The C_2 symmetry constraint between the monomers, and therefore, their dipoles
- The vector is fully in the best fitting plane of the chlorin macrocycle of the chlorophyll

- The open angle between the dipoles is fixed at $\theta = 39^\circ$

this solves for the 3 coordinates of both transition dipoles.

For the TD-DFT parameters, the *ab initio* transition dipoles were used directly from the calculation. As this method can only predict energy of the radiation interaction with the molecule up to its magnitude squared, then $|\vec{\mu} \cdot \vec{E}| = |-\vec{\mu} \cdot \vec{E}|$, the transition dipoles' direction can be freely inverted. Following the structural information, the transition dipoles are inverted to give an acute opening angle.

The protein static disorder (Stross et al., 2016) greatly influences the optical spectra, as it represents slight equilibrium variations of the structure within the crystal, and produces an inhomogeneous broadening, due to the resulting random variations in the site energies, according to eq. (1.2.51). This effect was considered by using a statistical distribution around the site energies with standard deviation σ .

For the non-vibronic modelling, three distributions were tested for profiling: Gaussian, Lorentzian and Voigtian. The static disorder parameter σ was estimated by varying it between 1.0 and 500.0 cm^{-1} with a 1.0 cm^{-1} step, and comparing the resulting spectra with the experimental one (Dinh & Renger, 2015).

To compare between spectra, three different curve matching metrics were evaluated as possible similarity figures of merit: the L^1 -norm, L^2 -norm and Procrustes distance (Gower & Dijkstra, 2004). For all the spectra, the similarity analysis is performed between the normalized calculated absorption spectrum and the experimental (Dinh & Renger, 2015) measured at 77 K; centering both at their maximum. Maximization of the similarity against the static disorder gives the estimated parameter for the protein.

To evaluate the quality of the parameters obtained by TD-DFT, linear absorption spectra were obtained using the numerically exact simulations through the hierarchical equations of motion (HEOM) method optimized for absorption spectra of the Chl b dimer in WSCP (Caycedo-Soler et al., 2022), considering the experimental spectral density determined by difference fluorescence line-narrowing spectroscopy (Δ -FLN) for both pigments (Kell et al., 2013; Pieper et al., 2011). The HEOM calculations were performed by Jaemin Lin, from the Institute of Theoretical Physics and IQST of the

Ulm University. This HEOM simulations consists a fully vibronic modelling with extremely high accuracy. All of the simulated spectra are rescaled for comparison so that the maximum absorption of the spectra is normalized to unity.

The fully vibronic spectra, along with the experimental, was then deconvolved into two absorption peaks, corresponding to the two excitonic bands expected according to the theory. The excitonic splitting and the relative height of the deconvolved bands were compared for TD-DFT parameters and experimental spectra to determined the best protocol to obtain a fully *ab initio* linear absorption spectra of the chromophoric system.

2.5 Closed System Dynamics

In the limit of null coupling to the environment, the hamiltonian of the total system is equivalent to the reduced system, and so, it has the form of the Frenkel hamiltonian previously analyzed (eq. (1.2.12)) and the reduced system dynamics are given by the direct solutions of eq. (1.3.15). Considering that $t_0 = 0$ fs, then the explicit reduced density matrix time evolution is given by,

$$\rho(t) = \exp\left[-\frac{it\hat{H}_{agg}}{\hbar}\right]\rho_0 \exp\left[\frac{it\hat{H}_{agg}}{\hbar}\right] \quad (2.5.1)$$

where $\rho_0 = \rho(t = 0)$ represents the initial conditions for the system. Several different choices can be considered for the starting state, in particular:

1. Single local excitation: the initial state is the single vertical excitation localized on one monomer. This is the most usual consideration, following the physical intuition of the process: first a photon excites a single chromophore to start the EET. Considering the site basis, the initial state takes the form $|n\rangle \langle n|$.
2. Single delocalized exciton: the initial state is one of the excitonic levels of the chromophoric aggregate, which is not necessarily localized on a single monomer, according to eq. (1.2.14). Considering the exciton basis, the initial state takes the form $|\alpha\rangle \langle \alpha|$.

3. Thermalized: in this condition, the reduced system is in thermal equilibrium with the bath, therefore the initial state coincides with the statistical equilibrium density matrix, according to eq. (1.3.7).

Here, the Liouville-von Neumann dynamics are analyzed for the Chl b WSCP (PDB ID: 6S2Z) using the previously obtained parameters using the TD-DFT methods. In particular, the functionals ω B97X-D3BJ, CAM-B3LYP and CAMh-B3LYP are considered.

The effects of the static disorder are essential to the description of dynamics, as slight variations can interfere with the delicate quantum dynamics (Cleary & Cao, 2013; Jing et al., 2012; S. Jang et al., 2001; Barvík et al., 1998). This is considered through the statistical average of 10^3 trials of the dynamics simulation. In each trial, the site energies are sampled from a normal distribution around the determined site energies with the optimized σ as standard deviation. The initial condition is set as the single local excitation over the first chromophore in each trial,

$$\rho_0 = |1\rangle \langle 1| = \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \quad (2.5.2)$$

for the Chl b dimer studied. The reduced system dynamics was simulated from 0 to 3000 fs on each trial with a 1 fs step, obtaining the matrix elements of ρ at each time. Then, the matrices at each fixed time are recursively averaged through the trials.

To evaluate the quantum effects in the dynamics, several quantum witnesses were analyzed. First, the total energy was determined using eq. (1.3.9). The populations of the sites were determined using the absolute values of the corresponding diagonal elements $|\langle n | \rho(t) | n \rangle|$, while the bipartite coherences between sites was calculated using the absolute values of the relative entropy of coherence, $\mathcal{C}_S(\rho(t))$, according to eq. (1.3.28). The purity of the state was assessed using the radius of its Bloch vector.

Quantum transport has been evaluated examining the frequencies of the excitonic coherence and populations beating. The excitonic coherence refers to bipartite coherence between the excitonic states, defined by $|\langle + | \rho(t) | - \rangle|$, where $|\pm\rangle$ are the excitonic states. This graph generally shows a decay added to the beatings, therefore, an exponential fitting was performed on the excitonic coherence data, and subtracted to obtain

the pure excitonic coherence beating. For the population and pure coherence beating, their Fourier transform was calculated using the Fast Fourier Transform for discrete data (FFT), to get their frequency components. A peak coincidence between both transforms is shown in their frequencies.

All witnesses were calculated over the averaged trajectory dynamics.

2.6 Open System Dynamics

To consider the effect of the environment, a first approach using the Redfield QME was employed. In this approach, the excitonic coupling is considered strong and the system-bath coupling is weak. In this limit, the relaxation is considered between excitonic states, and the EET dynamics are given by the Redfield equations (Cheng & Fleming, 2009; Breuer & Petruccione, 2002; Redfield, 1957),

$$\frac{d\rho_{\alpha\beta}(t)}{dt} = -i\omega_{\alpha\beta}\rho_{\alpha\beta}(t) - \sum_{\gamma\delta} R_{\alpha\beta,\gamma\delta}(t) \rho_{\gamma\delta}(t) \quad (2.6.1)$$

where $\omega_{\alpha\beta} = \frac{E_\beta - E_\alpha}{\hbar}$ is the energy gap frequency between the excitons, and the matrix elements $\rho_{\alpha\beta}$ are the reduce density matrix (RDM) elements in the exciton basis.

The first term of the right-hand side (RHS) refers to the evolution of coherently associated excitonic states, while the second term is referred as the dissipative term, and summarizes the dynamics of energy dissipation of the reduced system to the bath. The tensor \hat{R} with elements $R_{\alpha\beta,\gamma\delta}(t)$ is the Redfield relaxation tensor and describes the transfer rate from $\rho_{\gamma\delta}$ to $\rho_{\alpha\beta}$ at time t . By taking the weak bath approximation, a second order perturbative approach can be used to yield the tensor elements as,

$$R_{\alpha\beta,\gamma\delta} = - \int_0^t d\tau \left[\langle \Phi_{\delta\beta}(0) \Phi_{\alpha\gamma}(\tau) \rangle e^{-i\omega_{\delta\beta}\tau} + \langle \Phi_{\delta\beta}(\tau) \Phi_{\alpha\gamma}(0) \rangle e^{-i\omega_{\alpha\gamma}\tau} \right. \\ \left. - \delta_{\delta\beta} \sum_s \langle \Phi_{\delta s}(\tau) \Phi_{s\gamma}(0) \rangle e^{-i\omega_{s\gamma}\tau} - \delta_{\gamma\alpha} \sum_s \langle \Phi_{\delta s}(0) \Phi_{s\beta}(\tau) \rangle e^{-i\omega_{\delta s}\tau} \right] \quad (2.6.2)$$

where the operators Φ_α correspond to the bath operators coupled to the chromophores. Then, the tensor elements can be interpreted as,

- a) $R_{\alpha\alpha,\alpha\alpha}$ describes the depopulation of state $|\alpha\rangle$
- b) $R_{\alpha\alpha,\beta\beta}$ describes the population transfer from $|\beta\rangle$ to $|\alpha\rangle$
- c) $R_{\alpha\beta,\alpha\beta}$ ($\alpha \neq \beta$) describes the dephasing of the coherence between states $|\alpha\rangle$ and

$|\beta\rangle$, expressed in the decay of coherence $|\alpha\rangle\langle\beta|$

- d) $R_{\alpha\beta,\gamma\delta}$ ($\omega_{\alpha\beta} - \omega_{\gamma\delta} \neq 0$) describes the coherence transfer directly from $|\gamma\rangle\langle\delta|$ to $|\alpha\rangle\langle\beta|$

At long simulation times, the Redfield tensor relaxation is time-independent, and the coherence transfer terms are neglected, this is called the secular approximation. Also, this implies that the reduced system has no memory, and therefore the system is Markovian.

In the exciton basis, the WSCP dimer is a TLS and the environment can be approximated by a collection of quantum harmonic oscillators which ground states correspond to the collective bath vibrational states of the protein scaffold normal modes. For this system, the exciton states are dubbed $|+\rangle$ for the higher exciton level and $|-\rangle$ for the lower exciton level. Restricting to the secular approximation, eq. 2.6.1 reduces to (May & Kühn, 2011),

$$\frac{d\rho_{++}}{dt} = -k_{+\rightarrow-}\rho_{++} + k_{-\rightarrow+}\rho_{--} \quad (2.6.3)$$

$$\frac{d\rho_{+-}}{dt} = -i(\Omega - i\gamma)\rho_{+-} \quad (2.6.4)$$

where $\Omega = \frac{E_+ - E_-}{\hbar}$ and the other matrix elements follow the relations,

$$\rho_{--} = 1 - \rho_{++} \quad (2.6.5)$$

$$\rho_{-+} = \rho_{+-}^* \quad (2.6.6)$$

the transition rates ($k_{\alpha\rightarrow\beta}$) and dephasing rate (γ) are given by,

$$k_{+\rightarrow-} = 2(1 + n(\Omega))\mathcal{J}(\Omega) \quad (2.6.7)$$

$$k_{-\rightarrow+} = 2n(\Omega)\mathcal{J}(\Omega) \quad (2.6.8)$$

$$\gamma = \frac{1}{2}\left(k_{+\rightarrow-} + k_{-\rightarrow+}\right) + \gamma^{(\text{pd})} \quad (2.6.9)$$

where the $\gamma^{(\text{pd})}$ correspond to the pure dephasing rate, which comes from elastic interactions between the system and the bath that changes the coherence but not the energy content of the reduced system. The function $n(\omega)$ is the Bose-Einstein distribution function,

$$n(\omega) = \frac{1}{\exp\left[\frac{\hbar\omega}{k_B T}\right] - 1} \quad (2.6.10)$$

which indicates the average number of phonons in the vibrational state with frequency ω .

The function $\mathcal{J}(\omega)$ corresponds to the spectral density, and it describes the coupling strength between an electronic transition and the vibrational modes of the bath, as a function of the bath mode vibrational frequency ω . Therefore, $\mathcal{J}(\omega)$ contains all the necessary information to fully characterize the system-bath interaction.

The spectral density can be decomposed into two parts as $\mathcal{J}(\omega) = \mathcal{J}_l(\omega) + \mathcal{J}_h(\omega)$. The low energy part $\mathcal{J}_l(\omega)$ corresponds to a broad distribution, and the medium-to-high energy part $\mathcal{J}_h(\omega)$ has a discrete structure, with several peaks generally attributed to the intramolecular vibrations effects (Rosnik & Curutchet, 2015).

The low energy part depends on the specific protein, but can be well approximated by lognormal distribution functions (Kell et al., 2013),

$$\mathcal{J}_l(\omega) = \sum_{k=1}^N \frac{s_k}{\sigma_k \sqrt{2\pi}} \omega \exp\left[-\left(\frac{\ln \frac{\omega}{\omega_k}}{\sigma_k \sqrt{2}}\right)^2\right] \quad (2.6.11)$$

for the Chl b WSCP, $N = 3$ and $\{s_1, s_2, s_3\} = \{0.39, 0.23, 0.23\}$, $\{\sigma_1, \sigma_2, \sigma_3\} = \{0.40, 0.25, 0.20\}$ and $\{\omega_1, \omega_2, \omega_3\} = \{0.40, 0.25, 0.20\} \text{ cm}^{-1}$.

The high energy part can be considered from the experimental resonances observed via Δ -FLN (Kell et al., 2013). For each resonance, its energy ω_k and Huang-Rhys factor s_k is measured and then its broadened using the dressing function,

$$j_k(\omega) = \frac{4s_k\omega_k\Gamma\omega(\omega_k^2 + \Gamma^2)}{\pi [(\omega + \omega_k)^2 + \Gamma^2] [(\omega - \omega_k)^2 + \Gamma^2]} \quad (2.6.12)$$

then, $\mathcal{J}_h(\omega) = \sum_{k=1}^M j_k(\omega)$ for a system with M vibrations, with Γ being the inverse of the characteristic broadening lifetime of the vibrational modes, $\Gamma = \tau_{brd}^{-1}$. For the Chl b WSCP, 55 vibrations have been resolved, their complete distribution is given in Appendix B.

To simplify the structure of the spectral density, a coarse-grained spectral density is considered, where the high-frequency modes are approximated by a Lorentzian spectral density (Blau et al., 2018),

$$\mathcal{J}_{CG} = \frac{4s_{CG}\omega_{CG}\Gamma_{CG}\omega(\omega_{CG}^2 + \Gamma_{CG}^2)}{\pi [(\omega + \omega_{CG})^2 + \Gamma_{CG}^2] [(\omega - \omega_{CG})^2 + \Gamma_{CG}^2]} \quad (2.6.13)$$

for the WSCP, the parameters for coarse-graining are $\{\omega_{CG}, s_{CG}\} = \{1350 \text{ cm}^{-1}, 0.49\}$.

Here, 3 spectral densities are used for the simulation: an underdamped density ($\Gamma = (1 \text{ ps})^{-1}$), an overdamped density ($\Gamma = (50 \text{ fs})^{-1}$), and a coarse-grained density ($\Gamma_{CG} = (50 \text{ fs})^{-1}$). Fig. 2.2 shows a comparison between them. The pure dephasing was considered adding typical values according to Caycedo-Soler et al. (2022), using $\gamma^{(pd)} = 0 \text{ ps}^{-1}$ for no pure dephasing, and $\gamma^{(pd)} = (2 \text{ ps})^{-1}$ with finite pure dephasing.

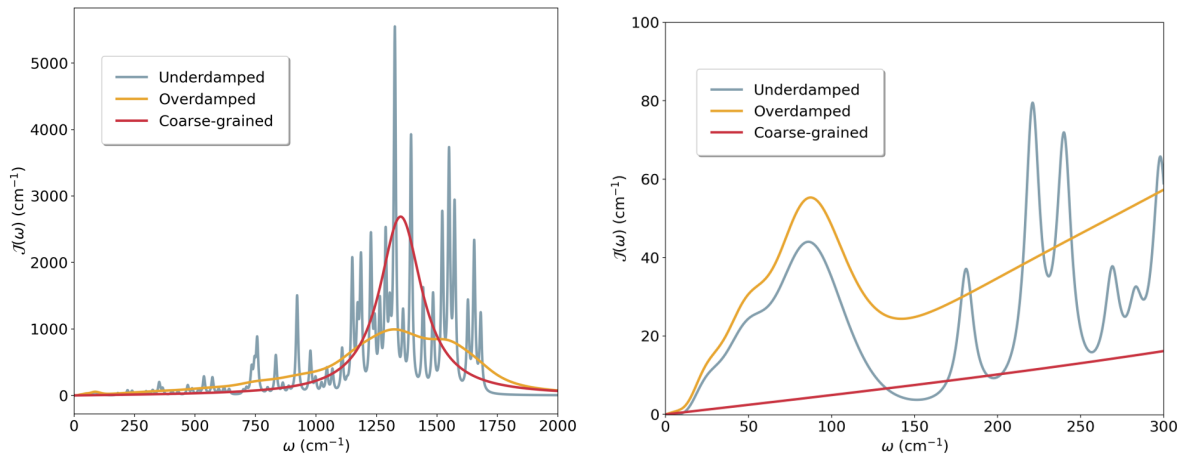


Figure 2.2: Spectral densities for the open system dynamics of the Chl b WSCP. **a)** full frequency range and **b)** low-energy region, respectively.

Considering that experimental measurements are done at low temperature, and by the principle of detailed balance, the upward transition rate is neglected; and the

eq. 2.6.3 can be directly integrated as,

$$\rho_{++}(t) = \rho_{++}(0) \exp[-k_{+\rightarrow-} t] \quad (2.6.14)$$

$$\rho_{+-}(t) = \rho_{+-}(0) \exp[-i(\Omega - i\gamma)t] \quad (2.6.15)$$

The matrix elements $\rho_{\alpha\beta}$ in the excitonic basis are related to the matrix elements in the site basis ρ_{mn} via the coefficients in eq. (1.2.14), that is,

$$\rho_{mn} = \sum_{\alpha\beta} c_{\alpha}^{(m)} c_{\beta}^{(n)*} \rho_{\alpha\beta} \quad (2.6.16)$$

For the approximate Redfield dynamics simulations, only the parameters for ω B97X-D3BJ were considered. The reduced system dynamics was simulated from 0 to 3000 fs, on each trial, and then averaged following the same procedure that for the closed system dynamics. The initial condition is the same that for closed dynamics, but in the excitonic basis,

$$\rho_{0,\pm} = |1\rangle \langle 1|_{\pm} = \frac{1}{2} \begin{bmatrix} 1 & 1 \\ 1 & 1 \end{bmatrix} \quad (2.6.17)$$

For the consideration of the static disorder, 10^3 trials were averaged in the excitonic basis, sampling the site energies from a normal distribution around the determined values with the optimized σ as standard deviation, and diagonalizing the hamiltonian in each trial. The averaged trajectory is then converted to the site basis, and the quantum witnesses calculated for each phenomenon of interest, following the same procedures as those for the closed system dynamics.

Chapter 3

Results and Discussion

3.1 TD-DFT Parametrization

3.1.1 Evaluation of Site energies

Table 3.1 summarized the relative error computed for different DFT functionals when compared to the experimental value of 15198 cm^{-1} (658 nm). For all the categories except GGA functionals, the relative errors are higher for values calculated using TDA than with the full TD-DFT calculation (paired t -test: $p = 4.65 \times 10^{-12}$). For GGA functionals, TDA gives better results than the full TD-DFT, however, previous work has attributed this to cancelation of errors (Shao et al., 2020). This implies that the full TD-DFT calculation is necessary for the accurate simulation of the absorption spectra.

Table 3.1: Normalized root-mean squared error (NRMSE) for the calculated site energies using TD-DFT methods.

Type	Full TD-DFT NRMSE (%)	TDA NRMSE (%)
GGA	3.3	2.3
meta-GGA	8.2	12.2
Hybrid	3.8	11.5
metaH-GGA	3.0	12.0
RS Hybrid	2.6	11.3
<i>Global</i>	4.7	10.8

Analyzing across the categories, the relative error is independent on its place in the Jacob’s ladder (Mardirossian & Head-Gordon, 2017), yielding to similar values for all the categories with the only exception of the meta-GGA functionals. Fig. 3.1 shows the relative error by functional, from which it is clear that the NRMSE in the meta-GGA group is significantly higher due to the B97M-V/D3BJ functionals. The B97M-V functional has been tested with good results in the prediction of kinetic and thermochemical properties of main-group compounds from the GMTKN55 database (Najibi & Goerigk, 2018), however, there is not enough previous information about its performance on excited states calculations. It should be noticed that for functional B97M-V, the dispersion corrections are parametrized using the VV10 non-local model as part of the correlation; for the D3BJ variant, the corrections are added post-SCF convergence,

conserving the vertical transition energy.

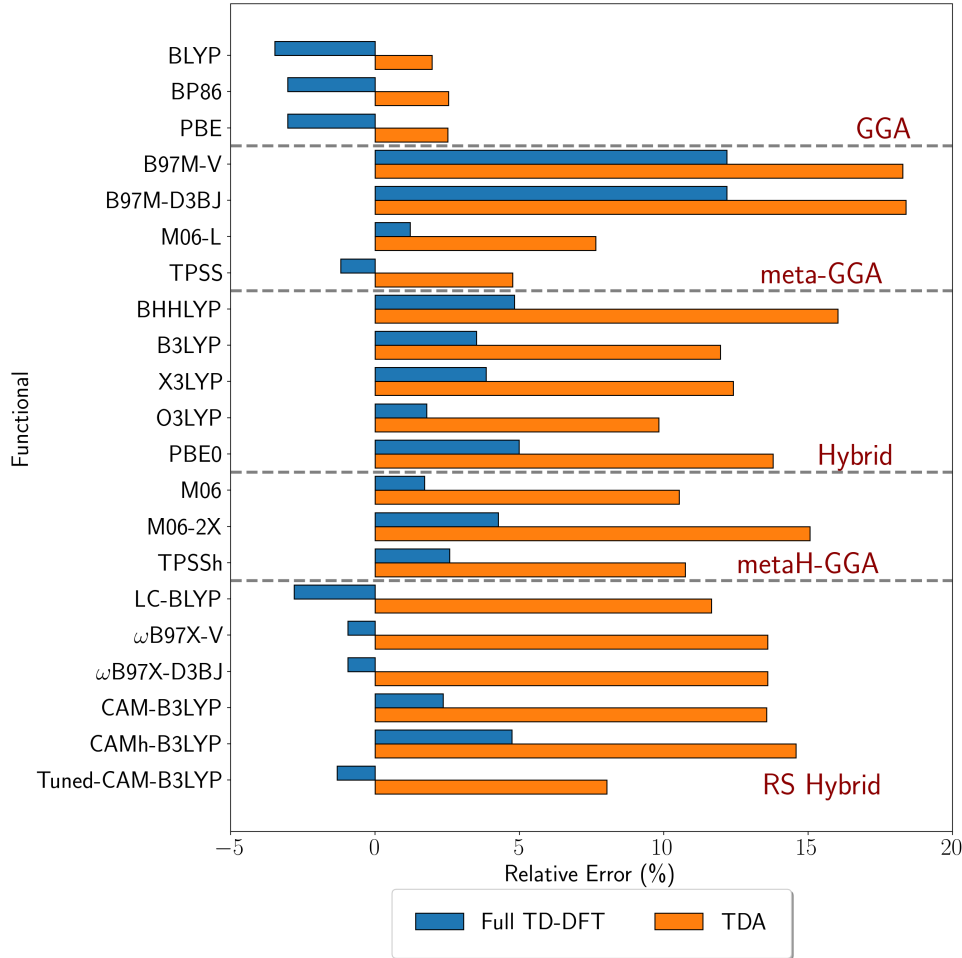


Figure 3.1: Relative errors of the calculated site energies for Chl b WSCP monomer pigment (PDB ID: 6S2Z) using TD-DFT methods.

Range-separated hybrid functionals show slightly better values than the rest of the groups. They are well known to improve the predicted values for vertical transition energies compared to hybrid functionals, correcting the charge-transfer (CT) states behaviour shown by the global hybrid functionals (Chai & Head-Gordon, 2008). This can be specially useful in PPCs, where the excitonic states can coexist with CT like excitations (Curutchet & Mennucci, 2017). In these schemes, the two-electron repulsion is separated into short and long range contributions as,

$$\frac{1}{r_{12}} = \frac{1 - [\alpha + \beta \text{erf}(\omega r_{12})]}{r_{12}} + \frac{\alpha + \beta \text{erf}(\omega r_{12})}{r_{12}} \quad (3.1.1)$$

The parameters α , β and ω in eq. (3.1.1) have been determined following particular statistical procedures on a benchmark training set. For example, for the CAM-B3LYP functional, the values $\alpha = 0.19$, $\beta = 0.46$ and $\omega = 0.33$ were optimized by minimizing the error for atomization energies of the small G2 set with 53 molecules (Yanai et al., 2004). However, it has been shown that these values are not appropriate for describing excited states of large molecules (Higashi et al., 2014), such as the chromophores in WSCP. To correct this, both CAMh-B3LYP ($\alpha = 0.19$, $\beta = 0.50$, $\omega = 0.33$) and Tuned-CAM-B3LYP ($\alpha = 0.0799$, $\beta = 0.9201$, $\omega = 0.150$) have been used to obtain better excited energies for dyes and biologically important chromophores, however, only the latter actually improves the calculated site energy for the WSCP, reproducing a behaviour previously reported on chlorin pigments upon reducing the value of ω on the CAM-B3LYP functional (Higashi et al., 2014).

The functionals that show better performance are ω B97X-V/D3BJ (-1.0% , -145 cm^{-1} , 6.32 nm), M06-L (1.0% , 149 cm^{-1} , 6.39 nm), TPSS (-1.2% , -182 cm^{-1} , 7.99 nm), Tuned-CAM-B3LYP (-1.3% , -200 cm^{-1} , 8.77 nm), M06 (1.7% , 261 cm^{-1} , 11.1 nm), and O3LYP (1.8% , 271 cm^{-1} , 11.5 nm). The observed errors are typical for TD-DFT calculations employing those functionals (Laurent & Jacquemin, 2013; Jacquemin et al., 2010, 2011, 2009). All of these are within 2% of the reported value. The detailed values are presented in Table 3.2.

Recently, higher-level calculations have been applied to photosynthetic pigments as an alternative to TD-DFT, such as the DLPNO-STEOM-CCSD (Sirohiwal, Berraud-Pache, et al., 2020; Sirohiwal, Neese, & Pantazis, 2020), however, this method shows a comparable accuracy with TD-DFT for the first excited states. Considering the computational cost and that higher-level methods require more extensive and careful considerations (for example, in the definition of the active space), TD-DFT represents the alternative with the most advantages in the *ab initio* calculation.

3.1.2 Evaluation of Excitonic Couplings

Using the T-TEDOPA method, a numerically exact model proposed to include the *full* vibronic contributions to the excitonic dynamics, an excitonic coupling of around

Table 3.2: Calculated site energies and global root-mean squared errors using TD-DFT methods. Experimental site energy of 15198 cm^{-1} .

Type	Functional	Full TD-DFT (cm^{-1})	TDA (cm^{-1})
<i>GGA</i>	BLYP	14669	15497
	BP86	14737	15584
	PBE	14738	15581
<i>meta-GGA</i>	B97M-V	17051	17977
	B97M-D3BJ	17051	17994
	M06-L	15347	16359
	TPSS	15016	15923
<i>Global Hybrid</i>	BHHLYP	15931	17634
	B3LYP	15732	17016
	X3LYP	15783	17084
	O3LYP	15469	16691
	PBE0	15956	17293
<i>metaH-GGA</i>	M06	15459	16800
	M06-2X	15846	17488
	TPSSh	15591	16831
<i>RS Hybrid</i>	LC-BLYP	14771	16969
	ω B97X-V	15054	17265
	ω B97X-D3BJ	15054	17265
	CAM-B3LYP	15557	17259
	CAMh-B3LYP	15919	17415
	Tuned-CAM-B3LYP	14998	16969
<i>RMSE (cm^{-1})</i>		724	1826
<i>NRMSE (%)</i>		4.7	10.8

$J = 140 \text{ cm}^{-1}$ was calculated to be able to predict correctly the absorption spectra of the Chl b dimer of the recombinant type IIa WSCP from cauliflower, according to Caycedo-Soler et al. (2022). This value accounts for the energy redistribution between the zero-phonon transition and its sidebands, and corresponds to a value of that is almost twice the previously determined value of $J = 69 \text{ cm}^{-1}$ by Renger et al. (2007). This is supported also by ZINDO QM/MMpol excited-state calculations along MD trajectories (Rosnik & Curutchet, 2015). Several methods for the calculation of the excitonic couplings are studied to assess the source of this significant discrepancy.

3.1.2.1 Coulombic methods

Table 3.3 contains the Coulombic couplings determined by 3 selected methods. In this case, PDA, TMA and TrEsp methods were used, as detailed in the Computational Methods.

Table 3.3: Excitonic Couplings for the WSCP (PDB ID: 6S2Z) calculated using Coulombic methods.

Method	J_{14} (cm^{-1})
PDA ($\theta_{\text{exp}} \approx 35.6^\circ$)	60.0
PDA ($\theta_{\text{Dinh}} \approx 39.0^\circ$)	51.7
TMA	73.6
TrEsp	75.3

The PDA method underestimates the value of excitonic coupling, this can be attributed to the breaking of the point-dipole model because of the short distance between chromophores; however, the calculated values follow the expected tendency, in which the increase in opening angle leads to a decrease of the coupling.

For both TMA and TrEsp the results can be considered equivalent, as both methods consist of the calculation of the energy between two sets of charges. The observed difference between the couplings comes from the methods employed to derive the charges. The normalized distribution of atomic charges in both methods is similar, however, their values are not; this yields to different couplings without considering the rescaling constant K . As previously discussed, the transition charges can be rescaled by a constant so that the calculated transition dipole moment coincides with the experimental transition dipoles. Upon rescaling, both methods yield to almost the same result. The values obtained are slightly higher than the previously reported value of 72 cm^{-1} obtained by Renger et al. (2007), as the latter was calculated using the WSCP structure from *Lepidinium virginicum* adjusted for the change in pigment Chl b (PDB ID: 2DRE).

To analyze the possible reasons for the discrepancies, the assumptions made in the derivation of the TrEsp method are challenged, and their relative importance in the results for the Chl b WSCP are addressed.

One of assumptions is that the transition charges are “recyclable”, that is, for a fixed level of theory, the transition charges determined at the equilibrium geometry can be reused for the calculation of the excitonic couplings in any other geometry. This approximation is arguably plausible: as long as the geometry of the pigment monomer fluctuates around its equilibrium geometry, the effect of geometrical variability on the electronic structure of the molecule and, hence, its transition density should not vary sufficiently enough to require a recalculation of the transition charges. This argument is used to justify the applicability of this method on molecular dynamics (MD) simulations (Olbrich & Kleinekathöfer, 2010).

To asses the validity of this assumption for the WSCP crystal structure, using the transition charges reported by Madjet et al. (2006) and Renger et al. (2007) and the geometries of the respective dimers in the crystal structures, one can reproduce the calculations of the couplings reported by Renger et al. (2007) (using the dipole strength of 4.0 D for Chl a and 3.6 D for Chl b). Then, once the reproducibility has been corroborated, the method with the same parameters can be applied to other systems that show similar structure and verify if the small change in geometry produces a considerably large change in the coupling or not. The results for this test on the different crystal structures of type II WSCP are summarized on table 3.4.

Table 3.4: Excitonic coupling calculated reproducing the conditions in the literature: TrEsp method, using the transition charges in (Madjet et al., 2006) and (Renger et al., 2007) and the geometries of the respective dimers in the crystal structures, using dipole strengths of 4.0 D for Chl a and 3.6 D for Chl b.

PDB Code	Organism	Pigment	$\alpha_{14}(\circ)$	$J_{14} (\text{cm}^{-1})$
6S2Z	<i>B. oleracea</i> var. <i>botrytis</i>	Chl b	33.62	75.3
2DRE	<i>L. virginicum</i>	Chl a	29.37	74.5
6S2Y	<i>L. virginicum</i>	Chl b	28.54	85.8
6GIW	<i>L. virginicum</i> (L91P)	Chl a	23.17	85.6
6GIX	<i>L. virginicum</i> (L91P)	Chl b	24.48	95.4

For the reproducibility assessment, the reference value is the 2DRE value for a Chl a complex. In this case, the reported value of $J_{14} = 77 \text{ cm}^{-1}$ is close to the one calculated of $J_{14} = 77.6 \text{ cm}^{-1}$, suggesting that the method is reproducible. However, it is unclear from (Renger et al., 2007) if this calculation was made using the geometrical

coordinates of the protein without further mapping to the “open-sandwich” model with the $r_{14} = 10.763$ Å and $\alpha_{14} = 29.37^\circ$ parameters; or if the calculation is done using explicit coordinates. From the fact that no coordinates are available for the 2DRE Chl b complex, the former is suggested. Here, the coupling is calculated using the native coordinates without further mapping. These small changes in the methods of calculation could explain the 0.6 cm^{-1} difference.

Comparing results between 6S2Z and 6S2Y, its clear that upon reducing the angles between the chromophores, the coupling increases. This tendency is conserved in 6GIX, where the angles are reduced even more, and is repeated across the Chl a complexes, 2DRE and 6GIW. Taking the PDA, this coincides with the increase of the geometrical parameter κ , which maximizes for $\alpha = 0^\circ$ for coplanar transition dipole moments. However, this increments are of no more than a 27%. Then, the small changes in the geometries between the models and the real crystal structure would not explain why the coupling has to be *doubled* to reach the T-TEDOPA new value $J = 140 \text{ cm}^{-1}$.

Another premise is that the transition charges have to be rescaled by a factor that gives the same experimental transition dipole to reach the correct coupling value. To test this, the coupling between pigments i and j without rescaling J_{ij}^0 can be calculated and from it, the corresponding rescaling transition dipole $\mu_{ij} = \sqrt{\mu_i \mu_j}$ can be estimated considering the target coupling of $J = 140 \text{ cm}^{-1}$. These results are summarized on table 3.5, and are only calculated for Chl b complexes, since the target value was only derived for type IIa WSCP reconstituted with Chl b.

Table 3.5: Estimates of experimental rescaling transition dipole moment to reach the proposed coupling of $J = 140 \text{ cm}^{-1}$. Conditions in the literature: TrEsp method, using the transition charges in Madjet et al. (2006) and Renger et al. (2007) and the geometries of the respective dimers in the crystal structures.

PDB Code	Organism	Pigment	J_{14}^0 (cm^{-1})	μ_{14} (D)
6S2Z	<i>B. oleracea</i> var. <i>botrytis</i>	Chl b	77.5	4.91
6S2Y	<i>L. virginicum</i>	Chl b	74.1	4.96
6GIX	<i>L. virginicum</i> (L91P)	Chl b	80.7	4.89

From the results on table 3.5, its clear that the coupling calculated without rescaling is near the rescaled one, presented on table 3.4. This is because the calculated transition

dipole for Chl b without rescaling ($\mu_{\text{Chl b}} = 3.67 \pm 0.04$ D) is similar to rescaling factor of 3.6 D used in the literature. To reach the target value of 140 cm^{-1} , the rescaling transition dipole has to be raised up to a minimum of 4.85 D, which represents an increase of ca. 35% from the reported value by Knox & Spring (2003).

It is difficult to precise the source of the discrepancy in the transition dipole values. The transition dipole can, in principle, be determined directly from the absorption spectra of the molecule. However, if the environment can polarize, the transition properties of the chromophores are changed and the Coulomb interactions are screened (Curutchet & Mennucci, 2017). The screening factor f is introduced to compensate for this effect (Hsu et al., 2001; Knox & van Amerongen, 2002; Adolphs & Renger, 2006; Renger et al., 2007; Friedl et al., 2022), describing the change of dipole strengths due to the chromophore interaction with the surrounding dielectric medium, so that $\vec{\mu} \cdot \vec{E} = f\mu_0 E$, where E is the average electrical field acting on the transition dipole $\vec{\mu}$ and μ_0 is the corresponding molecular transition dipole strength in the vacuum (Knox & van Amerongen, 2002).

Several approaches have been proposed to calculate the screening factor, as it can either increase or the decrease the excitonic coupling (Hsu et al., 2001). For example, an “empty cavity” approach calculates the correction screening factor to the local field around the pigment, considering it enclosed in an empty spherical cavity subjected to an external homogeneous field. For such a model, f is given by (Curutchet & Mennucci, 2017),

$$f = \frac{3\varepsilon}{2\varepsilon + 1} \quad (3.1.2)$$

with ε the dielectric constant of the medium (in this case, the solvent or the protein scaffold). This particular model is used to obtain the vacuum dipole of Chl a (4.6 D) and Chl b (3.8 D) further adjusted on Renger et al. (2007) to the ones used in Table 3.4. This leads to an effective screening factor of $f = 0.87$ for Chl a and $f = 0.95$ for Chl b, which correspond to effective dielectric constants of $\varepsilon = 0.69$ and $\varepsilon = 0.86$ using the empty cavity model. The argument for the selection these screening factors is not clear on Renger et al. (2007). The article states that the screening factor is selected “similar” to the one of BChl a determined in Adolphs & Renger (2006), but the latter

sets a dielectric constant of $\varepsilon = 2$ and a screening factor of $f = 0.8$. The artificial increase of the screening factor is not explained on Renger et al. (2007), neither is the relation of the screening factor to the dielectric constant, if any is used.

As stated before, other methods could lead to a different screening factors. In fact, extrapolating directly from the linear empirical relation given by Knox & Spring (2003), a protein refractive index of $n \approx 1.4954-1.5889$ can be derived for $\mu = 4.85-5.11$ D, this corresponds to a protein dielectric constant of $\varepsilon \approx 2.24 - 2.52$, which is in the range ($\sim 2 - 4$) of the internal dielectric region of a protein, according to the microscopic description literature (Laberge, 1998) and are close to the ones used ($\varepsilon = 3$) in previous works (Hughes et al., 2006). Recently, a large scale semiempirical calculation study derived a mean dielectric constant of 3.23 ± 0.04 for more than 150000 proteins (Amin & Küpper, 2020). This variability on the optimal value used for the dielectric constant of the protein reflects the lack of consensus on the matter, reaching values from the ones stated to as high as $\varepsilon \approx 15-40$ (Pitera et al., 2001), this is largely due to the dependence of the dielectric constant on the specific definition and model used to calculate it (Schutz & Warshel, 2001). Perhaps a better description of the dielectric constant of a protein is a field that reflects the complex protein structure and electrostatic properties of its residue sequence. This approach has lead to better results than using an homogeneous dielectric constant in pK_a 's prediction for tritable residues (L. Li et al., 2013).

All this calls for a more accurate description of the electrostatic properties of the protein scaffold and their relation to the transition dipole strength of the chromophore through better screening factors to *fully* explain the difference in excitonic couplings. Further research is recommended on this topic.

It has been reported that fully Coulombic methods (as TrEsp, TMA and their extensions as Poisson-TrEsp) significantly underestimate the total coupling, due to ignoring the short-range interactions (Kitoh-Nishioka et al., 2020; Fornari et al., 2017), which are enhanced in PPCs due to short distances, high orbital overlap, and high Coulombic couplings (Fornari et al., 2017). Therefore, the excitonic coupling is also calculated using diabatic approaches.

3.1.2.2 Diabatic methods

For the diabatic approach, the supermolecule model for dimers (Voityuk, 2014a) was used to estimate the couplings. In general, this method relies on the calculation of the excitonic states through a full TD-DFT calculation on the dimer, as well as over each monomer. TD-DFT has the advantage that the output gives the electric transition dipole moment coordinates, and also the energy and oscillator strength of the excitation. Therefore, the estimation of the coupling can be done using the transformation between states and their properties, avoiding extensive calculations of integrals between densities. Notice that this method works on the assumption that the diabatic states are fully localized on the monomers and the diabatic states are fully delocalized in the dimer. For the Chl b WSCP dimer studied, this can be seen in Fig. 3.2, where the MOs follow this scheme.

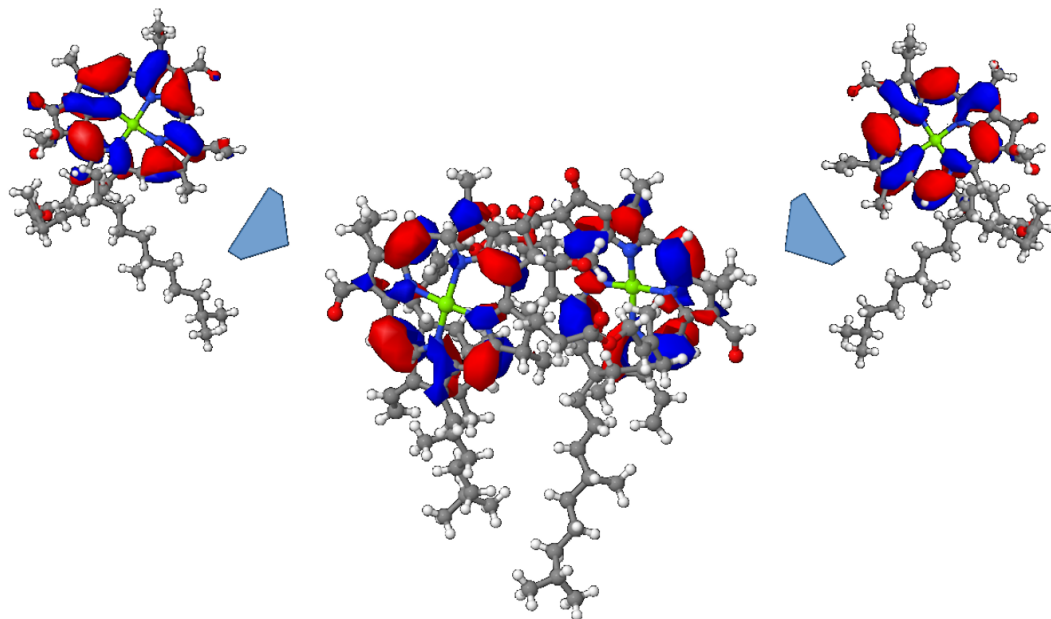


Figure 3.2: Molecular orbitals of the first excited states of the monomers and dimer of the Chl b WSCP, determined at TD-DFT/PBE0/def2-TZVP level of theory.

The diabaticization procedure also relies on the description of the supermolecule states, as being fully delocalized between chromophores; and representative of the excitonic states distribution as predicted by the Frenkel hamiltonian. Depending of the particular functional, density functional methods can lead to inaccurate description

of the states. As a comparison, the linear absorption spectra of the Chl b dimer of WSCP was calculated at TD-DFT/PBE0/def2-TZVP level, and also using TD-DFTB: a semiempirical version of TD-DFT which employs the tight-binding approximation, implemented on the DFTB+ suite (Hourahine et al., 2020; Niehaus et al., 2001). Both spectra are plotted on Fig. 3.3 using a Gaussian broadening. Both spectra show very different features: TD-DFT methods show only two transitions in the range of interest, with a predicted peak after broadening around 630 nm. It is clear that TD-DFTB predicts several more transitions in the excitonic band, against the expected two from the Frenkel theory. Also, the predicted peak after broadening is more shifted to the red. This can be attributed to the approximations made from the TD-DFT theory to get to the TD-DFTB level. As DFT is a level of theory that has a higher accuracy than DFTB, the former results are the ones recommended.

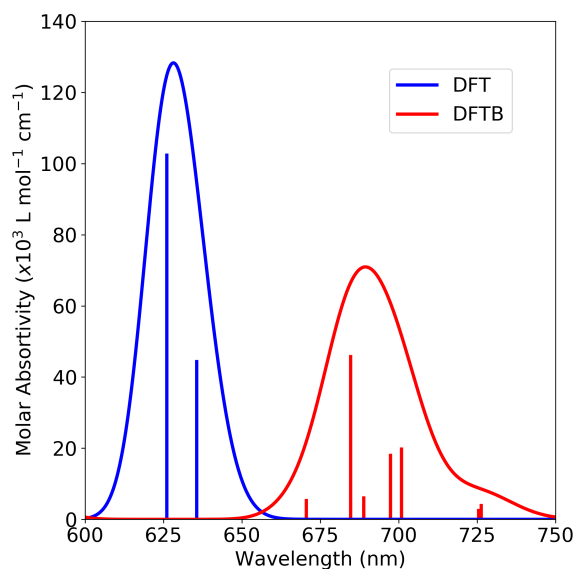


Figure 3.3: Absorption spectra for the 1–4 Chl b dimer of WSCP (PDB ID: 6S2Z) obtained using TD-DFT/PBE0/def2-TZVP and TD-DFTB methods. Vertical sticks show transition position and relative oscillator strength. Spectra plotted with Gaussian broadening with FWHM = 35 meV.

With all the advantages from this TD-DFT based diabatic method, come several disadvantages. As the calculations on the monomers and aggregate are done separately, typical errors present in TD-DFT calculations are present in all three separate calculations, increasing the possible deviations in the final result. Thus, quality metrics

are proposed to evaluate the validity of the excitonic coupling. For instance, the R parameter evaluates the ratio,

$$R = \frac{M_i^2 + M_j^2}{\mu_i^2 + \mu_j^2} \quad (3.1.3)$$

For the ideal case it follows that $R = 1$, therefore, a sufficient criteria is that the deviation $|R - 1|$ is less than certain limit. A suggested limit (Voityuk, 2014a) of 20% is applied in this work, beyond which the approximation is rendered invalid and the coupling is discarded. Moreover, in the particular case of the Chl b WSCP system studied, the coordinates of both chromophores are the same in their center-of-mass, therefore $\mu_i^2 = \mu_j^2$, and the different equations proposed for the estimation of the diabatic excitonic coupling (eq. (1.2.36)–(1.2.38)) should give similar results. As such, also a 20% maximum RSD is expected between expressions.

Using both criteria, values obtained using all GGA functionals, as well as B97M-V, B97M-D3BJ, X3LYP and M06, are discarded (see table 3.6). These functionals fail one or both criteria, which suggest that their description of the $S_0 \rightarrow S_1$ is not good enough to estimate valid excitonic couplings. As the diabatic states are not necessarily unique nor optimal, forcing the selection of the S_1 states results in the failure of the estimation, specially in diffuse transitions. Other methods of choosing the diabatic states have been proposed using transition charges (Fornari et al., 2016; Aragón & Troisi, 2015a,b).

The values determined by diabatization strategies for WSCP are closer to the one obtained using the T-TEDOPA procedure. This suggests that the short-range interactions have been greatly underestimated for this dimer. Other studies suggest that the contribution of short-range interactions can be around 15% of the total excitonic coupling, and can be as high as 70% for more closely coupled chromophores (Fornari et al., 2017). In particular, they state that if the minimum intermolecular distance is less than 7 Å, then the short-range interactions are significantly different than the method’s intrinsic errors. For the WSCP Chl b 1–4 dimer, the minimum intermolecular distance is of 0.97 Å (1.16 Å without considering H atoms); thus, short-range interactions are considered to be important.

Figure 3.4b shows the predicted excitonic coupling values by TD-DFT methods. In general, these methods gives higher couplings with respect to the ones determined by

Table 3.6: Calculated diabatic excitonic couplings and quality metrics using TD-DFT methods. In red, values that discard the respective coupling as valid, according to criteria outlined in the main text.

Type	Functional	J_{14} (cm^{-1})	R	%RSD
<i>GGA</i>	BLYP	55.7	0.802	21.24
	BP86	54.4	0.800	25.06
	PBE	53.2	0.800	26.84
<i>meta-GGA</i>	B97M-V	3.8	0.017	107.93
	B97M-D3BJ	98.2	0.125	39.03
	M06-L	81.8	0.819	4.86
	TPSS	60.4	0.814	19.00
<i>Global Hybrid</i>	BHHLYP	148.8	0.845	3.25
	B3LYP	104.8	0.821	1.27
	X3LYP	140.3	0.781	9.28
	O3LYP	88.5	0.829	6.08
	PBE0	118.1	0.834	3.91
<i>metaH-GGA</i>	M06	90.2	0.717	8.31
	M06-2X	131.4	0.826	4.37
	TPSSh	88.9	0.830	6.89
<i>RS Hybrid</i>	LC-BLYP	131.1	0.844	4.17
	ω B97X-V	139.5	0.848	3.89
	ω B97X-D3BJ	139.5	0.848	3.89
	CAM-B3LYP	135.6	0.844	3.62
	CAMh-B3LYP	129.8	0.841	3.65
	Tuned-CAM-B3LYP	112.3	0.833	3.87

Coulombic methods, this supports that the short-range contributions have been greatly overlooked in previous reports. Range-separated hybrids predict the best couplings compared to the 140 cm^{-1} target, and most of them give results near the target, consistent with the observed behaviour with the site energies.

The excitonic coupling depends not only on the magnitude but on the relative direction of the transition dipoles, this represents the opening angle between transition dipoles. Examining previously reported transition dipoles (Madjet et al., 2006; Dinh & Renger, 2015) the calculated opening angle is significantly different, almost doubling the reported angle. Figure 3.4 shows that the predicted direction and opening angle across functionals is very similar (average opening angle: $\theta = (65 \pm 6)^\circ$), therefore the deviations cannot account for the full variability in the excitonic couplings.

The length of the calculated transition dipoles determined ranges from 1.60 D to

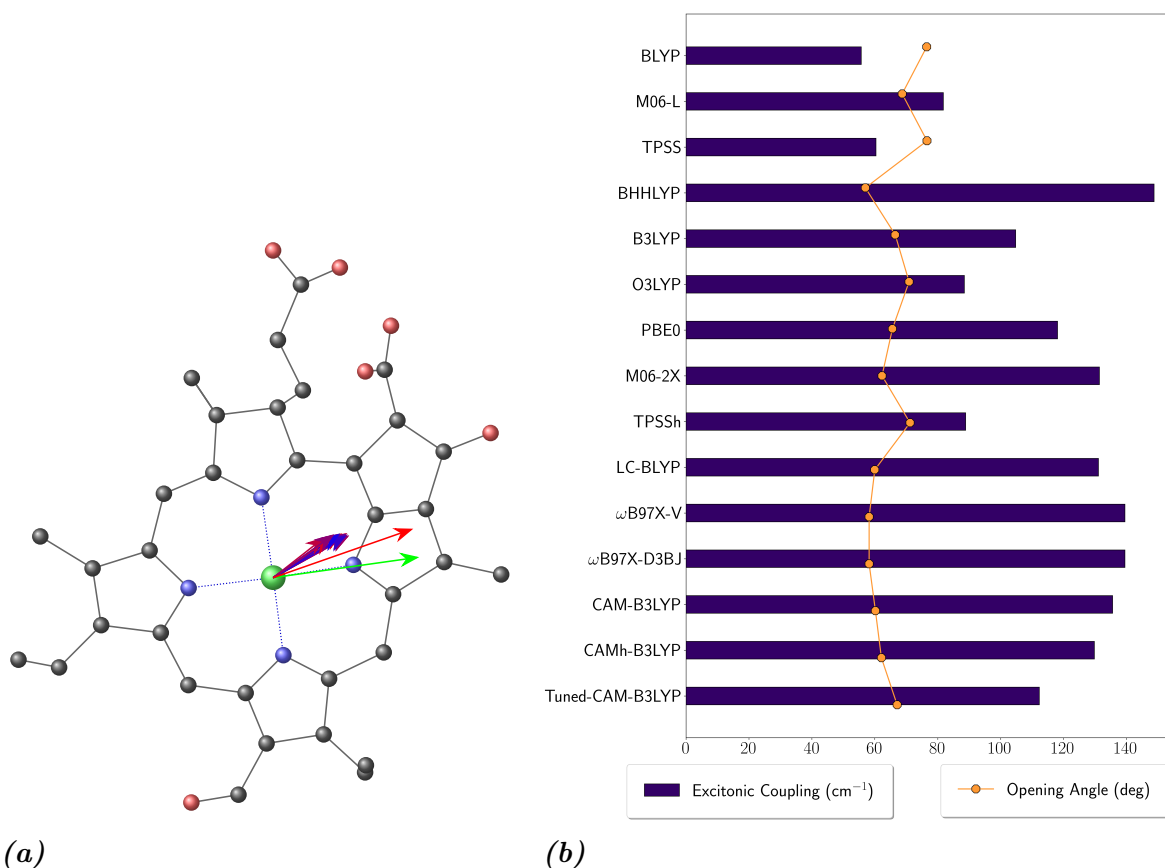


Figure 3.4: Excitonic couplings estimation by diabatic methods. **a)** Electric transition dipole moments determined by TD-DFT methods (group of blue to purple vectors) on the Chl b from WSCP structure. For reference, the transition dipole moment on the $N_A \rightarrow N_C$ axis (bright green) and the optimized for 39° of opening angle. Hydrogen atoms and phytyl tail have been omitted for clarity. **b)** Values of excitonic couplings and opening angle for valid functionals.

2.20 D, which is significantly lower compared to experimental data (Knox & Spring, 2003; Renger et al., 2007). Previously reported values (Renger et al., 2007; Friedl et al., 2022) of f range from around 0.80 to 1.40 for WSCP. However, taking the TD-DFT dipoles as the ones on the dielectric media, and the experimental (Knox & Spring, 2003) as the one on vacuum, predicted $f = 0.44 - 0.60$, which differ significantly. Thus, the introduction of the screening factor cannot explain the discrepancies between diabatic and Coulombic couplings.

Since neither the opening angle nor the dipole strength can explain the variability of the excitonic couplings, we attribute the increasing and variability of the determined excitonic couplings to the full supermolecule calculation, that accounts for all the

short-range and long-range contributions. Taking $J_{14} = 140 \text{ cm}^{-1}$ as reference, the functionals which predict better couplings are $\omega\text{B97X-V/D3BJ}$ (-0.4% , -0.5 cm^{-1}), CAM-B3LYP (-3.1% , -4.4 cm^{-1}), M06-2X (-6.1% , -8.6 cm^{-1}), LC-B3LYP (-6.4% , -8.9 cm^{-1}), CAMh-B3LYP (-7.3% , -10.2 cm^{-1}), and PBE0 (-16% , -21.9 cm^{-1}); which show that range-separated functionals give the most accurate excitonic couplings through the diabatic method, in line with the results for site energies.

3.1.3 Optimization of Linear Absorption Spectra

3.1.3.1 Estimation of the static disorder

The parameters previously obtained are used to predict the linear absorption spectra of Chl b WSCP using HEOM simulations (Caycedo-Soler et al., 2022). However, first the estimation of the static disorder parameters σ is necessary. This is performed neglecting the vibronic coupling according to equation (1.2.51).

The effect of the static disorder of the protein (Stross et al., 2016) is taken into account through statistical distributions around the site energies with standard deviation σ . Three distributions were considered:

- Gaussian profile:

$$\mathcal{F}(E, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{E^2}{2\sigma^2}} \quad (3.1.4)$$

- Lorentzian profile:

$$\mathcal{F}(E, \sigma) = \frac{2}{\pi} \frac{\sigma}{4E^2 + \sigma^2} \quad (3.1.5)$$

- Voigt profile:

$$\mathcal{F}(E, \sigma) = \int_{-\infty}^{\infty} \mathcal{G}(E', \sigma) \mathcal{L}(E - E', \sigma) dE' \quad (3.1.6)$$

where $\mathcal{G}(E, \sigma)$ and $\mathcal{L}(E, \sigma)$ are the Gaussian and Lorentzian profiles.

The estimation of σ comes from the optimization of the predicted spectra against the experimental. The election of the statistical distribution in (1.2.51) changes the shape of the predicted spectra. Fig. 3.5 shows the effect for the 3 different distributions used, obtained with the experimental site energy (15198 cm^{-1}) and TrEsp recalculated

coupling (75.3 cm^{-1}). Analogous curves for the TD-DFT derived parameters are shown on Appendix C. Notice that for the Lorentzian shows sharper peaks than Gaussian and Voigtian profiles, however, they are broader at the base. Also, Lorentzian profiles conserves the shoulder at much higher values of σ , while overestimating the shoulder height. For the Gaussian case, the shoulder only shows for $\sigma \leq 75 \text{ cm}^{-1}$; for the Voigtian, the shoulder occurs at even lower values of σ and both peaks fuse rapidly with increasing σ .

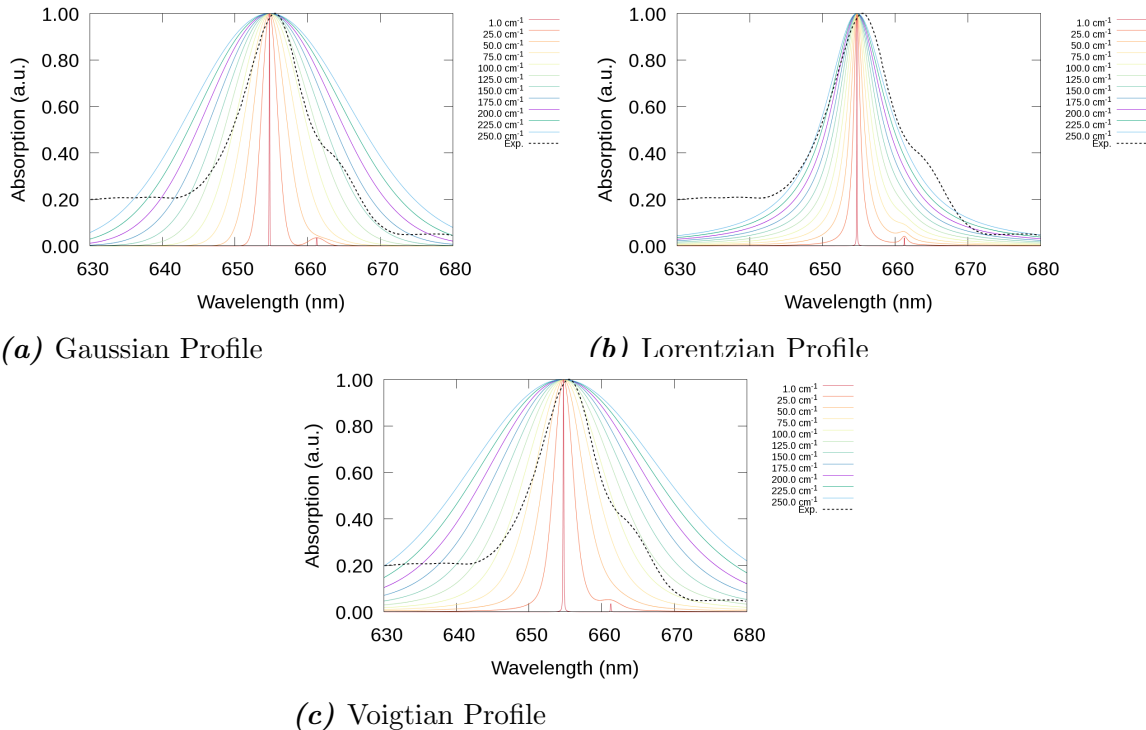


Figure 3.5: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy (15198 cm^{-1}) and TrEsp recalculated coupling (75.3 cm^{-1}).

The optimization of σ is performed by numerical iteration for every distribution and parameter set for each functional, minimizing the distance between the calculated and experimental spectra with respect to σ . Several metrics can be proposed to perform the shape comparison, based on the spatial distance between their corresponding points (Efrat et al., 2007; Vlachos et al., 2002): the lesser the distance, the greater the similarity.

A simple procedure to obtain the distance is calculating the Procrustes distance (Gower

& Dijksterhuis, 2004), which consists of the cartesian measure between 2 sets of points in n dimensions. Let \mathcal{S}_1 and \mathcal{S}_2 be two shapes in 2 dimensions so that the points $\{(x_i, y_i)\} \in \mathcal{S}_1$ and $\{(u_i, v_i)\} \in \mathcal{S}_2$, each set of k points, then to calculate the Procrustes distance between \mathcal{S}_1 and \mathcal{S}_2 , 3 transformations are performed:

1. Traslation: both shapes are centered around their centroids (\bar{x}, \bar{y}) and (\bar{u}, \bar{v}) , defined as,

$$\bar{x} = \sum_i \frac{x_i}{k} \quad ; \quad \bar{y} = \sum_i \frac{y_i}{k} \quad ; \quad \bar{u} = \sum_i \frac{u_i}{k} \quad ; \quad \bar{v} = \sum_i \frac{v_i}{k} \quad (3.1.7)$$

then, the transformations are so that,

$$(x_i, y_i) \mapsto (x_i - \bar{x}, y_i - \bar{y}) \quad ; \quad (u_i, v_i) \mapsto (u_i - \bar{u}, v_i - \bar{v}) \quad (3.1.8)$$

2. Scaling: both shapes are resized to the same scale. The statistical size of each shape can be estimated from the RMSD of the points. Let it be α_i for \mathcal{S}_i , then,

$$\alpha_1 = \sqrt{\frac{\sum_i (x_i - \bar{x})^2 + (y_i - \bar{y})^2}{k}} \quad ; \quad \alpha_2 = \sqrt{\frac{\sum_i (u_i - \bar{u})^2 + (v_i - \bar{v})^2}{k}} \quad (3.1.9)$$

then, the shape is divided by its size, so that both shapes are rescaled to size 1,

$$(x_i, y_i) \mapsto \left(\frac{x_i - \bar{x}}{\alpha_1}, \frac{y_i - \bar{y}}{\alpha_1} \right) \quad ; \quad (u_i, v_i) \mapsto \left(\frac{u_i - \bar{u}}{\alpha_2}, \frac{v_i - \bar{v}}{\alpha_2} \right) \quad (3.1.10)$$

3. Rotation: both shapes are rotated to the same orientation. To do this, one of the shape has to be selected as the reference, and the other is rotated to match the first one. Let $\{(X_i, Y_i)\}$ and $\{(U_i, V_i)\}$ be the traslated and rescaled sets, and take the first one as the reference, then the rotated shape with points $\{(W_i, Z_i)\}$ is given by,

$$\begin{bmatrix} W_i \\ Z_i \end{bmatrix} = \begin{bmatrix} \cos \theta & -\sin \theta \\ \sin \theta & \cos \theta \end{bmatrix} \begin{bmatrix} U_i \\ V_i \end{bmatrix} \quad (3.1.11)$$

the optimal rotation angle can be determined by minimizing the RMSD between

the rotated shape and the reference using a least squares procedure, then,

$$\tan \theta = \frac{\sum_i (Y_i U_i - X_i V_i)}{\sum_i (X_i U_i + Y_i V_i)} \quad (3.1.12)$$

After the transformations, the Procrustes distance d_P between both shapes is given by the Cartesian distance of the mapped points, given by,

$$d_P = \sqrt{\sum_i [(W_i - X_i)^2 + (V_i - Y_i)^2]} \quad (3.1.13)$$

in this case, the reference figure is the experimental linear absorption spectrum.

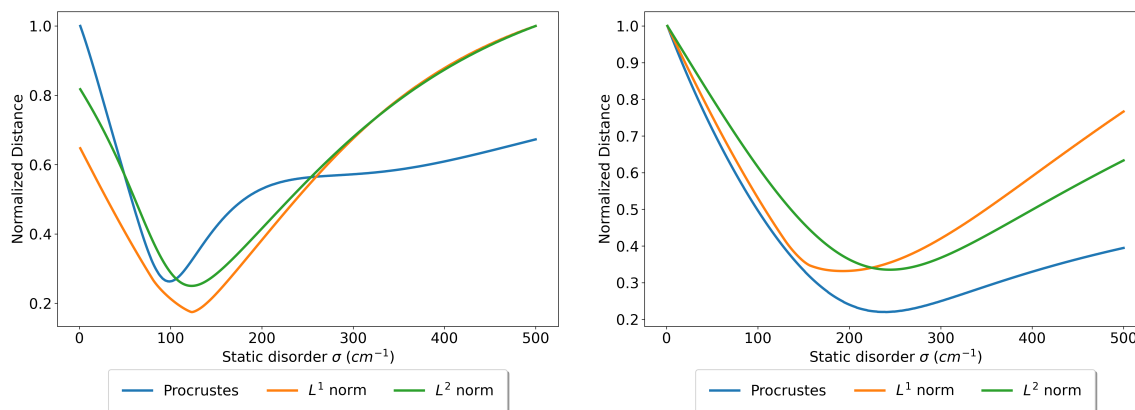
From measure theory, other metrics can be defined. In the case of two functions f, g that belong in a L^p metric space, both belong to the same equivalence class if the norm of their subtraction is zero (Rudin, 1987; Wheeden & Zygmund, 1977), that is,

$$\left(\int |f - g|^p d\mu \right)^{\frac{1}{p}} = 0 \quad (3.1.14)$$

then, the more similar the functions, the norm of their subtraction is closest to zero. The expression $\|f\|_p = \left(\int |f|^p d\mu \right)^{\frac{1}{p}}$ is called the L^p -norm of the metric space.

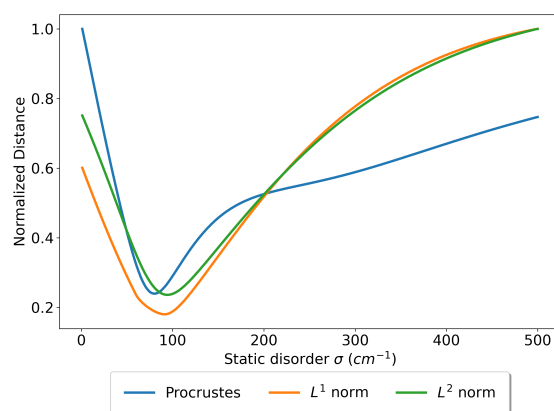
In particular, the Procrustes distance, the L^1 -norm and the L^2 -norm have been evaluated as similarity metrics between the estimated and experimental spectra. An example of the behaviour of the 3 metrics is shown of Fig. 3.6; analogous curves for the rest TD-DFT derived parameters are shown on Appendix C. For all conditions and metrics, the graph is different, however, in the vicinity of the minima, all of them form a well. For Lorentzian profiles, all metrics have similar graphs and are wider than for Gaussian and Voigtian profiles. Procrustes metric show narrower minima in all cases, which increases its method sensitivity, thus, this is the preferred metric.

Fig. 3.7 compares the different behaviour of the Procrustes distance for the different profiles. The distance is calculated for a wide range of values for σ , and then the minimal value is taken as optimal for every distribution. Curves for the rest TD-DFT derived parameters are shown on Appendix C. Again, Lorentzian profiling shows



(a) Gaussian Profile

(b) Lorentzian Profile



(c) Voigtian Profile

Figure 3.6: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy (15198 cm^{-1}) and $\omega\text{B97X-D3BJ}$ recalculated coupling (139.5 cm^{-1}).

remarkably different results than Gaussian and Voigtian, with much wider and shallower minimum, this suggest that the Lorentz distribution is completely inadequate for the approximation. Gaussian and Voigtian profiling show very similar results, with Voigtian giving slightly deeper minimum, which suggest a better spectrum.

Examining the results for the optimal values in table 3.7, similar optimal values are found across all the functionals, with percentual relative standard deviation (%RSD) of around 10% for static disorders and Procrustes distances alike. This indicates that the static disorder can be estimated as an independent parameter from the TD-DFT functional, only associated with the PPC and profiling. Comparing the averages, the Lorentzian profile give a slightly lower Procrustes distance, however, the corresponding

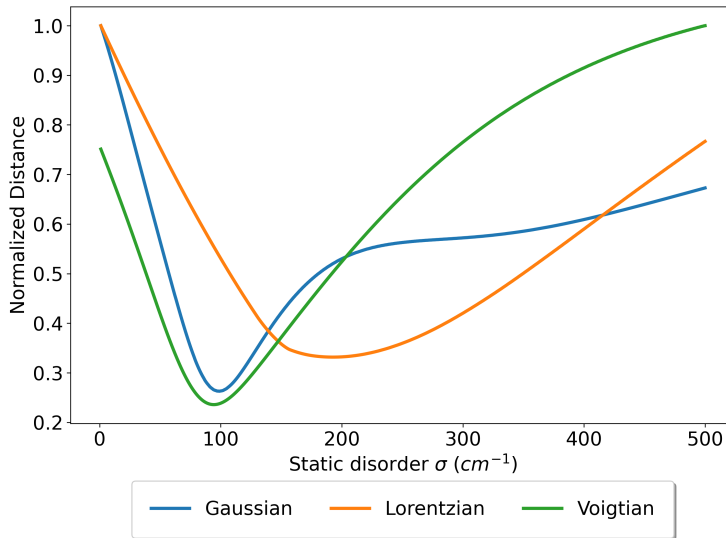


Figure 3.7: Example of the numerical optimization of σ by minimization of the Procrustes distance. *Conditions:* experimental site energy (15198 cm^{-1}) and $\omega\text{B97X-D3BJ}$ recalculated coupling (139.5 cm^{-1}).

static disorder is more than doubled from previous studies for WSCP (Dinh & Renger, 2015; Renger et al., 2009, 2007) and other PPCs (Khmelnitskiy et al., 2019; Adolphs & Renger, 2006; Raszewski et al., 2005; Novoderezhkin et al., 1999), which suggests is unphysical and an artifact of the numerical optimization, owing also to its low sensitivity, in accordance with previously seen behaviour. Therefore, the Lorentzian profile is discarded. For the other two profiles, the results are similar, but different statistically (paired t -test: $p = 0.00282$). Hence, the Voigtian profile gives better results, which optimized value for the static disorder is $(72 \pm 7) \text{ cm}^{-1}$, in accordance with previous studies (Caycedo-Soler et al., 2022).

Table 3.7: Optimal static disorder parameters σ (in cm^{-1}) and minimal Procrustes distances for the sets of parameters determined using TD-DFT methods.

Type	Functional	Gaussian		Lorentzian		Voigtian	
		σ	<i>Distance</i>	σ	<i>Distance</i>	σ	<i>Distance</i>
<i>meta-GGA</i>	M06-L	81	0.422	192	0.348	65	0.390
	TPSS	85	0.405	249	0.341	71	0.366
<i>Global Hybrid</i>	BHLYP	106	0.334	254	0.271	87	0.298
	B3LYP	81	0.399	206	0.333	67	0.366
	O3LYP	79	0.459	191	0.382	62	0.423
	PBE0	87	0.396	217	0.334	72	0.364
<i>metaH-GGA</i>	M06-2X	96	0.371	235	0.312	78	0.339
	TPSSh	83	0.459	195	0.386	65	0.427
<i>RS Hybrid</i>	LC-BLYP	93	0.362	225	0.309	65	0.427
	ω B97X-V	98	0.346	238	0.292	80	0.314
	ω B97X-D3BJ	98	0.346	238	0.292	80	0.314
	CAM-B3LYP	96	0.358	234	0.299	78	0.325
	CAMh-B3LYP	94	0.366	235	0.305	77	0.333
	Tuned-CAM-B3LYP	81	0.430	203	0.370	66	0.400
<i>Average</i>		90	0.390	222	0.327	72	0.363
<i>%RSD</i>		9.4	10.6	9.7	10.9	10.5	12.3

3.1.3.2 Vibronic Spectra

Optical processes dynamics are highly affected by vibronic effects, therefore, the correct lineshape theory must include the full description of all important PPC vibrations and their interplay with the excited states of the chromophores (May & Kühn, 2011). The Hierarchical equations of motion (HEOM) is an infinite set of Partial Differential Equations (PDEs) that describe the time-evolution of the reduced density matrix of the chromophoric aggregate in the bath of vibrational motions of its protein scaffold, by considering a linear coupling between the quantum system and the thermal bath of quantum harmonic oscillators (Jing et al., 2013; Chen et al., 2009).

Fig. 3.8 shows selected spectra obtained by numerically exact simulations, performed employing the HEOM method. The spectra for the rest TD-DFT derived parameters are shown on Appendix C. Qualitatively, functionals with $J_{14} \approx 140 \text{ cm}^{-1}$ show the correct features: the peak with a shoulder to red side, and a planar side to the blue side of the peak; meanwhile, lower excitonic couplings cannot reproduce the same behaviour, as is the case of TPSS. Neither functional can predict the relative height of the peak and its shoulder faithfully.

For a shifted hamiltonian with $E = 0 \text{ cm}^{-1}$, using equation (1.2.16), the higher (+) and lower (−) exciton dipole strenghts μ_{\pm} are given by,

$$\mu_{\pm} = \mu\sqrt{1 \pm \cos \theta} \quad (3.1.15)$$

where μ is the dipole strength of the monomer transition. This shows that the ratio of strengths (which determined the relative height of the peaks) is given by,

$$\frac{\mu_{+}}{\mu_{-}} = \sqrt{\frac{1 + \cos \theta}{1 - \cos \theta}} = \left| \cot \frac{\theta}{2} \right| \quad (3.1.16)$$

which decreases rapidly with increasing angle for $0 \leq \theta \leq \frac{\pi}{2}$. The ratio for the experimental data is approximately 2.86 (1/0.35), which solves for $\theta \approx 39^{\circ}$, that coincides with previous estimates (Dinh & Renger, 2015; Caycedo-Soler et al., 2022). The TD-DFT estimate for the opening angle is at least 60% higher, which leads to the discrepancies

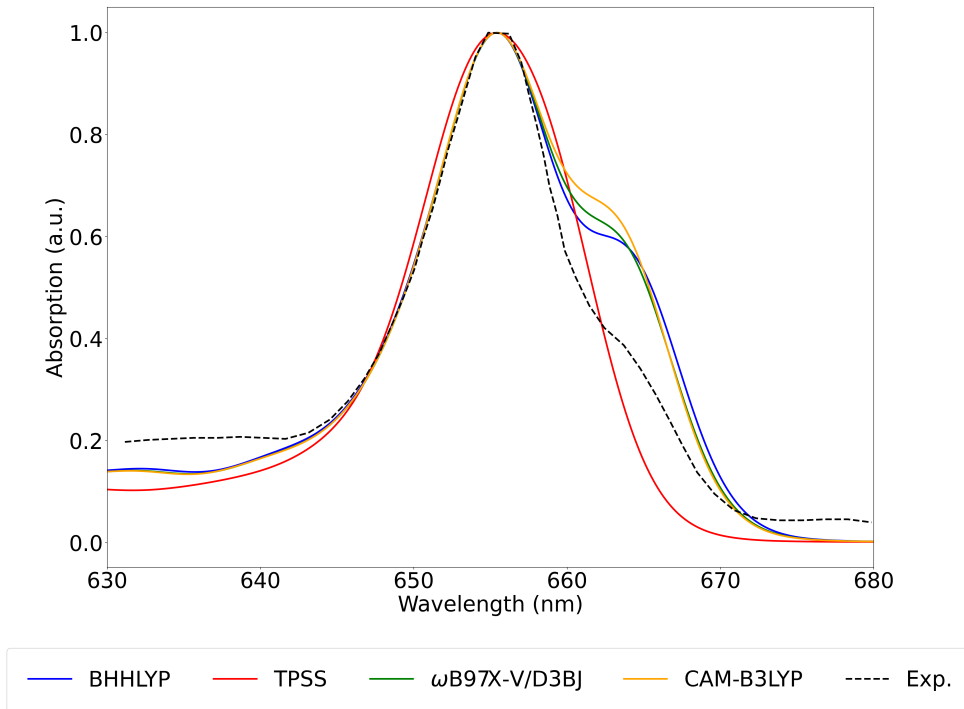


Figure 3.8: Simulated spectra for numerically exact lineshapes of linear absorption in the full vibronic picture. All site energies have been shifted so that the highest peak coincides with the experimental.

in the relative height of the peaks, reducing the ratio to 1.57 (1/0.64) on average. This comparison can be seen in Fig. 3.9. Therefore, the increase in opening angle explains the difference in relative height.

The orientation of the predicted transition dipoles by TD-DFT has not been explored thoroughly in the literature, but comparison to high level wavefunction theory calculations show deviations of around 9° on average, with maximal values near 34° for similar functionals (Robinson, 2018). This amount of errors in both the monomer transition dipoles could explain the large predicted opening angle. Methods to achieve better orientations of the transition dipoles have to be studied further, as small conformational changes can lead to large changes in the transition dipole (Brand et al., 2011).

To analyze the quality of HEOM-predicted spectra with TD-DFT parameters, de-

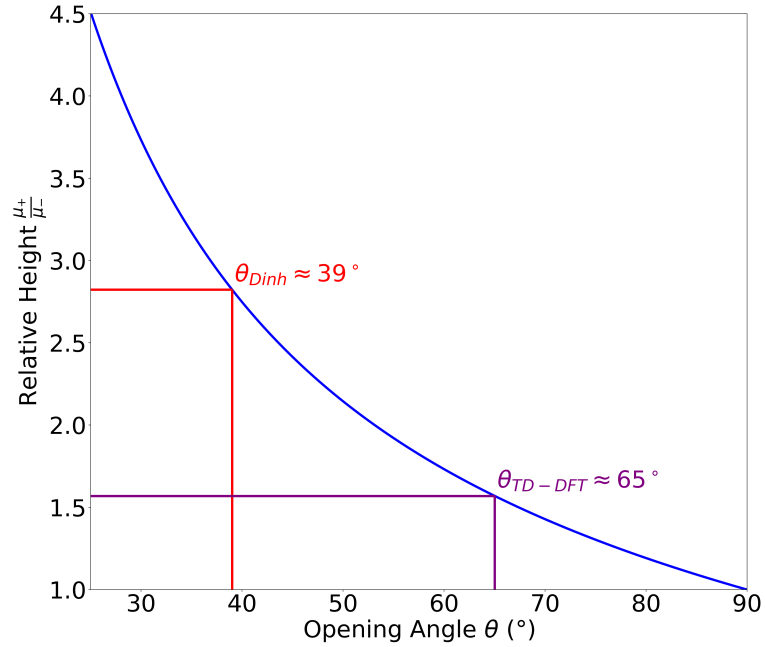


Figure 3.9: Dependence of the theoretical relative height between the peak and shoulder with the opening angle.

convolution of the spectra was performed into two Voigtian peaks of the form,

$$V(\omega) = A_0 \operatorname{Re} \left[W \left(\frac{\omega - \omega_0 + i\gamma}{\sigma\sqrt{2}} \right) \right] \quad (3.1.17)$$

where A_0 is the area under the peak, ω_0 is the frequency of the peak center, γ and σ are related to the underlying broadening through the standard deviations of respective Lorentzian and Gaussian profiles, and $W(z)$ is the Faddeeva function,

$$W(z) = e^{-z^2} \left(1 + \frac{2i}{\sqrt{\pi}} \int_0^z e^{t^2} dt \right) \quad (3.1.18)$$

The experimental spectra shows an almost horizontal zone between 630 nm and 640 nm, which leads to poor results in the curve-fitting procedure. To consider this effect, an artificial baseline $B(\omega)$ is inserted on the blue side of the major peak only, given by,

$$B(\omega) = (m\omega + b)[1 - H_s(\omega)] \quad (3.1.19)$$

where m and b define the linear regression of the first 1000 data points of each spectrum,

and $H_s(\omega)$ is the softened Heaviside function,

$$H_s(\omega) = 1 - \frac{1}{1 + e^{\lambda(\omega - \omega_s)}} \quad (3.1.20)$$

where λ is the softening parameter, which determines how sharp is the jump, and ω_s is the switch frequency at which the baseline is switched off. Thus, the full absorption spectra fitting function for deconvolution is,

$$\alpha(\omega) = B(\omega) + V_1(\omega) + V_2(\omega) \quad (3.1.21)$$

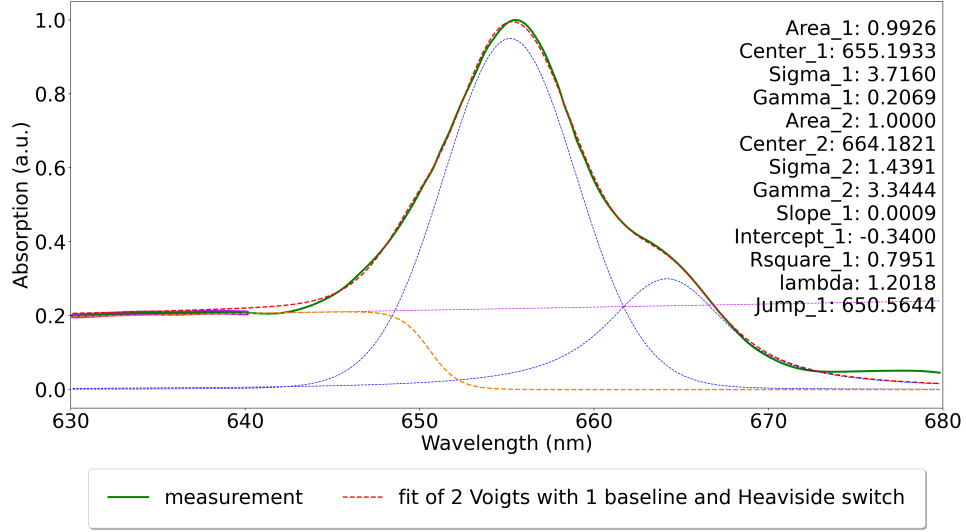
The curve-fitting was performed minimizing the residuals using the least-squares method. From each fit, 12 parameters are adjusted: 4 for each Voigtian peak $(A_0, \omega_0, \sigma, \gamma)$, and 4 for the baseline $(m, b, \lambda, \omega_s)$. Examples of the curve-fitting results are shown in Fig. 3.10. The curves for the rest of the functionals are shown on Appendix C.

From each peak, the center of the peak ω_0 and its height h_{max} are extracted, and compared to the experimental analogues, using the excitonic splitting E and the relative height P , defined as,

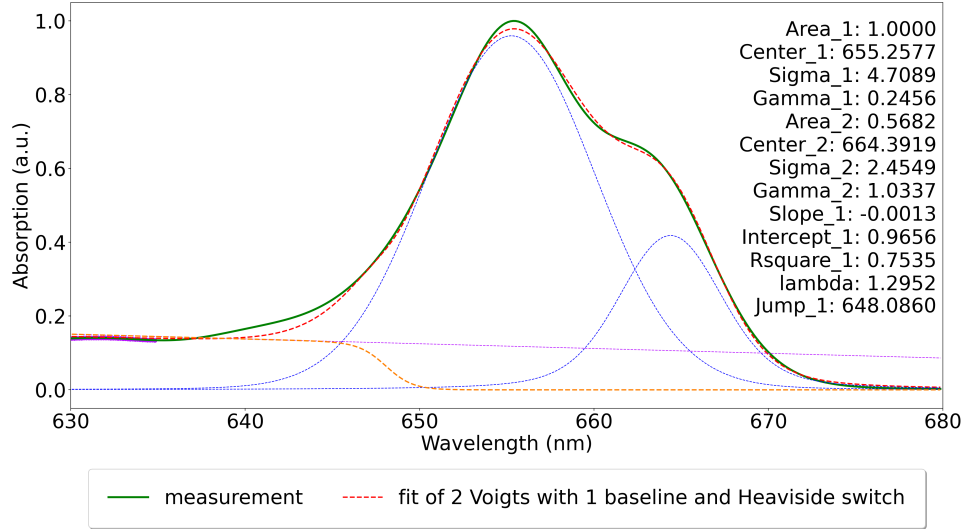
$$E = \omega_{0,+} - \omega_{0,-} \quad ; \quad P = \frac{h_{max,+}}{h_{max,-}} \quad (3.1.22)$$

as quality performance metrics. Fig. 3.11a shows the behaviour of the errors of both figures across the functionals, making the distance to the center the measurement of the full deviations. It is clear that range-separated hybrids perform best, as they are clustered near the center of the graph, which is in line with the observations on the performance for both site energies and excitonic couplings. Meanwhile, meta-GGA and metaH-GGA functionals perform the worst, as a consequence of the lower J_{14} predicted by these functionals. Global hybrids give mixed results: functionals like PBE0 have distances similar to RS Hybrids, however, this behaviour does not reproduce in other functionals of the same category.

A combined measurement of both contributions to the errors is the distance to the



(a) Experimental



(b) CAM-B3LYP

Figure 3.10: Deconvolution of simulated spectra for HEOM lineshapes obtained for experimental data and CAM-B3LYP calculated spectroscopical parameters.

center of the relative error plot, is given by,

$$d_{error} = \sqrt{\left(\frac{E}{E_{exp}} - 1\right)^2 + \left(\frac{P}{P_{exp}} - 1\right)^2} \quad (3.1.23)$$

This error distance is the one shown on Fig. 3.11b. It is clear that for meta-GGA functionals the distances are much greater than for the rest of functionals. The RS

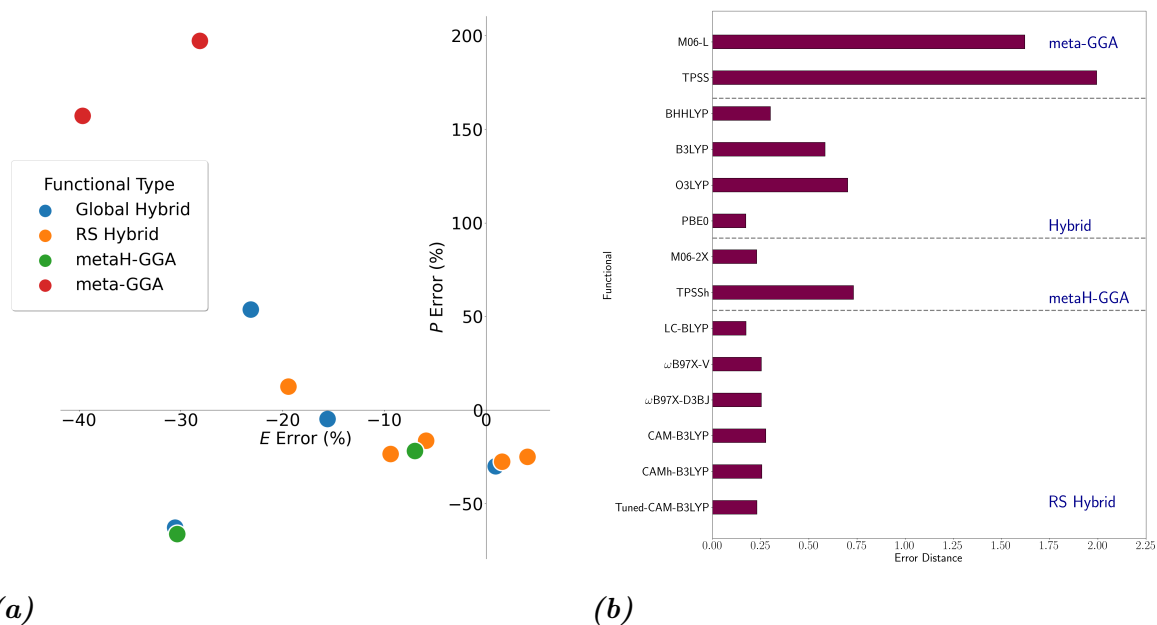


Figure 3.11: Relative errors for quality figures of merit for TD-DFT derived parameters in the prediction of linear absorption spectra, predicted HEOM lineshape theory. **a)** Metric percentage relative errors compared to the deconvolution of experimental data. **b)** Error distance as a measurement of the total deviation from experimental data.

hybrids perform the best, with very similar distances ($\%RSD = 17\%$), being LC-BLYP the best functional, followed by Tuned-CAM-B3LYP, ω B97X-V/D3BJ, CAMh-B3LYP and CAM-B3LYP.

Global hybrid functionals have very different performances between them. This variability is usually associated with the relative amount of Hartree-Fock (HF) exchange in the exchange–correlation contributions, and several benchmarks select functionals according to their HF exchange percentage (Laurent & Jacquemin, 2013; Jacquemin et al., 2009). For the functionals here assessed the HF exchanges are 50% for BHHLYP, 20% for B3LYP, 12% for O3LYP and 25% for PBE0. Thus, a positive correlation can be observed for the first 3 functionals between their performance and HF exchange, however, for PBE0 the error distance is abnormally low, being also the lowest of all the functionals across all categories. PBE0 is a functional that minimizes the effect of the self-interaction errors in the calculation of excited states, which explains the outlier behaviour (Adamo & Barone, 1999).

3.2 Quantum Effects in the WSCP EET

3.2.1 Liouville-von Neumann Dynamics

A first approach to analyze the EET dynamics in the system, is the limit of null coupling between the system and the bath, which leads to a closed system with non-dissipative dynamics. This gives information about the quantum characteristics of the system, and how the different parameters interplay with each other.

The energy landscape for the aggregate (Fig. 3.12a) shows significantly different energies for every functional, however the energy splittings are very similar, which suggests that the dynamics would also be similar for all cases. As the system is closed, the dynamics are non-dissipative and this energy must be conservative. This coincides with the behaviour observed in Fig. 3.12b, where the energy remains almost constant, owing its variability to the static disorder of the system. The disorder of the aggregate generates a statistical distribution of the hamiltonian, which implies a noisy distribution of the total energy. Indeed, the %RSD of all the energy values along the simulation is not greater than 0.01% for each tested functional. Notice that the value of energy depends on the functional, which coincides with the site energy of the first site, as indicated by the starting condition selected and the conservative nature of the system.

The EET dynamics can be seen directly from the site populations ($\rho_{nn}(t) = |\langle n | \rho(t) | n \rangle|$) and coherences. The former denotes the probability that the system is in certain state $|n\rangle$ at some time t , and the latter, the interaction between states. Fig. 3.13a and 3.13b show the dynamics for the site populations on the first site, for both the case with and without static disorder. In all cases, the population starts at 1, as expected, and oscillates sinusoidally around an offset of 0.5. This is a direct consequence of the form of the time-dependent Schrödinger equation and the initial state selected: for an initial state that is a superposition of the eigenstates of the system Hamiltonian, the time evolution yields a superposition of oscillations, or wave packet. The difference in phases of each coherent oscillation in the superposition produces the quantum beating observed in the populations, which indicates that the initial populations travel from one site

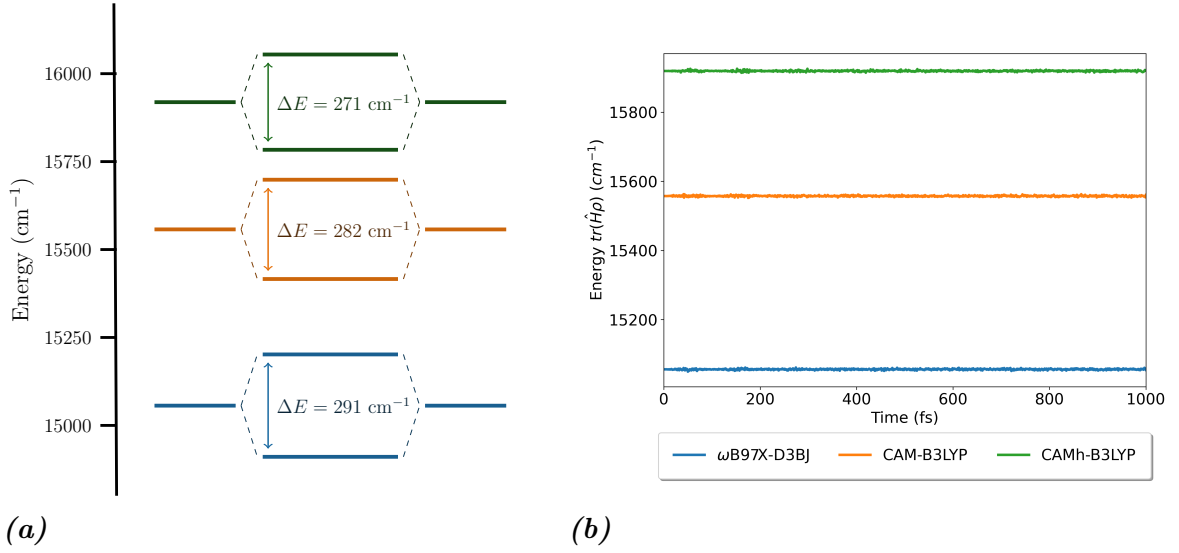


Figure 3.12: Energy distribution for the closed system dynamics of the Chl b WSCP. **a)** Energy landscape of the excitonic system determined from TD-DFT parameters. **b)** Total energy dynamics. Color symbology is the same for **a)** and **b)**.

to the other, back and forth with certain frequency. If the starting state were a pure eigenstate of the hamiltonian, then the time evolution would yield a time-independent solution for the populations (May & Kühn, 2011).

In both figures 3.13a and 3.13b the 3 oscillations do not have the same frequency Ω . The order is as follows $\Omega(\text{CAMh-B3LYP}) < \Omega(\text{CAM-B3LYP}) < \Omega(\omega\text{B97X-D3BJ})$, which is the same order than the energy splitting calculated. The inclusion of the static disorder results in a damping of the amplitude of the oscillations. This is owed to the difference in site energies in each trial: each sample lead to a different phase relation with the same average frequency, as the phase relations are averaged out for several trials, the result is a dephasing of the population and the amplitude decays exponentially (May & Kühn, 2011).

The populations dynamics can also be analyzed from the coherence witness, in this case, the relative entropy of coherence \mathcal{C}_S , according to eq. 1.3.28. Fig. 3.13c and 3.13d show the coherence dynamics in the site basis. The selection of the basis is extremely important, and must be considered in the interpretation of the results, as the witness quantifies the coherence between the basis states. As expected, the coherence starts at 0, since the starting state is a pure basis state. The oscillations are also present in this witness, however, the wave shape changes to a $\sin^2 \Omega t$ type. The maximal value for the

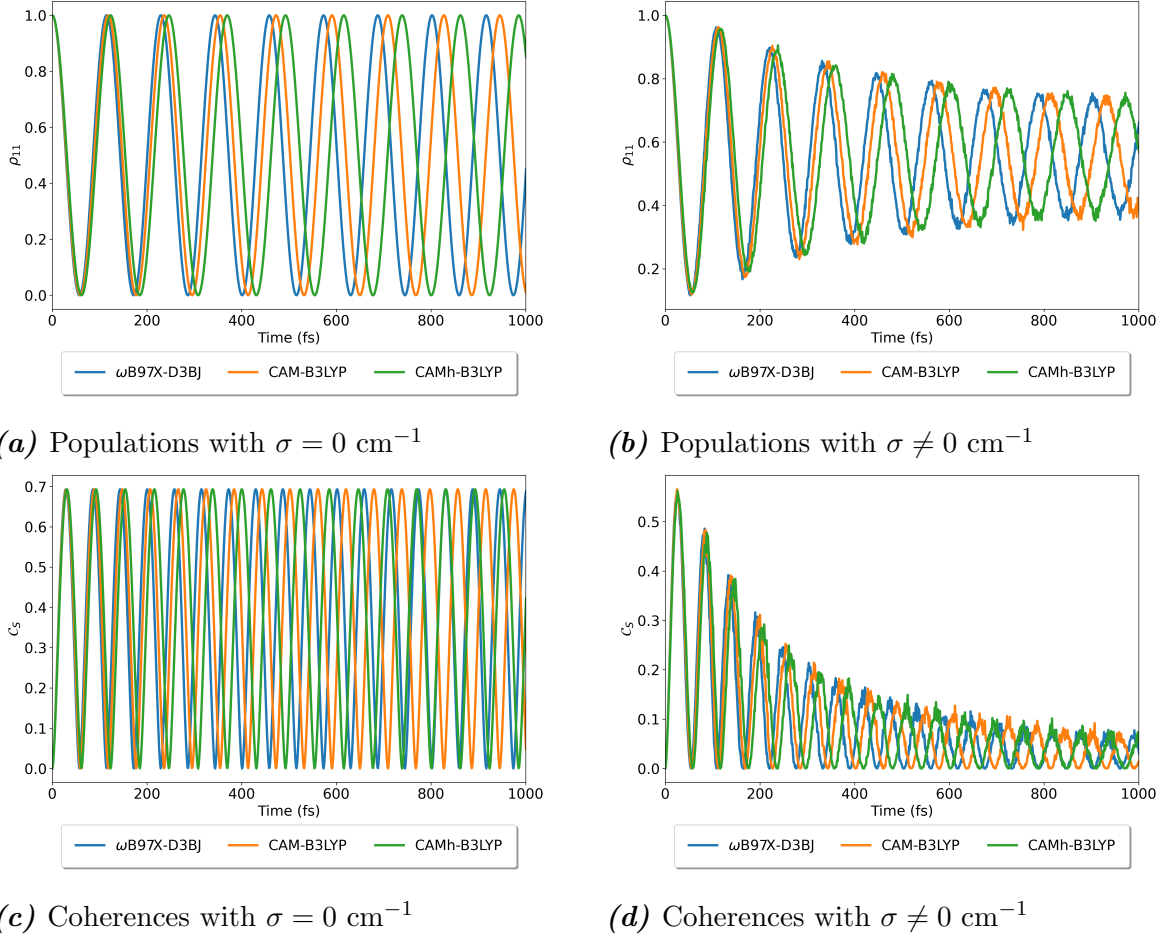


Figure 3.13: Populations and coherence for the closed system dynamics of the Chl b WSCP, and dependence with the TD-DFT parameters. The populations shown are for the first site, and the relative entropy of coherence is considered as coherence witness. **a)** and **b)** show population dynamics without and with static disorder, respectively. **c)** and **d)** show coherence dynamics without and with static disorder, respectively.

coherence corresponds to the maximum value of the von Neumann entropy,

$$S(\rho) = -\text{Tr} [\rho \ln \rho] \quad (3.2.1)$$

which in this case maximizes to $\ln 2 \approx 0.69$. The differences in frequencies are still present in the coherences, and follow the same order than before. The addition of the static disorder also produces a decay in the amplitude of the oscillations, however, the damping is more pronounced than in the populations. As stated before, this can be attributed to the dephasing of the multiple waves averaged, however it is clear that this is more correctly described as the decoherence of states due to the static disorder.

To further examine the effect of the static disorder, one can consider the purity of the state: the measurement of how much a state is a mixed. For a completely pure state, $\text{Tr} [\rho^2] = 1$, while for a mixed state $\text{Tr} [\rho^2] < 1$. The degree of mixing $\gamma = \text{Tr} [\rho^2]$ can be used to decide whether a system is mixed or not, for the maximally mixed state in a Hilbert space of dimension N ,

$$\rho_{\text{max. mixed}} = \frac{1}{N}I_N \Rightarrow \gamma = \frac{1}{N} \quad (3.2.2)$$

then, $\frac{1}{N} \leq \gamma \leq 1$. However, this measure is not necessarily monotonically decreasing upon mixing. To realize a more adequate witness of purity, the depiction of the state on the Bloch sphere can be analyzed (Nielsen & Chuang, 2010). For an arbitrary state with a density matrix ρ in the Hilbert space for $N = 2$, then,

$$\rho = \frac{I_2 + \vec{R} \cdot \vec{\sigma}}{2} \quad (3.2.3)$$

where $\vec{R} = (R_x, R_y, R_z)$ is the Bloch vector and $\vec{\sigma} = (X, Y, Z)$ is the vector which entries are the Pauli matrices. Then, the degree of purity is,

$$\gamma = \frac{1 + R_{\text{Bloch}}^2}{2} \quad (3.2.4)$$

where $R_{\text{Bloch}} = |\vec{R}|$, and therefore the state is pure when $R_{\text{Bloch}} = 1$, and the state is maximally mixed when $R_{\text{Bloch}} = 0$. Hence, the length of the Bloch vector decreases monotonically in the interval $[0, 1]$ when the state becomes less pure. Notice that the length of the Bloch vector can be recovered from,

$$R_{\text{Bloch}} = \sqrt{(\text{Tr} [\rho X])^2 + (\text{Tr} [\rho Y])^2 + (\text{Tr} [\rho Z])^2} \quad (3.2.5)$$

Fig. 3.14a and 3.14b show the purity dynamics without and with static disorder, using R_{Bloch} as a purity witness according to eq. (3.2.5). It is clear that for the case without static disorder the state remains pure in all cases, as the state system is set as pure at the beginning, and the unitary evolution does not alter the purity of the system,

as is the case of the closed system. However, the inclusion of the state disorder now produces an ensemble of wavefunctions, all valid for the system, as they represent the variability introduced in the static disorder and the dephasing. The beatings are still conserved, moreover, the frequencies of oscillation also follow the same order than for the populations and coherences. Also, the purity of the system starts at 1, as expected by the initial condition set; but the center of the oscillations decays exponentially. This is a clear indicative of the ensemble nature of the quantum state for the aggregate.

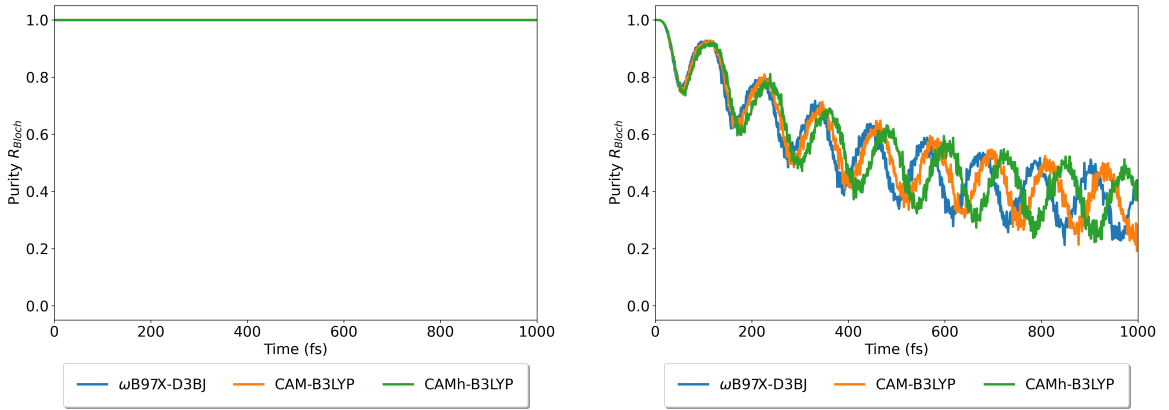
(a) Purity with $\sigma = 0 \text{ cm}^{-1}$ (b) Purity with $\sigma \neq 0 \text{ cm}^{-1}$

Figure 3.14: Purity for the closed system dynamics of the Chl b WSCP, and dependence with the TD-DFT parameters. The radius of the Bloch vector is used as purity witness. **a)** and **b)** show purity dynamics without and with static disorder, respectively.

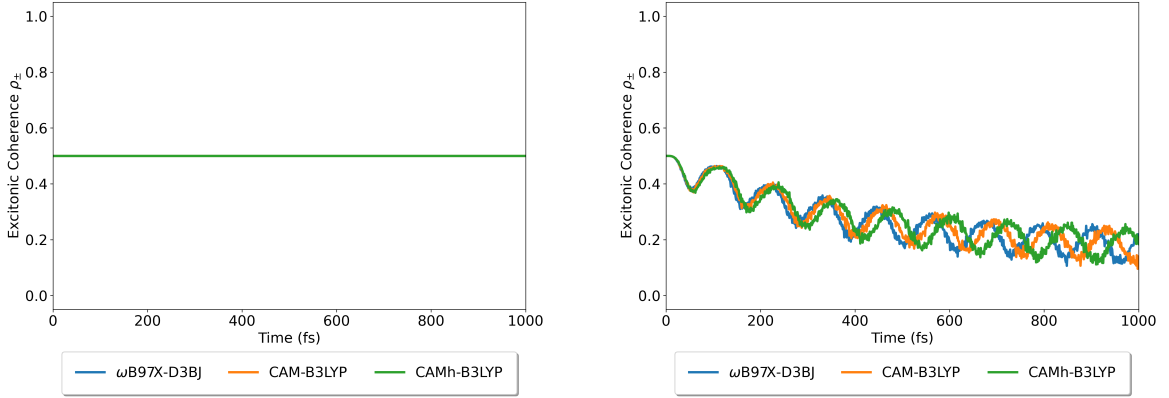
For the evaluation of quantum transport, the excitonic states are obtained from diagonalization of the average hamiltonian. As the Chl b WSCP is a dimer, the resulting aggregate is a two-level system (TLS), where the higher and lower excitons are represented by the states $|+\rangle$ and $|-\rangle$, respectively. The excitonic coherence is then given by,

$$\mathcal{C}_{ext} = \rho_{\pm} = |\langle + | \rho(t) | - \rangle| \quad (3.2.6)$$

where ρ_{\pm} represents the density matrix in the excitonic basis, this means that matrix elements $\rho_{\alpha\beta}$ of ρ_{\pm} are related to the matrix elements in the site basis ρ_{mn} via the coefficients in eq. (1.2.14), that is,

$$\rho_{\alpha\beta} = \sum_{mn} c_{\alpha}^{(m)} c_{\beta}^{(n)*} \rho_{mn} \quad (3.2.7)$$

Fig. 3.15 show the excitonic coherence dynamics, for the case with no static disorder, the excitonic coherence is constant a 0.5, which shows that the exciton is constantly delocalized between the two sites. Including the static disorder, makes the excitonic coherence decay exponentially and oscillates, sign of the decoherence phenomenon as discussed previously.



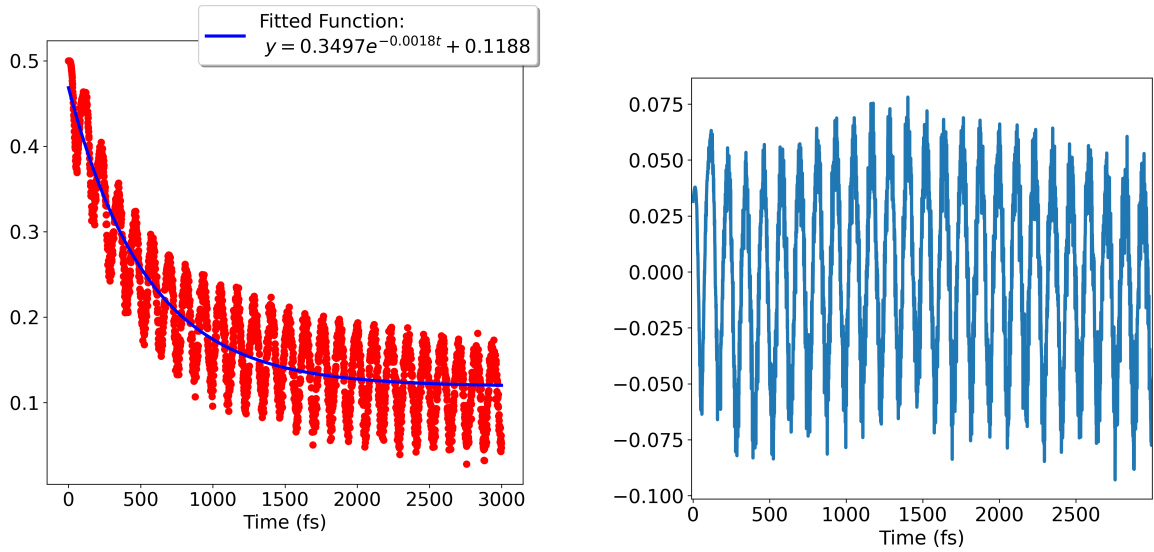
(a) Excitonic coherence with $\sigma = 0 \text{ cm}^{-1}$

(b) Excitonic coherence with $\sigma \neq 0 \text{ cm}^{-1}$

Figure 3.15: Excitonic coherence for the closed system dynamics of the Chl b WSCP, and dependence with the TD-DFT parameters. The relative entropy of coherence of ρ in the exciton basis is used as a coherence witness. **a)** and **b)** show excitonic coherence dynamics without and with static disorder, respectively.

As stated before, to witness quantum transport, the excitonic coherence must drive the population dynamics, and therefore must have the same beating frequency. As the excitonic coherence shows a decay mixed with the beating, an exponential fitting of the data is performed to extract only the coherence beating. Fig. 3.16 shows an example of this procedure. For the ordered condition ($\sigma = 0 \text{ cm}^{-1}$), the excitonic coherence is constant, and no beating is observed, therefore, the procedure fails.

Fourier analysis is performed on the population and excitonic coherence beating trajectories. Using the FFT, the frequency content of both signals is analyzed: to show coherence between them, their oscillation frequency and waveform must be the same. As the populations oscillate as an underdamped sine wave, only one frequency peak is expected; however, the excitonic coherence beating shows fast oscillations of almost constant amplitude around their average line, which also oscillates with a much slower frequency, therefore, two peaks are expected in the Fourier transform. Fig. 3.17 shows



(a) Excitonic coherence fit

(b) Extracted beating

Figure 3.16: Excitonic coherence beating extraction for the closed system dynamics of the Chl b WSCP. The exponential fit of the excitonic coherence is shown on **a)**, and **b)** shows the excitonic coherence beating extracted. *Conditions:* TD-DFT/CAM-B3LYP parameters with $\sigma = 78 \text{ cm}^{-1}$.

the FFTs of both witnesses for the analyzed conditions.

It is clear from Fig. 3.17 that the beating frequency of both witnesses coincide, which is a sign of the presence of quantum transport phenomena. This behaviour is independent on the choice of parameters, and therefore, it suggests that is a characteristic of the system in a closed conservative regimen.

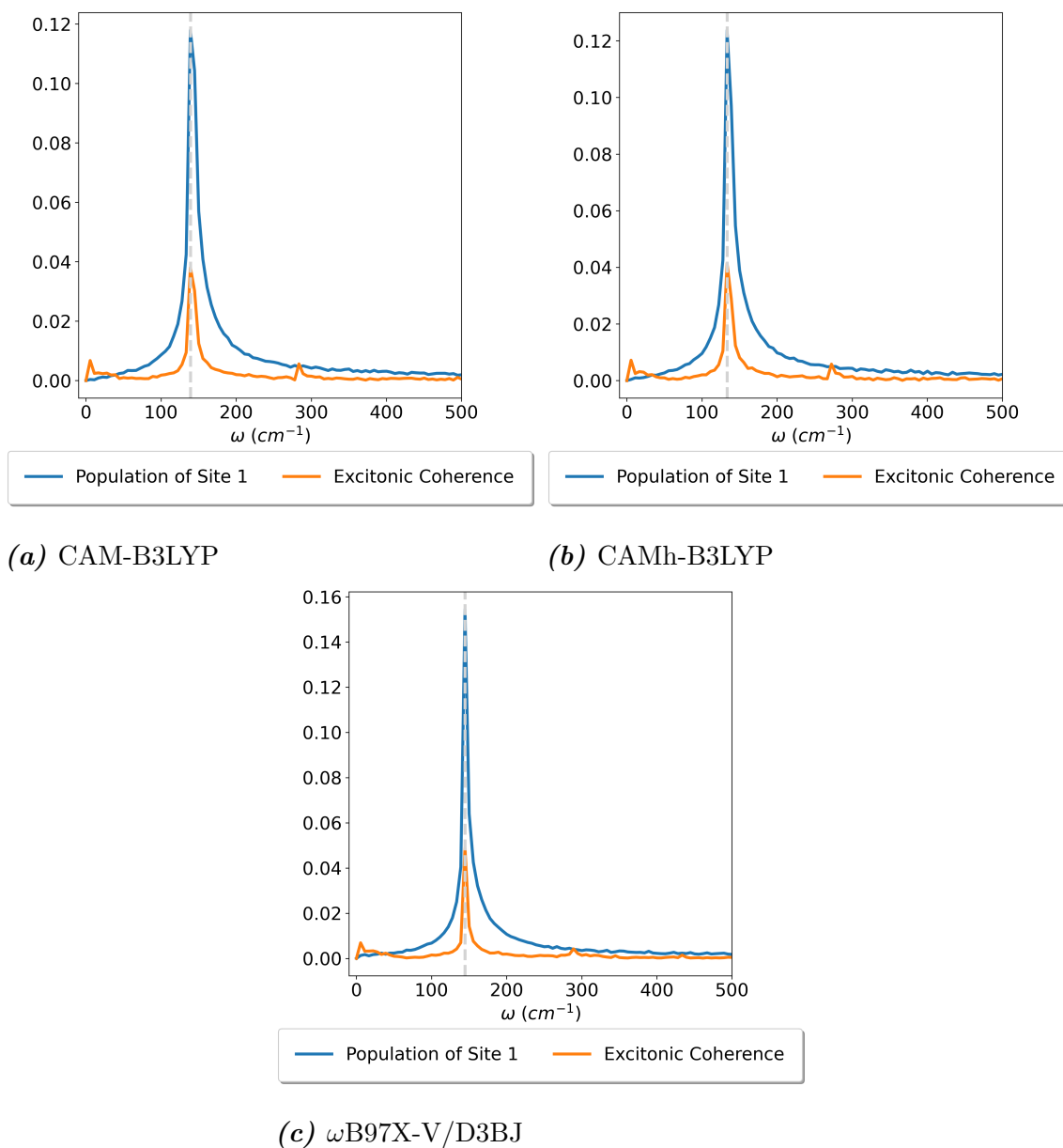


Figure 3.17: Quantum transport evaluation in the Chl b WSCP for closed system dynamics, and dependence on the TD-DFT parameters. The FFT of the population of site 1 and the excitonic coherence beating are shown. Dotted lined shows the frequency of the population beating.

3.2.2 Approximate Redfield Dynamics

The presence of a protein scaffold around the pigments in the WSCP leads to vibronic dynamics due to the coupling between the EET and the vibrational motions that change the electronic structure of each chromophore in time. This interaction then produces decoherence of the excitonic states, and has to be considered to accurately describe the EET dynamics. Therefore, an open quantum system approach has to be used to describe the dissipative dynamics. Here, the approximate secular Redfield dynamics is used for the low temperature two-level system (TLS), considering that the experimental spectra are measured at 77 K.

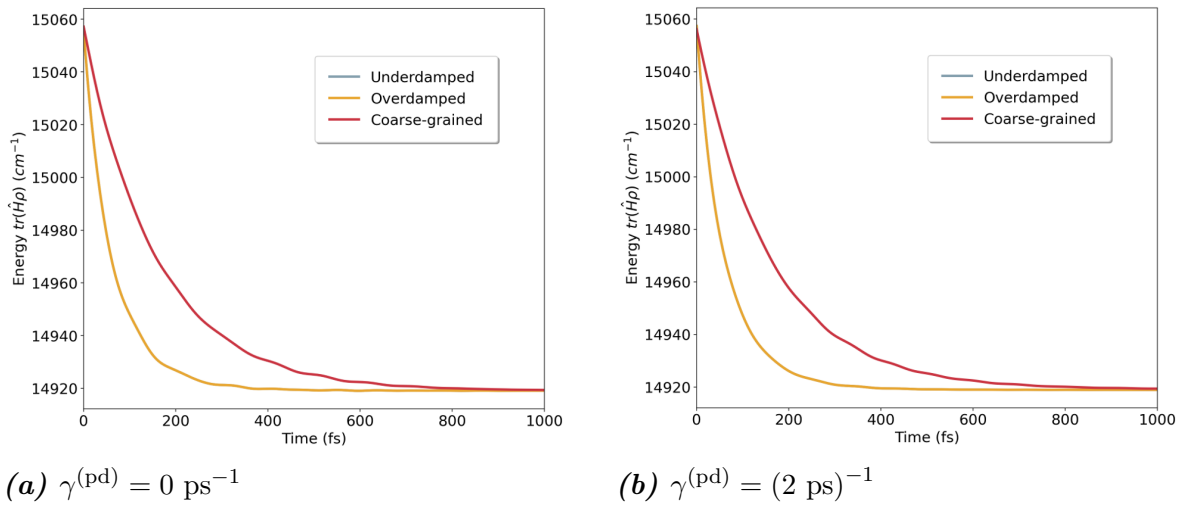


Figure 3.18: Energy for the open system dynamics of the Chl b WSCP, and dependence on the spectral density selection. **a)** and **b)** show energy dynamics without and with pure dephasing, respectively.

Fig. 3.18 shows the energy dynamics for the open system. It is clear that in this regimen, energy is lost to the environment until an equilibrium is achieved, consequence of the dissipative dynamics. As in the Redfield approach, the coupling to the environment is considered weak, the excitonic coupling is much higher than the environmental coupling, therefore the energy lost corresponds only to the excitonic coupling. This is a particular case for the resonant condition of the monomers: for a more general case, the energy value for the equilibrium is E_- , and the energy loss is half the excitonic splitting, $\frac{E_+ - E_-}{2}$.

The amount of energy lost to the environment is independent on the spectral den-

sity selection, nor the addition of pure dephasing affects it. However, the time to reach equilibrium is affected by the former. For the overdamped system, the equilibrium time is much shorter than for the underdamped and coarse-grained cases; this is expected, as the overdamped modes oscillate much faster, and so does the energy disperses. For underdamped and coarse-grained conditions, the behaviour is the same, this is consequence of similar values of $\mathcal{J}(\Omega)$.

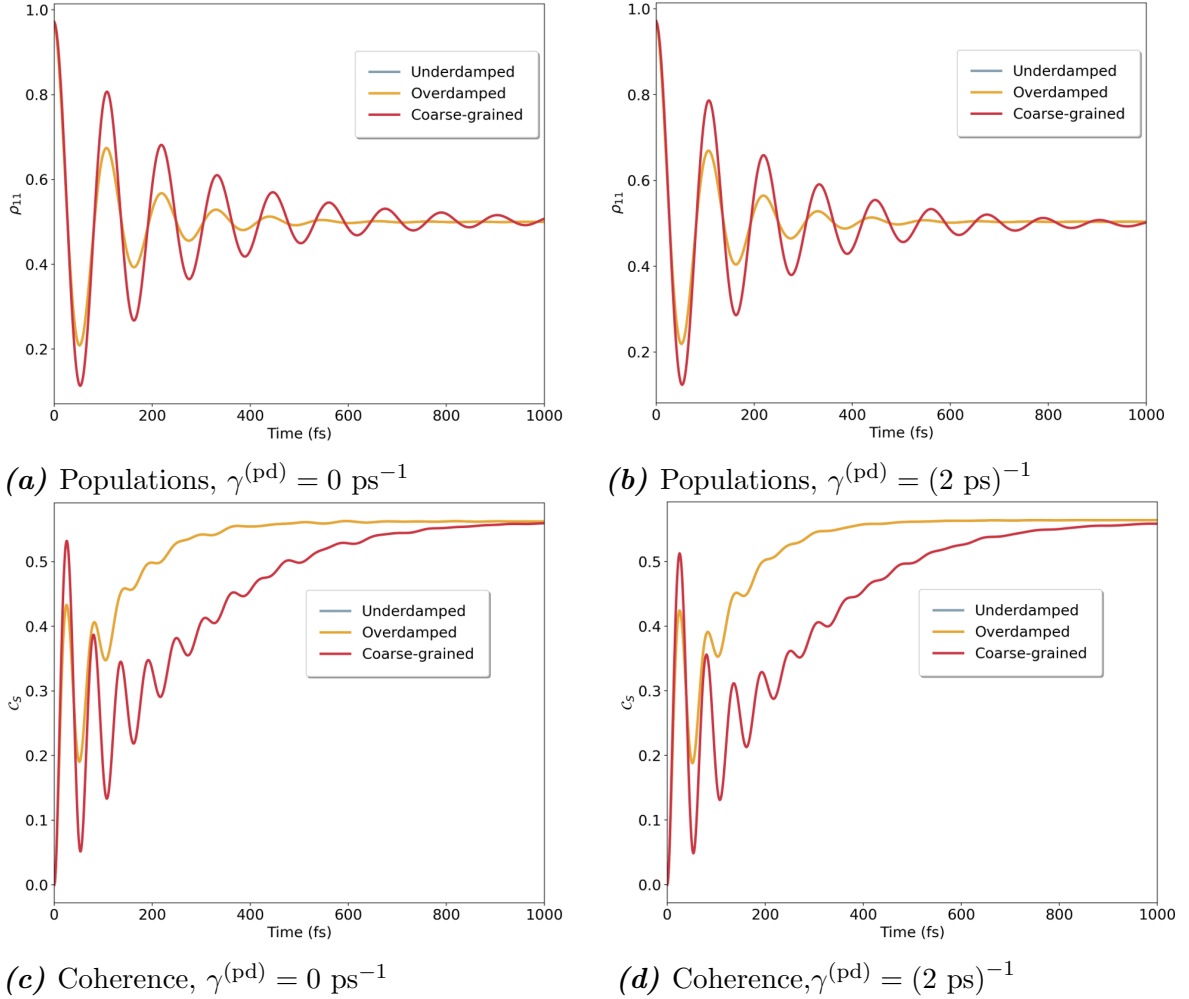


Figure 3.19: Populations and coherences for the open system dynamics of the Chl b WSCP, and dependence on the spectral density selection. **a)** and **b)** show populations for the first site dynamics without and with pure dephasing, respectively. For the bipartite coherence, the relative entropy of coherence is used as witness. **c)** and **d)** show coherence dynamics without and with pure dephasing, respectively.

It is worth noting that the coarsed-grained and the underdamped spectral densities have very different lineshapes, but result in the same behaviour: as the approximation

used here only needs one point of the spectral densities, all the complex attributes are lost. Higher level, numerically exact calculations can lead to different results by considering the contributions of the rest of couplings (Caycedo-Soler et al., 2022).

The population and coherence dynamics for the open system are shown on Fig. 3.19. The populations show the same underdamped sinusoidal wave behaviour than in the closed system case, however, their amplitude decrease much faster; even faster in the case of overdamped vibrations. This implies that the coupling to the environment suppresses the beating, and forces the system to reach equilibrium much faster. The addition of pure dephasing only slightly reduces the observed amplitudes, which implies that pure dephasing also contributes to the damping.

During the first femtoseconds of the dynamics, the coherences show similar oscillations than in the closed case. However, they are also damped because of the coupling to the environment. In this case, the value of the coherences without the beating increases until its stabilizes to a maximally coherent state. For a TLS, this state is of the form (Bai & Du, 2015),

$$|\phi\rangle = \frac{1}{\sqrt{2}} (|1\rangle \langle 1| + |2\rangle \langle 2|) \quad (3.2.8)$$

which coincides with the equilibrium state suggested by the populations, and also, is consistent with the Markovian nature of the secular approach used in the simulation. For the coherences, the same effect of the pure dephasing is observed as in the case of the populations, where only slightly damps the oscillations.

Finally, Fig. 3.20 show the quantum transport evaluation for the open system, performed with the same procedure than in the closed system case. For all the spectral densities, presence of quantum transport is clear in the case of no pure dephasing, however, the addition of it completely suppresses the presence of quantum transport. This suggests that pure dephasing is the principal mechanism that breaks quantum transport. Further research is suggested with numerically exact, non-Markovian methods to study in detail the relative importance of decoherence mechanisms in the presence of quantum transport.

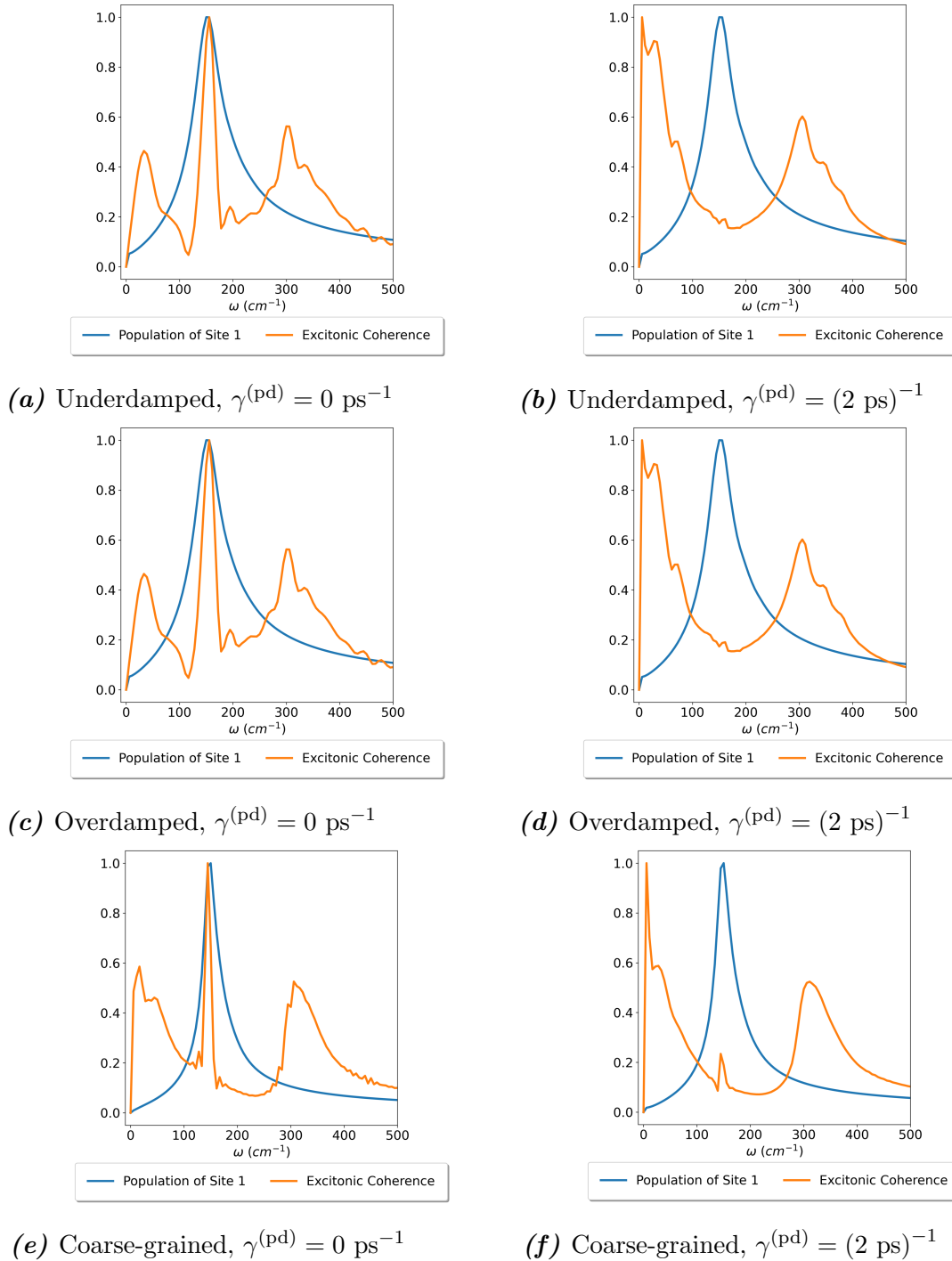


Figure 3.20: Quantum transport evaluation in the Chl b WSCP for open system dynamics, and dependence on the spectral density selection. **a)** and **b)** shows the evaluation for the underdamped spectral density ($\tau_{brd} = 1 \text{ ps}$) without and with pure dephasing, respectively. **c)** and **d)** shows the evaluation for the overdamped spectral density ($\tau_{brd} = 50 \text{ fs}$) without and with pure dephasing, respectively. **e)** and **f)** shows the evaluation for the coarse-grained spectral density ($\tau_{brd} = 50 \text{ fs}$) without and with pure dephasing, respectively.

Chapter 4

Concluding Remarks

In this work, the quantification of presence and prevalence of quantum effects in PPCs was evaluated through Quantum Chemical and Computational techniques.

First, the relevant spectroscopical parameters for the chromophoric aggregates were obtained using *ab initio* methods in the Frenkel model framework. For the site energies, the calculations show excellent agreement with the experimental values at the TD-DFT/def2-TZVP level, with better values predicted by range-separated hybrid functionals. It was also demonstrated that the Tamm Dancoff approximation is insufficient for the quantitative prediction of site energies. For completion, it is recommended to perform calculations employing double hybrid methods and parametrizations for range separated functionals to assess their performance.

For the prediction of the excitonic couplings, a numerically exact fully vibronic method was considered as reference for the evaluation of different techniques. Coulombic methods give almost half of the reference value, which is not explained by structural differences; however, the influence of the dielectric properties of the protein scaffold on the transition dipole moment is not clear, which can affect the rescaling of the couplings.

Diabatic methodologies, using TD-DFT calculations, show excellent results for the calculation of the excitonic couplings. This is attributed to the inclusion of long and short range interactions, in contrast to the Coulombic methods, that only account for long range interactions. Range separated functionals give better results overall, while global hybrids give mixed results; it is recommended to fully study the nature of the predicted excited states to understand the source of these discrepancies.

For the prediction of the linear absorption spectra of the PPC, first, the static disorder was estimated using a non-vibronic model. It was demonstrated that this parameter can be estimated independently of the TD-DFT functional, and is dependent on the statistical distribution selected for the broadening. Voigtian broadening show the best results, with the Procrustes distance as the best metric to asses quality of the spectra. The static disorder obtained coincides with previous reports. Vibronic linear absorption spectra were simulated using the obtained parameters, showing that range-separated functionals give the best results in the accurate prediction of the spectra; with the ex-

ception of the relative height of the peaks, which shows significant discrepancies, owing to the opening angle predicted. It is recommended to investigate the source of this discrepancies and possible solutions to give more accurate transition dipoles.

To study the presence of quantum coherence and transport in the EET dynamics, the time evolution of the system was obtained under closed and open system paradigms. The closed system dynamics show that in this regimen the energy is conservative. The populations and coherence show sinusoidal oscillations with a frequency dependent on the excitonic splitting. The introduction of the static disorder effects leads to dephasing and decoherence in the dynamics, resulting in a mixing of the states in a statistical ensemble. Through Fourier analysis, it was shown that the closed system presents quantum transport in the disordered case, independently of the functional selected for the parameters calculation.

The approximate Redfield dynamics simulation shows that the coupling to the environment damps the quantum beatings and rapidly forces the system to an equilibrium state, which corresponds to a maximally coherent state. The use of overdamped spectral densities greatly lowers the lifetime of the oscillations, while pure dephasing only slightly contributes to the damping. The evaluation of quantum transport shows that the absence of pure dephasing allows the quantum transport, while its inclusion completely suppresses it. Further research is recommended using numerically exact, non-Markovian methods to fully account for the intermediate couplings to the environment and vibronic effects, in order to fully assess the relative importance of decoherence and dephasing sources to the suppression of quantum transport.

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Appendices

Appendix A

Coordinate Files

A.1 6S2Z Chl b dimer

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1 272
2 PDB ID: 6s2zFH      Chain: AD      Ligand: CHL      ID: 1001
3 MG      11.312      3.415      15.292
4 C      13.274      3.48      18.06
5 C      8.663      3.899      17.325
6 C      9.255      2.753      12.689
7 C      13.989      2.054      13.481
8 N      11.025      3.866      17.237
9 C      11.892      3.973      18.135
10 C     11.419      4.528      19.414
11 C     9.942      4.464      19.23
12 C     9.86      4.044      17.832
13 C     9.339      3.415      20.128
14 C     12.03      5.859      19.83
15 C     11.425      6.505      21.05
16 C     11.983      6.137      22.392
17 O     12.926      6.67      22.805
```

18	O	11.308	5.202	23.219
19	N	9.261	3.37	15.041
20	C	8.317	3.551	15.951
21	C	6.935	3.393	15.517
22	C	7.143	3.052	14.141
23	C	8.588	3.067	13.957
24	C	5.668	3.529	16.291
25	C	6.124	2.768	13.117
26	C	5.14	1.973	13.304
27	N	11.558	2.562	13.414
28	C	10.644	2.351	12.497
29	C	11.15	1.735	11.275
30	C	12.534	1.53	11.494
31	C	12.665	2.056	12.843
32	C	10.47	1.341	10.034
33	O	9.328	1.556	9.844
34	C	13.537	0.906	10.574
35	C	13.557	-0.567	10.747
36	N	13.255	2.873	15.602
37	C	14.216	2.339	14.891
38	C	15.454	2.119	15.67
39	C	15.011	2.63	16.954
40	C	13.79	3.018	16.815
41	C	16.834	1.621	15.369
42	C	15.441	2.851	18.345
43	O	16.577	2.621	18.796
44	C	14.32	3.427	19.101
45	C	14.011	2.644	20.329
46	O	14.164	3.098	21.395
47	O	13.541	1.325	20.289

48	C	13.547	0.54	21.421
49	C	11.843	4.148	23.965
50	C	10.68	3.524	24.654
51	C	10.616	2.22	24.889
52	C	11.729	1.347	24.508
53	C	9.442	1.618	25.548
54	C	8.779	0.644	24.613
55	C	8.529	1.166	23.223
56	C	7.881	0.09	22.374
57	C	8.843	-0.526	21.384
58	C	6.634	0.602	21.693
59	C	5.555	0.757	22.707
60	C	4.232	0.778	22.003
61	C	3.144	1.441	22.819
62	C	2.773	0.638	24.038
63	C	1.925	1.643	21.949
64	C	0.955	2.629	22.576
65	C	-0.303	2.81	21.744
66	C	-1.022	4.074	22.153
67	C	-1.59	4.764	20.962
68	C	-2.145	3.715	23.055
69	H	10.477	6.299	21.056
70	H	12.977	5.725	19.992
71	H	0.712	2.32	23.463
72	H	11.954	6.477	19.086
73	H	2.198	1.966	21.076
74	H	9.473	5.288	19.437
75	H	11.711	4.034	20.196
76	H	-2.758	3.124	22.59
77	H	-1.798	3.266	23.841

78	H	-2.614	4.52	23.324
79	H	-0.874	4.995	20.349
80	H	-2.219	4.176	20.516
81	H	-2.047	5.572	21.243
82	H	-0.39	4.662	22.595
83	H	9.719	2.549	19.915
84	H	-0.073	2.851	20.803
85	H	-0.888	2.045	21.86
86	H	1.394	3.487	22.685
87	H	1.48	0.792	21.81
88	H	2.453	-0.236	23.765
89	H	3.552	0.533	24.606
90	H	2.075	1.099	24.529
91	H	3.484	2.294	23.13
92	H	4.327	1.245	21.158
93	H	3.966	-0.132	21.796
94	H	9.53	3.632	21.054
95	H	5.585	0.026	23.344
96	H	5.681	1.577	23.21
97	H	6.813	1.452	21.262
98	H	6.355	-0.015	20.998
99	H	9.179	0.162	20.788
100	H	9.585	-0.93	21.861
101	H	8.384	-1.206	20.866
102	H	7.617	-0.621	22.979
103	H	7.956	1.948	23.261
104	H	9.365	1.447	22.82
105	H	8.379	3.388	19.995
106	H	9.331	-0.151	24.551
107	H	7.932	0.371	24.999

108	H	9.714	1.165	26.361
109	H	8.814	2.311	25.806
110	H	11.872	1.404	23.55
111	H	12.534	1.627	24.972
112	H	11.52	0.431	24.75
113	H	9.945	4.089	24.94
114	H	12.295	3.508	23.393
115	H	12.498	4.469	24.605
116	H	14.76	1.85	12.928
117	H	14.456	0.447	21.746
118	H	13.0	0.955	22.106
119	H	13.189	-0.336	21.209
120	H	14.472	4.302	19.492
121	H	16.784	0.715	15.026
122	H	17.248	2.195	14.706
123	H	17.365	1.63	16.18
124	H	13.794	-0.782	11.663
125	H	12.679	-0.928	10.547
126	H	14.211	-0.955	10.145
127	H	8.712	2.82	11.888
128	H	13.321	1.126	9.654
129	H	14.418	1.27	10.753
130	H	10.981	0.887	9.346
131	H	4.497	1.822	12.594
132	H	5.037	1.521	14.156
133	H	6.203	3.207	12.256
134	H	5.663	2.889	17.019
135	H	5.603	4.428	16.651
136	H	4.912	3.36	15.707
137	H	11.506	7.466	20.948

138	H	7.92	4.039	17.932
139	MG	11.312	-3.415	23.258
140	C	13.274	-3.48	20.49
141	C	8.663	-3.899	21.225
142	C	9.255	-2.753	25.861
143	C	13.989	-2.054	25.069
144	N	11.025	-3.866	21.313
145	C	11.892	-3.973	20.415
146	C	11.419	-4.528	19.136
147	C	9.942	-4.464	19.32
148	C	9.86	-4.044	20.718
149	C	9.339	-3.415	18.422
150	C	12.03	-5.859	18.72
151	C	11.425	-6.505	17.5
152	C	11.983	-6.137	16.158
153	O	12.926	-6.67	15.745
154	O	11.308	-5.202	15.331
155	N	9.261	-3.37	23.509
156	C	8.317	-3.551	22.599
157	C	6.935	-3.393	23.033
158	C	7.143	-3.052	24.409
159	C	8.588	-3.067	24.593
160	C	5.668	-3.529	22.259
161	C	6.124	-2.768	25.433
162	C	5.14	-1.973	25.246
163	N	11.558	-2.562	25.136
164	C	10.644	-2.351	26.053
165	C	11.15	-1.735	27.275
166	C	12.534	-1.53	27.056
167	C	12.665	-2.056	25.707

168	C	10.47	-1.341	28.516
169	O	9.328	-1.556	28.706
170	C	13.537	-0.906	27.976
171	C	13.557	0.567	27.803
172	N	13.255	-2.873	22.948
173	C	14.216	-2.339	23.659
174	C	15.454	-2.119	22.88
175	C	15.011	-2.63	21.596
176	C	13.79	-3.018	21.735
177	C	16.834	-1.621	23.181
178	C	15.441	-2.851	20.205
179	O	16.577	-2.621	19.754
180	C	14.32	-3.427	19.449
181	C	14.011	-2.644	18.221
182	O	14.164	-3.098	17.155
183	O	13.541	-1.325	18.261
184	C	13.547	-0.54	17.129
185	C	11.843	-4.148	14.585
186	C	10.68	-3.524	13.896
187	C	10.616	-2.22	13.661
188	C	11.729	-1.347	14.042
189	C	9.442	-1.618	13.002
190	C	8.779	-0.644	13.937
191	C	8.529	-1.166	15.327
192	C	7.881	-0.09	16.176
193	C	8.843	0.526	17.166
194	C	6.634	-0.602	16.857
195	C	5.555	-0.757	15.843
196	C	4.232	-0.778	16.547
197	C	3.144	-1.441	15.731

198	C	2.773	-0.638	14.512
199	C	1.925	-1.643	16.601
200	C	0.955	-2.629	15.974
201	C	-0.303	-2.81	16.806
202	C	-1.022	-4.074	16.397
203	C	-1.59	-4.764	17.588
204	C	-2.145	-3.715	15.495
205	H	10.477	-6.299	17.494
206	H	12.977	-5.725	18.558
207	H	0.712	-2.32	15.087
208	H	11.954	-6.477	19.464
209	H	2.198	-1.966	17.474
210	H	9.473	-5.288	19.113
211	H	11.711	-4.034	18.354
212	H	-2.758	-3.124	15.96
213	H	-1.798	-3.266	14.709
214	H	-2.614	-4.52	15.226
215	H	-0.874	-4.995	18.201
216	H	-2.219	-4.176	18.034
217	H	-2.047	-5.572	17.307
218	H	-0.39	-4.662	15.955
219	H	9.719	-2.549	18.635
220	H	-0.073	-2.851	17.747
221	H	-0.888	-2.045	16.69
222	H	1.394	-3.487	15.865
223	H	1.48	-0.792	16.74
224	H	2.453	0.236	14.785
225	H	3.552	-0.533	13.944
226	H	2.075	-1.099	14.021
227	H	3.484	-2.294	15.42

228	H	4.327	-1.245	17.392
229	H	3.966	0.132	16.754
230	H	9.53	-3.632	17.496
231	H	5.585	-0.026	15.206
232	H	5.681	-1.577	15.34
233	H	6.813	-1.452	17.288
234	H	6.355	0.015	17.552
235	H	9.179	-0.162	17.762
236	H	9.585	0.93	16.689
237	H	8.384	1.206	17.684
238	H	7.617	0.621	15.571
239	H	7.956	-1.948	15.289
240	H	9.365	-1.447	15.73
241	H	8.379	-3.388	18.555
242	H	9.331	0.151	13.999
243	H	7.932	-0.371	13.551
244	H	9.714	-1.165	12.189
245	H	8.814	-2.311	12.744
246	H	11.872	-1.404	15.0
247	H	12.534	-1.627	13.578
248	H	11.52	-0.431	13.8
249	H	9.945	-4.089	13.61
250	H	12.295	-3.508	15.157
251	H	12.498	-4.469	13.945
252	H	14.76	-1.85	25.622
253	H	14.456	-0.447	16.804
254	H	13.0	-0.955	16.444
255	H	13.189	0.336	17.341
256	H	14.472	-4.302	19.058
257	H	16.784	-0.715	23.524

258	H	17.248	-2.195	23.844
259	H	17.365	-1.63	22.37
260	H	13.794	0.782	26.887
261	H	12.679	0.928	28.003
262	H	14.211	0.955	28.405
263	H	8.712	-2.82	26.662
264	H	13.321	-1.126	28.896
265	H	14.418	-1.27	27.797
266	H	10.981	-0.887	29.204
267	H	4.497	-1.822	25.956
268	H	5.037	-1.521	24.394
269	H	6.203	-3.207	26.294
270	H	5.663	-2.889	21.531
271	H	5.603	-4.428	21.899
272	H	4.912	-3.36	22.843
273	H	11.506	-7.466	17.602
274	H	7.92	-4.039	20.618

Appendix B

Spectral Densities

B.1 Parameters for the modeling of Chl b WSCP spectral density

Table B.1: Parameters for the log-normal approximation of the low-energy part of the spectral density of the Chl b WSCP from Δ -FLN. Taken from Kell et al. (2013).

k	s_k	ω_k (cm^{-1})	σ_k
1	0.39	26	0.40
2	0.23	51	0.25
3	0.23	85	0.20

Table B.2: Frequencies and Huang-Rhys factors of the Chl b WSCP from Δ -FLN. Taken from Pieper et al. (2011).

Energy (cm^{-1})	HRF	Energy (cm^{-1})	HRF
181	0.0173	221	0.0246
240	0.0182	269	0.0064
283	0.0036	298	0.0104
325	0.0112	352	0.0249
366	0.0112	405	0.0061
430	0.0050	470	0.0075
488	0.0061	515	0.0045
537	0.0157	572	0.0132
598	0.0036	620	0.0047
641	0.0033	700	0.0019
713	0.0025	734	0.0107
746	0.0112	757	0.0229
800	0.0022	834	0.0140
863	0.0033	887	0.0019
922	0.0291	977	0.0110
998	0.0036	1023	0.0022
1045	0.0056	1068	0.0050
1108	0.0087	1128	0.0011
1150	0.0244	1172	0.0121
1186	0.0226	1227	0.0249
1243	0.0090	1264	0.0126
1288	0.0224	1305	0.0093
1326	0.0509	1360	0.0093
1393	0.0328	1443	0.0121
1484	0.0107	1522	0.0185
1550	0.0241	1573	0.0182
1628	0.0081	1654	0.0135
1681	0.0067		

Appendix C

Linear Absorption Spectra Optimization

C.1 Estimation of the static disorder parameter

C.1.1 Spectra dependence on the statistical distribution

The spectra for all valid parameters are presented, and their dependence on the static disorder and statistical distribution selected. All site energies have been shifted so that the site energy matches the experimental one (15198 cm^{-1}).

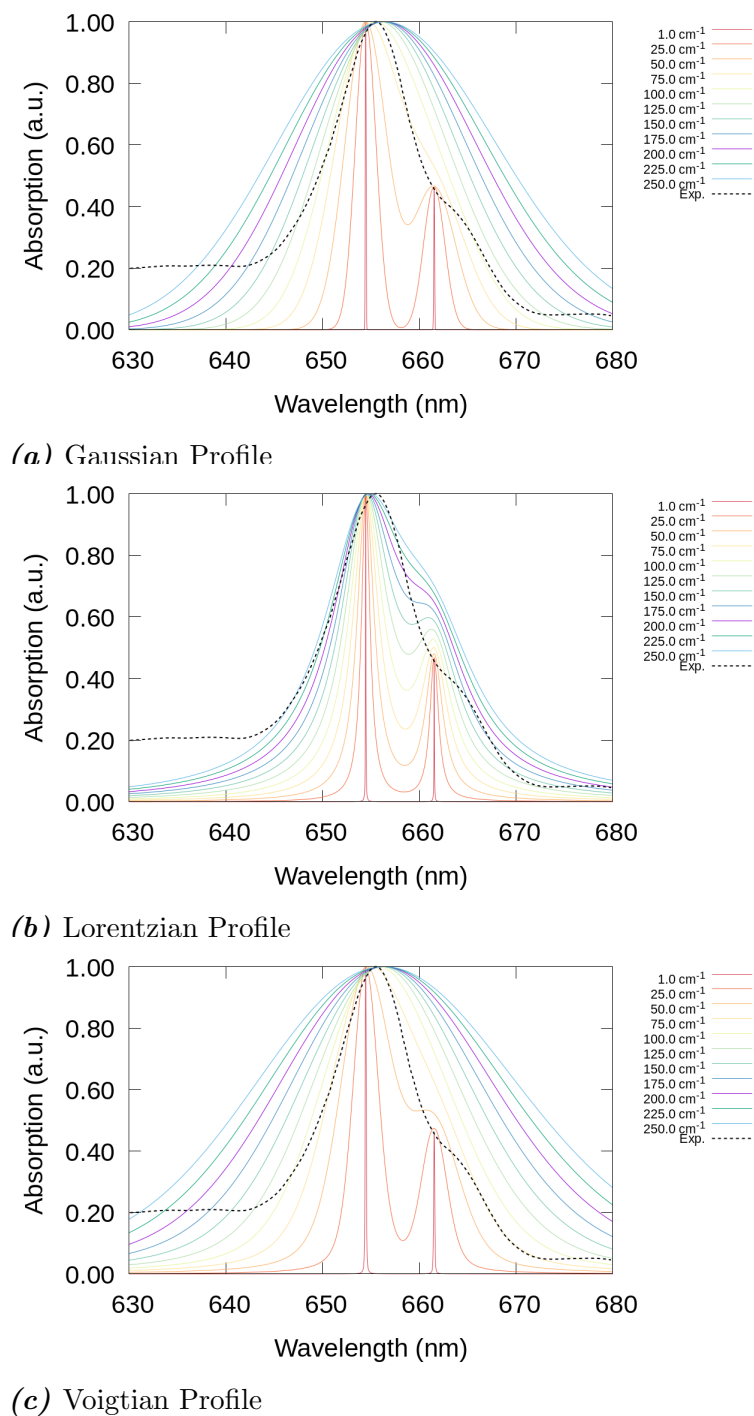


Figure C.1: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional M06-L.

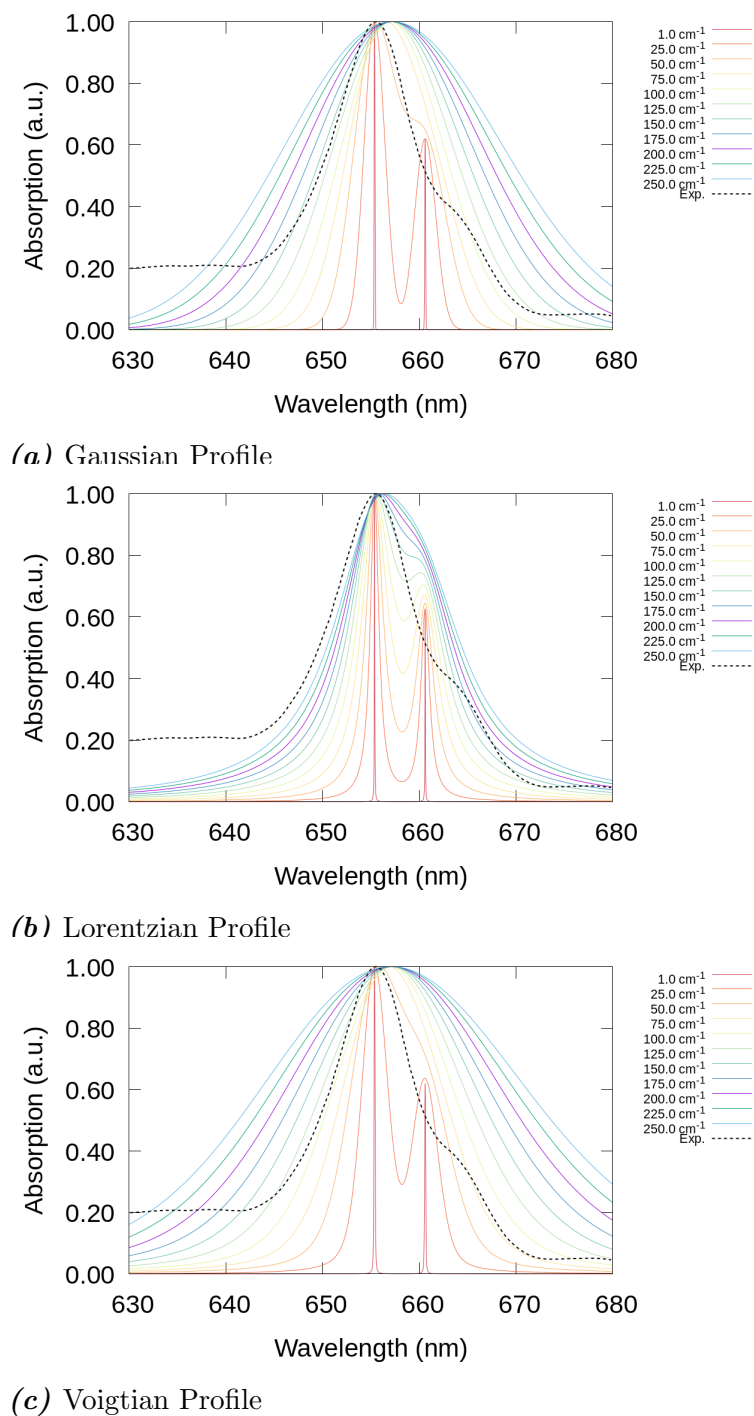


Figure C.2: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional TPSS.

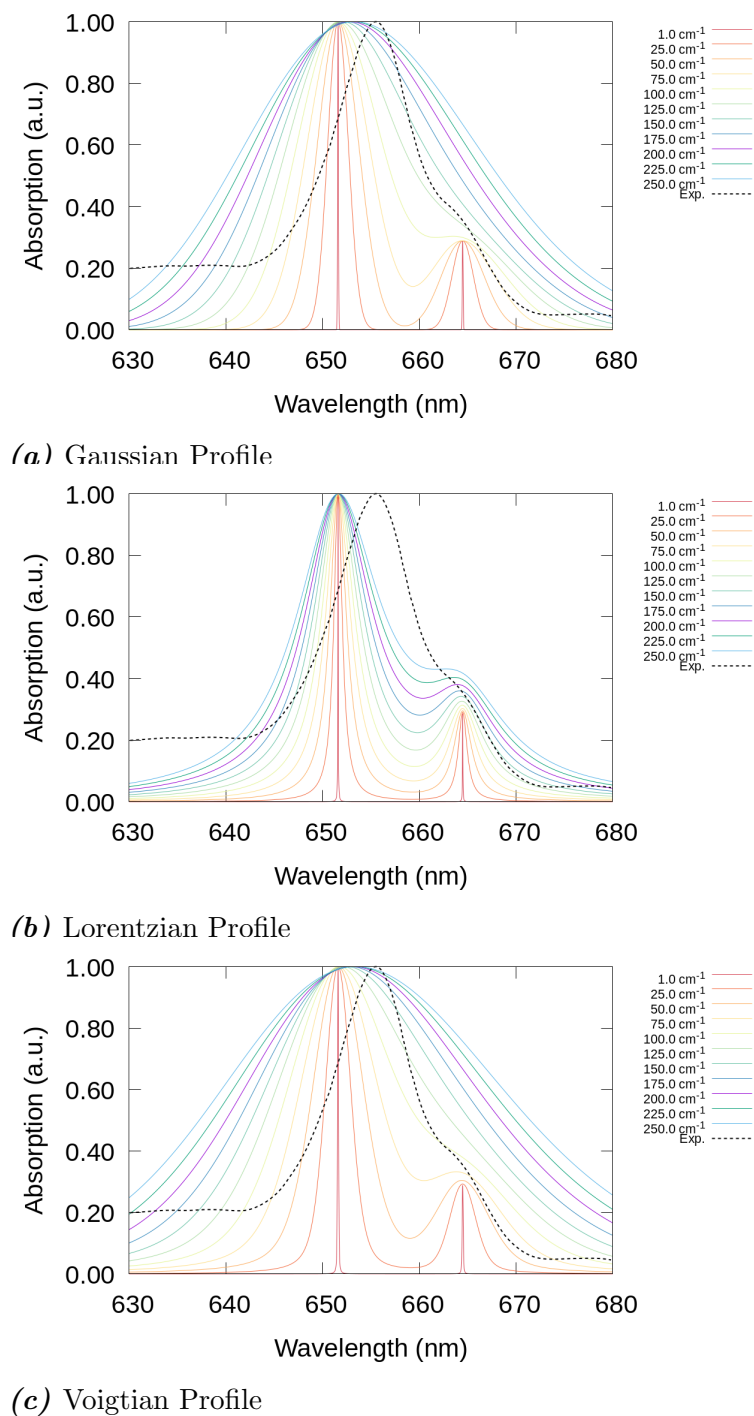


Figure C.3: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional BHHLYP.

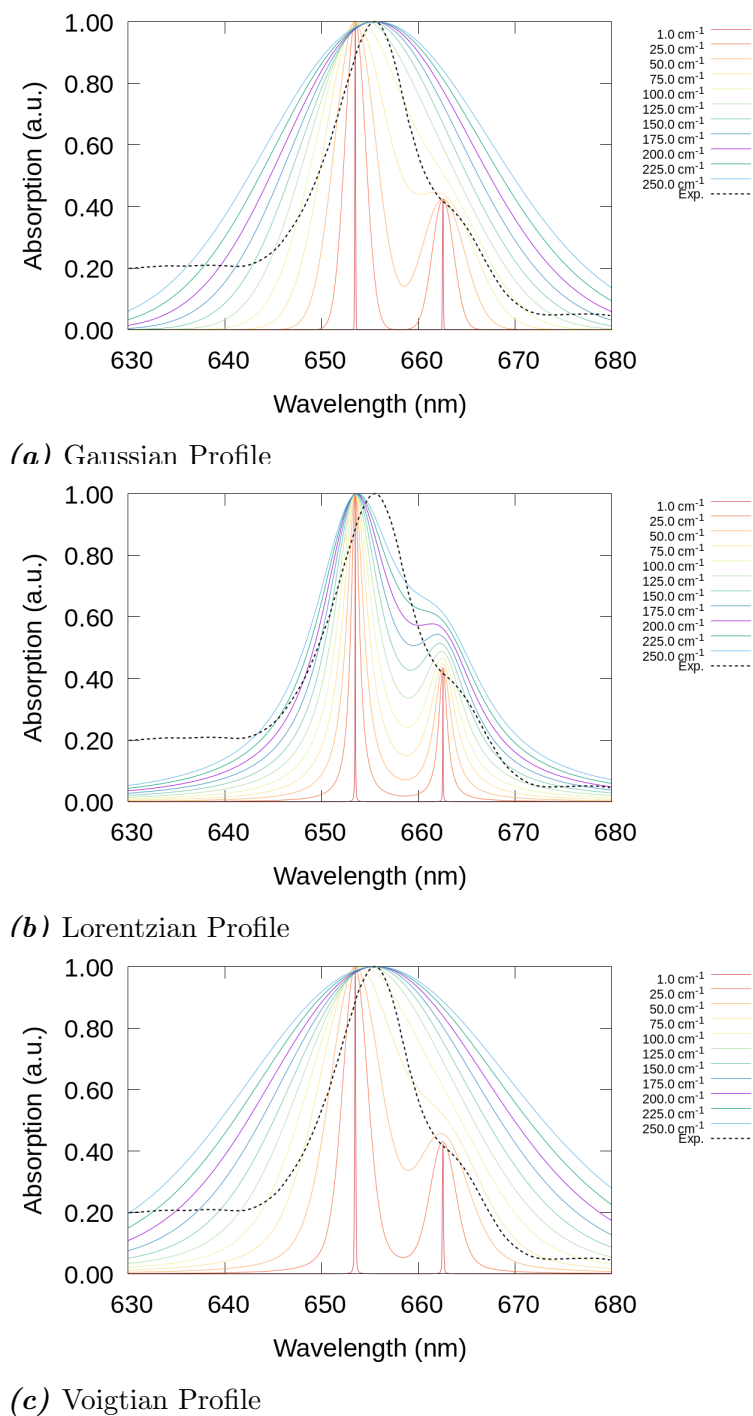


Figure C.4: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional B3LYP.

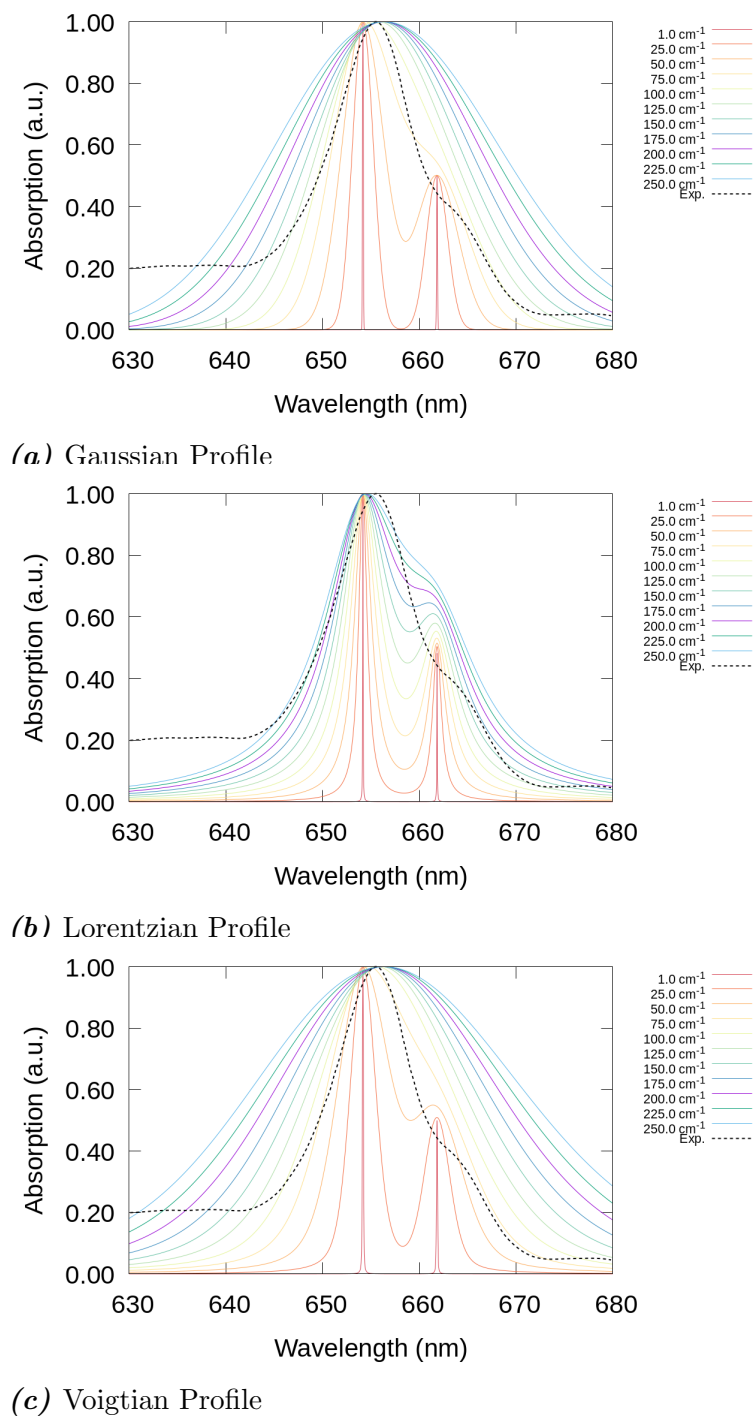


Figure C.5: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional O3LYP.

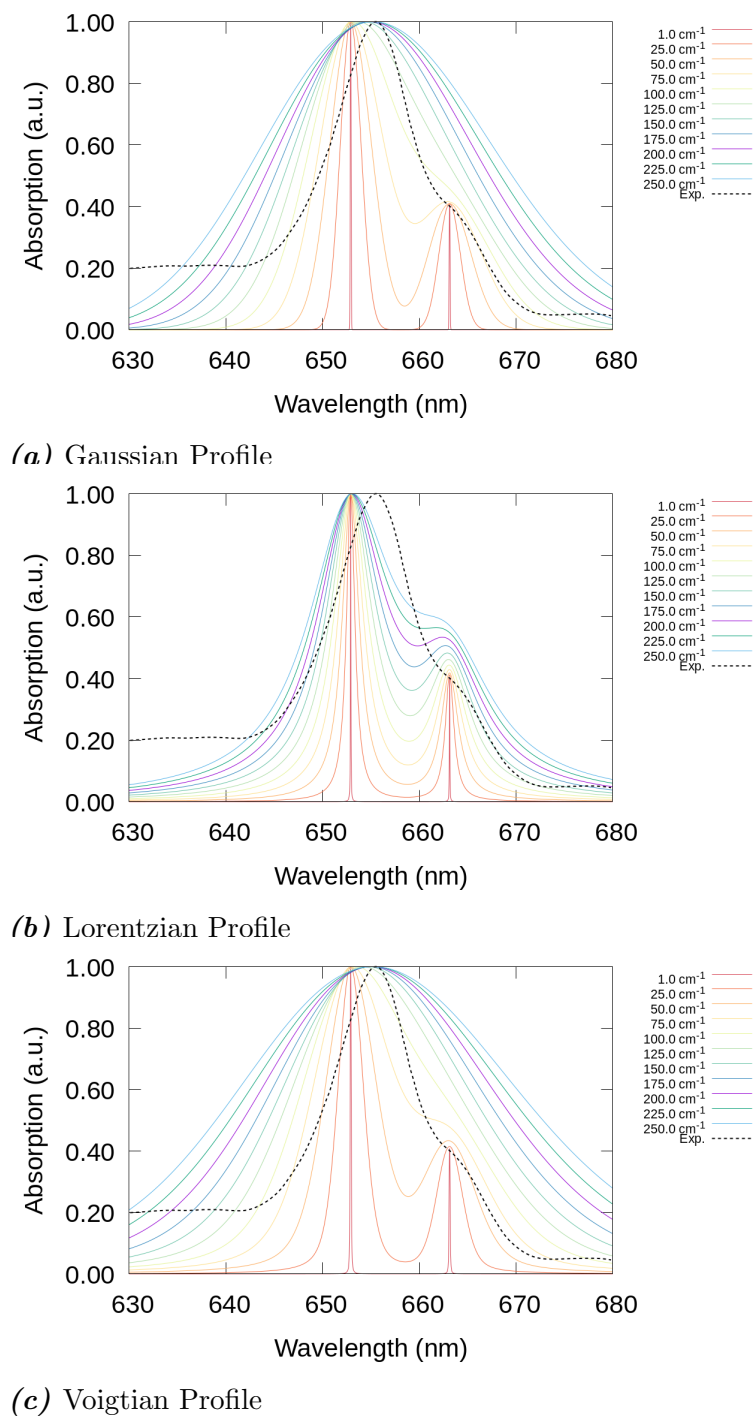


Figure C.6: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional PBE0.

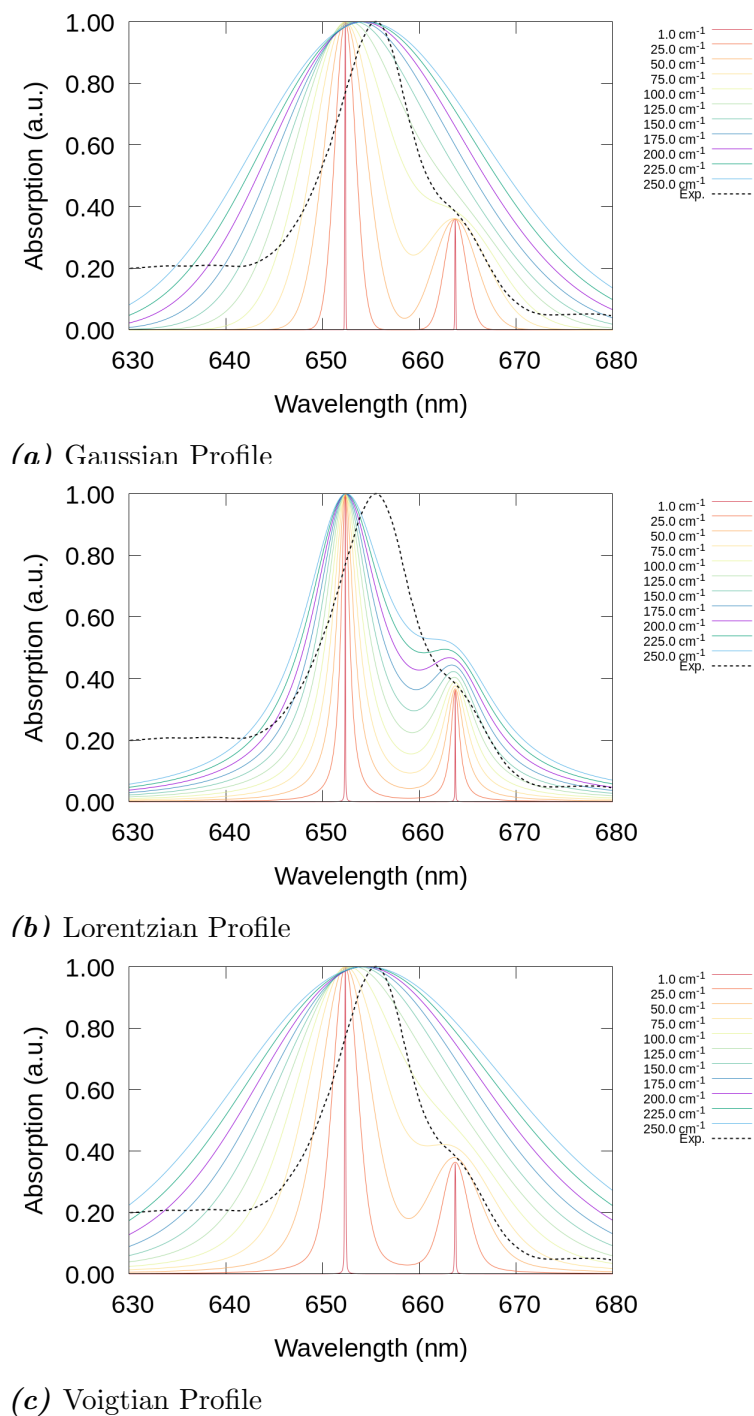


Figure C.7: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . Conditions: site energy and diabatic excitonic coupling using functional M06-2X.

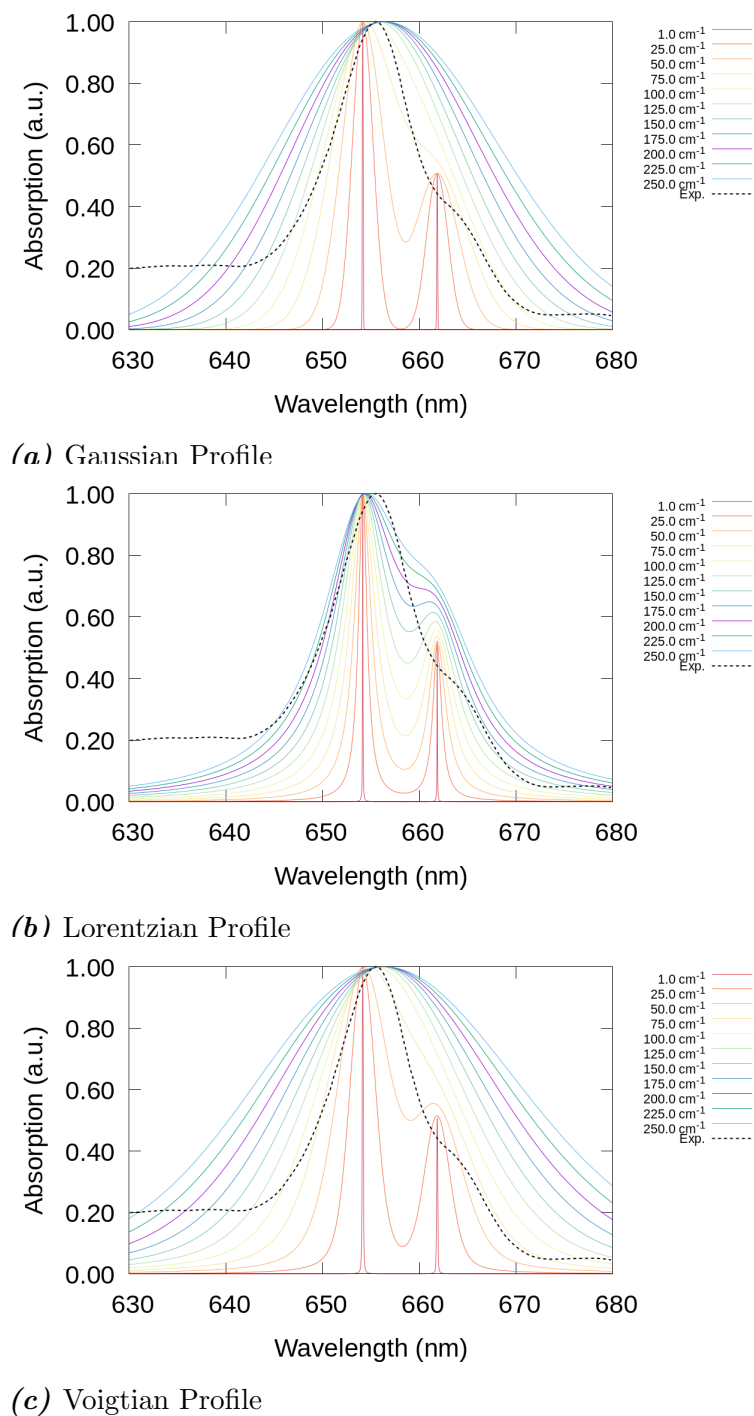


Figure C.8: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional TPSSh.

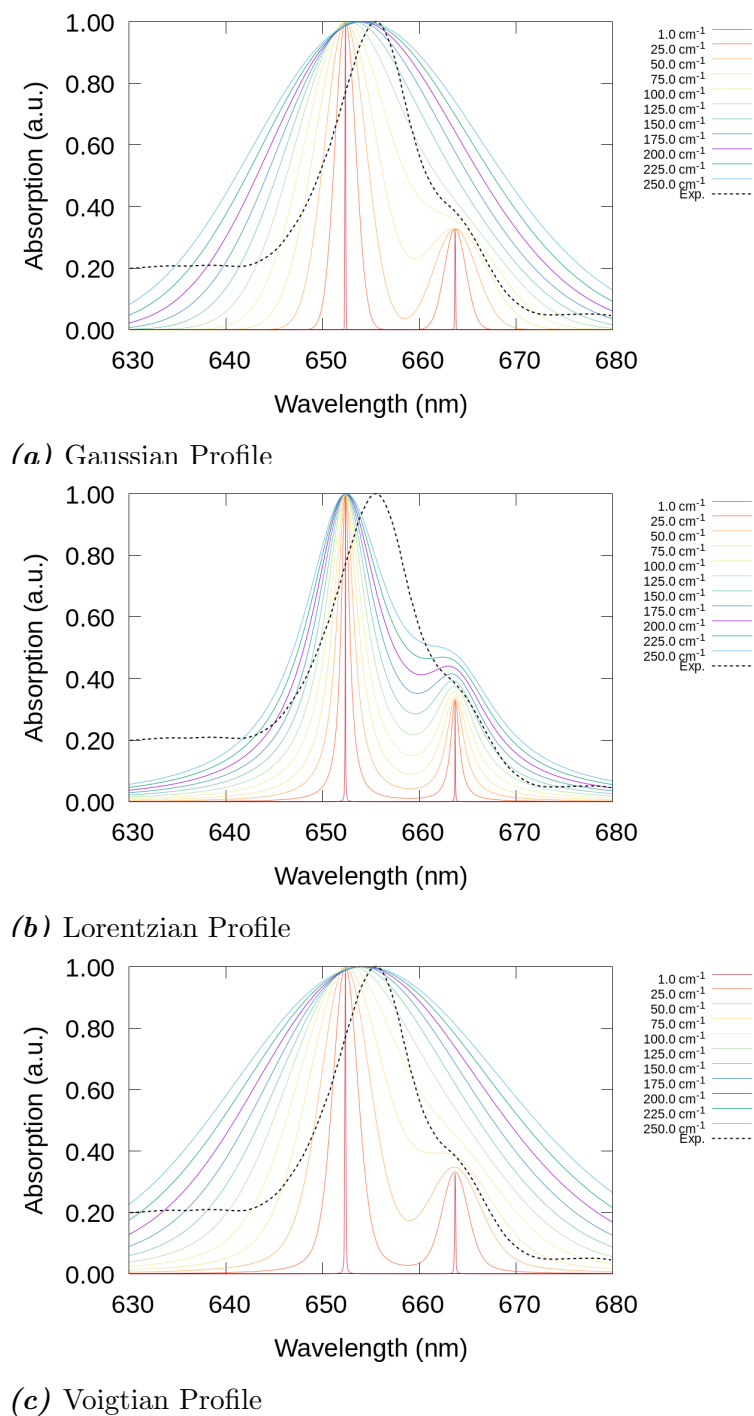


Figure C.9: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional LC-BLYP.

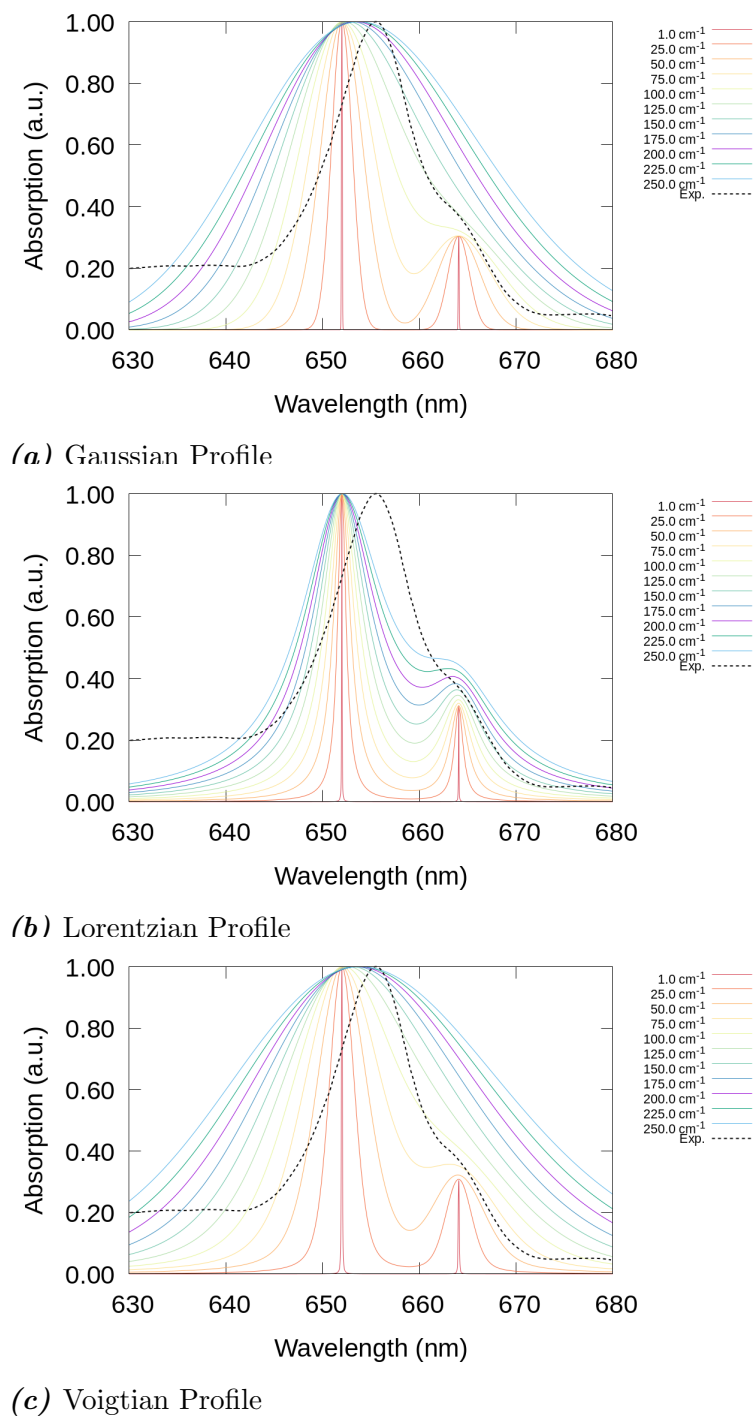


Figure C.10: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional ω B97X-V.

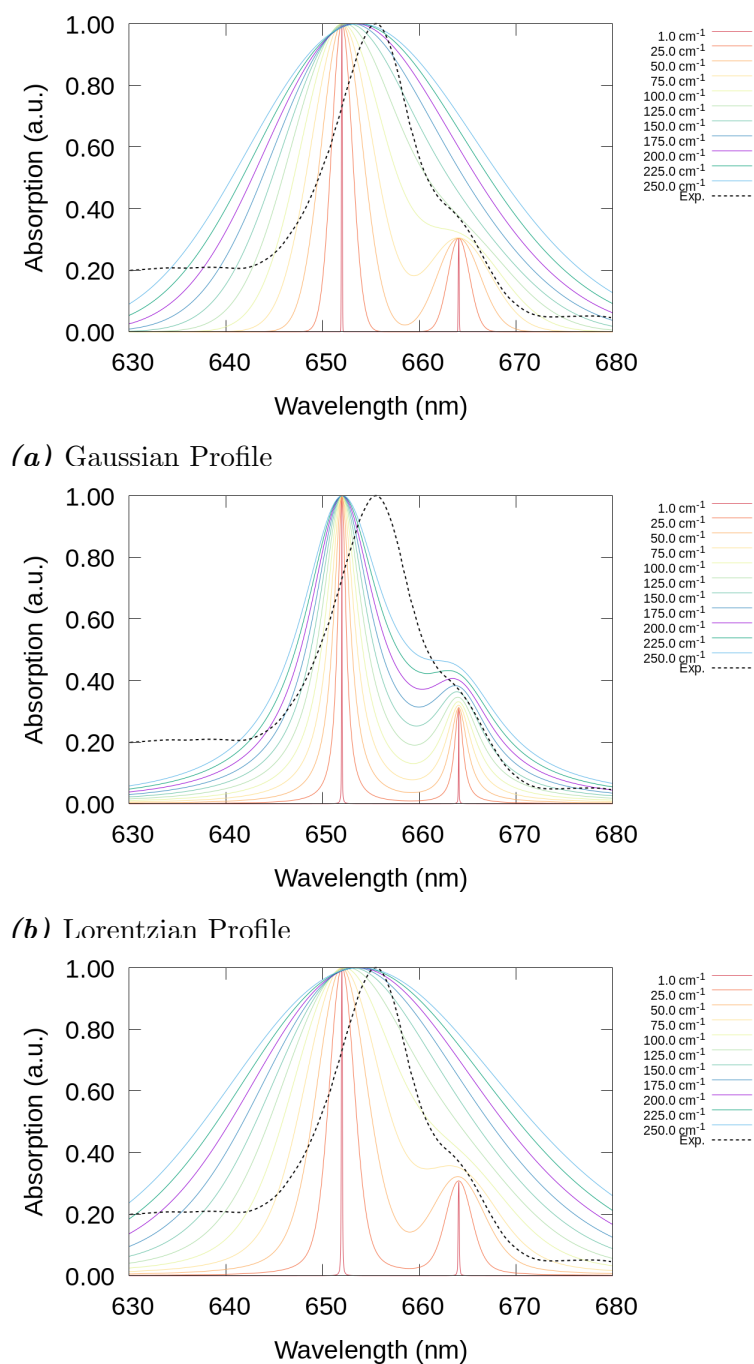
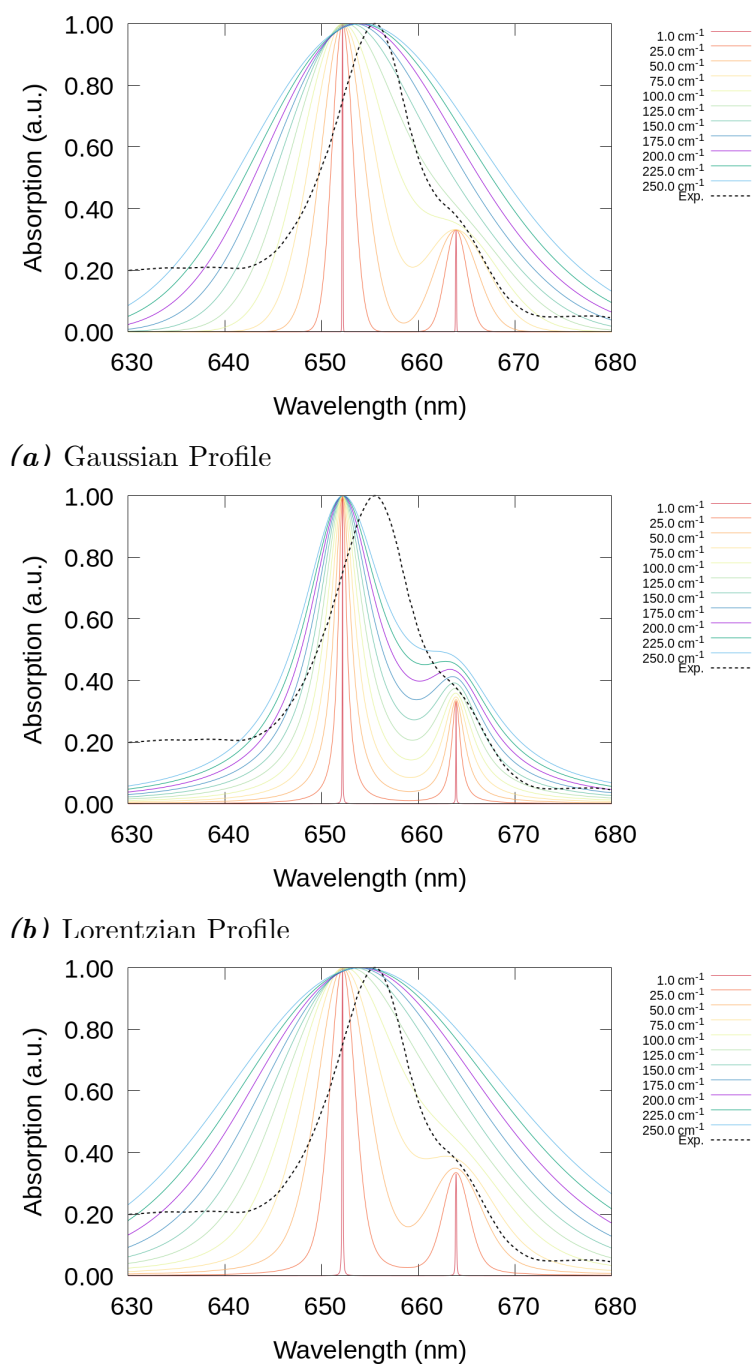
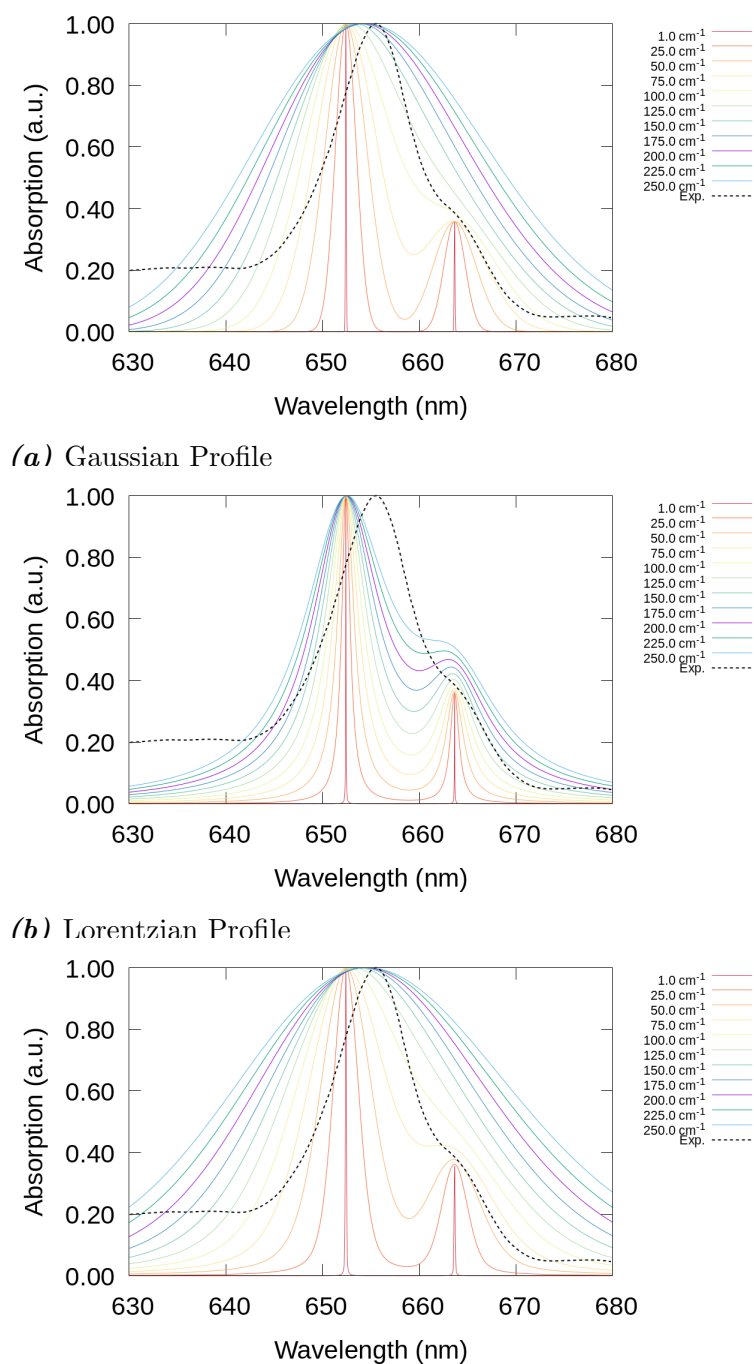


Figure C.11: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional ω B97X-D3BJ.



(c) Voigtian Profile

Figure C.12: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . Conditions: site energy and diabatic excitonic coupling using functional CAM-B3LYP.



(c) Voigtian Profile

Figure C.13: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional CAMh-B3LYP.

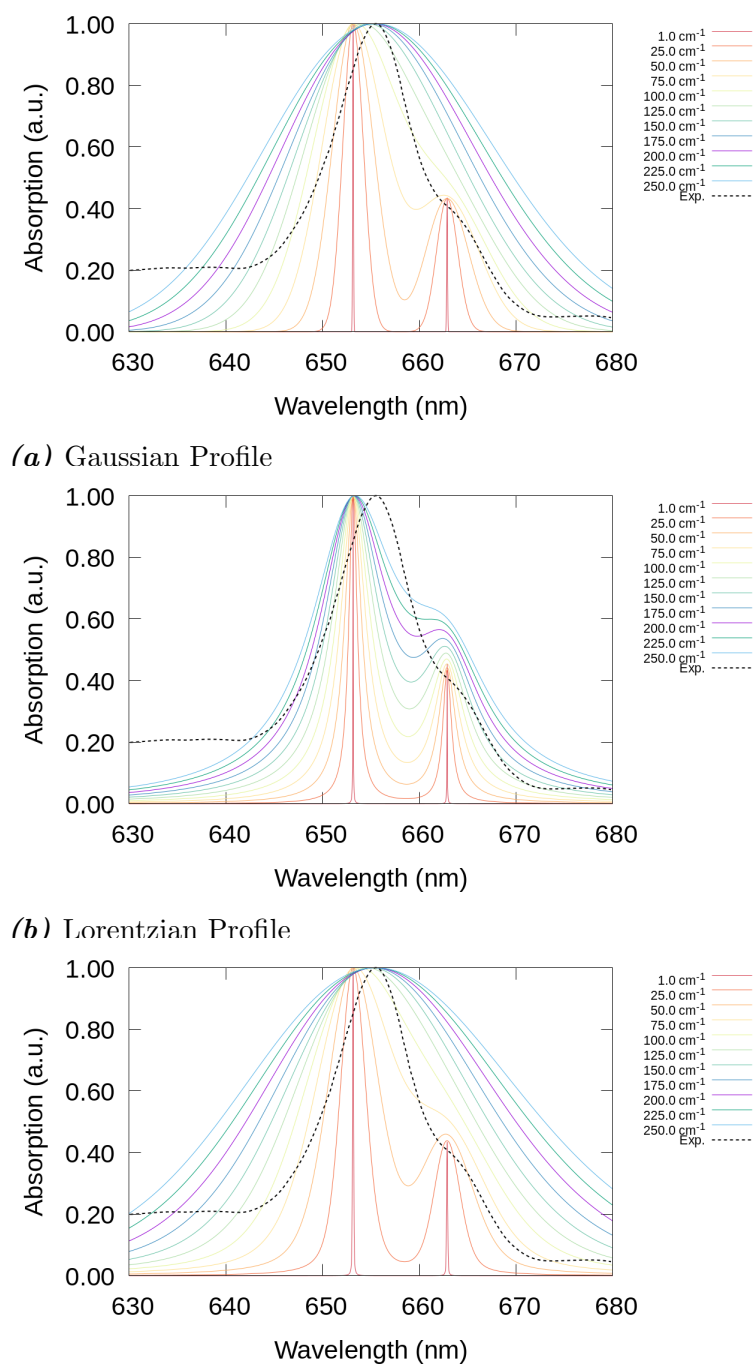
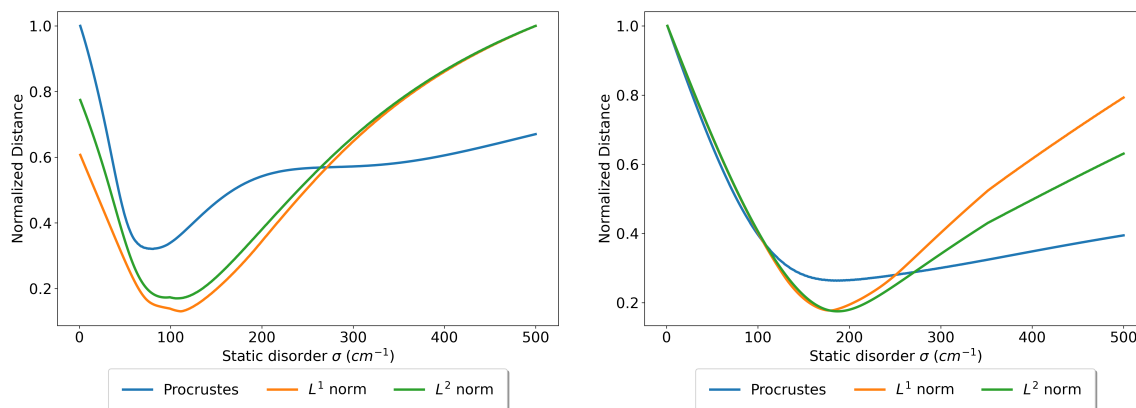


Figure C.14: Simulated spectra for approximate lineshapes of absorption spectra in the non-vibronic case. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* site energy and diabatic excitonic coupling using functional Tuned-CAM-B3LYP.

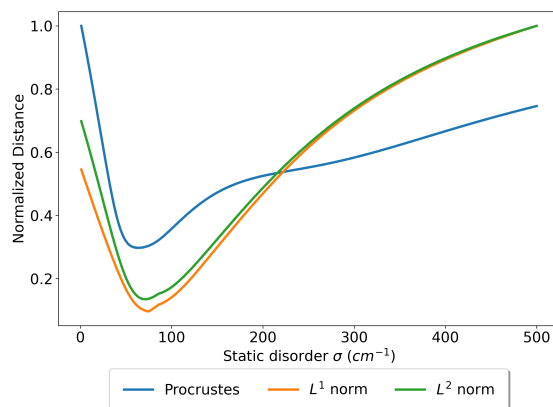
C.1.2 Similarity metrics behaviour

Comparison of the different similarity metrics is presented, and their dependence on the static disorder and statistical distribution selected. All site energies have been shifted so that the site energy matches the experimental one (15198 cm^{-1}).



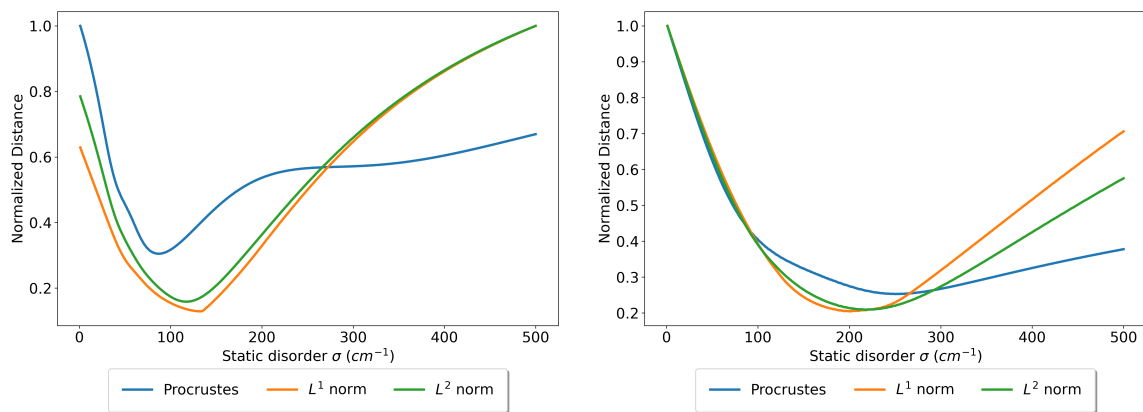
(a) Gaussian Profile

(b) Lorentzian Profile



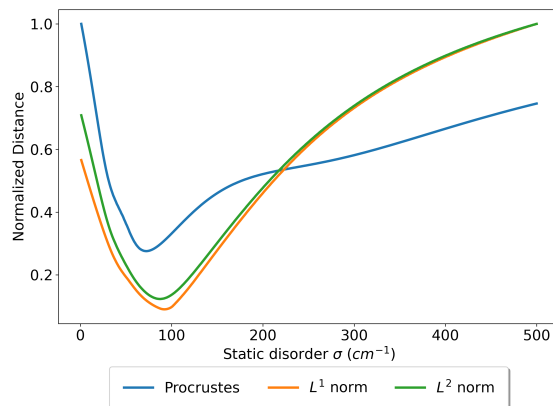
(c) Voigtian Profile

Figure C.15: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional M06-L.



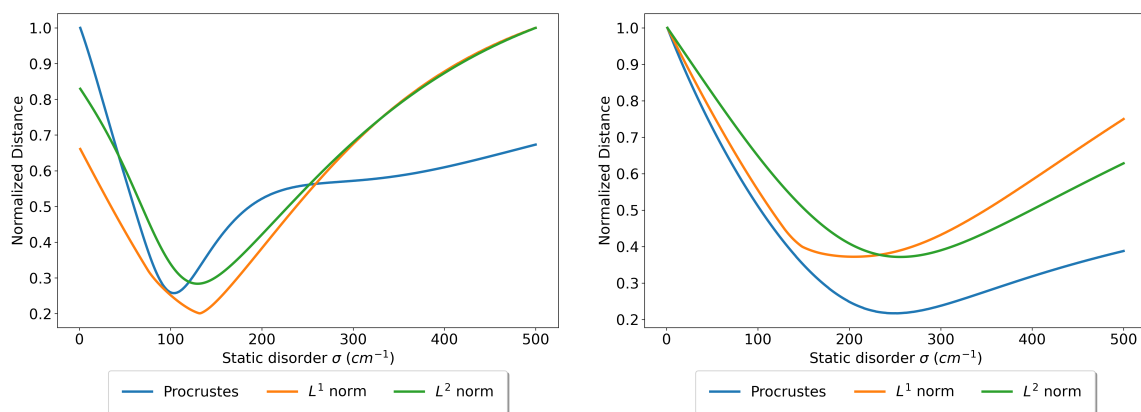
(a) Gaussian Profile

(b) Lorentzian Profile



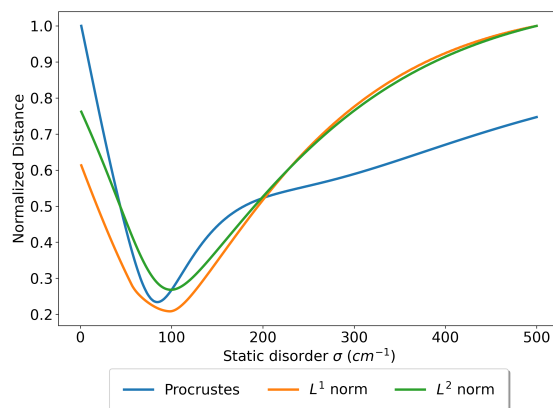
(c) Voigtian Profile

Figure C.16: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional TPSS.



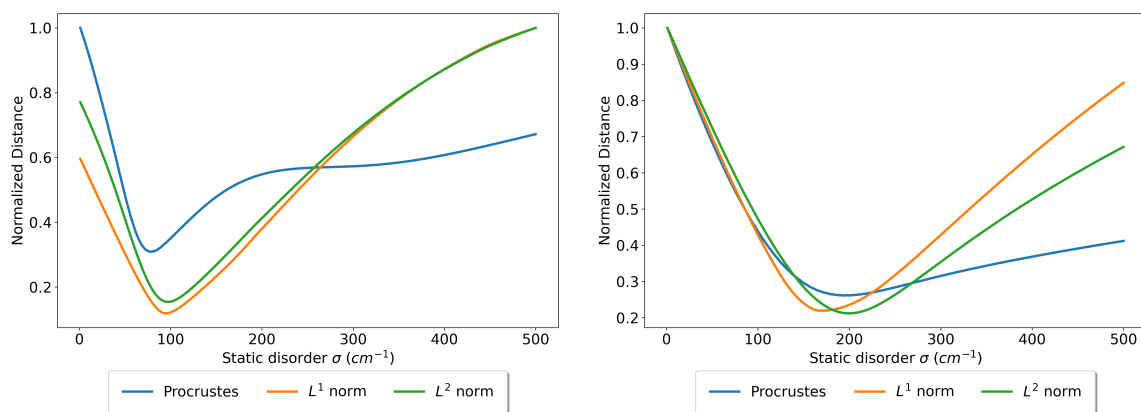
(a) Gaussian Profile

(b) Lorentzian Profile



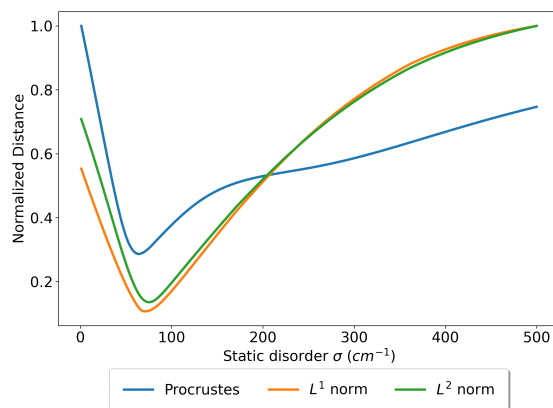
(c) Voigtian Profile

Figure C.17: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional BHLYP.



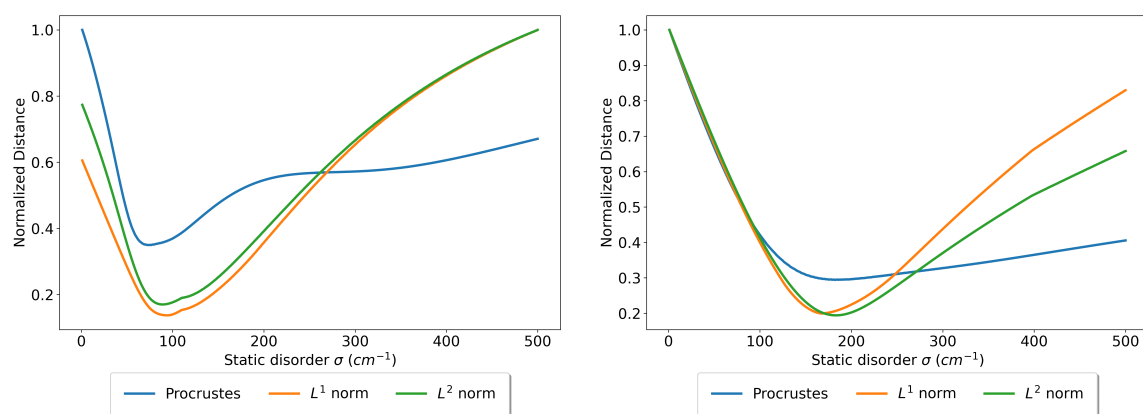
(a) Gaussian Profile

(b) Lorentzian Profile



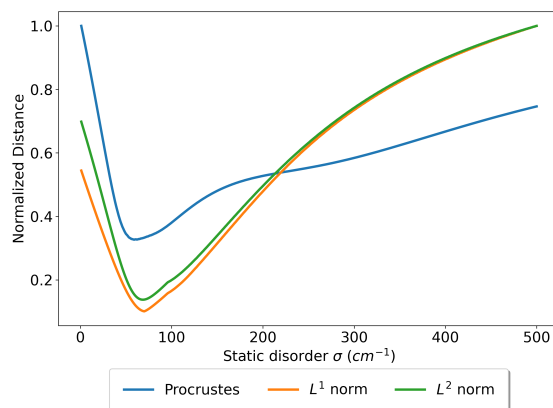
(c) Voigtian Profile

Figure C.18: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional B3LYP.



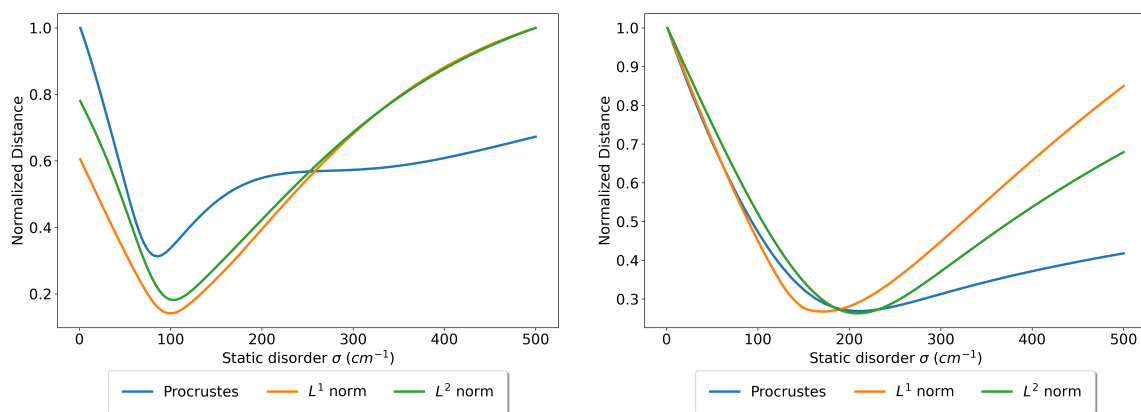
(a) Gaussian Profile

(b) Lorentzian Profile



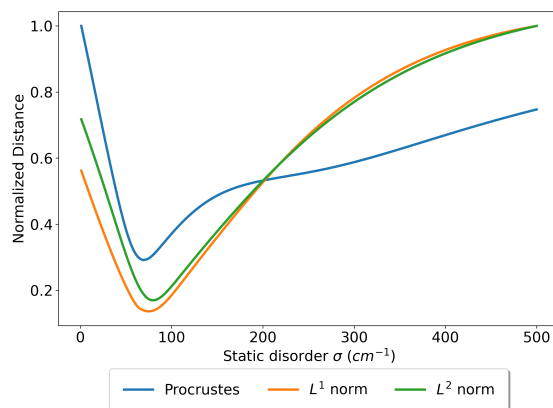
(c) Voigtian Profile

Figure C.19: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional O3LYP.



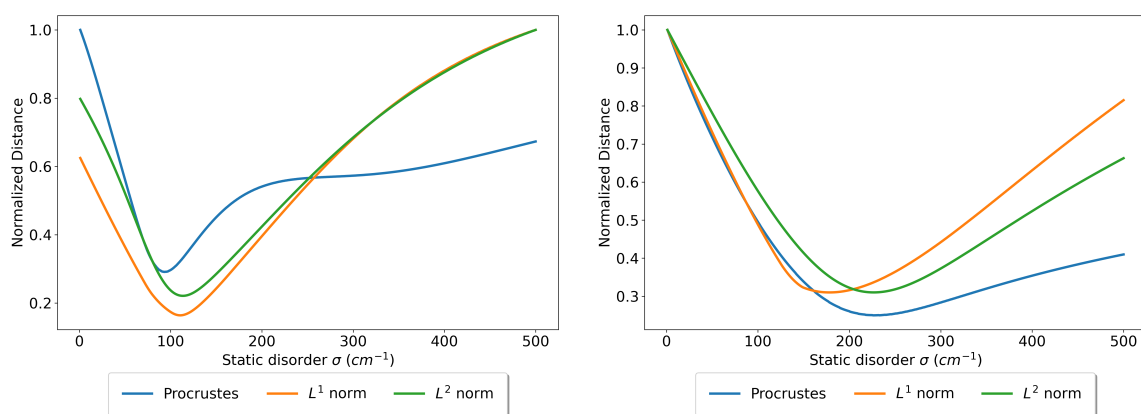
(a) Gaussian Profile

(b) Lorentzian Profile



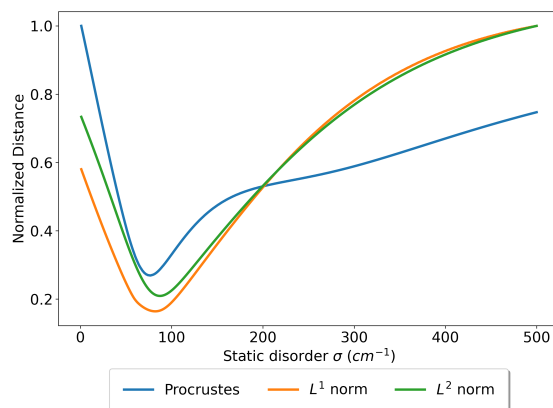
(c) Voigtian Profile

Figure C.20: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional PBE0.



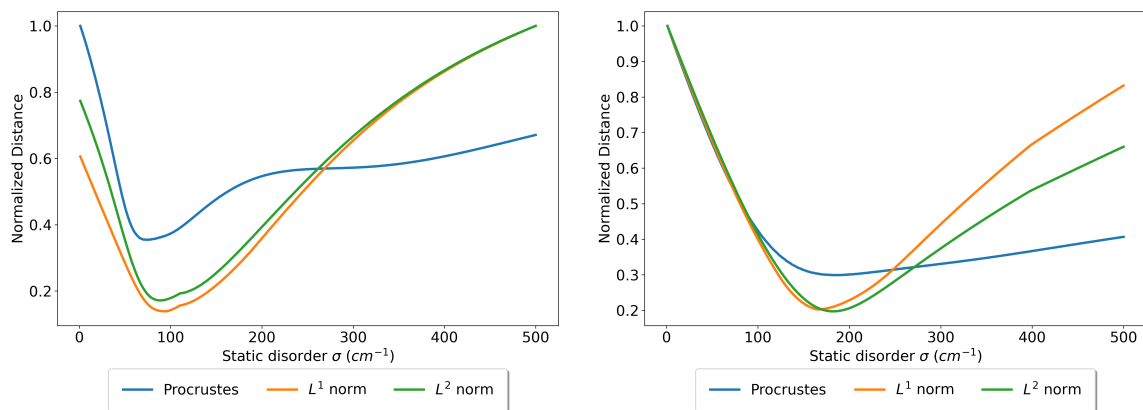
(a) Gaussian Profile

(b) Lorentzian Profile



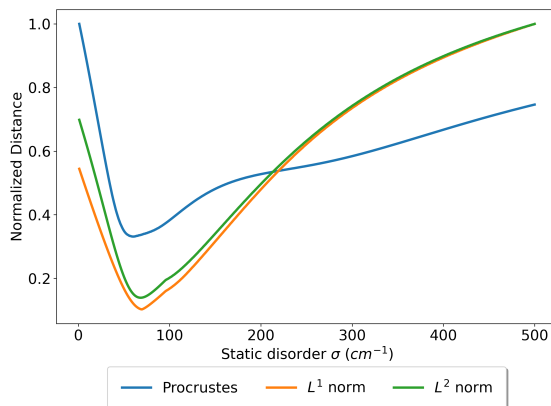
(c) Voigtian Profile

Figure C.21: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional M06-2X.



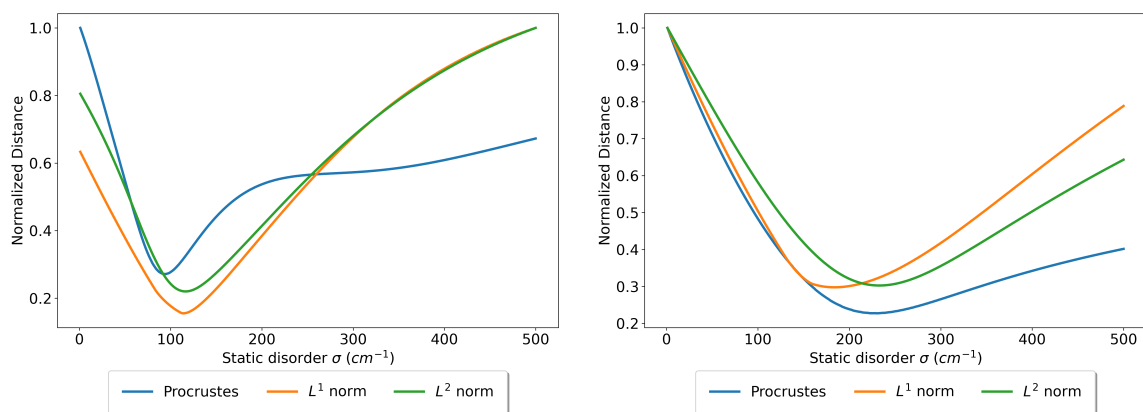
(a) Gaussian Profile

(b) Lorentzian Profile



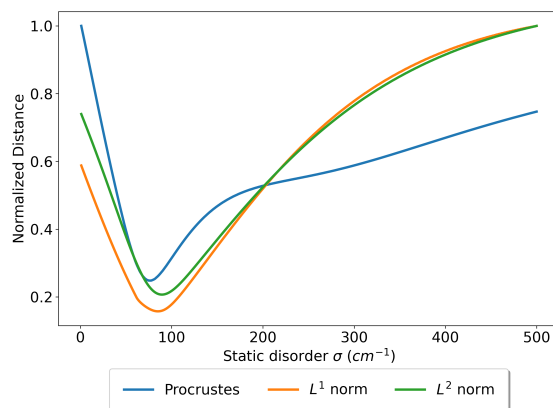
(c) Voigtian Profile

Figure C.22: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional TPSSh.



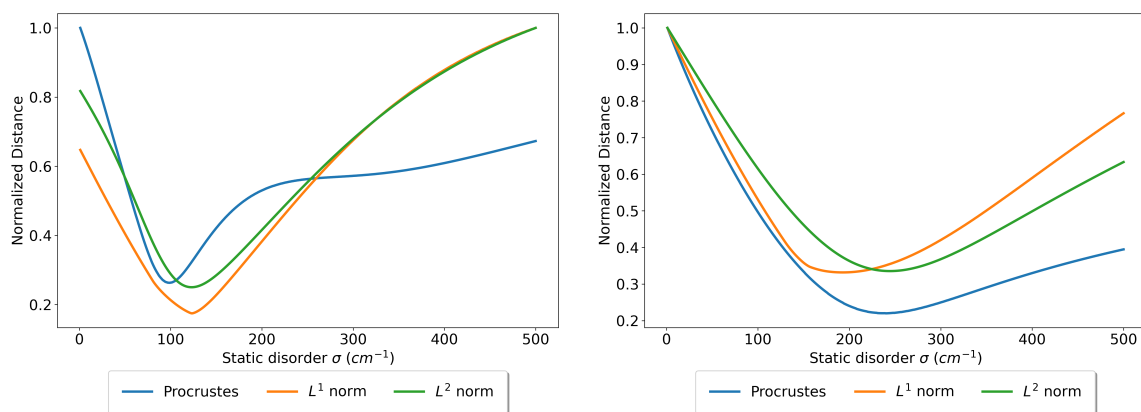
(a) Gaussian Profile

(b) Lorentzian Profile



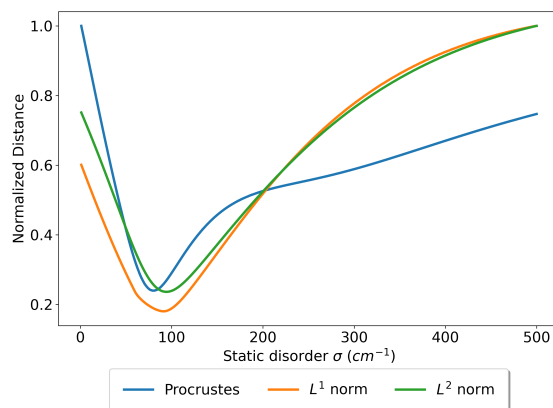
(c) Voigtian Profile

Figure C.23: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional LC-BLYP.



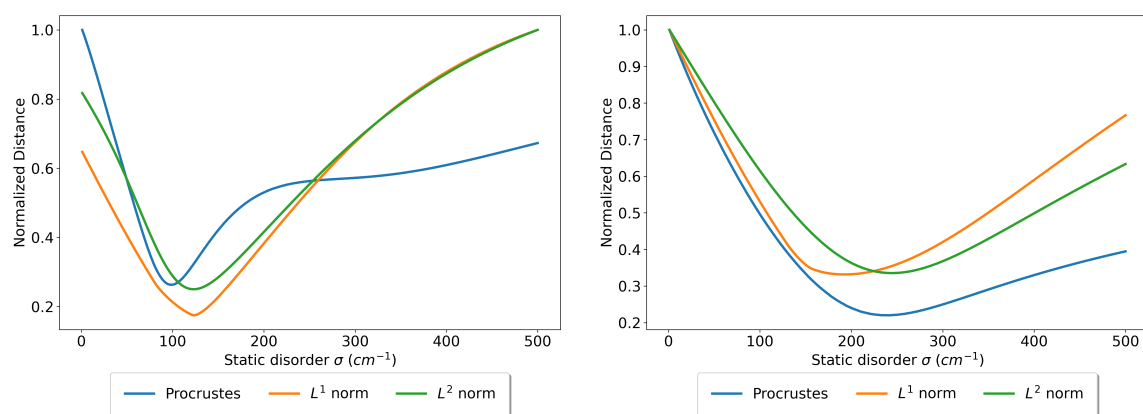
(a) Gaussian Profile

(b) Lorentzian Profile



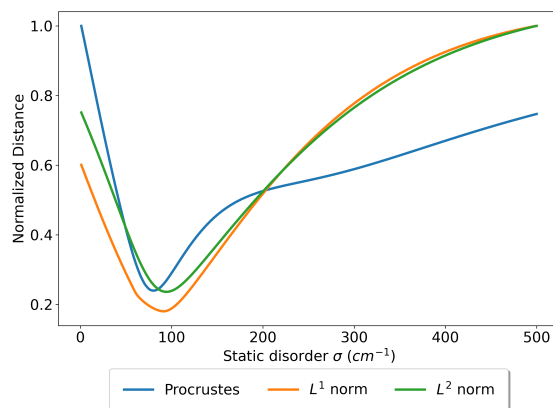
(c) Voigtian Profile

Figure C.24: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional ω B97X-V.



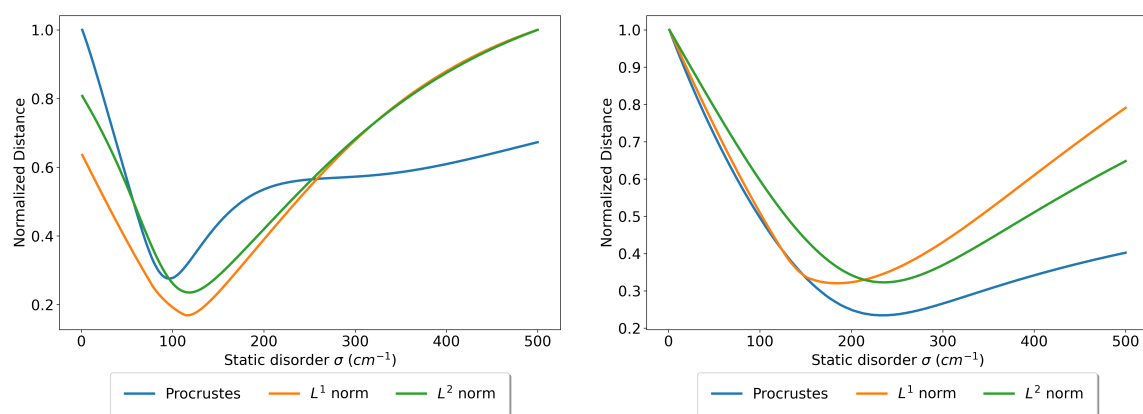
(a) Gaussian Profile

(b) Lorentzian Profile



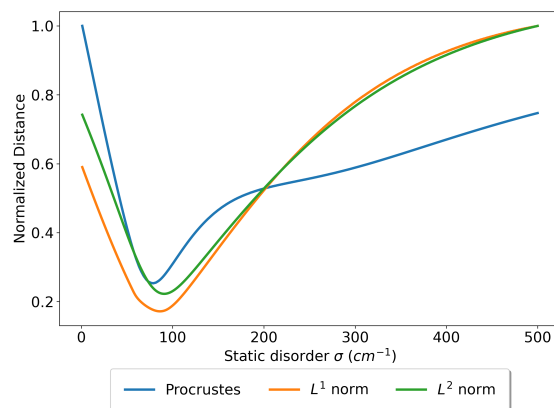
(c) Voigtian Profile

Figure C.25: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional ω B97X-D3BJ.



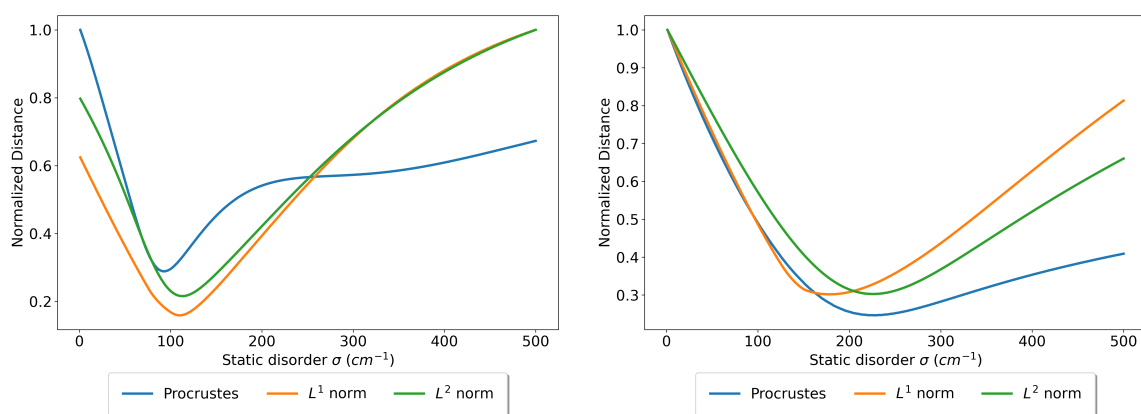
(a) Gaussian Profile

(b) Lorentzian Profile



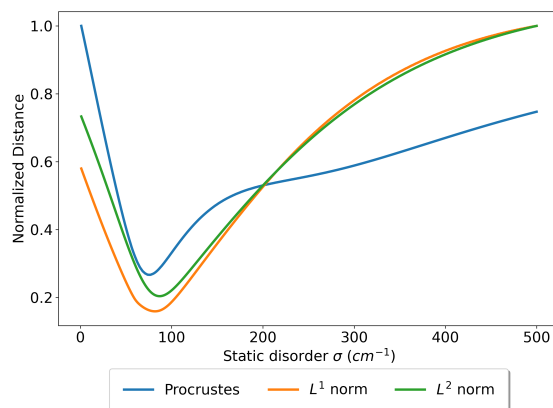
(c) Voigtian Profile

Figure C.26: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional CAM-B3LYP.



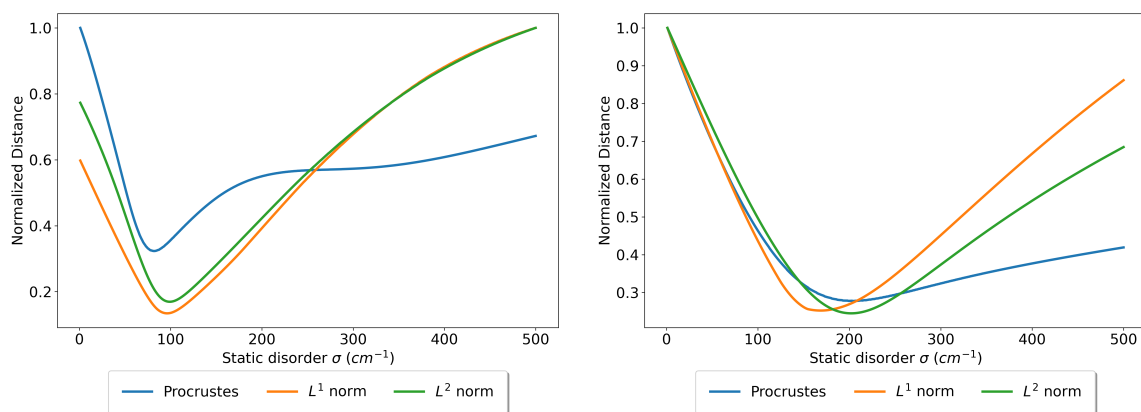
(a) Gaussian Profile

(b) Lorentzian Profile



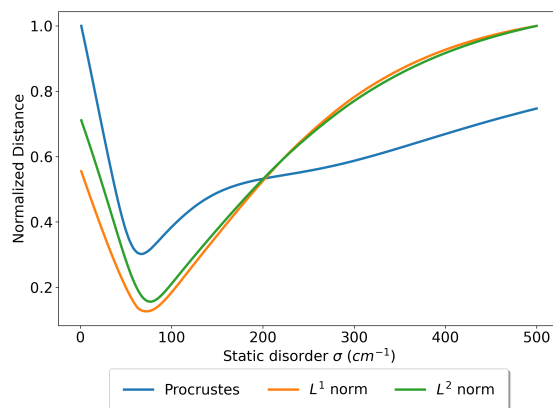
(c) Voigtian Profile

Figure C.27: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional CAMh-B3LYP.



(a) Gaussian Profile

(b) Lorentzian Profile



(c) Voigtian Profile

Figure C.28: Behaviour of different similarity metrics for the optimization of approximate spectral lineshapes. Effect of the statistical distribution and static disorder parameter σ . *Conditions:* experimental site energy and diabatic excitonic coupling using functional Tuned-CAM-B3LYP.

C.1.3 Static disorder optimization

Numerical optimization of the σ by minimization of the Procrustes distance is presented. This is performed for all the statistical distributions selected. All site energies have been shifted so that the site energy matches the experimental one (15198 cm^{-1}).

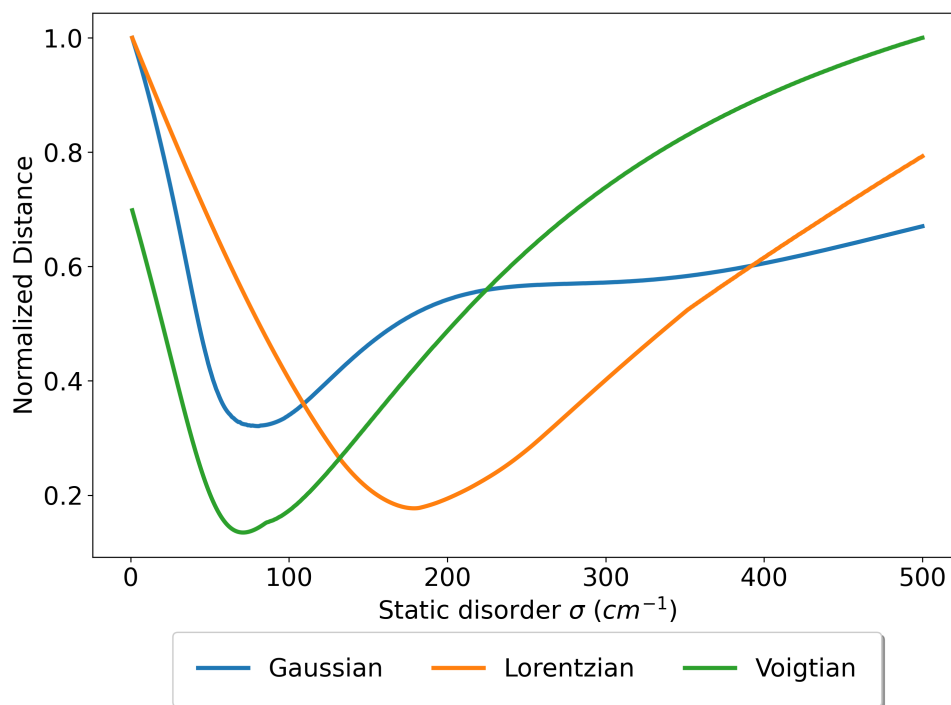


Figure C.29: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and M06-L diabatic excitonic coupling.

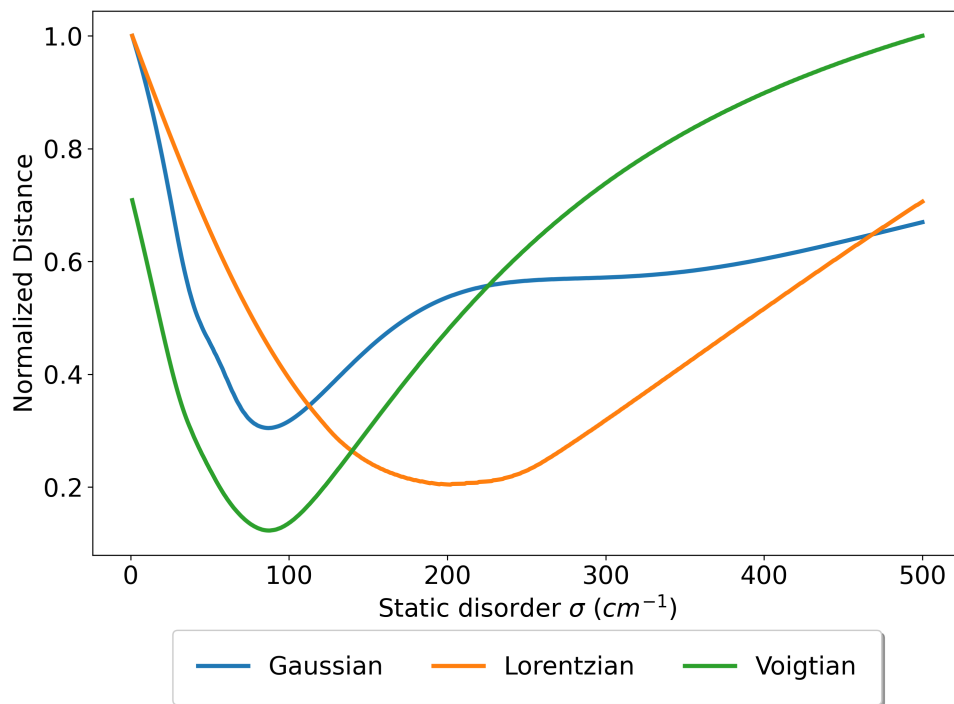


Figure C.30: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and TPSS diabatic excitonic coupling.

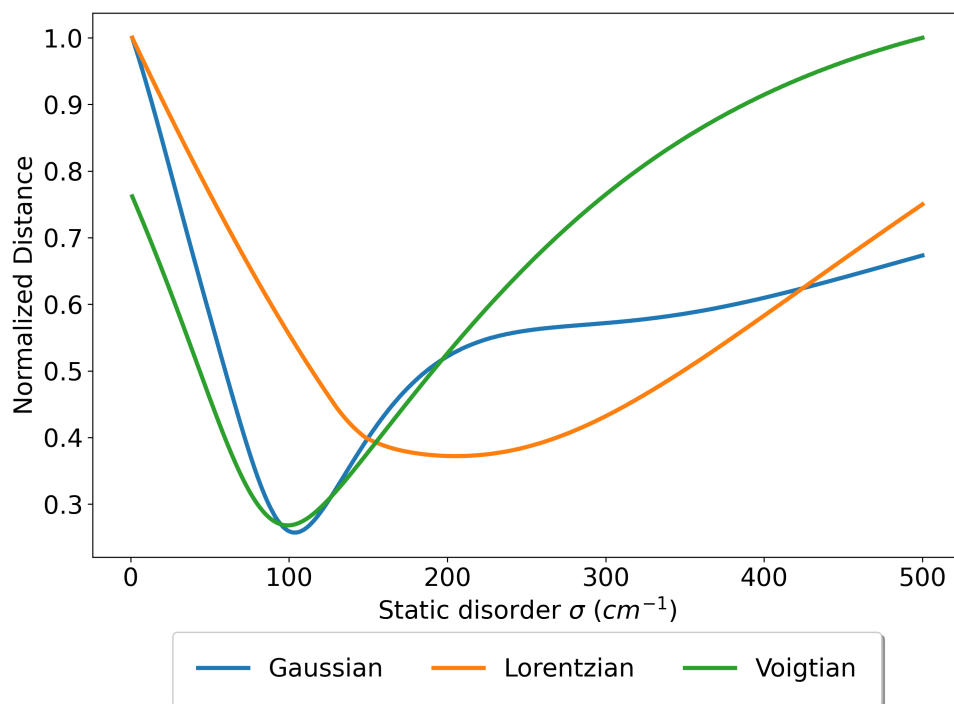


Figure C.31: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and BHHLYP diabatic excitonic coupling.

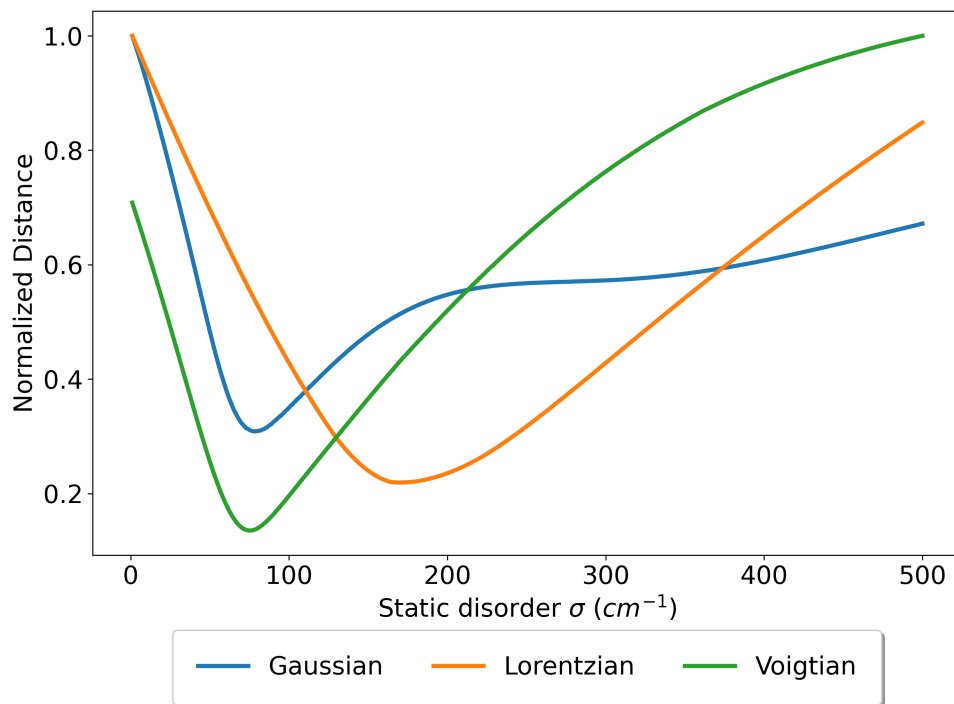


Figure C.32: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and B3LYP diabatic excitonic coupling.

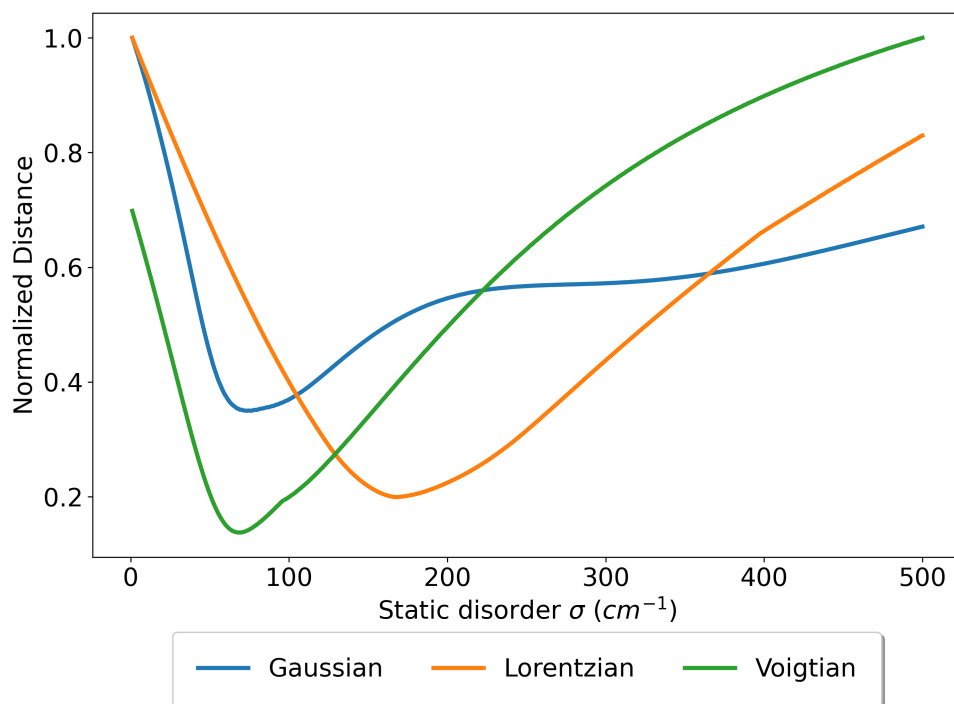


Figure C.33: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and O3LYP diabatic excitonic coupling.

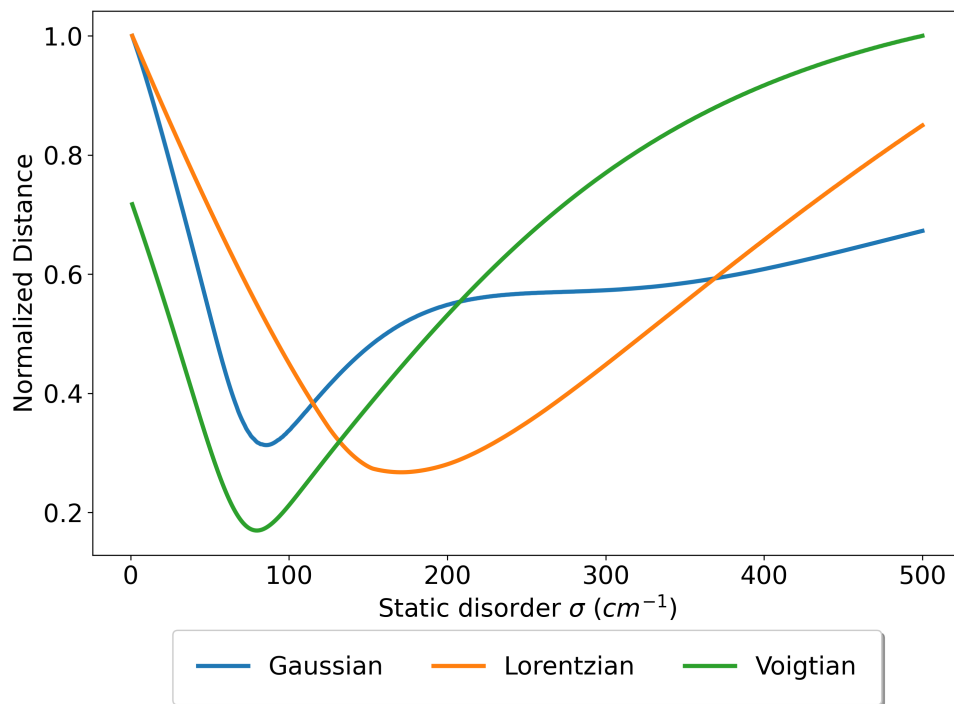


Figure C.34: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and PBE0 diabatic excitonic coupling.

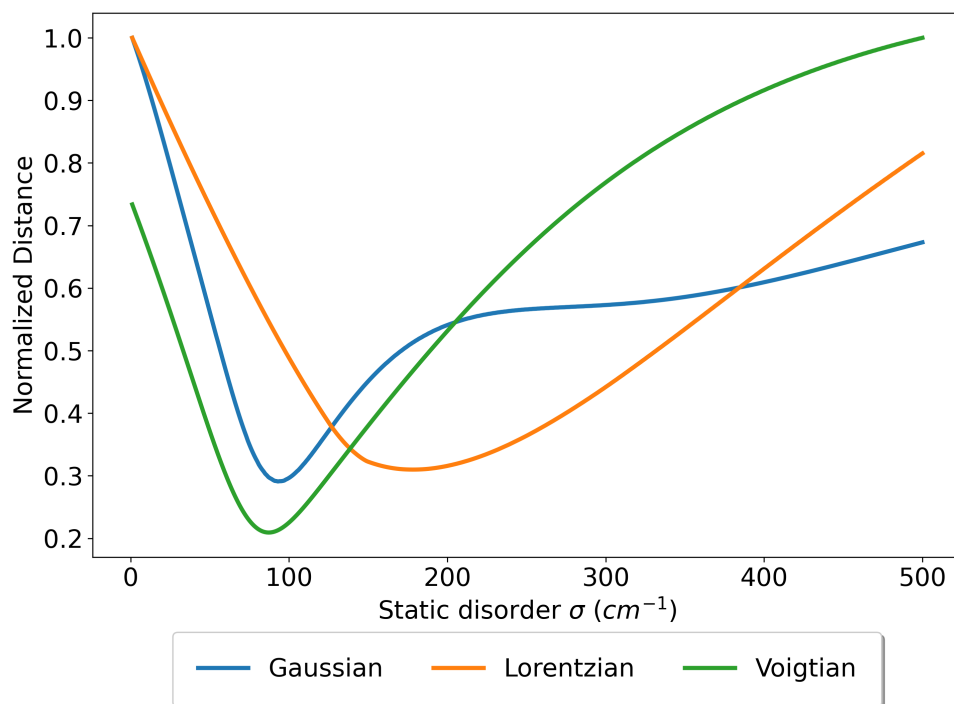


Figure C.35: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and M06-2X diabatic excitonic coupling.

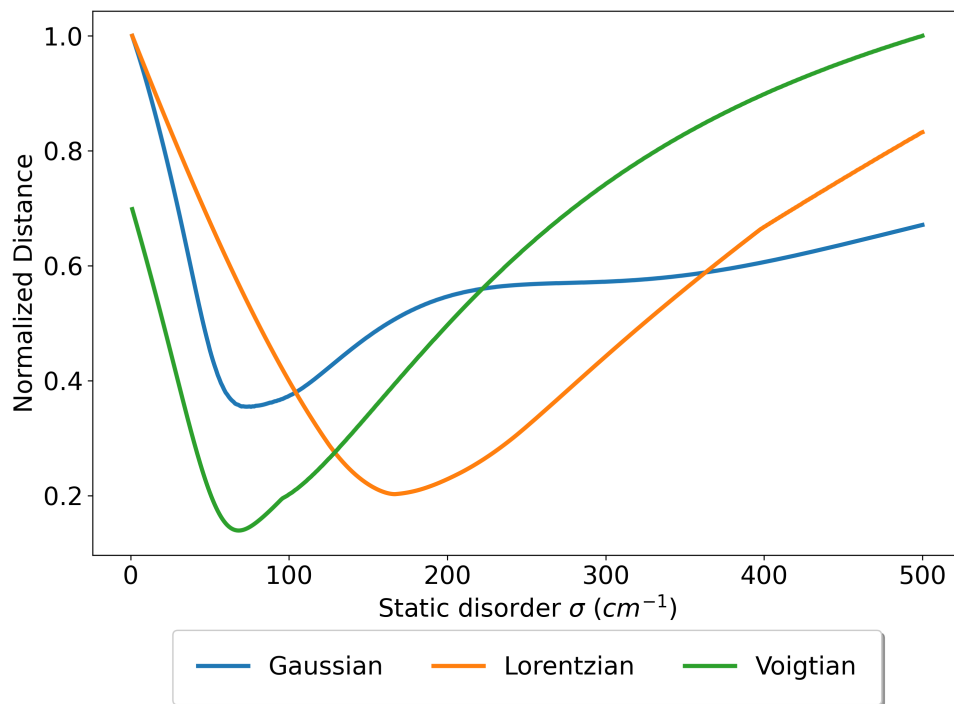


Figure C.36: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and TPSSh diatomic excitonic coupling.

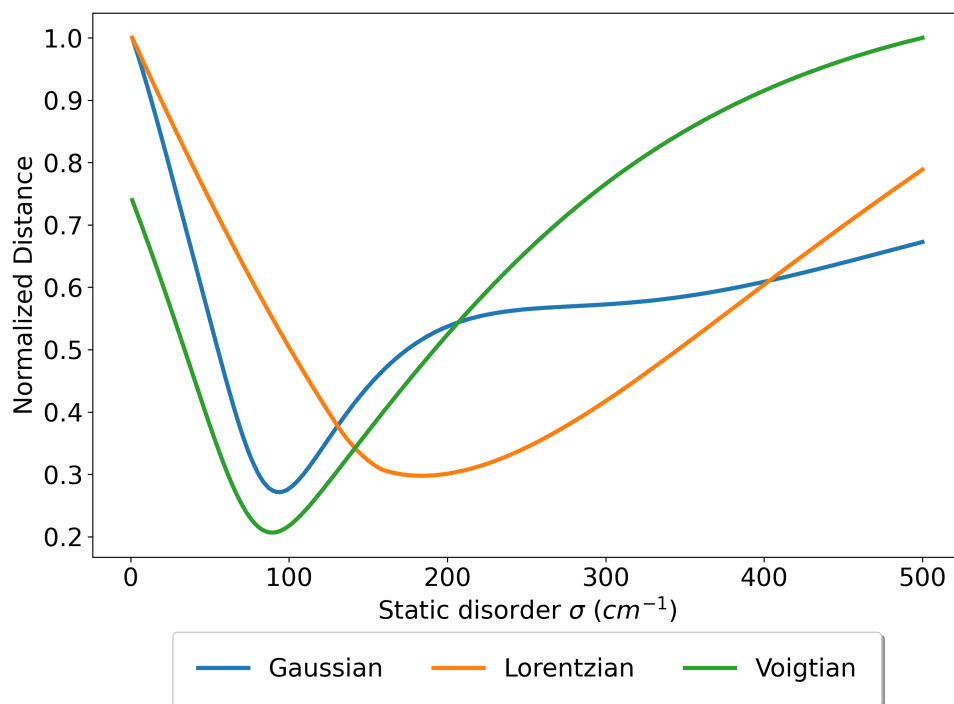


Figure C.37: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and LC-BLYP diatomic excitonic coupling.

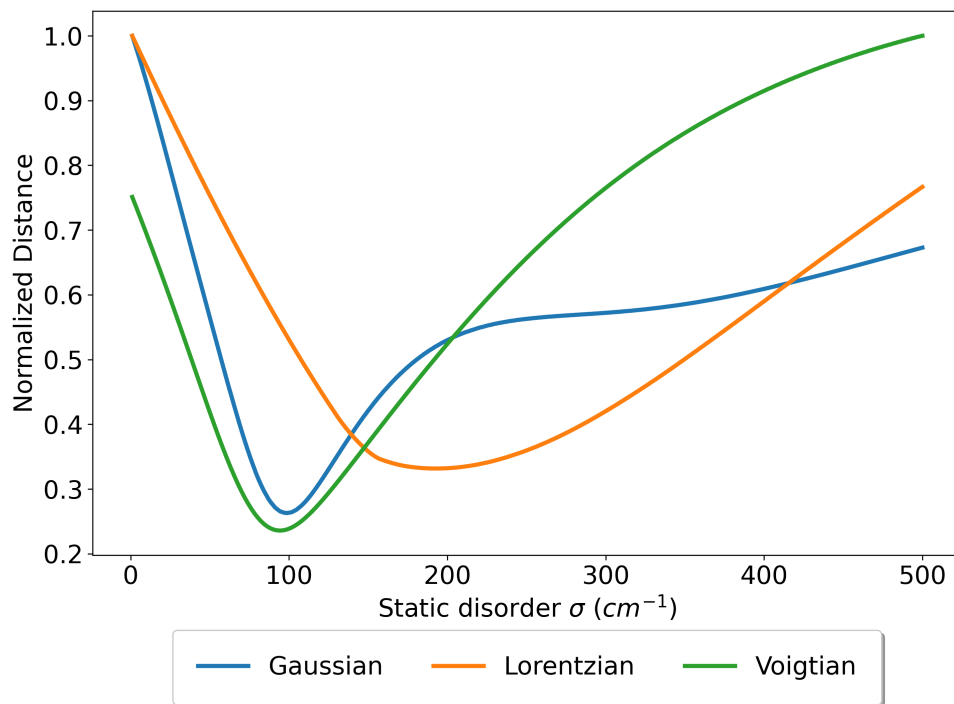


Figure C.38: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and $\omega\text{B97X-V}$ diabatic excitonic coupling.

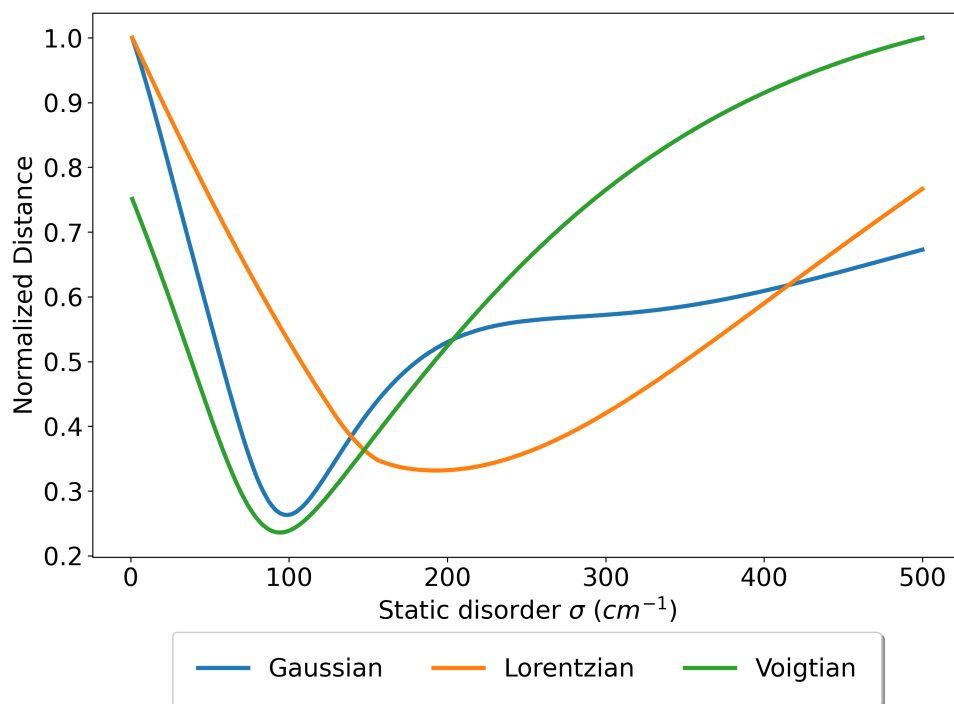


Figure C.39: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and $\omega\text{B97X-D3BJ}$ diabatic excitonic coupling.

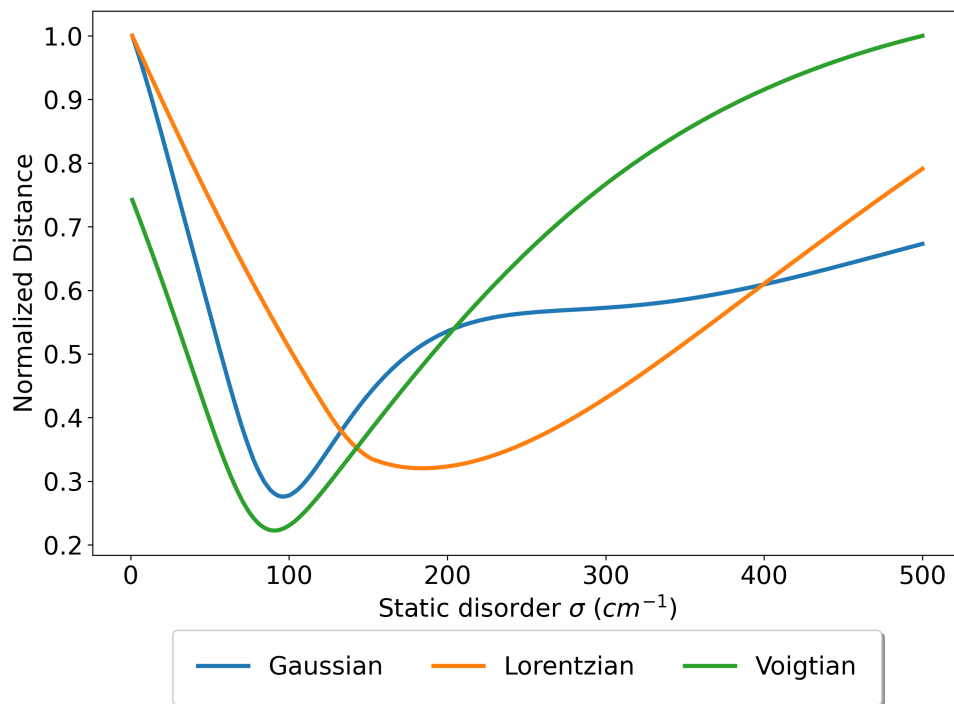


Figure C.40: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and CAM-B3LYP diabatic excitonic coupling.

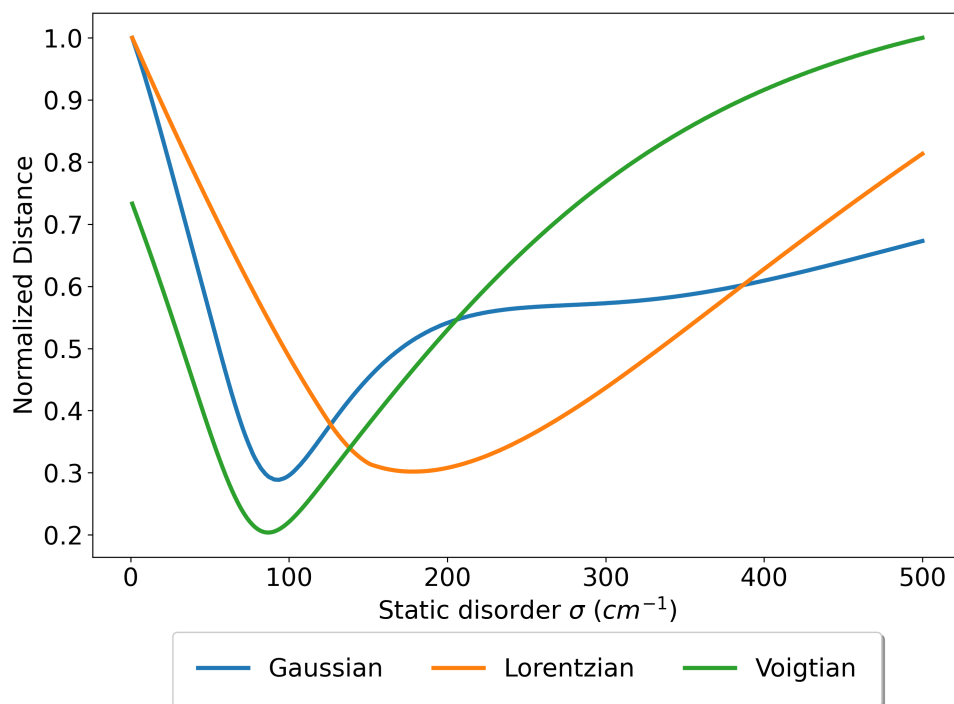


Figure C.41: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and CAMh-B3LYP diabatic excitonic coupling.

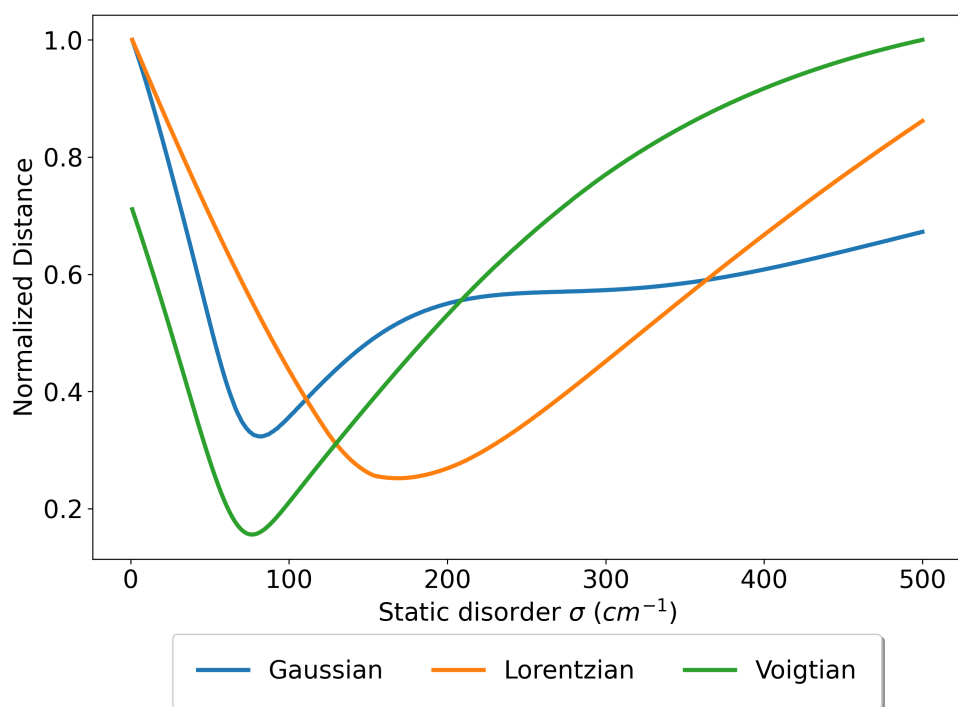


Figure C.42: Numerical optimization of σ . *Conditions:* experimental site energy (15198 cm^{-1}) and Tuned-CAM-B3LYP diabatic excitonic coupling.

C.2 Vibronic Spectra

C.2.1 HEOM spectra

Vibronic spectra was simulated using the HEOM method. This method is based on the extension of the Frenkel hamiltonian to a vibronic picture, using the excitonic spectral density to account for the exciton-vibrational couplings. This model takes as parameters the site energy, excitonic coupling, static disorder, and the opening angle between transition dipoles. In this case, all site energy have been shifted to match the highest peak with the experimental spectrum. The parameters used for the simulation are summarized in table C.1. For all simulations, σ was kept at 80 cm^{-1} .

Table C.1: Summary of parameters used in the HEOM simulation of absorption spectra. E_{calc} is the site energy as calculated by TD-DFT, E_{opt} is the optimized site energy, J is the excitonic coupling, and θ is the opening angle between transition dipoles.

Type	Functional	$E_{\text{calc}} \text{ (cm}^{-1}\text{)}$	$E_{\text{opt}} \text{ (cm}^{-1}\text{)}$	$J \text{ (cm}^{-1}\text{)}$	$\theta \text{ (}^\circ\text{)}$
<i>meta-GGA</i>	M06-L	15382	15887	81.8	68.7
	TPSS	15016	15909	60.4	76.6
<i>Global Hybrid</i>	BHHLYP	15931	15836	148.8	57.0
	B3LYP	15731	15866	104.8	66.5
	O3LYP	15469	15884	88.5	70.9
	PBE0	15956	15857	118.1	65.6
<i>metaH-GGA</i>	M06-2X	15846	15846	131.4	62.3
	TPSSh	15591	15884	88.9	71.2
<i>RS Hybrid</i>	LC-BLYP	14771	15846	131.1	60.0
	ω B97X-V	15054	15841	139.5	58.2
	ω B97X-D3BJ	15054	15841	139.5	58.2
	CAM-B3LYP	15556	15844	135.6	60.8
	CAMh-B3LYP	15919	15849	129.8	62.1
	Tuned-CAM-B3LYP	14998	15862	112.3	67.1

The simulated spectra are shown in the following.

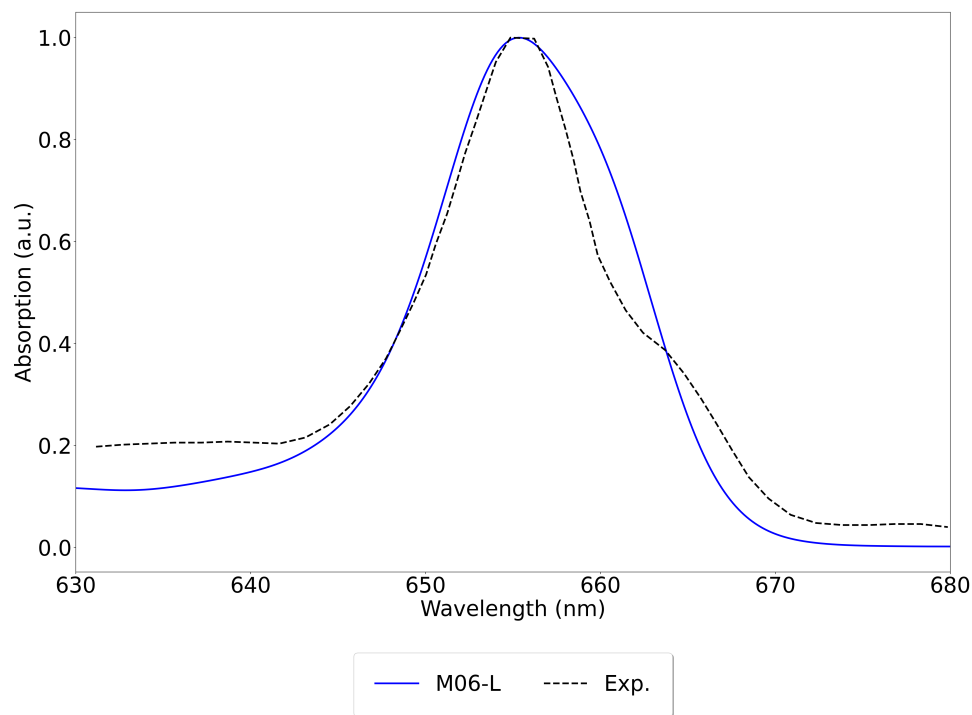


Figure C.43: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and M06-L diabatic excitonic coupling.

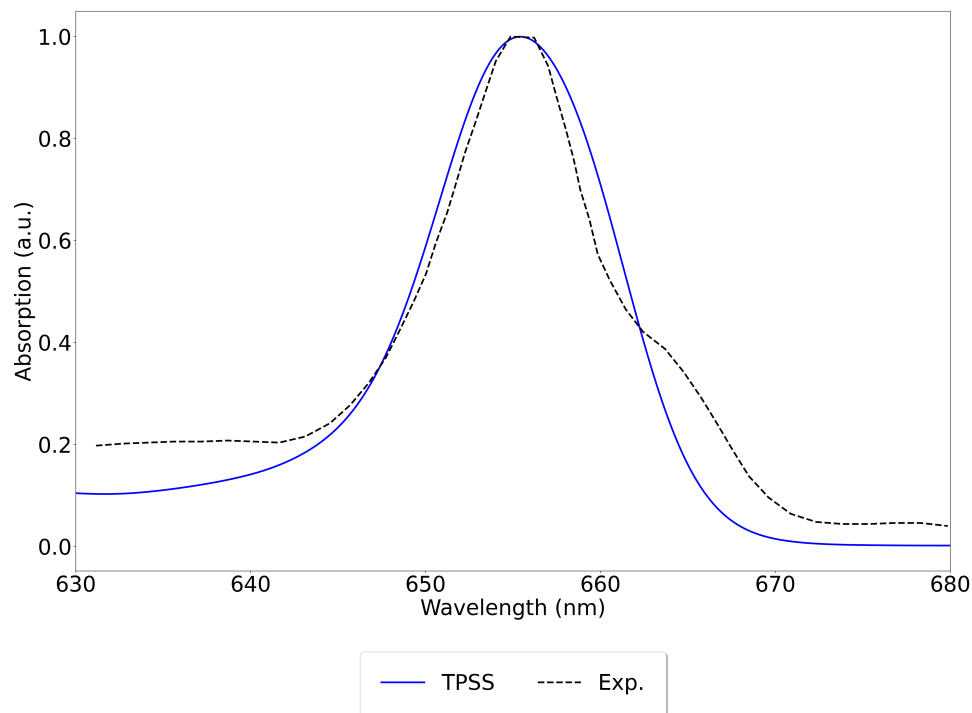


Figure C.44: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and TPSS diabatic excitonic coupling.

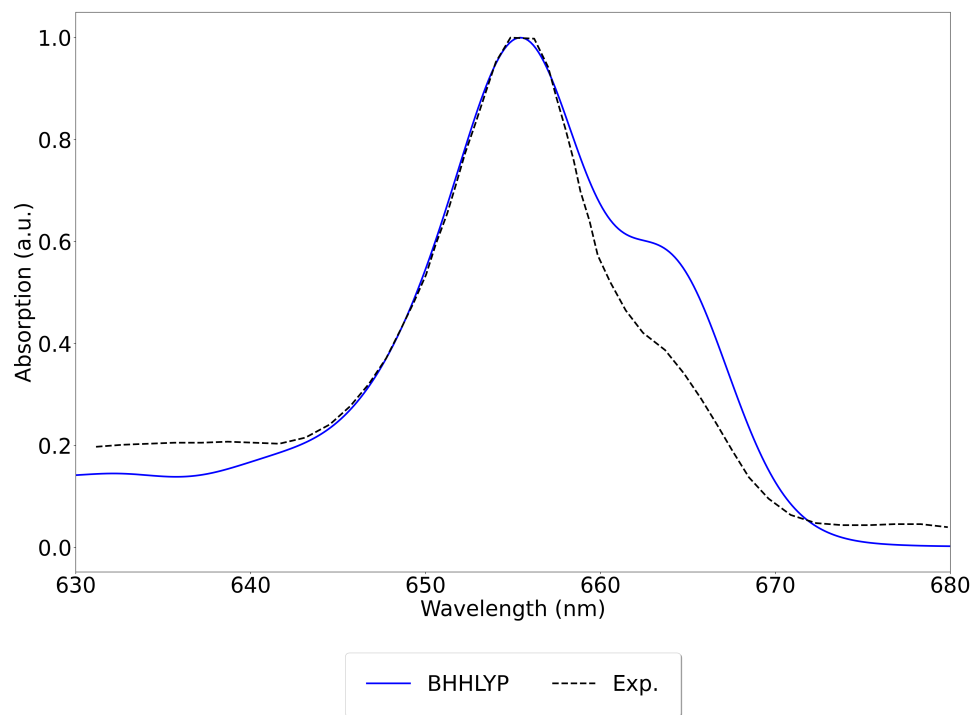


Figure C.45: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and BHHLYP diabatic excitonic coupling.

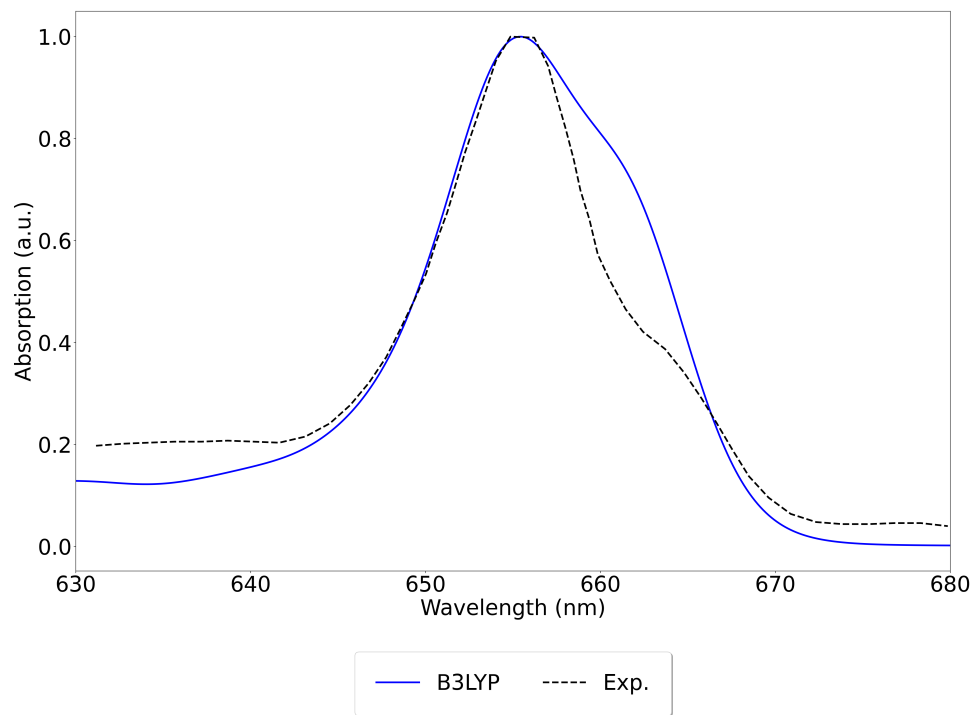


Figure C.46: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and B3LYP diabatic excitonic coupling.

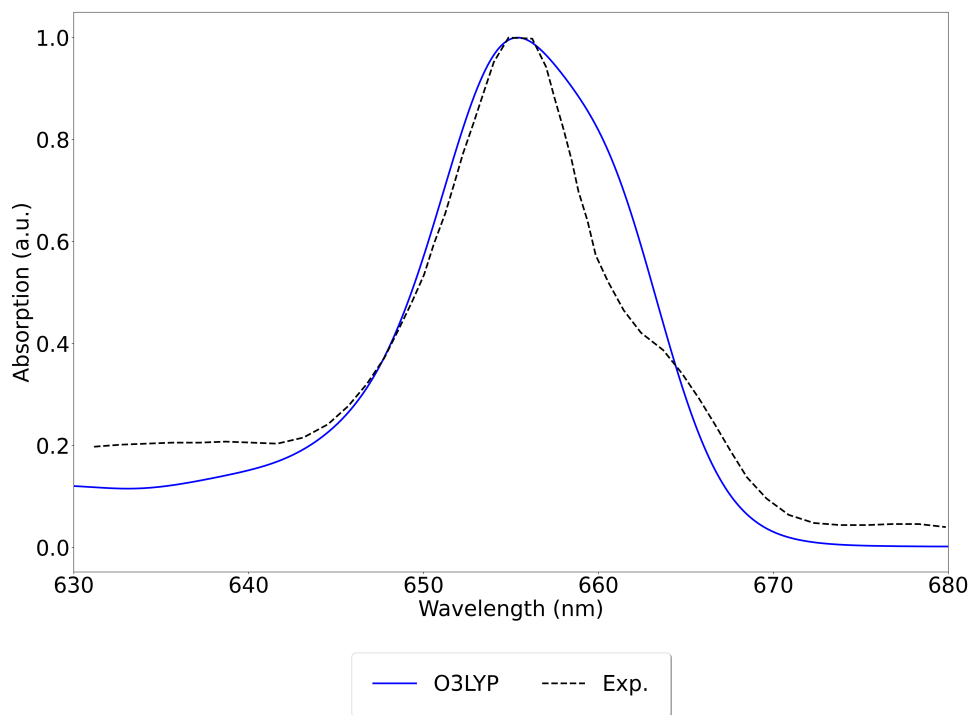


Figure C.47: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and O3LYP diabatic excitonic coupling.

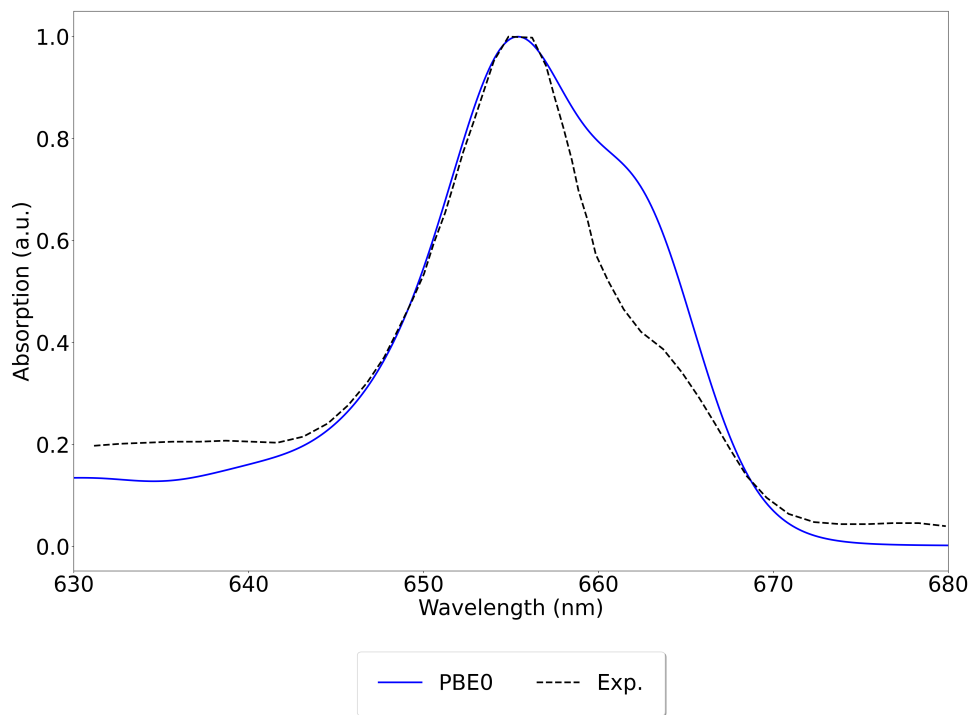


Figure C.48: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and PBE0 diabatic excitonic coupling.

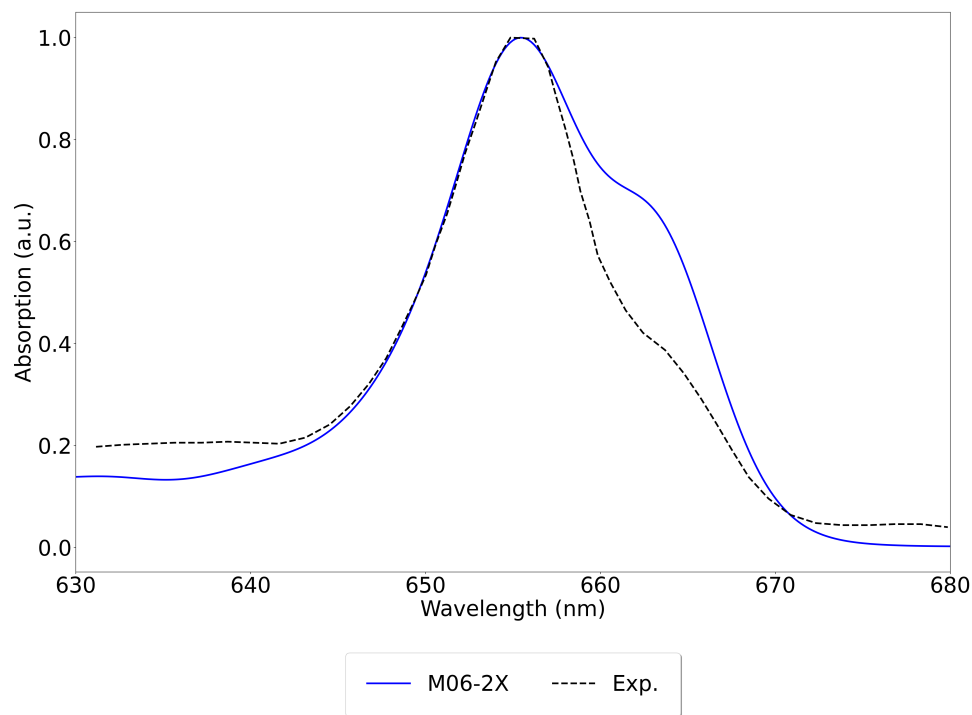


Figure C.49: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and M06-2X diabatic excitonic coupling.

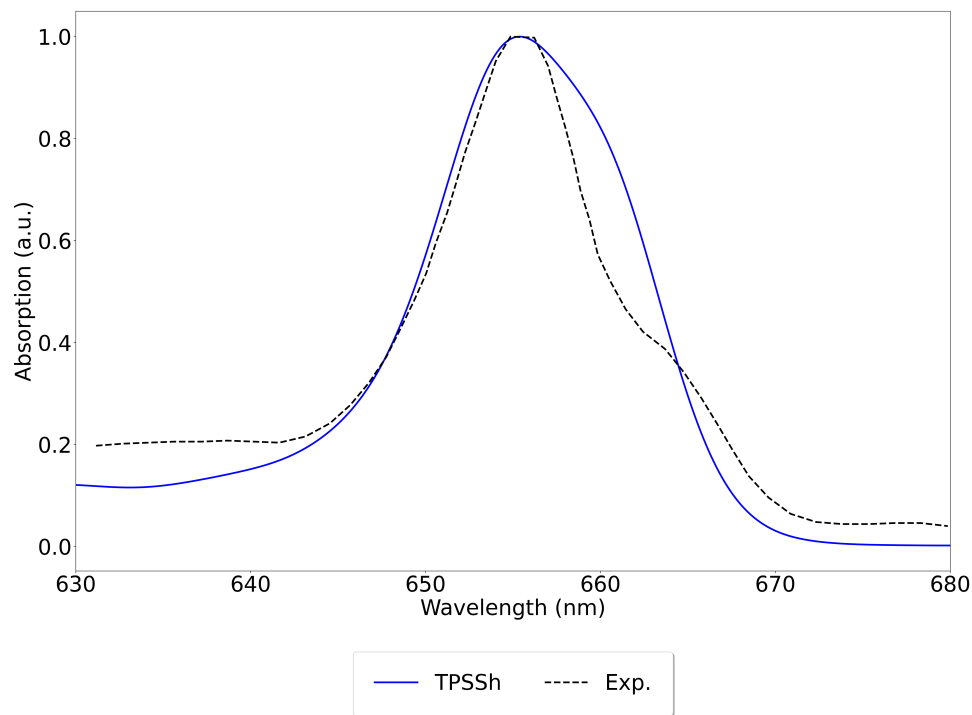


Figure C.50: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and TPSSh diabatic excitonic coupling.

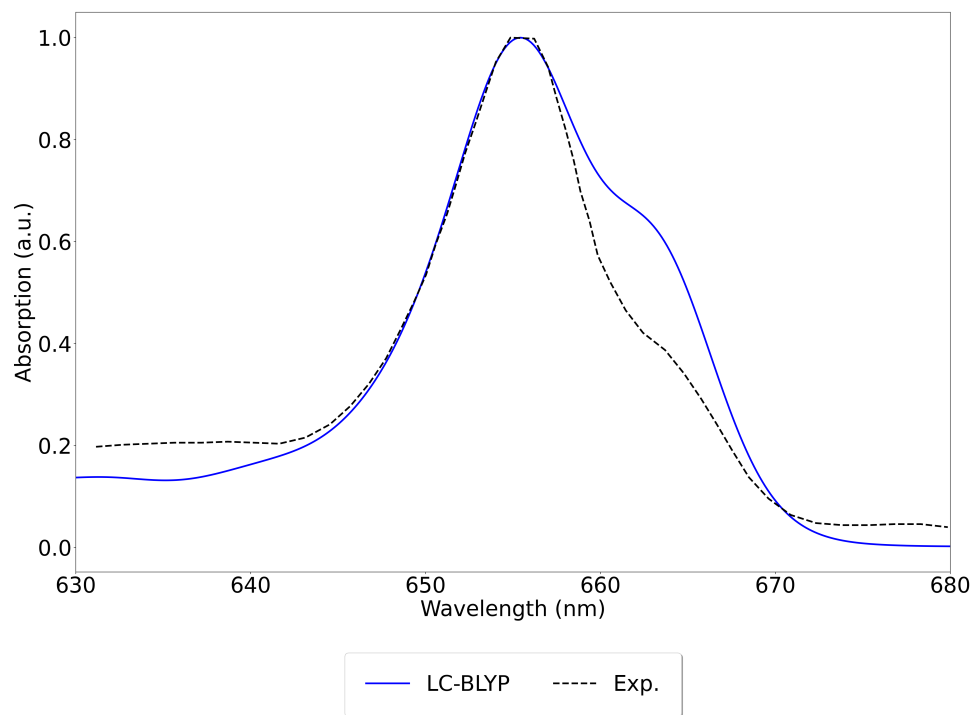


Figure C.51: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and LC-BLYP diabatic excitonic coupling.

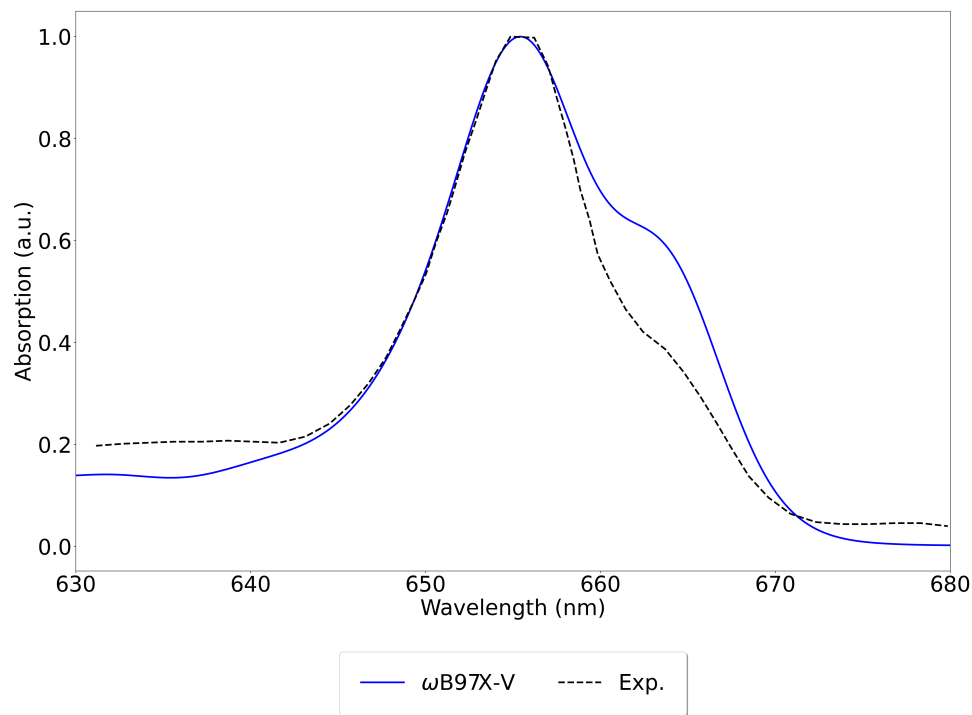


Figure C.52: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and ω B97X-V diabatic excitonic coupling.

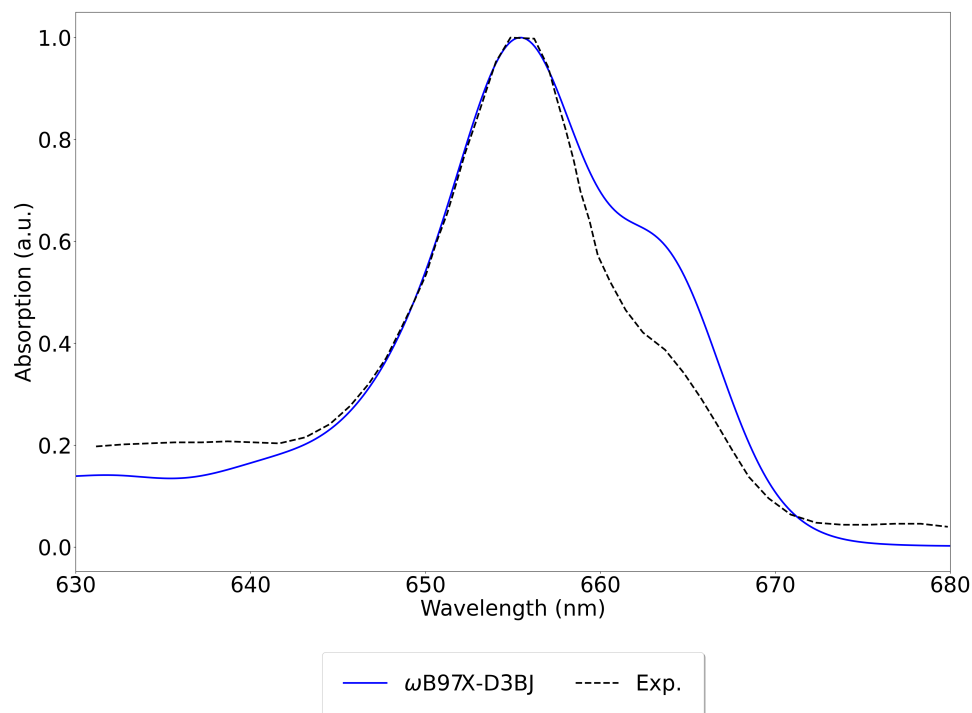


Figure C.53: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and ω B97X-D3BJ diabatic excitonic coupling.

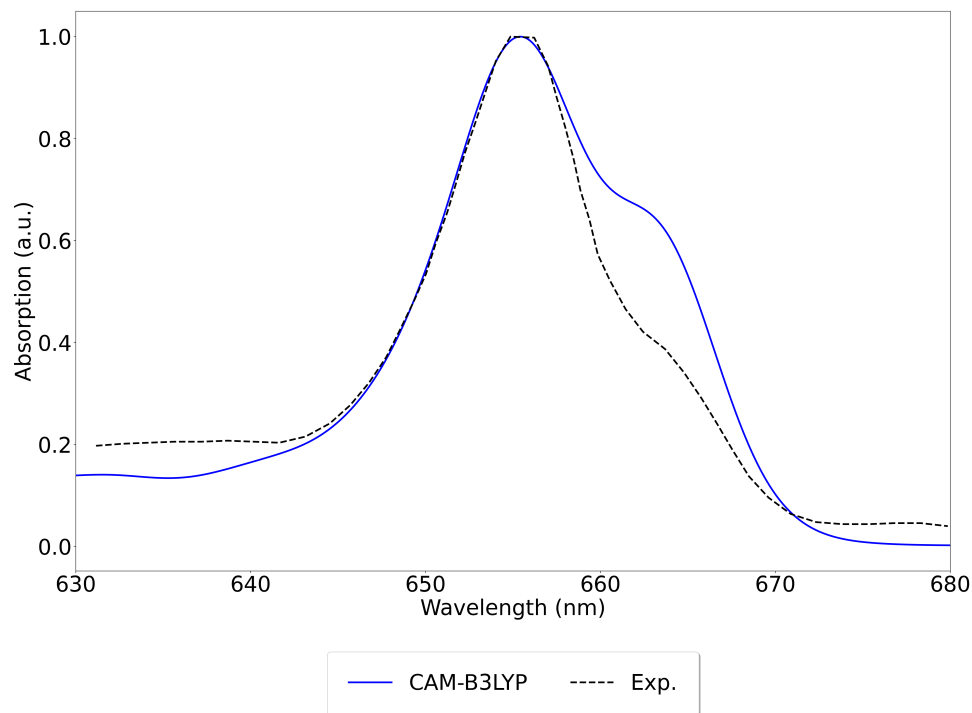


Figure C.54: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and CAM-B3LYP diabatic excitonic coupling.

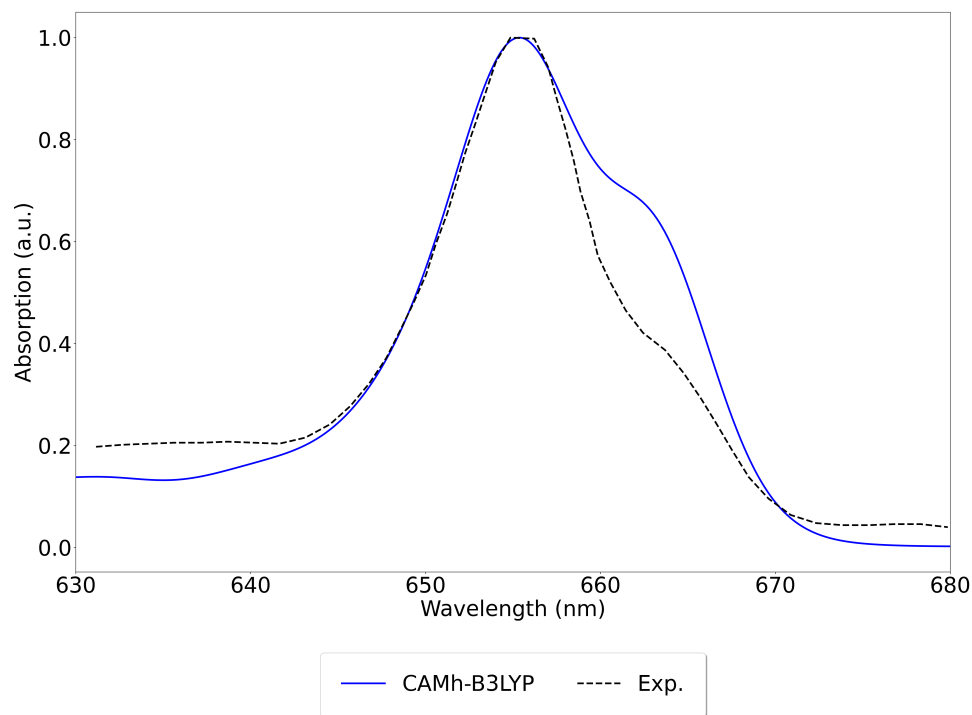


Figure C.55: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and CAMh-B3LYP diabatic excitonic coupling.

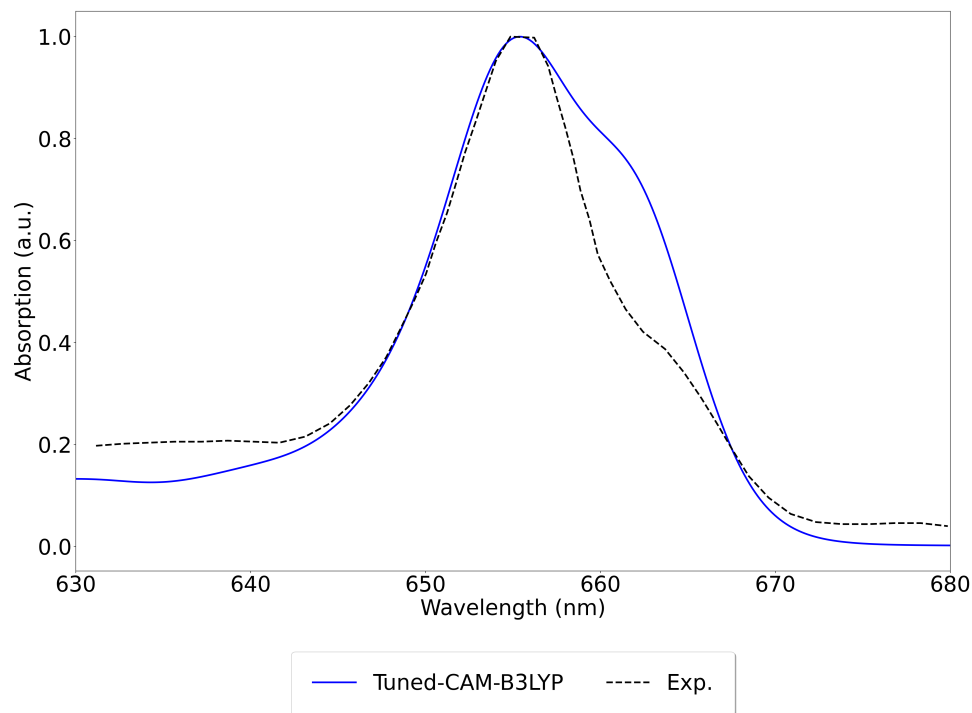


Figure C.56: Linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and Tuned-CAM-B3LYP diabatic excitonic coupling.

C.2.2 Deconvolution of HEOM spectra

Deconvolution of the HEOM spectra is shown, along with their fitting parameters, according to the scheme described in section 3.1.3.2 of the Main Text. In this case, all site energies have been shifted to match the highest peak with the experimental spectrum. The parameters used for the simulation are summarized in table C.1. For all HEOM simulations, σ was kept at 80 cm^{-1} . The curve-fitting was made using the least-squares procedure.

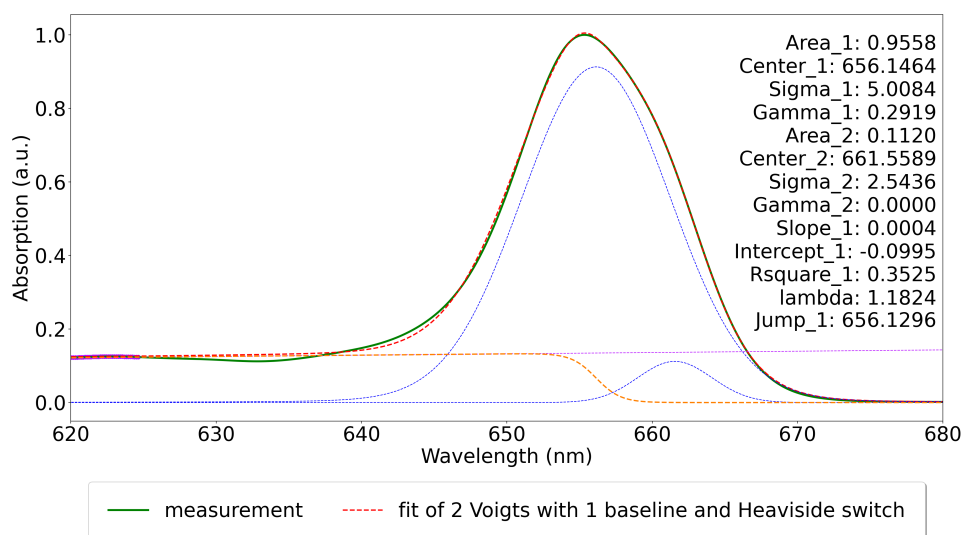


Figure C.57: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and M06-L diabatic excitonic coupling.

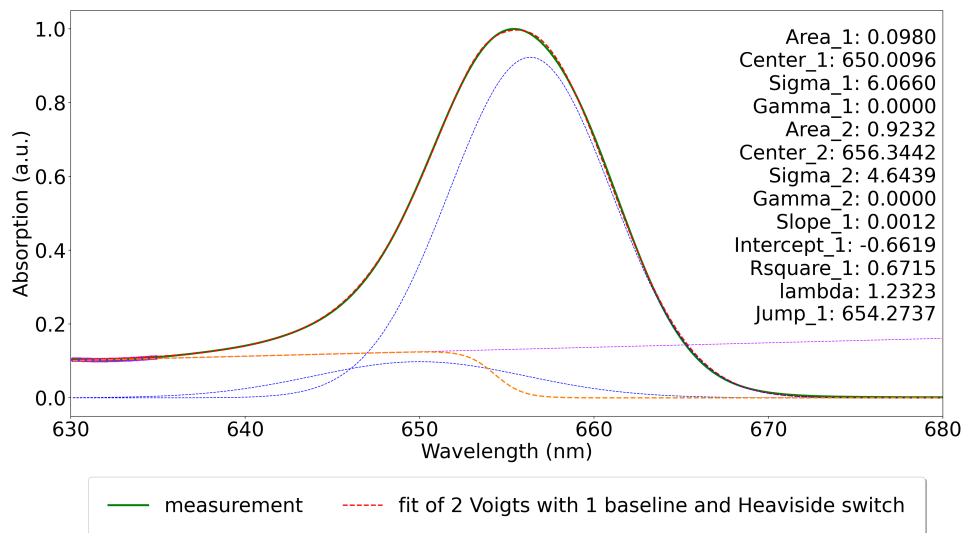


Figure C.58: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and TPSS diabatic excitonic coupling.

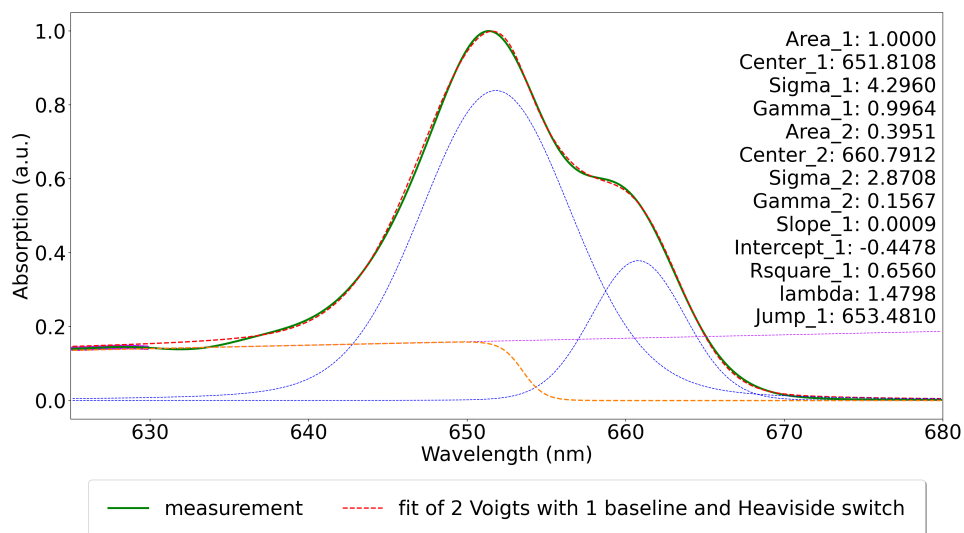


Figure C.59: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and BHLYP diabatic excitonic coupling.

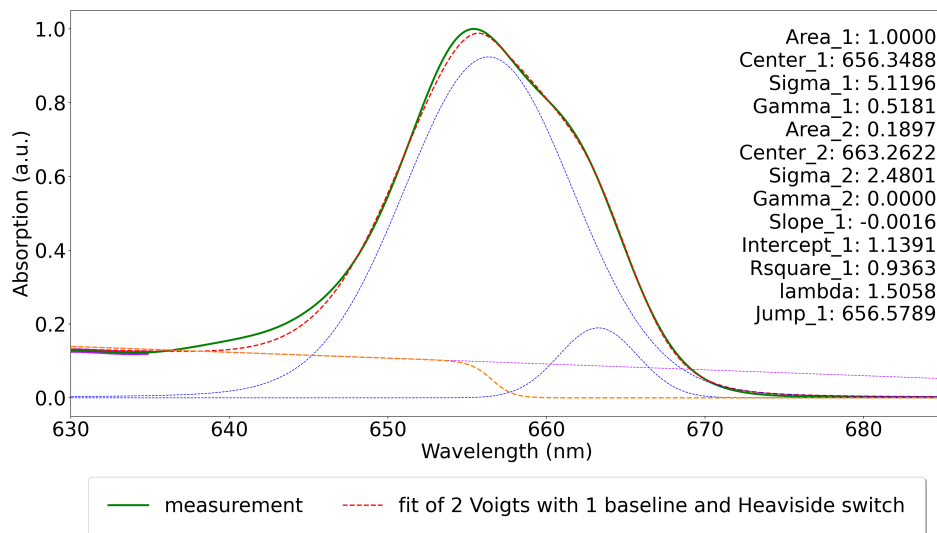


Figure C.60: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and B3LYP diatomic excitonic coupling.

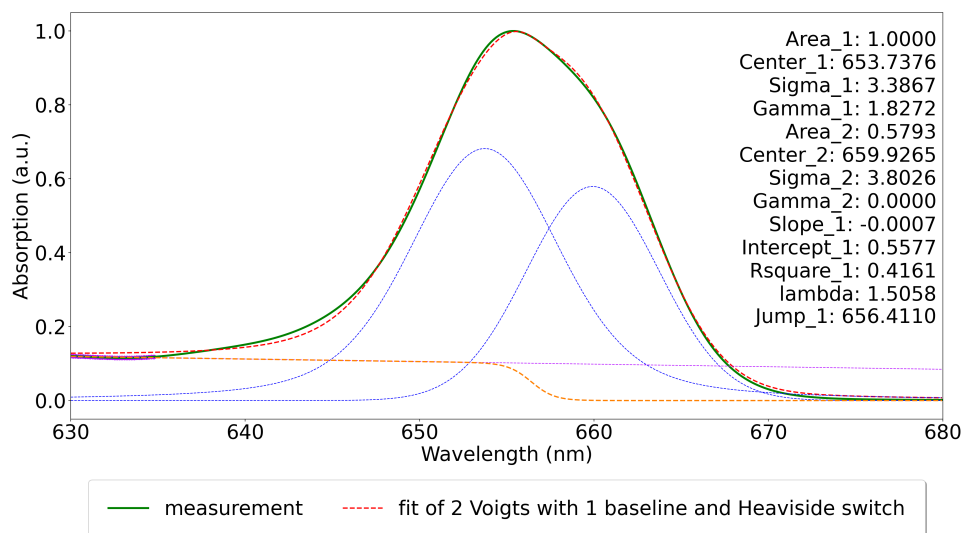


Figure C.61: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and O3LYP diatomic excitonic coupling.

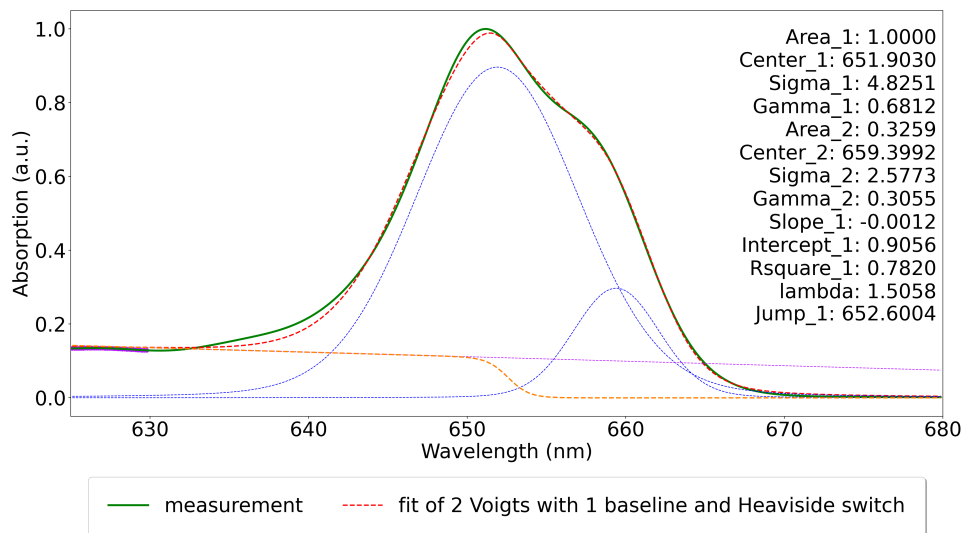


Figure C.62: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and PBE0 diabatic excitonic coupling.

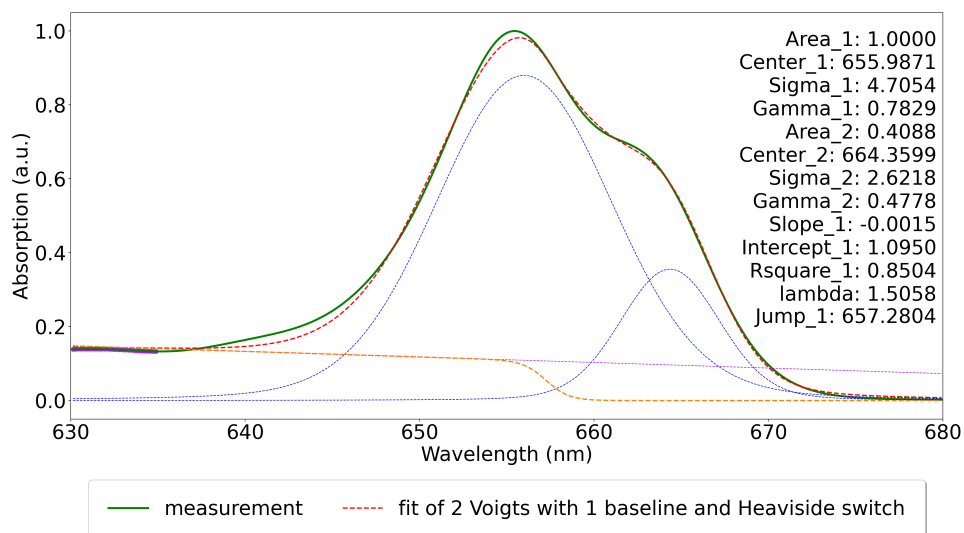


Figure C.63: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and M06-2X diabatic excitonic coupling.

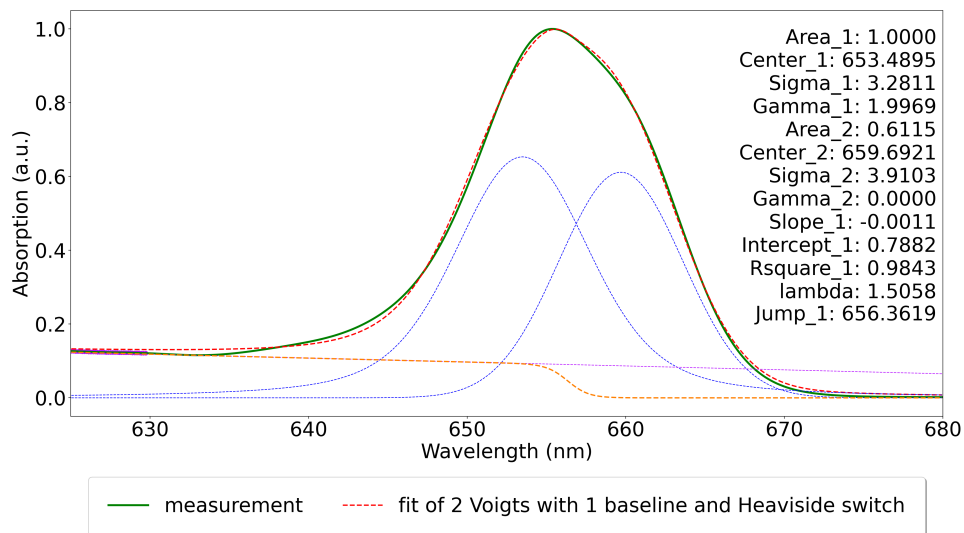


Figure C.64: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and TPSSh diabatic excitonic coupling.

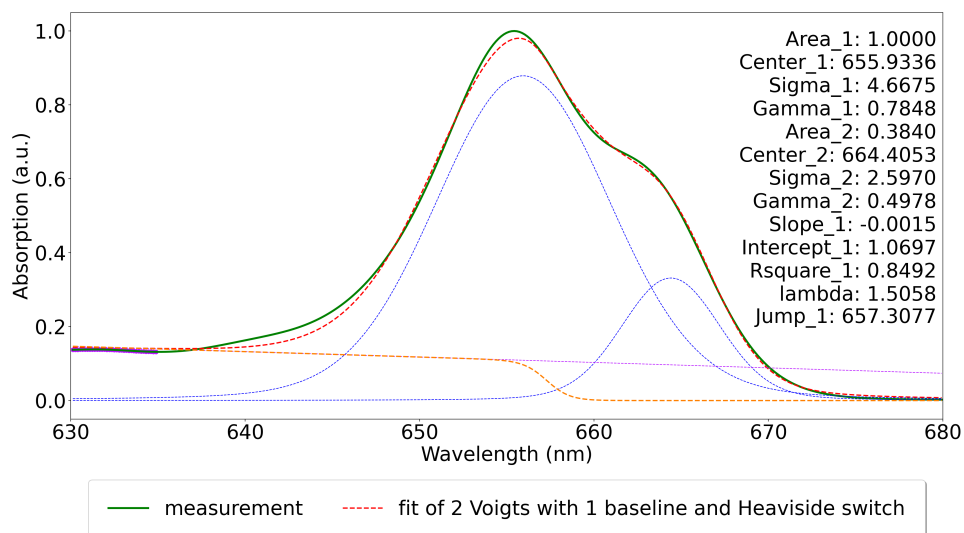


Figure C.65: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and LC-BLYP diabatic excitonic coupling.

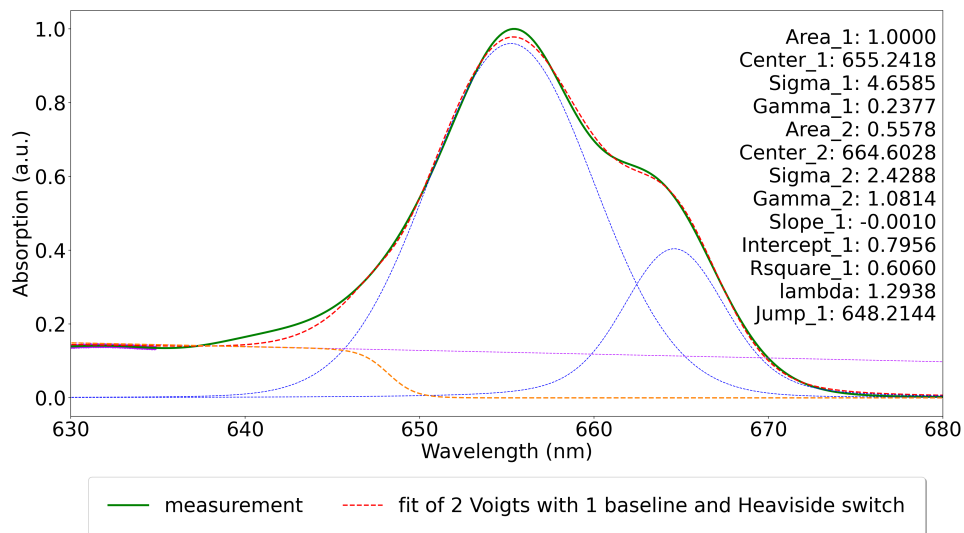


Figure C.66: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and ω B97X-V diabatic excitonic coupling.

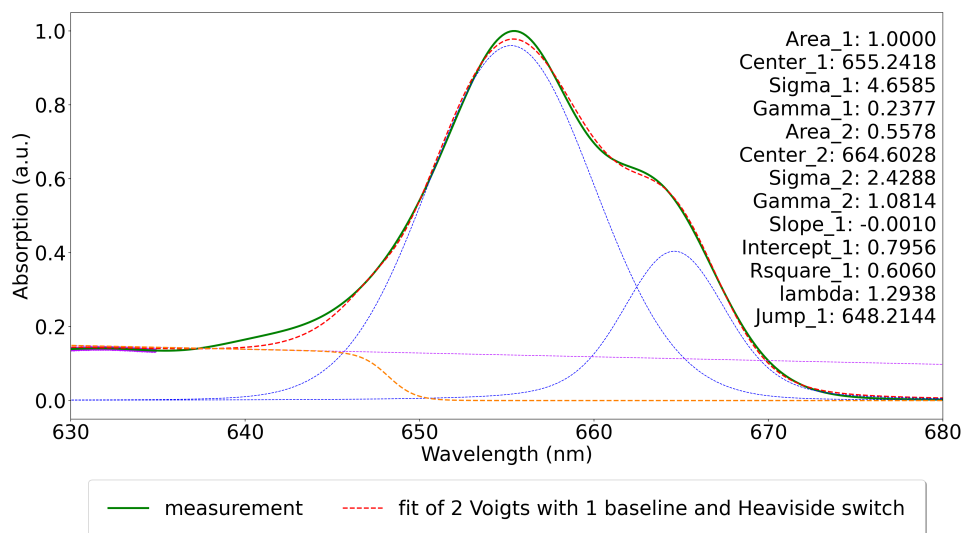


Figure C.67: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and ω B97X-D3BJ diabatic excitonic coupling.

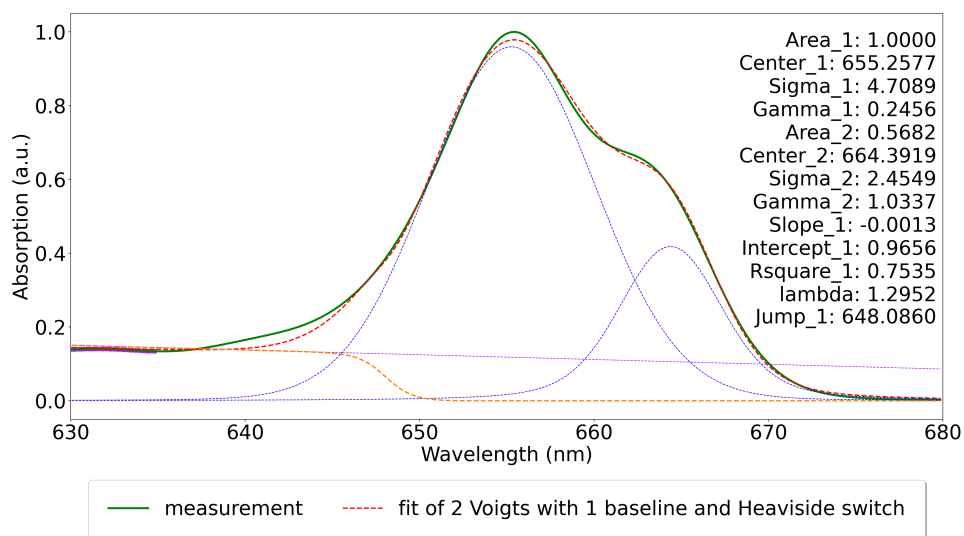


Figure C.68: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and CAM-B3LYP diabatic excitonic coupling.

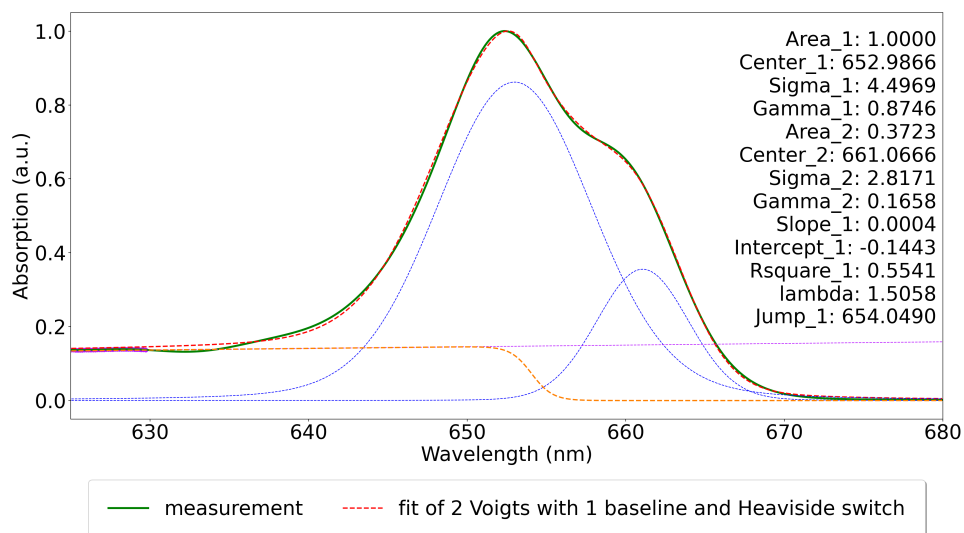


Figure C.69: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and CAMh-B3LYP diabatic excitonic coupling.

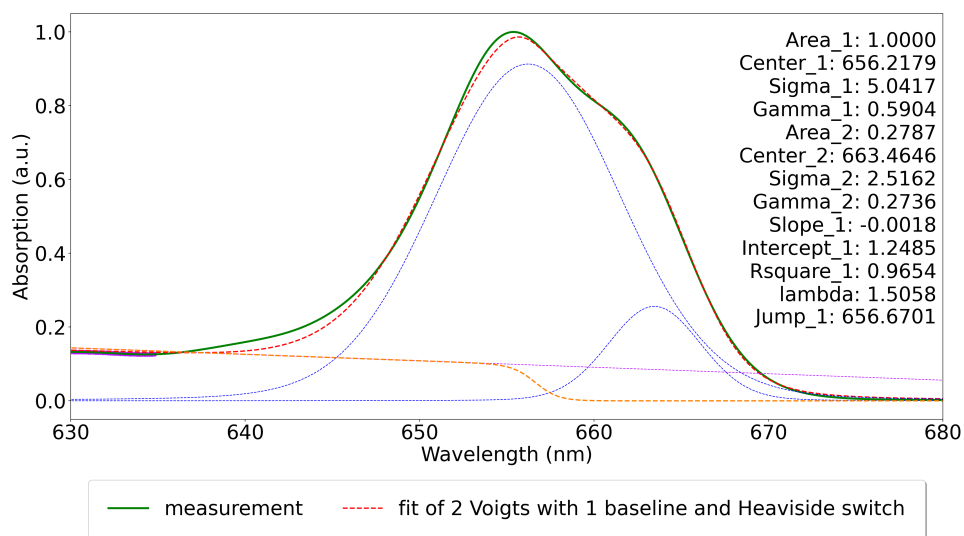


Figure C.70: Deconvolution of the linear absorption spectra simulated by the HEOM method. *Conditions:* site energy shifted and Tuned-CAM-B3LYP diabatic excitonic coupling.