INCREASING THE COMPUTATIONAL EFFICIENCY OF AB INITIO METHODS WITH GENERALIZED MANY-BODY EXPANSIONS

DISSERTATION

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By

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ABSTRACT

It is well known that a hierarchy of *ab initio* methods exist and can be used to achieve high accuracy, but at high cost. This is because correlated methods scale as $O(N^p)$, where $N$ is a measure of system size and typically $p \geq 3$, making high accuracy prohibitive for all but the smallest of systems. One strategy for circumventing this non-linear scaling is to use fragment based methods, which are a group of methods that rely on the “nearsightedness” of electronic matter to decompose a system of size $N$, to $N_{Frag}$ systems of size $n$. This decomposition allows *ab initio* methods to be performed on larger systems than before because the scaling is reduced from $O(N^p)$ to $N_{Frag} \times O(n^p)$; furthermore, each of the $N_{Frag}$ fragments is independent and can be divided amongst processors decreasing the overall wall time of the calculation. Here we focus on exploring a general, theoretical framework that elucidates the differences between various, ostensibly different, fragment methods, with a particular emphasis being placed on high accuracy applications.
I would like thank my adviser, John Herbert, for insightful discussions, mentoring, and all-around helping me reach this point in my academic career. I would also like to thank the entire Herbert group (both past and present members) for help and support along the way. Additionally, I would like to thank The Ohio State University for the educational opportunity, and funding. And finally, the Ohio Supercomputing Center for gratuitous amounts of computer time.
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CHAPTER 1

Preliminaries

1.1 Introduction

Chemistry is typically thought of as the science dedicated to elucidating the composition, properties, and behavior of matter (anything made up of atoms or molecules). It is often known as the central science because it serves as an interface between physics and other sciences such as biology and geology. Because of the centralized role of chemistry within science, it is common for chemists to adhere to one of two ideologies when describing matter. Perhaps the more common ideology is based on a phenomenological approach in which a “chemical intuition” is honed by studying a vast array of chemical processes and then using this intuition to make predictions. The other ideology attempts to use the laws of physics to predict and explain chemical behavior. It is this latter ideology we adopt here and we proceed by briefly recapitulating the relevant laws of physics.

Prior to the nineteenth century, it was a commonly held belief that most, if not all, of science could be explained in terms of Sir Issac Newton’s iconic second law of motion:

\[
-\frac{dV(\vec{r},\vec{p},t)}{dt^2} = m \frac{d^2\vec{r}(t)}{dt^2},
\]  

(1.1)
where $\vec{r}(t)$ is the trajectory of a system, having mass $m$, and momentum $\vec{p}$, at time $t$, moving in a potential $V$. Given a system’s momentum and initial position, $\vec{r}_0$, Eq. (1.1) allows us to determine the trajectory of the system for all $t$. By the mid to late nineteenth century, numerous physical phenomenon had defied explanation in terms of Eq. (1.1), with two of the more infamous examples being: the failure of the Rayleigh-Jeans law*, and the need for arbitrary parameters when describing the procession of the perihelion† of the planet Mercury. The failure of classical physics for these and other phenomenon ushered in a new era in science, now known as modern physics.

Modern physics is usually thought of as being comprised of two branches. The first of these two branches, general relativity, is concerned with the physics of very large objects and deals with planets, stars, and other celestial objects. It can be used to explain the anomalous procession of Mercury’s perihelion without recourse to arbitrary parameters. The other branch, quantum mechanics, can be conversely thought of as the branch of modern physics that describes the motion and behavior of the smallest known objects, *e.g.* molecules, atoms, and subatomic particles. Because these are the objects comprising matter, it is no surprise that the physics of chemistry is typically thought of in terms of quantum mechanics.

*The classical law which attempted to describe black-body radiation. Black-body radiation is electromagnetic radiation emitted from an opaque, non-reflective object (at room temperature the object will therefore appear black, giving rise to the name), which is in thermal equilibrium with its environment. It is known that at a given temperature the black-body radiation will have a wavelength that depends only on the temperature. The Rayleigh-Jeans law instead diverges to infinity for small wavelengths, regardless of the temperature. The Rayleigh-Jeans law is used to explain black-body radiation and is based on the assumption that the object is in thermal equilibrium with its environment.

†Point of a planet’s orbit, closest to the sun.
1.2 Fundamentals of Quantum Mechanics

Similar to how most of classical physics relies on Eq. (1.1), Newton’s second law of motion, quantum mechanics appeals to the Schrödinger equation\(^\dagger\), which is defined as\(^\S\):

\[
i \hbar \frac{\partial |\Phi \rangle}{\partial t} = \hat{H} |\Phi \rangle,
\]

where \(i = \sqrt{-1}\), \(\hbar\) is Planck’s constant divided by \(2\pi\), \(|\Phi \rangle\) is the wave function of the system, and \(\hat{H}\) is the Hamiltonian operator of the system. In general, both \(\hat{H}\) and \(|\Phi \rangle\) depend on the coordinates of all objects within the system as well as on time. Given the initial state, \(|\Phi_0 \rangle\), and the Hamiltonian, the Schrödinger equation, Eq. (1.2), gives us a way to calculate the wave function of the system at any future time \(t\). Instinctively at this point one wants to draw a comparison between \(|\Phi \rangle\) and the classical trajectory; however, such a comparison is not the correct way of viewing the wave function and the actual interpretation is more complicated.

\(^\dagger\)We are only interested in non-relativistic phenomenon presently and ignore complications caused by special relativity.

\(^\S\)We assume the reader has some familiarity with bra-ket notation. For our purposes the ket, \(|\Psi \rangle\), represents a function, \(\Psi\) and the bra, \(\langle \Psi |\), represents the complex conjugate transpose of that function. When the bra and ket appear together, such as in \(\langle \Psi |\Psi \rangle\), it is interpreted as the inner product of \(\Psi^\dagger\) with \(\Psi\), where the \(\dagger\) denotes the Hermitian conjugate of \(\Psi\). If an operator appears between the bra and ket, such as \(\langle \Psi |\hat{X}|\Psi \rangle\), \(\hat{X}\) first acts on \(|\Psi \rangle\) to generate some new function, say \(|\Theta \rangle\). So that \(\langle \Psi |\hat{X}|\Psi \rangle = \langle \Psi |\Theta\rangle\), which is then interpreted as the inner product of \(\Psi^\dagger\) and \(\Theta\).

\(^\dagger\)The solution of any differential equation is only defined up to an overall multiplicative constant. This constant then takes on a particular value only when boundary conditions are introduced. Within quantum mechanics, this constant is usually fixed by mandating that the wave function is normalized. Presently we absorb this “normalization” constant into the wave function in an attempt to simplify the equations.
Within the physics community there is some room for discussion on how to interpret the wave function; however, within the chemistry community nearly all interpretations utilize the Born interpretation, which says: given a system with wave function $|\Phi\rangle$, the probability of finding the system with coordinates $\tau$, is given by $|\Phi|^2d\tau$, i.e. the probability is proportional to the square modulus of the wave function. This means it is not $|\Phi\rangle$ itself that we prescribe meaning to, but rather the square modulus of the wave function. The manifestation of probability in quantum mechanics is a reoccurring theme that is distinctly different then the deterministic formalism and interpretation of Newton’s laws of motion. In general, this probabilistic nature means that in quantum mechanics we can only state how likely an observation is to occur at a given future time, not when it will occur. We therefore talk in terms of expected values. The expectation (most probable) value, $\langle X \rangle$, of observable $X$, with operator $\hat{X}$, is postulated to be:

$$\langle X \rangle = \langle \Phi | \hat{X} | \Phi \rangle.$$  \hspace{1cm} (1.3)

Eqs. (1.2) and (1.3) together provide the basis for all of quantum mechanics. A system is prepared in some initial state, $|\Phi_0\rangle$. The time evolution of the state is then directly calculated via the Schrödinger equation, Eq. (1.2). The resulting wave function along with Eq. (1.3) can then be used to calculate the expectation value of a property of interest, at a time of interest, or as a function of time. This way of thinking establishes the wave function as the quantity we are solving for and means we need an explicit form for the Hamiltonian operator of the system.
Without loss of generality, we can write down a Hamiltonian for any system comprised of matter. For a system comprised of $N_e$ electrons, each of mass $m_e$ and charge $-e$, as well as $N_A$ atoms (nuclei), the $I$th nucleus having mass $m_I$ and charge $Z_I$, the Hamiltonian can be written as:

$$\hat{H}(\vec{r}, \vec{R}, t) = -\frac{\hbar^2}{2m_e} \sum_{i=1}^{N_e} \hat{\nabla}^2_i - \frac{\hbar^2}{2} \sum_{I=1}^{N_A} \frac{1}{m_I} \hat{\nabla}^2_I + \frac{1}{2} \sum_{i,j=1}^{N_e} \frac{e^2}{4\pi\epsilon_0 ||\vec{r}_i - \vec{r}_j||} + \frac{1}{2} \sum_{I,J=1}^{N_A} \frac{Z_I Z_J e^2}{4\pi\epsilon_0 ||\vec{R}_I - \vec{R}_J||} - \sum_{i=1}^{N_e} \sum_{I=1}^{N_A} \frac{Z_I e^2}{4\pi\epsilon_0 ||\vec{r}_i - \vec{R}_I||} + \hat{V}_{\text{Ext}}(\vec{r}, \vec{R}, t).$$

(1.4)

Within Eq. (1.4) lower case indicies index electrons, capital indicies index nuclei, $\hat{\nabla}^2$ is the Laplacian operator, $\epsilon_0$ is the permittivity of free space, $\vec{r}$ is the vector of electron positions, $\vec{r}_i$ is the vector from the origin to the position of electron $i$, $\vec{R}$ is the vector of nuclear positions, $\vec{R}_I$ is the vector from the origin to the position of atom $I$, $\hat{V}_{\text{Ext}}$ is the total external potential, and $||X||$ is the absolute value of $X$. We can identify each of the terms as an energetic contribution to the overall energy of the system, which allows us to identify the Hamiltonian operator as the operator tied to the observable energy. Respectively, the terms in Eq. (1.4) can be identified as: the kinetic energy of the electrons, the kinetic energy of the nuclei, the electron-electron repulsion, the nucleus-nucleus repulsion, the nucleus-electron attraction and the external potential.

For our current purposes, we will not be interested in time-dependent external potentials. In such cases, it is clear from Eq. (1.4) that the Hamiltonian itself does not depend on time. Consequentially, the wave function is necessarily factorable into a spatially independent part, $|U(t)\rangle$ and a time-independent part, $|\psi(\vec{r}, \vec{R})\rangle$, the
Schrödinger equation, Eq. (1.2), can then be manipulated to yield:

\[ | \Phi(\vec{r}, \vec{R}, t) \rangle = | U(t) \rangle | \psi(\vec{r}, \vec{R}) \rangle \] \hspace{1cm} (1.5a)

\[ \hat{H} | \psi(\vec{r}, \vec{R}) \rangle = E | \psi(\vec{r}, \vec{R}) \rangle \] \hspace{1cm} (1.5b)

\[ | U(t) \rangle = e^{-iE t / \hbar} \] \hspace{1cm} (1.5c)

where \( E \) is a scalar, and can be identified with the energy of the system in state \( | \psi(\vec{r}, \vec{R}) \rangle \).

It is a general result from the study of differential equations, that the general solution of a differential equation can be written as a linear combination of particular solutions. In terms of the Schrödinger equation, this means we can solve Eq. (1.5b) for the complete set of time independent wave functions and their corresponding energies, form the time dependent phase factors, Eq. (1.5c), and write a general solution to the Schrödinger equation as:

\[ | \Phi(\vec{r}, \vec{R}) \rangle = \sum_{I=1} c_I e^{-iE_I t / \hbar} | \psi_I(\vec{r}, \vec{R}) \rangle, \] \hspace{1cm} (1.6)

where the \( c_I \) are the expansion coefficients. So long as our set of time-independent wave functions is a complete basis set for the time-independent problem, we will always be able to exactly represent the time-dependent problem’s wave function by Eq. (1.6). As such, finding solutions to the Schrödinger equation is then facilitated by finding solutions to Eq. (1.5b).
1.3 Born-Oppenheimer Approximation

As written, Eq. (1.5b), is still a formidable problem because it will depend on $3 \times N_A \times N_e$ degrees of freedom. If it was not for Coulombic attraction between the nuclei and electrons the Hamiltonian would be separable into a nuclear Hamiltonian and an electronic Hamiltonian. Assuming this separability, the eigenfunction of Eq. (1.5b) could be written as a product of two eigenfunctions one for the nuclear degrees of freedom and one for the electronic degrees of freedom. This would then allow us to separate Eq. (1.5b) into two eigenvalue equations, markedly decreasing the complexity of the problem.

In 1927, Born and Oppenheimer suggested that such a separation is justified. The conventional justification is that the nuclei are much more massive than the electrons, and if they have similar momenta, then it must be the case that the nuclei move slower. This slower movement means the nuclei are standing still from the perspective of the electrons and can be considered an external potential that the electrons move around in. This explanation is hand waving at best, and the real justification for this approximation comes from the fact that the electronic and nuclear energy scales are usually well separated.

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**Eq. (1.5b) is an example of a type of equation known as an eigenvalue equation, which we assume the reader has some familiarity with. Within the nomenclature of eigenvalue equations, the wave function is known as the eigenfunction and the energy of that wave function is known as the eigenvalue.**

**The hydrogen atom’s nucleus (the lightest nucleus) is about 1,800 times more massive than the electron.**
Regardless of which justification is used, for the work considered here, the Born-Oppenheimer approximation is fully justified and we can talk of the electronic structure problem which is defined as:

\[ \hat{H}_{\text{Elec}} \left| \psi_{\text{Elec}}(\vec{r}; \vec{R}) \right\rangle = E_{\text{Elec}} \left| \psi_{\text{Elec}}(\vec{r}; \vec{R}) \right\rangle \]  

(1.7)

with:

\[ \hat{H}_{\text{Elec}}(\vec{r}; \vec{R}) \equiv -\frac{\hbar^2}{2m_e} \sum_{i=1}^{N_e} \nabla_i^2 + \frac{1}{2} \sum_{i,j=1}^{N_e} \frac{e^2}{4\pi\epsilon_0 ||\vec{r}_i - \vec{r}_j||} - \sum_{i=1}^{N_e} \sum_{I=1}^{N_A} \frac{Z_I e^2}{4\pi\epsilon_0 ||\vec{r}_i - \vec{R}_I||} + \hat{V}_{\text{Ext}}(\vec{r}; \vec{R}). \]  

(1.8)

At this point it is important to note that the nuclei appear as parameters in Eq. (1.7) and not variables. Consequentially, this means we can think of the total energy as a function of \( R \) because changing the nuclear positions, changes the energy. \( E(\vec{R}) \) is known as the potential energy surface and its evaluation is at the heart of what is known as electronic structure theory.

### 1.4 Electronic Structure Theory

To illustrate some key concepts within electronic structure theory we focus on the solution of Eq. (1.5b) for atomic systems, which by adapting a center of mass reference frame, are rigorously independent of nuclear motion. This allows us to develop a set of concepts rigorously, which can in turn then be applied to molecules in the Born-Oppenheimer framework, just introduced, approximately. By doing this, it is our intent to illustrate the basics of electronic structure theory for atoms and molecules.
1.4.1 Atoms

The simplest electronic structure problem is the hydrogen atom, the Hamiltonian for which can be written as\textsuperscript{††}:

\[
\hat{H}_H(\vec{r}, \vec{R}) = -\frac{\hbar^2}{2\mu} \nabla^2 - \frac{e^2}{4\pi\epsilon_0 ||\vec{r} - \vec{R}||},
\]

(1.9)

where \(\mu\) is the reduced mass of the hydrogen atom. This Hamiltonian combined with Eq. (1.5b) is an analytically solvable problem and the result is a set of wave functions, \(\{ |\psi(\vec{r}, \vec{R})\rangle\}\) and corresponding energies. With trivial modifications, the solutions obtained from this problem, can be adapted to analytically describe any one nucleus and one electron atom. Therefore, we turn our attention to the next simplest electronic structure problem, the two-electron, one nucleus system, for which the helium atom is the canonical example.

For the helium atom the Hamiltonian is\textsuperscript{‡‡}:

\[
\hat{H}_{He}(\vec{r}) = -\frac{\hbar^2}{2m_e} \nabla^2_1 - \frac{\hbar^2}{2m_e} \nabla^2_2 + \frac{e^2}{4\pi\epsilon_0 ||\vec{r}_1 - \vec{r}_2||} - \frac{2e^2}{4\pi\epsilon_0 ||\vec{r}_1||}
\]

\[
= \hat{h}_1 + \hat{h}_2 + \frac{e^2}{4\pi\epsilon_0 ||\vec{r}_1 - \vec{r}_2||},
\]

(1.10)

(1.11)

where \(\hat{h}_1\) and \(\hat{h}_2\) are one-electron operators, each of which has the same solutions (accounting for the different nuclear charge) as Eq. (1.9); however, the presence of

\textsuperscript{††}We are implicitly assuming the center of mass is at the origin and that we are considering a reference frame in which the center of mass is at rest.

\textsuperscript{‡‡}We have made the usual approximations, \(i.e.\ \mu \approx m_e\) and that the nucleus is infinitely heavy (neglect of the so called mass polarization term). As with the hydrogen atom, we again consider the center of mass reference frame, which is now centered at the nucleus.
the electron-electron repulsion term makes the overall solution of Eq. (1.5b) for the helium atom non-separable. Furthermore, the helium atom problem is isomorphic with the “three-body problem” of classical mechanics, which, in 1887, was shown by the mathematician Henri Poincaré to have no analytic solution in terms of known functions. Consequentially, we are forced to resort to approximate methods to solve the helium atom problem.

One way to proceed is to take the set of wave functions obtained for the hydrogen atom, which are a complete one-electron basis, and use them as a basis for expanding the helium atom’s two electron wave function. Because the helium Hamiltonian is approximately additively separable, we naively may assume that the ground state\[\text{§§}\] for the helium atom, \( | \psi_{0}^{He} \rangle \), can be written as a product of two hydrogen ground state orbitals\[\text{¶¶}\], \( | \psi_{0}^{H} \rangle \):

\[
| \psi_{0}^{He} \rangle = | \psi_{0}^{H} (1) \rangle | \psi_{0}^{H} (2) \rangle,
\]

(1.12)

where the number in parenthesis corresponds to which electron occupies the hydrogenic state. At this point, we have to account for two experimental observations which we present here by fiat. First, electrons are indistinguishable particles, and our wave function must not distinguish between them (this is violated because we claim that electron one is in the first orbital and electron two is in the second). Second, the electron has an intrinsic angular momentum known as spin, which is of half-integer

\[\text{§§}\]The lowest energy solution.

\[\text{¶¶}\]A one-electron wave function.
value; consequentially, no two electrons can occupy the same state. We can simultaneously satisfy these two points if we let $| \psi^H_0 \rangle$ be a wave function with spin $\alpha = +\frac{1}{2}$ and $| \psi^H_0 \rangle$ be a wave function with spin $\beta = -\frac{1}{2}$, furthermore we use a wave function that is a determinant:

$$| \psi^{He}_0 \rangle = | \psi^H_0 (1) \psi^H_0 (2) \rangle \equiv \frac{1}{\sqrt{2}} \begin{vmatrix} \psi^H_0 (1) & \overline{\psi^H_0 (1)} \\ \psi^H_0 (2) & \overline{\psi^H_0 (2)} \end{vmatrix} \tag{1.13}$$

This wave function is acceptable and we can use it to solve Eq. (1.5b), the result would be an energy value markedly higher than the true value. We now turn our attention to improving this approximate energy.

Within quantum mechanics, the variational principle says: given a trial wave function, $| \tilde{\psi} \rangle$, the following relationship holds (assuming the trial wave function is normalized):

$$\langle \tilde{\psi} | \hat{H} | \tilde{\psi} \rangle \geq E_0, \tag{1.14}$$

where $E_0$ is the true ground state energy. What this means is that if we introduce a parameter into our wave function, and minimize the energy with respect to this parameter, the resulting energy, is the best possible approximation to the ground state energy using this parameterized wave function. When using hydrogenic orbitals as trial wave functions, one common choice of variational parameter is the nuclear charge. The justification for this choice is the idea that each electron does not actually experience the full Coulombic attraction to the nucleus because other electrons are “using up” some of the nucleus’s charge; therefore, each electron experiences an effective nuclear charge. Rather than pursue the helium problem in more detail it is
now our intent to return the current focus to molecules and use these ideas to obtain 
molecular energies.

### 1.4.2 Molecules

Extending the helium Hamiltonian to more than two electrons presents no new con-
ceptual difficulties. In all cases the problem is still not analytically solvable and we 
must still resort to some approximate method. The next way to make the electronic 
structure problem more complicated is then to start adding in additional nuclei, form-
ing molecules. Because the nuclei are being treated as stationary point charges within 
the Born-Oppenheimer approximation this only adds minor additional conceptual 
complication to the electronic structure problem. For any molecule, the electronic 
Hamiltonian can be written:

\[
\hat{H}_{\text{Elec}}(\vec{r}; \vec{R}) = \sum_{i=1}^{N_e} \hat{h}_i + \frac{1}{2} \sum_{i,j=1}^{N_e} \frac{e^2}{4\pi\epsilon_0||\vec{r}_i - \vec{r}_j||}
\]  

(1.15a)

\[
\hat{h}_i(\vec{r}; \vec{R}) \equiv -\frac{\hbar^2}{2m_e} \nabla_i^2 + \hat{V}_{\text{Ext}}(\vec{r}_i; \vec{R}),
\]

(1.15b)

that is it can be written as a sum of one-electron terms and the total electron-electron 
repulsion. The final energy will also depend on an additive constant equal to the 
repulsion of the atomic nuclei (recall the nuclei are fixed, so this term is trivial to 
compute). Additionally, note that the $\hat{V}_{\text{Ext}}$ will minimally contain the interaction 
of the electrons with the nuclei in addition to whatever other fields may be present. 
Phrased this way, the molecular problem’s similarity to the helium atom problem is 
apparent, we have a sum of one-electron terms, that would be “easy” to solve if it was 
not for the two-electron repulsion. Ultimately, it will turn out that all of electronic
structure theory can be thought of as a series of systematic approximations to treating this two-electron term.

Returning to our strategy for the helium atom, the variational principle, we intend to apply it in the same way, except now we need a molecular basis set. From the helium problem it is clear how we could form a basis set for an arbitrary atom; however, it is not clear how to form a basis for an arbitrary molecule. Historically, the usual way of creating molecular orbitals (one-electron wave functions that span a molecule) is to create them from atomic orbitals, by taking a linear combination of $N_B$ atomic orbitals (from this point forward we are ignoring consequences of spin other than the fact that it mandates our wave function be a determinant and with each orbital maximally occupied by at most two electrons):

$$|\chi_i\rangle = \sum_{j=1}^{N_B} c_{ij} |\psi_j\rangle.$$ (1.16)

This gives us $N_B$ molecular orbitals. It is these $N_B$ molecular orbitals that serve the same purpose as the atomic orbitals did for the helium atom.

One can imagine that there is a vast number of ways of creating molecular orbitals and the question now is how to find the way that produces the wave function with the best approximate ground state energy. As we did for the helium atom, we appeal to the variational principle; however, now we are not varying parameters within the atomic orbitals, $|\psi_j\rangle$, as we did for helium, but rather varying the $c_{ij}$'s, the so-called molecular orbital coefficients. It can be shown mathematically that the optimal choice for the set of molecular orbital coefficients, $\{c_{ij}\}$, is given by solving the matrix
equations (assuming all electrons are paired):

\[ FC = SC\epsilon \]  \hspace{1cm} (1.17a)

\[ C_{ij} = c_{ij} \] \hspace{1cm} (1.17b)

\[ F_{ij} = \langle \psi_i(\vec{r}_1; \vec{R}) \mid \hat{f}(\vec{r}_1; \vec{R}) \mid \psi_j(\vec{r}_1; \vec{R}) \rangle \] \hspace{1cm} (1.17c)

\[ S_{ij} = \langle \psi_i \mid \psi_j \rangle \] \hspace{1cm} (1.17d)

with:

\[ \hat{f}(\vec{r}_1; \vec{R}) = \hat{h}_1(\vec{r}_1; \vec{R}) + \sum_{kl} P_{lk} \langle \psi_k(\vec{r}_2; \vec{R}) \mid \left( \hat{1} - \frac{1}{2} \hat{P}_{12} \right) (||\vec{r}_i - \vec{r}_j||)^{-1} \mid \psi_l(\vec{r}_2; \vec{R}) \rangle \] \hspace{1cm} (1.18a)

\[ P = CC^\dagger \] \hspace{1cm} (1.18b)

where \( \epsilon_{ii} \) is the energy of molecular orbital \( i \) and \( \hat{P}_{12} \) is an operator that permutes electrons one and two. These equations are known as the restricted Hartree-Fock (HF) equations. Using them we can obtain the total energy of the system as:

\[ E = \sum_{i=1}^{N_e/2} h_{ii} + \epsilon_{ii} + \frac{1}{2} \sum_{I,J=1}^{N_A} \frac{Z_I Z_J e^2}{4\pi \epsilon_0 ||\vec{R}_A - \vec{R}_B||} \] \hspace{1cm} (1.19)

where:

\[ h_{ii} = \langle \psi_i(\vec{r}_1; \vec{R}) \mid \hat{h}_1(\vec{r}_1; \vec{R}) \mid \psi_i(\vec{r}_1; \vec{R}) \rangle. \] \hspace{1cm} (1.20)

One of the more predominant features of these equations is the fact that they are non-linear due to the occurrence of the molecular orbital coefficients in Eq. (1.18a), via the density matrix, \( P \). This means that the HF equations must be solved iteratively.
Formally, in the limit that $N_b$ is very large, setting up the four-index, two-electron matrix is the bottleneck of a HF calculation because this matrix can be set-up by looping over four indices, each of which run from one to $N_b$. Resultantly, the total time to set up the matrix will be proportional to $N_b^4$ [this is usually denoted as $O(N_b^4)$]. Perhaps the most important point about the HF equations is with regards to what part of the exact energy they are missing.

Formally the difference between the exact energy and the HF energy is known as the correlation energy. The name “correlation energy” is probably best thought of as a historic artifact because it is a bit of a misnomer, as we will see. It is straightforward to show that the HF equations do not prohibit electrons with different spin from occupying the same region of space. In other words, we find that the HF equations predict that the probability of one electron’s location is independent of the position of all other electrons. The justification for this is that each electron only experiences the average repulsion of every other electron and not the instantaneous repulsion felt when two electrons approach one another. Statistically speaking, this means the probability of finding an electron is uncorrelated with the probability of finding another (hence the origin of the term correlation energy). This is a non-physical result. In reality there is a correlation between the position of two electrons because

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*** In practice most electronic structure packages take advantage of the fact that a lot of these matrix elements are negligible and thus can be ignored. This means the HF method actually scales something like $O(N_b^2)$ with respect to the number of basis functions.

††† The proof proceeds by showing that the overall probability factors into the square moduli of each molecular orbital, which is non-zero for electrons having opposite spins. If one repeats this exercise with orbitals of the same spin, one finds that the same probability is identically zero because of cross terms introduced by exchange. Therefore the statement that the HF equations include no correlation is over zealous because they include some correlation for electrons of the same spin.
all electrons have the same charge and like charges repel. This tendency for electrons to avoid each other is known as dynamic correlation because it involves the dynamical motion of the electrons. It is one of two components of the correlation energy, often the larger component.

Now consider the process of homolytically cleaving the bond of a diatomic molecule. When the atoms are infinitely far apart the total wave function must be the sum of the wave function of two neutral atoms; however at the beginning of this section we discussed that the wave function for an atom was a determinant. This means that the total wave function of the separated atoms must be the sum of two determinants, a result that is obviously impossible to obtain with a single determinant wave function. This is known as static correlation (as opposed to dynamic correlation just explained) and to properly account for it also requires a description beyond the HF equations. Together static and dynamic correlation represent the total correlation energy of a system. The goal of the next section is to briefly explain how one can determine the correlation energy of a system and to emphasize the cost of doing so.

1.5  Post-HF methods

At this point, we will simply mention some of the common methods used to go beyond the HF equations. The actual working equations of these post-HF methods, as they are known, are irrelevant for our current purpose and represent a substantial detour from our current objective. Here we limit our focus to introducing the abbreviations, brief descriptions, and the cost of each method. In general a given electronic structure
method will have a scaling that is proportional to $O(N_A^a N_B^b)$. For reasons analogous to those presented for HF, $b$ is at most 4 for all methods. Consequentially it is usually $a$ that forms the bottleneck in a calculation and we focus on it exclusively in this section.

1.5.1 Density functional theory (DFT)

In recent years a post-HF method known as DFT has become increasingly popular. It can be shown that the energy of a system is a functional of the density of the system. Furthermore, it can be shown that by introducing a one-electron effective potential (known as the exchange-correlation potential) into the electronic Hamiltonian we can construct a non-interacting (single determinant) system that has the same density as the true system. This means by solving a HF like equation, with a modified potential, we can, in theory, obtain the exact energy.

Unfortunately, the exact form of the exchange-correlation potential is unknown, and likely unknowable, therefore we are forced to use approximate potentials. More often then not, these approximate potentials are simply fit to test sets of data and have little to no physical basis. Consequentially, DFT methods make accurate predictions in some cases, and fail to be accurate in other cases. A priori, there is usually no way to know how well a particular DFT method will work for a given system. Furthermore, when a DFT method is identified as making poor predictions, in general there is no way of knowing how to make it better. Given the similarity to HF, DFT also can be made to scale as $O(N_A^3)$, but its lack of systematic improvability distinctly limits its applicability. Nevertheless it remains a popular post-HF method today.
1.5.2 Configuration interaction (CI)

DFT represents the least costly way of calculating correlated energies. On the other end of the spectrum of post-HF methods are the CI methods. These methods can be thought of as the brute force approach to including the correlation energy. For HF we considered one determinant, which was the best single determinant we could use for our wave function. However, there exists a whole set of determinants (one for each combination of $N_e$ molecular orbitals). The set of all such determinants is a complete basis-set for the energy. This means if we expand our molecular wave function in terms of all such determinants we will get the best possible energy for our given atomic basis set (if our atomic basis set is complete, we will get the exact answer). However, it is easy to see that the number of determinants we need to consider scales exponentially. The method just described is known as full-CI and is readily seen to be intractable for all, but the smallest of systems.

One could argue that it should be possible to obtain a decent wave function without using all of the possible determinants. It is a general rule of quantum mechanics that states of similar energies tend to mix, and so we should only need to consider determinants that are similar in energy to the HF ground state if we want to improve our HF description. The determinants that should be closest in energy to the HF ground state are the determinants that differ by one molecular orbital; however, it can be shown via Brillouin’s theorem, that such determinants do not improve the description of the HF ground state. Never the less, in an attempt to introduce a systematic nomenclature, such a method will be known as CI singles (CIS).
The next set of determinants closest in energy to the HF ground state are the determinants that differ by two molecular orbitals. They do improve the HF description of the ground state and the corresponding method is known as CI doubles (CID). Even though the singly excited determinants do not change the description of the HF ground state directly, they do influence the doubly excited determinants and so including the singly excited determinants along with doubly excited ones provides a better wave function than just the double excitations alone. This is known as CIS doubles (CISD). At this point a clear hierarchy of CI methods are apparent with the cost increasing rapidly every time another excitation is taken into account.

1.5.3 Perturbative methods

CI represents a brute force approach, but one could instead seek a more physically motivated approach. Two rather intimately related ways of doing this are in common use. The first method is known as Møller-Plesset perturbation theory and it uses the fact that the exact Hamiltonian can be written as the sum of the Fock operator and a correlation potential (difference between the exact Hamiltonian and the Fock operator). Then assuming this correlation potential is small, one employs perturbation theory. In theory, this allows us to systematically include more correlation by going out to higher orders of perturbation theory. In practice, only Møller-Plesset perturbation theory at second order (MP2) sees regular use. This can be attributed to: the cost of extending Møller-Plesset perturbation theory out to higher orders,

\[^{+++}\text{One typically views determinants that differ from the HF ground state as being caused by excitations of electrons. If it differs by two molecular orbitals, it means the resulting determinant can be formed by exciting two electrons from their ground state orbitals.}\]
the erratic convergence behavior of the series, and the existence of the next method, which often times can provide better results for about the same computational cost. MP2 scales as $O(N_4^5)$.

The final method we introduce here is coupled-cluster (CC) theory, which uses an exponential wave function created from the HF ground state determinant, the form of which comes from explicitly coupling pairs of electrons. Although not clear at this superficial of a level, CC theory has many parallels to CI and Møller-Plesset perturbation theory. However unlike CI and Møller-Plesset perturbation theory CC, for example, will include some quadruple excitations at the double excitation level. This is a direct consequence of the nature of the wave function and results from the action of two separate double excitation operators on the HF ground state. CC with single and double excitations is known as CCSD and scales as $O(N_6^6)$ (same cost as MP5). CCSD with perturbative triples, CCSD(T), scales as $O(N_7^7)$, and CCSD with exact triples, CCSDT, scales as $O(N_8^8)$.

Choosing the level of electronic structure theory that is needed for a given problem is highly dependent on the property of interest and also the desired level of accuracy. For most properties, CCSD(T) extrapolated to the complete basis set (CBS), CCSD(T)/CBS, is considered the “gold-standard”. This is particularly true for interactions between molecules, which is what we will be predominantly interested in for the remainder of this dissertation. However, this method is too costly for all but the smallest of molecules making its applicability extremely limited. The remainder of this dissertation is dedicated to a series of approximations that can be
made to circumvent the highly non-linear scaling of \textit{ab initio} methods (methods that make predictions by only relying on first principles). In Chapter 2 we introduce the many-body expansion (MBE) and the generalized MBE (GMBE). In Chapter 3 we illustrate that the GMBE is capable of chemical accuracy for several small systems. In Chapter 4 we compare and contrast the accuracy of the MBE and the GMBE. The final two chapters focus on using the MBE to obtain high accuracy benchmarks.
CHAPTER 2

Fragment Methods

2.1 Introduction

As we mentioned in the last chapter, the cost of ab initio electronic structure calculations increases steeply as a function of both system size (number of atoms, $N_A$) and also one-particle basis size (number of basis functions per atom, $N_B$). The computational cost of a given ab initio method can be characterized as $O(N_A^a N_B^b)$, where typically $b = 2$–4 and $a \geq 3$, depending upon the ab initio method in question.

Fragment-based methods\textsuperscript{5} represent a promising path toward reducing the computational scaling with respect to $N_A$. In such methods, the energy of a large molecule or cluster is decomposed in terms of the energies of a collection of smaller subsystems, known as fragments, each of which is assumed to be representative of the local electronic environment. This idea has an undeniable intuitive appeal, as chemists are accustomed to reasoning in terms of functional groups, localized orbitals, and electron pairs, and is consistent with Kohn’s notion of the “nearsightedness” of electronic matter.\textsuperscript{6,7} If the $N_A$-atom system can be decomposed into $N_F$ smaller fragments (each of size $n_A$, say), then the computational scaling for a fixed basis set is reduced
from $\mathcal{O}(N_A^a)$ to $N_F \times \mathcal{O}(n_A^a)$. This is potentially a huge speed-up, even more so because the $N_F$ smaller calculations are completely independent and therefore qualify as “embarrassingly parallelizable”, i.e. can be run on separate processors with minimal processor to processor communication.

Of course, the proverbial devil lies in the as-yet-unspecified details. While these ideas have been around for a long time, the past decade has seen a flurry of activity resulting in a tremendous variety of fragment-based quantum chemistry methods that seek better approximations to the total system energy. (See Ref. [5] for a lengthy review, albeit one that still falls short of an exhaustive list of fragment-based methods.) Relationships between these methods are not always clear, and the primary aim of the current chapter is to develop a common theoretical framework to describe this plethora of methods in a concise, systematic way.

The systematic theoretical framework we develop in this chapter is in no way unique and any number of equivalent frameworks could be developed. None the less, we find that our framework is particularly well suited for providing adequate disambiguation of existing fragment methods and thus allowing meaningful comparisons across fragment-based methods. Before we can introduce this framework, we need to agree on a nomenclature. Given the plethora of fragment-based methods, it is perhaps unsurprising that there is no consensus in this regard. For that reason, in Section 2.2, we briefly list and define the majority of the fragment-based terms that we will use for the remainder of this document. In doing so, we have taken care to try
to use the more commonly encountered terms (Ref [5] describes existing fragment-based methods in their native terms, and serves as a useful starting point for anyone attempting to learn alternative nomenclatures).

After introducing our nomenclature, we introduce the reader to the many-body expansion in Sec. 2.3. Up until this point, the many-body expansion has served as the backbone of many of the more rigorously derived fragment-based approaches. As we will see in Sec. 2.4, there exists a more general, many-body expansion. Its derivation by our group represents our first contribution to the theory of fragment-based methods and will serve as the backbone of our theoretical framework. In Sec. 2.5, we conclude this introductory chapter by presenting a literature review of existing fragment-based methods, but using our newly developed framework.

### 2.2 Nomenclature

As mentioned in the last section, there exists many fragment-based methods and within each, most authors choose to develop their own unique terminology. If we are to attempt to describe a common framework, that transcends all fragment-based methods, we must first agree on basic terminology. The following list of terms are the ones we will use in this work, along with a brief definition of each. We note that some of the following terms are, confusingly, used in different contexts in other studies. In creating the following list we have attempted to use and define terms in the way they are most commonly encountered in the fragment literature.

**Supersystem**
This is the molecular system, whose physical properties we are interested in. It will be useful to think of the supersystem as a rigorous, mathematical, set of atoms. In this work the supersystem set will be labeled: $\mathcal{U}$, following conventional set-theory notation for the universe.

**Groups**

In all algorithmic approaches to fragment-based methods, the first step (aside from choosing a supersystem) is to divide the supersystem up into a set of subsystems. The smallest of these subsystems are usually termed groups. Groups typically represent sets of atoms that are thought to behave as a collective moiety, such as methyl (CH$_3$) and methylene (CH$_2$) units in a hydrocarbon, carbon-carbon double bonds in alkenes, or hydroxyl groups in alcohols. The concept of a group is very similar to the concept of a fragment and we further disambiguate the two after defining a fragment.

**Fragments**

Despite being the most universally used term in the existing literature, the term “fragment” does not appear to have a universal definition. It is common in the fragment literature to use the term in two different ways. The first definition, and the one we use, defines a fragment as the smallest set, actually appearing in the equations derived later. The other definition defines the term fragment, in the same way we use the word group. The important conceptual distinction between groups and fragments (using our definitions) is that groups are a construct used in algorithms to simplify the fragmentation problem and
fragments are the smallest subsets actually used to derive physical properties. We will label fragment \( I \) using the notation \( F^{(1)}_I \), where the meaning of the superscript will become clear shortly. We note that the term monomer is used interchangeably with the term fragment.

**Dimer**

Ultimately, the working equations of fragment-based methods will be presented in a linear expansion in the inter-fragment interactions. The most important of these interactions will be the pair-wise interactions. Mathematically, we can exactly calculate the inter-fragment interaction, \( \Delta E^{(1)}_{IJ} \), of two fragments, \( F^{(1)}_I \) and \( F^{(1)}_J \), by:

\[
\Delta E^{(1)}_{IJ} = E \left( F^{(1)}_{IJ} \right) - E \left( F^{(1)}_I \right) - E \left( F^{(1)}_J \right) \tag{2.1}
\]

where \( E(X) \) is the energy of system \( X \) and \( F^{(1)}_{IJ} \equiv F^{(1)}_I \cup F^{(1)}_J \). \( F^{(1)}_{IJ} \) is termed a dimer because it is created from two fragments.

**Trimer, Tetramer,..., n-mer**

Following from the definition of a dimer we can define a trimer, \( F^{(1)}_{IJK} \), as the union of three fragments:

\[
F^{(1)}_{IJK} \equiv F^{(1)}_I \cup F^{(1)}_J \cup F^{(1)}_K. \tag{2.2}
\]

Similarly we can define a tetramer as the union of four fragments and so on. In general, the union of \( n \) fragments is termed an \( n \)-mer and the \( I \)-th \( n \)-mer denoted as \( F^{(n)}_I \). At this point it helps to define the superscript. The superscript
is a “bookkeeping” index that tells us what the subscripts are indexing, e.g. a superscript of 1 means the subscripts are indexing monomers, a superscript of 2 means the subscripts are indexing dimers, etc. In the literature, the usual notation is to explicitly list all fragments contributing to a term (hence terms in the literature would always have superscripts of 1); however, this notation becomes cumbersome for general formulaic manipulations and we feel our notation alleviates a large portion of this cumbersomeness.

**Fragmentation Method**

In defining dimers, trimers, etc. we have defined them in terms of the algorithms for creating them (unions of fragments); however, we have not defined how to actually create a fragment from the supersystem. In practice, one can envision many ways of doing just that. The majority of these algorithms use either a bond-based or distance-based threshold for determining which groups form a fragment. Regardless of how the algorithm actually works, the algorithm for assigning groups to fragments is termed a fragmentation method.

**Cap**

When fragmenting large molecules, it is common that a fragment will “sever” a covalent bond. For example, consider two groups that are bonded to one another. If our fragmentation algorithm assigns one of the two groups to $F_i^{(1)}$ and the other to $F_j^{(1)}$, the covalent bond between the two groups will be severed. Furthermore, calculations on either fragment, as is, would lead to the fragments having a non-physical radical and/or ionic nature. In order to avoid this...
problem, one typically adds an atom or a group of atoms to the fragment at the position of the missing group. This additional atom or group of atoms is termed a cap, and in most fragment-based methods is typically a hydrogen atom, so as to perturb the system as little as possible. The idea of capping severed valencies with hydrogen atoms has seen utility in other areas of electronic structure theory, particularly in the context of QM/MM (mixed quantum-mechanical and molecular mechanics) calculations\textsuperscript{12}.*

Capping Method

In the last section we defined a cap, and suggested one possible way of assigning and creating caps. In practice a whole host of methods exist for this task and we term these algorithms capping methods. Each capping method determines the spatial location and atomistic identity of the cap.

Embedding method

It will be seen shortly, that the number of calculations grows exponentially with system size. One way of avoiding this is to truncate the inter-fragment interaction expansion as soon as possible. It was quickly realized\textsuperscript{5,16–21} that polarization comprises the vast majority of these missing interactions. For $F^{(1)}_I$, 

\textsuperscript{*}Within the QM/MM community the majority of problems associated with the introduction of caps have been resolved. For example, each cap introduces three additional degrees of freedom (DoF) to the total system; however, these DoFs can be directly mapped to DoFs of the atoms being replaced.\textsuperscript{13} Another common criticism, particularly when using hydrogen atoms as caps, is that the electronic environment of a hydrogen atom is a poor approximation to that of the atom it is replacing. The usual solution is to modify the properties of the cap (usually the nuclear charge) to better represent the atom being replaced.\textsuperscript{14} If necessary, these solutions could be directly applied to fragment methods (and some already have); however, it has been shown,\textsuperscript{15} that, in the context of fragment methods, caps represent a smaller perturbation then they do for QM/MM calculations, due to the nature of the working fragment equations, \textit{vide infra}. 

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one way to cheaply include the polarization effects of all other fragments is to determine atomic-point charges for the other fragments in $\mathcal{U}$ and add them to the calculation of $F_i^{(1)}$. Again, many different ways of accomplishing this are possible and we term the algorithm that does this the embedding method.

2.3 Many-body expansion

The terms defined in Sec 2.2 provide us with the foundation to discuss how the majority of fragment methods in the literature go about computing the supersystem property of interest from a set of fragments. For our purpose we limit the property of interest to the energy of the supersystem, but note that a large number of other useful properties can be formulated in terms of the energy and its derivatives.\textsuperscript{22} As we will see all equations arising in fragment methods are linear, which makes the evaluation of their derivatives straightforward\textsuperscript{‡}.

The vast majority of methods in existence appeal to an interaction energy expansion known as the many-body expansion (MBE), where the name comes from the fact that it decomposes the total energy, $E^{(0)}$, into its “many-body” components. The purpose of this section is to introduce the MBE, and discuss its fundamental properties.

\textsuperscript{†}Although the embedding point charges are present in each fragment electronic structure calculation, and therefore polarize the fragment wave functions, the self-energy (mutual Coulomb interaction) of these embedding charges should \textit{not} be included in the fragment energy, as this amounts to overcounting of electron–electron interactions.

\textsuperscript{‡}See Footnote ‡‡ for comments on the effect of self-consistent charges with respect to this claim.
The MBE is defined as:

\[ E^{(0)} \equiv \sum_{I=1}^{N_F} E^{(1)}_I + \sum_{I<J} \Delta E^{(1)}_{IJ} + \sum_{I<J<K} \Delta E^{(1)}_{IJK} + \cdots \]  

(2.3)

where \( \Delta E^{(1)}_{IJ} \) is defined as:

\[ \Delta E^{(1)}_{IJ} \equiv E^{(1)}_{IJ} - E^{(1)}_I - E^{(1)}_J \]  

(2.4)

and \( \Delta E^{(1)}_{IJK} \) is defined as:

\[ \Delta E^{(1)}_{IJK} \equiv E^{(1)}_{IJK} - \Delta E^{(1)}_{IJ} - \Delta E^{(1)}_{IK} - \Delta E^{(1)}_{JK} - E^{(1)}_I - E^{(1)}_J - E^{(1)}_K \]  

(2.5)

In the above equations, \( I, J, \) and \( K \) index fragments. We have simplified the energy notation introduced in Sec. 2.2 by absorbing the indexes of the fragment onto the energy, \( i.e. \) \( E^{(1)}_I \) is the energy of fragment \( I \), \( E^{(1)}_{IJ} \) is the energy of the dimer formed from the union of fragments \( I \) and \( J \), and \( E^{(1)}_{IJK} \) is the energy of the trimer formed from union of fragments \( I, J, \) and \( K \).

The terms in Eq. (2.3) have simple interpretations. The first summation is the sum of the fragment energies; its total is the energy of a system of non-interacting fragments. Truncation of Eq. 2.3 at this point is known as the one-body approximation, because it only accounts for one-body interactions. Eq. (2.4) suggests that \( \Delta E^{(1)}_{IJ} \) can be thought of as the two-body interaction between fragments \( I \) and \( J \); therefore, the sum of all such \( \Delta E^{(1)}_{IJ} \) terms is the total two-body interaction energy for the supersystem and subsequent truncation of Eq. (2.3) at this term is known as the two-body approximation because it accounts for a set of fragments interacting pairwise. Similar analysis of Eq. (2.5) shows that \( \Delta E^{(1)}_{IJK} \) is the three-body interaction.
of fragments $I$, $J$, and $K$ and truncation of Eq. (2.5) at this point is known as the three-body approximation.

This interpretation of the various $\Delta E_{IJK\ldots n}^{(1)}$ terms as $n$-body interactions provides us with a straightforward way to write down a recursive form for an arbitrary $\Delta E$ that arises from $n$ fragments: $I, J, K, \ldots, n$. The form of the $n$-body interaction amongst the set of $n$ fragments is then given by:

$$
\Delta E_{IJK\ldots n}^{(1)} \equiv E_{IJK\ldots n}^{(1)} - \sum_{\{IJK\ldots(n-1)\} \in \{IJK\ldots n\}} \Delta E_{IJK\ldots(n-1)}^{(1)} - \ldots - \sum_{I \in \{IJK\ldots n\}} \Delta E_{I}^{(1)}
$$

(2.6a)

$$
\equiv E_{I}^{(n)} - \sum_{F_{I}^{(n-1)} \in F_{I}^{(n)}} \Delta E_{I}^{(n-1)} - \ldots - \sum_{F_{I}^{(1)} \in F_{I}^{(n)}} \Delta E_{I}^{(1)}
$$

(2.6b)

The notation $\sum_{\{IJK\ldots(n-1)\} \in \{IJK\ldots n\}}$ means summations over all unique sets of $(n-1)$ monomers that can be formed from the set of $n$ monomers. Eq. (2.6b) demonstrates how our superscript indexing notation can be used to simplify the appearance of equations greatly. Such an equation is useful in formal manipulations and allows for a straightforward proof of the exact equality of Eq. (2.3):

$$
E^{(0)} = \sum_{I=1}^{N_{F}} E_{I}^{(1)} + \sum_{I<J} \Delta E_{IJ}^{(1)} + \sum_{I<J<K} \Delta E_{IJK}^{(1)} + \ldots + \Delta E_{IJK\ldots N_{F}}^{(1)}
$$

(2.7)

$$
= \sum_{I=1}^{N_{F}} E_{I}^{(1)} + \sum_{I<J} \Delta E_{IJ}^{(1)} + \sum_{I<J<K} \Delta E_{IJK}^{(1)} + \ldots + E_{I}^{(N_{F})} - \sum_{F_{I}^{(N_{F}-1)} \in F_{I}^{(N_{F})}} \Delta E_{I}^{(N_{F}-1)} - \ldots - \sum_{F_{I}^{(1)} \in F_{I}^{(N_{F})}} \Delta E_{I}^{(1)}
$$

(2.8)

$$
= E_{I}^{(N_{F})} = E^{(0)}
$$

(2.9)
In its current form Eq. (2.3) is of little use because it will contain $N_F$ summations [one over all $N_F$ (i.e. $N_F C_1$) fragments, one over all $N_F C_2$ dimers, one over all $N_F C_3$ trimers and so on up until a summation over all $N_F C_{N_F}$, $N_F$-mers] and will require $2^{N_F} - 1$ energy calculations including one that is the entire supersystem (see Eq. (2.8)). In practice, it is not the exactness of the MBE equation that is useful, but rather the fact that we can truncate it at some order $n$, typically around $n = 2$ or $n = 3$. If truncating at a low order does not negatively impact the accuracy of our approximate energy, then the utility of the MBE becomes apparent. Furthermore, because each energy calculation in Eq. (2.3) is an independent energy calculation, the MBE is “embarrassingly parallelizable.” In later chapters we will see that these properties lead to the MBE representing a significant increase in computational efficiency over the traditional supersystem calculation.

There are at least two ways to make the MBE truncate faster: use of intersecting fragments (see next section) or via embedding methods, which we briefly introduced in Sec. 2.2. Of these two strategies, embedding methods have seen far more use.\textsuperscript{5,16–21} We return to embedding methods in Sec. 2.5.3 and focus on intersecting fragments in the next section.

2.4 Generalized MBE

In the last section we introduced the MBE and mentioned that intersecting fragments will cause it to converge faster. To understand this consider a simple fragment

\textsuperscript{5}The notation $N C_m$ is the number of ways of arranging $N$ objects into $m$ groups, i.e. $N$ choose $m$. This is also commonly denoted as $\binom{N}{m}$; however, here we prefer the former notation because it is more compact.
calculation of normal butane. Letting the carbons be numbered from end to end sequentially, we consider two ways of fragmenting the molecule:

\[
\text{Disjoint Scheme} = \begin{cases} 
F_1^{(1)} &= \{1, 2\} \\
F_2^{(1)} &= \{3, 4\}
\end{cases} \tag{2.10a}
\]

\[
\text{Intersecting Scheme} = \begin{cases} 
F_A^{(1)} &= \{1, 2\} \\
F_B^{(1)} &= \{2, 3\} \\
F_C^{(1)} &= \{3, 4\}
\end{cases} \tag{2.10b}
\]

where the numbers in brackets refer to the numbers of the carbons included in the fragment (hydrogens attached to the carbons are included as well). Eq. (2.10a) breaks butane into two fragments that do not intersect, whereas pair-wise, some of the fragments in the second scheme share a common atom.

At this point, if we were to approximate the energy of butane at the one-body level, it is clear that Eq. (2.10a) would be lacking the interactions between carbons 2 and 3. It would be necessary to proceed to the dimer level before this interaction would actually appear in the MBE. On the other hand, Eq. (2.10b), does include the carbon 2, carbon 3 interaction at the monomer level. What this means is that in general by considering intersecting instead of disjoint fragments more of the interaction space is accounted for at a given truncation level and the overall description of the interactions is more complete.

The MBE, presented in Sec. 2.3, only works for the case where all fragments are disjoint. If our fragments were described analogous to those in Eq. (2.10b), simply inserting the energies of the three fragments into a one-body expansion Eq. (2.3) results in double-counting the one-body interactions of carbons 2 and 3. Heuristically, we could correct for this by simply subtracting out the one-body energies of carbons.
2 and 3. In theory, such an approach should always work, but as the fragmentation patterns become more complicated it is not always immediately apparent how many times a given interaction is over-counted. The remainder of this section is devoted to deriving an expression that is analogous to the MBE, but true regardless of whether or not the fragments are disjoint.

Our starting point is the mandate that such a generalized MBE (GMBE) should have a similar form to the MBE:

\[
E^{(0)} \equiv \mathcal{E}^{(1)} + \Delta E^{(2)} + \Delta E^{(3)} + \ldots + \Delta E^{(N_F)}
\]  

(2.11a)

\[
\Delta E^{(2)} \equiv \mathcal{E}^{(2)} - \mathcal{E}^{(1)}
\]  

(2.11b)

\[
\Delta E^{(3)} \equiv \mathcal{E}^{(3)} - \mathcal{E}^{(2)}
\]  

(2.11c)

\ldots

\[
\Delta E^{(\alpha)} \equiv \mathcal{E}^{(\alpha)} - \mathcal{E}^{(\alpha-1)}
\]  

(2.11d)

\ldots

\[
\Delta E^{(N_F)} \equiv \mathcal{E}^{(N_F)} - \mathcal{E}^{(N_F-1)}.
\]  

(2.11e)

In the above equations we define a series of new quantities: the \(\alpha\)-mer “intersection-corrected” energies, \(\mathcal{E}^{(\alpha)}\), which are interpreted as the total energy of all of the \(\alpha\)-mers, corrected so as to not double count any energetic contribution. Realizing that \(\mathcal{E}^{(N_F)} = E^{(0)}\) proves the exactness of Eq. (2.11a) and identifies the entire expansion as a creative way of adding zero. However, we still do not have a form for any of the \(\mathcal{E}^{(\alpha)}\) terms except \(\alpha = N_F\).

To proceed in deriving a general form for \(\mathcal{E}^{(\alpha)}\), it is important to realize that
the general framework for correcting $\mathcal{E}^{(\alpha)}$ for the intersections does not depend on the value of $\alpha$, but rather on the number of $\alpha$-mers. That is to say a brute-force approach would compare every pair of $\alpha$-mers and subtract out any interactions in the intersection. By doing this, however, it is easily seen that any interaction appearing in the intersection of more than one pair of $\alpha$-mers, are subtracted out too many times. Adding these interactions back in, subsequently leads to any interaction appearing in the intersection of three or more pairs of $\alpha$-mers being added back in too many times. This of course would continue until we have considered interactions that appear in the intersection of all $N_F$ $\alpha$-mers.

An example helps to illustrate this further. Let us assume we made $N_F$ fragments, we then take all possible unions of $\alpha$ fragments to form the set of $\alpha$-mers. For simplicity, we assume that doing so results in two unique such $\alpha$-mers. Furthermore, let the atoms in $\alpha$-mer $I$ be denoted by the set $F_I^{(\alpha)}$ and those in $\alpha$-mer $J$ be denoted as $F_J^{(\alpha)}$. It is clear by inspection that:

$$E^{(\alpha)} \approx E_I^{(\alpha)} + E_J^{(\alpha)} - E_{I \cap J}^{(\alpha)}$$

(2.12)

where $E_I^{(\alpha)}$ is the energy of the atoms in set $F_I^{(\alpha)}$ and $F_{I \cap J}^{(\alpha)}$ denotes the intersection of sets $F_I^{(\alpha)}$ and $F_J^{(\alpha)}$. $\alpha$ is arbitrary in this example and can take on any allowed value and the approximate (this term is necessarily approximate because it involves two $\alpha$-mers, we clarify this point shortly) equality would still hold. This shows us that the form of the correction only depends on the number of $\alpha$-mers, not the value of $\alpha$.

\footnote{We show that only the unique $n$-mers contribute to the final expression later, so it may be that we created more than two $\alpha$-mers, but the other $\alpha$-mers are proper subsets of the two $\alpha$-mers}
It is now our intent to derive a general $\mathcal{E}^{(\alpha)}$ energy expression for an arbitrary number of $\alpha$-mers. It turns out that progress in this direction is greatly facilitated by working directly with the Hamiltonian. For compactness, let $m = N_{\alpha}C_\alpha$ denote the number of $\alpha$-mers. In general it will be possible to obtain any integer value of $m$, except for $m = 2$ (see next paragraph) and we need to derive a form for each $m$; however, we will show, via induction, that the Hamiltonian has the same form regardless of $m$.

Before proceeding with the derivation, we mention a few technical points that need addressing. The Hamiltonian is a two-particle operator; therefore, if we are to be able to expand the Hamiltonian exactly in terms of $\alpha$-mers every pair of particles must appear in at least one $\alpha$-mer. If for example particles $i$ and $j$ never appear together in a fragment, the final Hamiltonian will be missing the interactions of particles $i$ and $j$. Although this requirement sounds restrictive, it can be trivially satisfied by mandating $\alpha \geq 2$, therefore this derivation applies to most existing methods. For applications that do not include each pair in at least one $\alpha$-mer, the following equalities are only approximately true, with the strength of the approximation depending on which pairs are missing. Finally we note that there is actually no physical way to have $\alpha \geq 2$ and have $m = 2$, so that step in the forthcoming derivation is not physically meaningful, despite being mathematically defined and well behaved. We include it for completeness and because it can occur for approximate equalities.

If $m = 1$, then the entire supersystem ($\mathcal{U}$) is contained in a single $\alpha$-mer, so

$$\hat{H}(\mathcal{U}) = \hat{H}(F_{1}^{(\alpha)})$$  \hspace{1cm} (2.13)
where $\hat{H}(S)$ denotes the Hamiltonian for the set $S$ of particles.

For the $m = 2$ case the universe is divided into two sets, $F_1^{(a)}$ and $F_2^{(a)}$:

$$U = F_1^{(a)} \cup F_2^{(a)}.$$  \hspace{1cm} (2.14)

However, the system can also be partitioned according to

$$U = \left( F_1^{(a)} \setminus F_2^{(a)} \right) \cup \left( F_2^{(a)} \setminus F_1^{(a)} \right) \cup \left( F_1^{(a)} \cap F_2^{(a)} \right).$$  \hspace{1cm} (2.15)

These three sets are, respectively, the part of $F_1^{(a)}$ that is not in $F_2^{(a)}$, the part of $F_2^{(a)}$ that is not in $F_1^{(a)}$, and the part that they share in common. Note that these three sets are disjoint, and since $\hat{H}$ is additively separable, we can therefore write $\hat{H}(U)$ as a sum of three Hamiltonians, partitioned according to Eq. (2.15). We then obtain

$$\hat{H}(U) = \hat{H}(F_1^{(a)} \setminus F_2^{(a)}) + \hat{H}(F_2^{(a)} \setminus F_1^{(a)}) + \hat{H}(F_1^{(a)} \cap F_2^{(a)})$$

$$+ \hat{H}(F_1^{(a)} \cap F_2^{(a)}) - \hat{H}(F_1^{(a)} \cap F_2^{(a)})$$

$$= \hat{H}\left[(F_1^{(a)} \setminus F_2^{(a)}) \cup (F_1^{(a)} \cap F_2^{(a)})\right]$$

$$+ \hat{H}\left[(F_2^{(a)} \setminus F_1^{(a)}) \cup (F_1^{(a)} \cap F_2^{(a)})\right] - \hat{H}(F_1^{(a)} \cap F_2^{(a)})$$

$$= \hat{H}(F_1^{(a)}) + \hat{H}(F_2^{(a)}) - \hat{H}(F_1^{(a)} \cap F_2^{(a)}).$$  \hspace{1cm} (2.16)

From here we proceed by induction. Let us assume that the following is true for all $m \leq x$:

$$\hat{H}(U) = \sum_{I=1}^{x} \hat{H}(F_I^{(a)}) - \sum_{I<J=1}^{x} \hat{H}(F_I^{(a)} \cap F_J^{(a)}) + \cdots + (-1)^{x-1} \hat{H}\left( \bigcap_{I=1}^{x} F_I^{(a)} \right).$$  \hspace{1cm} (2.17)

We have already verified this explicitly for the $m = 1$ and $m = 2$ cases. To show that Eq. (2.17) actually provides a general expression for $\hat{H}(U)$, it suffices to show that
this expression is valid for the case of \( m = x + 1 \) \( \alpha \)-mers. In other words, we need to show that

\[
\hat{H} \left( \bigcup_{I=1}^{x+1} F_I^{(\alpha)} \right) = \sum_{I=1}^{x+1} \hat{H}(F_I^{(\alpha)}) - \sum_{I<J=1}^{x+1} \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)}) \\
+ \cdots + (-1)^x \hat{H} \left( \bigcap_{I=1}^{x+1} F_I^{(\alpha)} \right).
\]

\[(2.18)\]

We will show that the left side of the Eq. (2.18) can be rearranged to yield the right side. First, note that

\[
\hat{H} \left( \bigcup_{I=1}^{x+1} F_I^{(\alpha)} \right) = \hat{H} \left( \bigcup_{I=1}^{x} F_I^{(\alpha)} \cup F_{x+1}^{(\alpha)} \right) \\
= \hat{H} \left( \bigcup_{I=1}^{x} F_I^{(\alpha)} \right) + \hat{H}(F_{x+1}^{(\alpha)}) - \hat{H} \left( \bigcup_{I=1}^{x} F_I^{(\alpha)} \cap F_{x+1}^{(\alpha)} \right),
\]

\[(2.19)\]

which is similar to the manipulations that we performed in the \( m = 2 \) case. The final term in this equation can be rewritten as

\[
\hat{H} \left( \bigcup_{I=1}^{x} F_I^{(\alpha)} \cap F_{x+1}^{(\alpha)} \right) = \sum_{I=1}^{x} \hat{H}(F_I^{(\alpha)} \cap F_{x+1}^{(\alpha)}) - \sum_{I<J=1}^{x} \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)} \cap F_{x+1}^{(\alpha)}) \\
+ \cdots + (-1)^{x-1} \hat{H} \left( \bigcap_{I=1}^{x} F_I^{(\alpha)} \cap F_{x+1}^{(\alpha)} \right),
\]

\[(2.20)\]

using the inductive hypothesis, Eq. (2.17). Substituting this into Eq. (2.19) gives:

\[
\hat{H}(U) = \hat{H}(F_{x+1}^{(\alpha)}) + \sum_{I=1}^{x} \hat{H}(F_I^{(\alpha)}) - \sum_{I<J=1}^{x} \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)}) \\
+ \cdots + (-1)^{x-1} \hat{H} \left( \bigcap_{I=1}^{x} F_I^{(\alpha)} \right) - \sum_{I=1}^{x} \hat{H}(F_I^{(\alpha)} \cap F_{x+1}^{(\alpha)}) \\
+ \sum_{I<J=1}^{x} \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)} \cap F_{x+1}^{(\alpha)}) - \cdots + (-1)^x \hat{H} \left( \bigcap_{I=1}^{x} F_I^{(\alpha)} \cap F_{x+1}^{(\alpha)} \right).
\]

\[(2.21)\]
In deriving this expression, we have once again used the inductive hypothesis for \( x \), this time to expand the first term on the right in Eq. (2.19). Combining terms,

\[
\hat{H}(\mathcal{U}) = \sum_{I=1}^{x+1} \hat{H}(F^{(\alpha)}_I) - \sum_{I<J=1}^{x+1} \hat{H}(F^{(\alpha)}_I \cap F^{(\alpha)}_J) + \cdots + (-1)^{x-1} \hat{H}\left( \bigcap_{I=1}^{x} F^{(\alpha)}_I \right) \\
+ \sum_{I<J=1}^{x} \hat{H}(F^{(\alpha)}_I \cap F^{(\alpha)}_J \cap F^{(\alpha)}_{x+1}) - \cdots + (-1)^x \hat{H}\left( \bigcap_{I=1}^{x+1} F^{(\alpha)}_I \right). \tag{2.22}
\]

At this point we need to generalize this procedure for combining terms and collapsing intersections, in order to deal with the terms represented by ellipses in Eq. (2.22). Let us denote by \( T_{1,y} \) a term represented by the first ellipses with an index \( y < x \):

\[
T_{1,y} = (-1)^{y-1} \sum_{I<\cdots<y=1}^{x} \hat{H}\left( \bigcap_{I=1}^{y} F^{(\alpha)}_I \right). \tag{2.23}
\]

Within the second set of ellipses there will be a term (call it \( T_{2,z} \)), indexed by \( z = y-1 \), of the form

\[
T_{2,z} = (-1)^z \sum_{I<\cdots<z=1}^{x} \hat{H}\left( \bigcap_{I=1}^{z} F^{(\alpha)}_I \cap F^{(\alpha)}_{x+1} \right). \tag{2.24}
\]

The sum of these two terms is

\[
T_{1,y} + T_{2,z} = (-1)^{y-1} \left[ \sum_{I<\cdots<y=1}^{x} \hat{H}\left( \bigcap_{I=1}^{y} F^{(\alpha)}_I \right) + \sum_{I<\cdots<y-1=1}^{x} \hat{H}\left( \bigcap_{I=1}^{y-1} F^{(\alpha)}_I \cap F^{(\alpha)}_{x+1} \right) \right]. \tag{2.25}
\]

The first term on the right generates all Hamiltonians involving \( y \) fragments, in which none of the \( y \) fragments are \( F^{(\alpha)}_{x+1} \). The second term will produce all Hamiltonians involving the intersection of \( y \) fragments and \( F^{(\alpha)}_{x+1} \) is included. Together, these two terms are the sum over all Hamiltonians resulting from the intersection of \( y \) fragments, if there are \( x+1 \) fragments to choose from. Thus the two terms can be combined to
afford

\[ T_{1,y} + T_{2,z} = (-1)^{y-1} \sum_{I_1 \ldots < I_y = 1}^{x+1 \choose y} \hat{H}\left( \bigcap_{I=1}^{y} F^{(\alpha)}_I \right). \tag{2.26} \]

This result demonstrates that the \( y \)th term in the first set of ellipses [Eq. (2.22)] will combine with the \( z \)th term in the second set of ellipses, to afford a term of the form appearing in Eq. (2.26). In deriving Eq. (2.22), we have already combined the \( y = 1 \) term with the \( z = 0 \) term and the \( y = 2 \) term with the \( z = 1 \) term, as these appeared explicitly in Eq. (2.21). The remaining terms can be combined, as outlined above, to afford

\[ \hat{H}(\mathcal{U}) = \sum_{I=1}^{x+1} \hat{H}(F^{(\alpha)}_I) - \sum_{I<J=1}^{x+1 \choose 2} \hat{H}(F^{(\alpha)}_I \cap F^{(\alpha)}_J) + \cdots + (-1)^x \hat{H}\left( \bigcap_{I=1}^{x+1} F^{(\alpha)}_I \right). \tag{2.27} \]

This is the desired result for the case \( m = x + 1 \) case. By induction, the form of \( \hat{U} \) given in Eqs. (2.17) and (2.27) must be valid for all \( m \), that is, for an arbitrary number of \( \alpha \)-mers of fragments.

Ultimately what we have shown is that we can always exactly rewrite the super-system Hamiltonian in terms of the Hamiltonians of the \( \alpha \)-mers plus or minus their mutual intersections (so long as \( \alpha \geq 2 \)). The form of Eq. (2.27) is reminiscent of the inclusion/exclusion principle of set theory, which is an equation for calculating the cardinality (number of elements in a set) of a superset in terms of the cardinalities of that set’s subsets. Mathematically, the similarity between the inclusion/exclusion principle and Eq. (2.27) is not a coincidence, but arises from the fact that care has been taken in both cases to ensure that no element [interactions for Eq. (2.27), cardinalities for the inclusion/exclusion principle] has been double counted. Alternatively, in an interpretation analogous to Eq. (2.16), we may interpret Eq. (2.27) as the
mathematical consequence of mandating our Hamiltonian be expressed in terms of
the Hamiltonians of our non-disjoint fragments. For example, for a system of three
molecules, \( A, B, \) and \( C, \) whose Hamiltonian, \( \hat{H}_{ABC}, \) is given by:

\[
\hat{H}_{ABC} = \hat{H}_A + \hat{H}_B + \hat{H}_C + \hat{H}_{A-B} + \hat{H}_{A-C} + \hat{H}_{B-C}, \tag{2.28}
\]

with \( \hat{H}_{X-Y} \) defined as the interactions between molecules \( X \) and \( Y, \) the requirement
that this Hamiltonian be written in terms of the dimer Hamiltonians:

\[
\hat{H}_{AB} = \hat{H}_A + \hat{H}_B + \hat{H}_{A-B} \tag{2.29a}
\]
\[
\hat{H}_{AC} = \hat{H}_A + \hat{H}_C + \hat{H}_{A-C} \tag{2.29b}
\]
\[
\hat{H}_{BC} = \hat{H}_B + \hat{H}_C + \hat{H}_{B-C}, \tag{2.29c}
\]

means that we need to add zero in the forms:

\[
0 = \hat{H}_A - \hat{H}_A \tag{2.30a}
\]
\[
0 = \hat{H}_B - \hat{H}_B \tag{2.30b}
\]
\[
0 = \hat{H}_C - \hat{H}_C \tag{2.30c}
\]

to \( \hat{H}_{ABC} \) obtaining:

\[
\hat{H}_{ABC} = \left( \hat{H}_A + \hat{H}_B + \hat{H}_{A-B} \right) + \left( \hat{H}_A + \hat{H}_C + \hat{H}_{A-C} \right) + \left( \hat{H}_B + \hat{H}_C + \hat{H}_{B-C} \right) - \hat{H}_A - \hat{H}_B - \hat{H}_C \tag{2.31}
\]
\[
= \hat{H}_{AB} + \hat{H}_{AC} + \hat{H}_{BC} - \hat{H}_A - \hat{H}_B - \hat{H}_C. \tag{2.32}
\]

These values of zero are immediately recognizable as the parts of each dimer Hamiltonian that occur in more than one dimer, \( i.e. \) the intersections. From this point of
view, we have simply added zero, albeit very creatively, to our original Hamiltonian. Regardless of how Eq. (2.27) is interpreted we still need to obtain an energy from it.

As is usual in quantum mechanics, we calculate the energy of a Hamiltonian by taking its ground-state expectation value, \( \mathcal{E}^{(\alpha)} = \langle \Psi_0 | \hat{H}(U) | \Psi_0 \rangle \):

\[
\mathcal{E}^{(\alpha)} = \sum_{I=1}^{m} \langle \Psi_0 | \hat{H}(F_I^{(\alpha)}) | \Psi_0 \rangle - \sum_{I<J=1}^{m} \langle \Psi_0 | \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)}) | \Psi_0 \rangle + \cdots + (-1)^{m+1} \langle \Psi_0 | \hat{H}\left( \bigcap_{I=1}^{m} F_I^{(\alpha)} \right) | \Psi_0 \rangle .
\]

This can be rewritten as

\[
\mathcal{E}^{(\alpha)} = \sum_{I=1}^{m} E_I^{(\alpha)} - \sum_{I<J=1}^{m} E_{I \cap J}^{(\alpha)} + \cdots + (-1)^{m+1} E_{I_1 \cap J_1 \cap \cdots \cap m}^{(\alpha)} ,
\]

where the energies are to be interpreted as the expectation values of the individual fragment Hamiltonians, with respect to the ground-state supersystem wave function. In practical calculations of interest, \( |\Psi_0 \rangle \) is not available (and its determination would require us to solve the supersystem problem) so we approximate each expectation value in Eq. (2.34) with a fragment electronic structure calculation. For a given term in Eq. (2.34), say the intersection of \( \alpha \)-mers I and J, we can view this approximation as:

\[
\langle \Psi | \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)}) | \Psi \rangle \approx \langle \Psi_{I \cap J}^{(\alpha)} | \hat{H}(F_I^{(\alpha)} \cap F_J^{(\alpha)}) | \Psi_{I \cap J}^{(\alpha)} \rangle .
\]

Here, \( |\Psi_{I \cap J}^{(\alpha)} \rangle \) is the ground-state wave function for the subsystem that is constructed from the intersection of \( \alpha \)-mers \( F_I^{(\alpha)} \) and \( F_J^{(\alpha)} \). This approximation is essentially an appeal to Kohn’s principle of the “locality of electronic matter”\(^6,7\) Note also that the
same motivation works if point charges are included as part of each “subset” Hamiltonian, $\hat{H}(S)$, as part of a charge-embedding scheme designed to better approximate the electronic structure of each local region of the system.

As with the MBE, the GMBE is not particularly useful as written in Eq. (2.11a) because of the number of terms involved. Analogous to the MBE we speculate that the $\Delta E^{(\alpha)}$ terms become less and less important as $\alpha$ increases. As was the case for the MBE, we assume we can truncate the GMBE at order $n$ and in doing so, we arrive at an $n$-body approximation to the ground-state energy. Applying such a truncation, it is straightforward to show that Eq. (2.11a) reduces to:

$$E_{n} = \sum_{I=1}^{m} E^{(n)}_{I} - \sum_{I<J=1}^{mC_2} E^{(n)}_{I\cap J} + \ldots + (-1)^{m+1} E^{(n)}_{I\cap J\cap \ldots \cap m} .$$ (2.36)

Here, we are interested in GMBE calculations at the $n = 2$ truncation order exclusively, and we next show that in that case, the two-body GMBE is equivalent to the traditional two-body expansion, if the monomers do not intersect. For the $n = 2$ case of Eq. (2.36), assuming disjoint monomers, we obtain the following:

$$E_{0} \approx \sum_{I=1}^{m} E^{(2)}_{I} - \sum_{I<J=1}^{mC_2} E^{(2)}_{I\cap J} + \ldots + \sum_{I<J<\ldots<N_{F}-1=1}^{mC_{N_{F}-1}} (-1)^{N_{F}} E^{(2)}_{I\cap J\cap \ldots \cap (N_{F}-1)} .$$ (2.37)

We have simplified this expression somewhat by noting that at most $N_{F} - 1$ dimers may intersect. If the monomers are disjoint, then we can evaluate the intersections in terms of the monomers by realizing that the same monomer must appear in all dimers or else the intersection is an empty set. Taking all unions of monomers that do not result in empty sets, and making use of the identity

$$\sum_{\alpha=0}^{n} (-1)^{\alpha} \, aC_{\alpha} = 0 ,$$ (2.38)
Eq. (2.37) reduces to Eq. (2.3), the traditional two-body energy formula expressed in closed form.

Finally we show that when using the GMBE it is not necessary to include any \(n\)-mer that is a subset of another \(n\)-mer. More generally, if \(A \subseteq B\), then one can show that

\[
E_0 = \sum_{I=1}^{m-1} E_I^{(n)} - \sum_{I \neq A}^{m-1} C_2 E_{I \cap J}^{(n)} + \cdots + (-1)^{\gamma+1} \sum_{I \neq A, B}^{m-1} C_\gamma E_{I \cap J \cap \cdots \cap \gamma}^{(n)} + \cdots \tag{2.39}
\]

This equation says that one obtains the same energy if \(A\) is not considered at all.

### 2.5 Elemental classification of fragment methods

Having introduced the GMBE, along with establishing our nomenclature, we are now in a position to approach our second goal for the chapter, namely reviewing the existing literature within the framework we have just established. It is our opinion that such a review is facilitated by decomposing existing fragment methods into four main components: a fragmentation method, a capping method, an embedding method, and the GMBE truncation order. In doing so we note that, unless otherwise stated, the working equations of all of these methods can be derived from the GMBE.
2.5.1 Fragmentation methods

As suggested in Sec. 2.2, fragmentation methods rely primarily on either a bond-based or a distance based criteria for assigning the groups to fragments. At least four variants of these two fragmentation methods are commonly used in the literature.

The systematic molecular fragmentation (SMF) method of Collins and co-workers\textsuperscript{23–26} is an example of a bond-based fragmentation method that uses the bonding network to dictate where fragment boundaries are drawn. As described in the various SMF references, the method commonly called SMF is actually a hierarchy of methods ("levels one, two, three, etc." in the language of that paper). At level $X$, each atom and all atoms within $X$ covalent bonds are placed into the same fragment. Fragments that are subsets of other fragments are discarded. The resulting fragments in general will intersect because the fragmentation algorithm loops over all atoms in $U$. The fact that the fragments intersect in SMF is actually what led to the need to define a hierarchy of levels. SMF uses a heuristically derived variant of the GMBE that is only capable of treating monomers. Collins et al. consequently found it necessary to define a hierarchy of fragmentation methods so that they could increase the overall accuracy of SMF. This was a direct consequence of SMF being unable to treat dimers, or higher $n$-mers. Consequentially, SMF is the first example of a method that does not rigorously conform to the GMBE. For the purpose of notation, we denote fragmentation according to the SMF algorithm as SMF1, SMF2, and SMF3.

The generalized energy based fragmentation (GEBF) approach of Li and co-workers\textsuperscript{27–29} is an example of a distance based fragmentation method. The GEBF
fragmentation method starts with a group, $G_1$, and creates a fragment that includes $G_1$ and all other groups that lie within some specified distance, $\xi$, of the atoms in $G_1$ (The recommended $\xi$ from Ref. [27] is $\xi = 3.0$ Å.). As was the case with SMF, the fragments created with GEBF will in general intersect and the energy expression derived in the GEBF study was only amenable to monomers. Consequentially, increasing the accuracy of GEBF calculations was done by increasing $\xi$ quite analogous to how SMF increased the level. Although not apparent immediately, the GEBF energy expression is exactly equal to a one-body GMBE expansion.

Gadre et al.$^{30}$ introduced the *cardinality-guided molecular tailoring approach* (CG-MTA) in 2006. This method uses a distance-based fragmentation method that is similar to GEBF, except that CG-MTA utilizes two parameters to create the “best” fragments. The final energy expression was again derived heuristically by comparing to the inclusion-exclusion principle of probability by suggesting there exists a relationship between cardinality and energy; however no attempt to discern this relationship was made. Again, CG-MTA was not capable of treating dimers, trimers, etc.

For the sake of completeness we also define a trivial fragmentation method, which we call “user-defined” (UD). The UD method is by far the most used fragmentation method and simply means the user specifies each fragment manually (or that the authors did not explicitly indicate how they choose their fragments). The UD method has the distinct drawback that it can not be automated, as it requires user input and thus is not a feasible option for the fragmentation of large systems. However, it is useful for small systems such as the ones typically considered when benchmarking.
2.5.2 Capping methods

After deciding how the fragments are formed, each method must decide how any severed covalent bonds are dealt with. Usually this is done by a simple capping method; however, the widely popular fragment molecular orbital (FMO) approach\textsuperscript{31–33} is perhaps the striking exception to this. We term this capping scheme: “FMO capping”.\textsuperscript{31} In the FMO capping approach, one computes localized molecular orbitals (MOs) on related molecules (for example the severing of a carbon-carbon bond would use localized MOs from methane). These MOs are then added to the fragment calculation to account for orbitals “lost” to severed covalent bonds.

One of the only other methods that is typically thought of as not relying on hydrogen caps was introduced in 2003 by Zhang and Zhang,\textsuperscript{34} and is known as the molecular fractionation with conjugate caps (MFCC) approach. The original formulation of MFCC was only applied to proteins, and involved capping each fragment with the amino acids on either side. The capping amino acids, called conjugate caps in MFCC, were then capped with hydrogen atoms at the severed peptide bond of the cap. In MFCC, the fragments themselves are single amino acids, and resultanty the energy was computed by the MBE. However, the resulting capped-fragments do intersect, specifically with four other fragments (the ends of a linear peptide only intersect with two other fragments). MFCC accounted for this intersection by adding an \textit{ad hoc} correction to the energy formula, designed to ensure that the caps are not double counted. The need for this correction is a consequence of thinking of MFCC
as a capping method, as it usually is. However, if MFCC is thought of as a fragmentation method (amino acids are groups, each fragment is a group and its bonded groups) then application of the GMBE to the resulting fragments exactly reproduces the energy equation proposed by MFCC. This is just one example of how the GMBE simplifies and unifies existing fragment methods.

As already mentioned, most fragment methods use hydrogen caps to deal with severed bonds. One of the earliest adapters of this idea was the kernel energy method (KEM), which was introduced by Huang et al.,

In 2009, Suárez et al. rigorously showed that KEM was simply a normal many-body expansion in which the fragments are re-branded as “kernels” and distance based cut-offs (n-mers further than some distance cut-off are not considered) were employed. It turns out that this is only part of the story, because the capping scheme used by KEM is primarily restricted to KEM. The KEM capping method places hydrogen atoms at the positions of the atoms they replace. Due to the cut-offs employed in KEM, this is not problematic; however, this can actually be quite problematic if the cut-offs are relaxed. For example, consider symmetrically fragmenting pentane into two ethane fragments around carbon 3. The result leads to two caps necessarily residing on top of each other, in the dimer calculation. In truth, such a complication exists in the MFCC method as well, but due to the buffer region introduced by the larger caps (assuming we are thinking of it as a capping method), it is likely that this effect is more isolated from the system of interest.

∥As equations in Ref. [34] show, the interaction of these two overlying hydrogens cancels
The SMF method of Collins and co-workers\textsuperscript{23–26} introduced a modification of this capping method which circumvents the problem explained in the previous paragraph. In the SMF capping method, when a covalent bond between an atom located at \( \mathbf{r}_1 \), resides in the fragment and a covalently bonded atom located at \( \mathbf{r}_2 \) does not, a hydrogen atom is placed at position \( \mathbf{r}_{\text{cap}} \) defined by

\[
\mathbf{r}_{\text{cap}} = \mathbf{r}_1 + \left( \frac{R_1 + R_H}{R_1 + R_2} \right) (\mathbf{r}_2 - \mathbf{r}_1),
\]

where \( R_x \) is the atomic radius of atom \( x \) using some standard list of atomic radii. Because the SMF capping method moves the caps towards the fragment, the difficulties associated with the KEM capping method are avoided.

### 2.5.3 Embedding methods

As mentioned in Sec. 2.3, the number of terms in the MBE grows exponentially and it is beneficial if we do not have to include too many higher orders. We previously mentioned that embedding methods can aid in this dilemma by incorporating higher-order interactions at lower-order expansions, albeit at an approximate level. In general embedding methods are either iterative or non-iterative. We choose to focus on iterative methods first.

Iterative methods usually work by first computing a set of charges using gas-phase monomers. Next each monomer’s density is calculated in the field of all of these charges. In general, this modifies the fragment’s density, resulting in a slightly different set of charges. These charges can then be used to calculate a new density. Eventually, the charges and density become self-consistent to a specified accuracy.
ending the cycle. This means that the fragments are no longer uncorrelated because modifying one changes it’s resulting charges, which influences the other fragments.

Historically, the coupling introduced by iterative methods has caused many complications. Perhaps the most infamous manifestation of these complications arises in the series of embedding methods used with the FMO method and the resulting derivatives. When the FMO method debuted,\textsuperscript{31} it did so with a self-consistent embedding method that used the actual fragment electron densities to compute inter-fragment Coulomb interactions. This was repeated until self-consistency. We term this the “FMO99 embedding method”, although it is really just density embedding. In 2002\textsuperscript{39} two approximations were introduced into the FMO99 embedding method at intermediate and long range. The intermediate interactions use FMO99 embedding, but also exploit a Mulliken approximation for the two-electron integrals. The distant region replaces the FMO99 embedding with self-consistent Mulliken point charge embedding. Short range uses FMO99 with no approximations. The actual range separation is handled via distance parameters. We will refer to this three-region scheme as the “FMO02 embedding method”. Correct analytic gradients for the fragment molecular orbital method\textsuperscript{5,31–33} were reported only recently,\textsuperscript{40} following several “approximate” versions of the gradient.\textsuperscript{41,42}

The GEBF approach uses an electrostatic embedding method based on charges derived from natural population analysis.\textsuperscript{43} The embedding charges, which could in principle be converged self-consistently with the fragment self-consistent field (SCF) wave functions, by means of a “dual SCF” procedure\textsuperscript{44,45} are found to be converged,
or very nearly so, after only one iteration.\textsuperscript{27} Unfortunately, the charge-embedding procedure that is used in the GEBF method leads to non-variational\textsuperscript{**} means SCF wave functions, because the embedding potential is simply grafted onto the SCF equations without proper account for how the embedding charges vary with respect to changes in the SCF wave function.\textsuperscript{44–46} As a result, the derivatives $\delta E_{\text{SCF}}/\delta \phi^A_i$, where $\phi^A_i$ represents the $i$th occupied molecular orbital (MO) on molecule $A$, are not zero, even if they are iterated to fully self-consistent convergence with the fragment SCF wave functions. As such, correct analytical gradients ought to require the solution of coupled-perturbed equations—even at the SCF level—whose dimension equals the dimension of the entire supersystem. Although we are not the first to make this observation,\textsuperscript{40, 47} this point is not discussed in any of the GEBF papers,\textsuperscript{27–29} nor in the majority of other papers where the embedding charges are iterated to self-consistency.\textsuperscript{25, 26, 48} It implies that putative analytic gradients published for some of these methods are formally incorrect\textsuperscript{††}.

To our knowledge the first method to use a non-iterative embedding method, in

\textsuperscript{**}Variational in this context has a slightly different meaning then that used in Chapter 1. Here a functional is variational if its first variation with respect to some parameter is zero.

\textsuperscript{††} The GEBF analytic gradient expressions that appear in Refs. \cite{28, 29} are formally incorrect because they do not include the response terms that arise from the embedding charges, which are present even for an infinitesimal perturbation since $\delta E_{\text{SCF}}/\delta \phi^A_i \neq 0$ at convergence. These incorrect gradient expressions were subsequently used for geometry optimizations and harmonic frequency calculations.\textsuperscript{29, 49, 50} In some cases, results compared favorably to supersystem calculations. For large systems, however, the “errors” reported in Ref. \cite{29} are actually differences in GEBF calculations using two different fragment sizes, rather than differences with respect to supersystem calculations. The magnitude of the errors due to neglect of the response terms therefore remains to be determined. A self-consistent embedding procedure that has been introduced in the context of SMF calculations,\textsuperscript{25, 26} based on distributed multipole analysis,\textsuperscript{51} is also non-variational, for the same reason.
the context of fragment methods was the *electrostatically-embedded many-body* (EE-MB) method of Dahlke and Truhlar.\(^{17}\) EE-MB actually introduced two embedding methods, called EE-MB-a and EE-MB-b. EE-MB-b embedding employs gas-phase (monomer) Mulliken charges, and is the method we will use primarily for the remainder of this document. EE-MB-a embedding charges are computed using the entire cluster instead of a single monomer. Using either of the EE-MB embedding schemes avoids the problems with iterative charges, because the charge values do not change as each fragment changes.

Table 1 summarizes how each of the methods discussed up till this point can be decomposed using our nomenclature. \(^{‡‡}\)

2.6 Notation

For the majority of the remainder of this document we will need to compare and contrast a variety of fragment based methods and here we introduce a compact notation that differentiates various methods. As a first step we dictate that we only use the GMBE to define our energy formula. Specifically this means that we are not using the approximate formulas introduced by SMF or other methods. We adopt the notation “XYZ(\(n\))” to mean that fragmentation method XYZ has been used in conjunction with an \(n\)-body truncation of the GMBE; only the \(n = 1\) and \(n = 2\) cases of the GMBE are considered here, but we do invoke \(n = 3\) cases of the MBE. If we

\(^{‡‡}\)We omit a detailed discussion of group formation. Most fragment-based methods construct groups to ensure that fragments do not cut across multiple bonds, although exceptions have been considered in order to treat extended \(\pi\) systems.\(^{52}\) The systems treated here do not contain multiple bonds so this issue does not arise.
Table 1: Classification of existing fragment-based methods.

<table>
<thead>
<tr>
<th>Method</th>
<th>Literature Reference</th>
<th>Fragment Method</th>
<th>Capping Method</th>
<th>Embedding Method</th>
</tr>
</thead>
<tbody>
<tr>
<td>FMO</td>
<td>[31]</td>
<td>UD</td>
<td>FMO99</td>
<td>FMO99</td>
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<tr>
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<td>[39]</td>
<td>UD</td>
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<td>[35]</td>
<td>UD</td>
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<td>N/A</td>
</tr>
<tr>
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<td>[30]</td>
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<td>KEM</td>
<td>N/A</td>
</tr>
<tr>
<td>EE-MB</td>
<td>[17]</td>
<td>UD</td>
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<td>EE-MB-(a or b)</td>
</tr>
<tr>
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<td>UD</td>
<td>N/A</td>
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<tr>
<td>GEBF</td>
<td>[27]</td>
<td>GEBF</td>
<td>SMF</td>
<td>XPOL</td>
</tr>
</tbody>
</table>

use embedding we add the prefix “EE” to method name such as “EE-GEBF(2)” to specify an embedded, two-body, GEBF calculation.\textsuperscript{55}

2.7 Summary

This chapter has focused on a concise summary of the existing fragment literature using a nomenclature and mathematical framework first worked out by our group. We propose the rigorously derived GMBE as a foundation for rationalizing many of the existing fragment methods and have shown that in many cases it provides a simpler picture of the methods, because it avoids the \textit{ad hoc} or heuristic derivations that are unique to a given fragment method.

The remainder of this dissertation is decomposed as follows. In Chapter 3, we

\textsuperscript{55}The notation GEBF(\textit{n}) is used in Ref. [29] in a different (and unrelated) sense.
briefly review another purposed intersecting fragment method that was developed concurrently with our method. Ultimately it will be shown that for most cases both methods are capable of chemical accuracy; however, only GMBE is robust across various fragment methods and is rigorously correct. The data in that chapter demonstrates the feasibility of GMBE as a useful *ab initio* method. Chapter 4 compares and contrasts GMBE and MBE results. It will be seen that the GMBE is more accurate for a given truncation order, as was suggested in this chapter, on the basis of theoretical arguments alone. The remaining two chapters focus on using the MBE to reproduce high quality benchmarks. In Chapter 5 we demonstrate the quintessential role of basis set superposition error corrections in this endeavor. Ultimately this will lead us to propose a new MBE based basis set superposition error correction, which is then compared to an existing MBE based correction in Chapter 6.
CHAPTER 3

Feasibility of the GMBE

Having introduced the generalized many-body expansion (GMBE) in Chapter 2, it is now our intent to explore whether or not the GMBE offers a reasonable approximation to conventional \textit{ab initio} methods. To this end, we seek to first establish the extent to which the GMBE is capable of replicating supersystem energetics. Presently, we focus on replicating the absolute supersystem energy. Our goal here is to be able to replicate these quantities to within chemical accuracy (here defined as approximately 1 kcal/mol).

This chapter also has a secondary focus, namely a comparison of another intersecting many-body method, the many-overlapping body expansion (MOBE),\textsuperscript{53} to the GMBE. We start this chapter by briefly reviewing the details of the MOBE. Next, we offer a theoretical comparison of the two methods. Finally, we compare the GMBE and MOBE for a set of test systems focusing on their abilities to replicate supersystem energetics. Ultimately, it will be concluded that both the GMBE and MOBE are in general capable of replicating supersystem properties, but only the GMBE is theoretically robust enough to be able to describe all fragmentation schemes considered here.
3.1 MOBE theory

The MOBE expansion, derived heuristically in Ref. [53] by comparing to the MBE, and generalizing it to the case of intersecting fragments. The MOBE is then defined as having the form:

\[
E_0 = \sum_{I=1}^{M} c_I E_I^{(1)} + \sum_{I<J}^{M} c_I c_J \Delta E_{IJ}^{(1)} + \sum_{I<J<K}^{M} c_I c_J c_K \Delta E_{IJK}^{(1)} + \cdots .
\] (3.1)

The coefficients \( c_I \) are discussed below, and \( M \) denotes the total number of fragments that are considered. (We denote this as \( M \) rather than \( N_F \), for reasons that will become clear.) The remaining terms in Eq. (3.1) are defined as

\[
\Delta E_{IJ}^{(1)} = E_{I\cup J}^{(1)} - E_I^{(1)} - E_J^{(1)} + E_{I\cap J}^{(1)}
\] (3.2)
and

\[ \Delta E^{(1)}_{IJK} = E^{(1)}_{I \cup J \cup K} - \Delta E^{(1)}_{I} - \Delta E^{(1)}_{J} - \Delta E^{(1)}_{K} - E^{(1)}_{I} - E^{(1)}_{J} - E^{(1)}_{K} + E^{(1)}_{I \cap J} + E^{(1)}_{I \cap K} + E^{(1)}_{J \cap K} - E^{(1)}_{I \cap J \cap K}. \]  

(3.3)

To comprehend the MOBE, Eq. (3.1), one must understand how traditional fragmentation ideas are modified in order to use it. First, as with all fragment-based methods, a large system is partitioned into \( N_F \) subsystems (fragments), capping severed valencies if the fragmentation method cuts across covalent bonds. Then, according to the MOBE procedure, one next adds \( M - N_F \) additional fragments to this set, constructed from all possible intersections involving 2, 3, \ldots, \( N_F \) fragments out of the original \( N_F \). In general, this means that one must consider \( M = 2^{N_F} - 1 \) fragments in Eq. (3.1). This also leads to the origin of the coefficients in Eq. (3.1), since more than one intersection might give rise to the same fragment. Specifically, the coefficient \( c_I \) equals the number of times that fragment \( I \) appears in the summation, with a sign equal to \((-1)^{\alpha + 1}\) where \( \alpha \) is the number of unique fragments whose intersection gave rise to fragment \( I \). (By convention, or since \( I \cap I = I \), each of the original \( N_F \) fragments gets a coefficient \( c_I = 1 \).)

Owing to the difficulty in treating intersections as fragments and keeping them distinct, it is difficult to analyze the MOBE in an analogous manner to the one presented in Chapter 2 for the GMBE. However, some properties of the MOBE can be deduced from a simple example that demonstrates the utility of this approach. Consider a system composed of three fragments labeled 1, 2, and 3. According to the
prescription of Mayhall and Raghavachari, the one-body energy for this system is given by:

$$E_{MOBE}^{(1)} = \sum_{I=1}^{3} E_{I}^{(1)} - E_{1\cap 2}^{(1)} - E_{1\cap 3}^{(1)} - E_{2\cap 3}^{(1)} + E_{1\cap 2\cap 3}^{(1)}.$$  

(3.4)

Intersections appearing in this expression become fragments when evaluating dimers and higher order \(n\)-mers. Referring to these fragments (including intersections) collectively as “monomers”, the total number of monomers is \(2^{N_F} - 1\) and the number of dimers is \(2^{N_F-1}C_2\), although not all of these need be unique and these numbers are best thought of as upper bounds.

For our three-body example, the seven terms in Eq. (3.4) lead to \(7C_2 = 21\) corrections of the form \(\Delta E_{IJ}^{(1)}\) [Eq. (3.2)]. Naïvely, then, the MOBE in Eq. (3.1), when truncated at the two-body level, consists of \(7 + 4 \times 21 = 91\) separate electronic structure calculations, but in fact many of these are redundant. First, note that if \(A \supset B\) then \(\Delta E_{AB}^{(1)} = 0\) according to Eq. (3.2). The identities

$$A \cap (B \cup C) = (A \cap B) \cup (A \cap C) \quad \text{(3.5a)}$$

$$A \cup (B \cap C) = (A \cup B) \cap (A \cup C) \quad \text{(3.5b)}$$

can then be used to reduce these 91 separate terms down to just 13. A completely general two-body MOBE energy expression for a three-fragment system is

$$E_{MOBE}^{(2)} = E_{1u2}^{(1)} + E_{1\cap 3}^{(1)} + E_{2\cap 3}^{(1)}$$

$$- E_{(1\cup 2)\cap (1\cup 3)}^{(1)} - E_{(1\cup 2)\cap (2\cup 3)}^{(1)} - E_{(1\cup 3)\cap (2\cup 3)}^{(1)}$$

$$+ E_{(1\cap 2)\cup (1\cap 3)}^{(1)} + E_{(1\cap 2)\cup (2\cap 3)}^{(1)} + E_{(1\cap 3)\cup (2\cap 3)}^{(1)}$$

$$- E_{1\cap 2}^{(1)} - E_{1\cap 3}^{(1)} - E_{2\cap 3}^{(1)} + E_{1\cap 2\cap 3}^{(1)}.$$  

(3.6)
Equation (3.6) demonstrates that when using the MOBE, one does need to consider \( n \)-mers that are subsets of other \( n \)-mers, in contrast to the GMBE. To see this, consider the seventh, eighth, and ninth terms in Eq. (3.6), which represent the dimers formed as unions of monomer intersections. Each of the resulting dimers is a proper subset of the sets represented by the first three terms in Eq. (3.6). These terms do not cancel out as they would in the GMBE.

This lack of cancellation has an important consequence, namely, that given a set of \( N_F \) monomers, an \( N_F \)-body approximation to the MOBE does not afford the exact ground-state energy, as it would in the case of the traditional MBE or the GMBE. One can understand this because the MOBE potentially generates \( 2^{N_F} - 1 \) monomers, so that the exact energy is recovered only at order \( 2^{N_F} - 1 \). If the monomers are disjoint, this issue goes away and the MOBE reduces to the traditional many-body expansion, Eq. (2.3).

### 3.1.1 Comparison of the GMBE and the MOBE

A two-body truncation of the GMBE, for the system of three monomers considered in Eq. (3.6), affords an energy expression

\[
E_{\text{GMBE}}^{(2)} = E_{1 \cup 2}^{(1)} + E_{1 \cup 3}^{(1)} + E_{2 \cup 3}^{(1)} - E_{(1 \cup 2) \cap (1 \cup 3)}^{(1)} - E_{(1 \cup 2) \cap (2 \cup 3)}^{(1)} + E_{(1 \cup 2) \cap (1 \cup 3) \cap (2 \cup 3)}^{(1)}.
\]  

(3.7)

Note that the final “triple intersection” term does not appear in \( E_{\text{MOBE}}^{(2)} \), Eq. (3.6), but the latter does include some terms that are absent from \( E_{\text{GMBE}}^{(2)} \). This demonstrates
conclusively that the MOBE and the GMBE are not equivalent; nevertheless, for many of the systems considered in Section 3.2, we find that $E_{\text{GMBE}}^{(2)} \approx E_{\text{MOBE}}^{(2)}$. This suggests that

$$E_{(1 \cup 2) \cap (1 \cup 3) \cap (2 \cup 3)}^{(1)} \approx$$

$$E_{(1 \cap 2) \cup (1 \cap 3)}^{(1)} + E_{(1 \cap 2) \cup (2 \cap 3)}^{(1)} + E_{(1 \cap 3) \cup (2 \cap 3)}^{(1)}$$

$$- E_{1 \cap 2}^{(1)} - E_{1 \cap 3}^{(1)} - E_{2 \cap 3}^{(1)} + E_{1 \cap 2 \cap 3}^{(1)} .$$

This suggests that perhaps higher-order intersections such as $(1 \cup 2) \cap (1 \cup 3) \cap (2 \cup 3)$ can be approximated in terms of lower-order intersections, which might be exploited in order to reduce the number of intersections that appear in the GMBE. Results in Section 3.2, however, reveal that this would have to be done with care, as we are able to find fragmentation schemes for which $E_{\text{GMBE}}^{(2)}$ is a significantly better approximation to the supersystem energy than is $E_{\text{MOBE}}^{(2)}$.

By way of comparison, it is also worth noting that for $N_F$ monomers, the maximum number of $n$-mers generated by the GBME is $m = N_F C_n$ (though some may not be unique), and thus the final energy expression consists of at most $2^m - 1$ terms. (In practical applications, many of these may be redundant; the redundant terms are not generated by our fragmentation code.) In contrast, the MOBE generates $2^{N_F} - 1$ monomers and thus the maximum number of $n$-mers is $m = 2^{N_F - 1} C_n$. The final MOBE energy expression is a linear combination of all of these $n$-mers, along with all $(n - 1)$-mers, $(n - 2)$-mers, etc., on down to monomers. For $n > 1$ and $N_F > 1$, the GMBE will have fewer terms to evaluate, as compared to the MOBE. For example, in
the case considered above \((N_F = 3 \text{ and } n = 2)\), \(E^{(2)}_{\text{GMBE}}\) contains 7 terms as compared to 13 terms for \(E^{(2)}_{\text{MOBE}}\).

As a final point of comparison, we consider a system composed of seven \textit{groups} (indestructible units).\(^5\) Let us assign \(N_F = 3\) fragments as follows:

\[
F^{(1)}_1 = \{1, 2, 3, 4\} \quad (3.9a)
\]

\[
F^{(1)}_2 = \{1, 3, 5, 7\} \quad (3.9b)
\]

\[
F^{(1)}_3 = \{1, 4, 6, 7\} . \quad (3.9c)
\]

These particular assignments were chosen so that, at the \(n = 1\) level, no intersection is empty and at the \(n = 2\) level, no dimer constitutes the entire system. Given these fragments, the two-body MOBE is

\[
E^{(2)}_{\text{MOBE}} = E^{(1)}_{123457} + E^{(1)}_{123467} + E^{(1)}_{134567} - E^{(1)}_{12347} - E^{(1)}_{13457} - E^{(1)}_{13467} + E^{(1)}_{134} + E^{(1)}_{137} + E^{(1)}_{147} \quad (3.10)
\]

where the indices refer to groups.

Relative to the GMBE, the MOBE omits the final term in Eq. \((3.7)\), involving the intersection of three dimers, or at best approximates this term as in Eq. \((3.8)\). Since we know that the GMBE precisely accounts for each term in the supersystem Hamiltonian (see Chapter 2), let us examine this triple intersection term to determine whether the corresponding terms in the Hamiltonian appear in the MOBE. For the fragments selected in Eq. \((3.9)\), the triple intersection \((F^{(1)}_1 \cup F^{(1)}_2) \cap (F^{(1)}_1 \cup F^{(1)}_3) \cap (F^{(1)}_2 \cup F^{(1)}_3) \cap \ldots \cap (F^{(1)}_n \cup F^{(1)}_n)\)
($F^{(1)}_2 \cup F^{(1)}_3$) evaluates to \{1, 3, 4, 7\}. The simplest type of interaction that could appear in the Hamiltonian is the appearance of a single group, and it is easily verified that each of the seven groups appears only once in the MOBE. A similar exercise shows that all interactions between pairs of groups also appear only once. However, when we repeat this check for interactions amongst three groups, we see that any interaction that is a net result of the mutual interaction between groups 3, 4, and 7 is counted zero times. Similarly, the interaction amongst all four groups is not counted either. Since these interactions were present in the initial dimers ($F^{(1)}_1 \cup F^{(1)}_2$, etc.) they ought to show up in the final energy expression.

3.2 Numerical results

3.2.1 Computational details

We next make a numerical comparison of the GMBE and the MOBE, based on the fragmentation scheme suggested in Eq. (3.9). That is, each system considered here is first divided into seven groups, from which we construct three overlapping fragments as suggested in Eq. (3.9).

We have written a program, called FRAGME\cap T, that can fragment a given system according to any one of several possible fragmentation methods. Various embedding and capping methods are also available, as described in Ref. [54]. The FRAGME\cap T program generates all required electronic structure input files, calls an electronic structure package, and finally computes the energy according to the GMBE. Electronic structure calculations were performed using Q-Chem, v. 4.0.55 The MOBE
has not been implemented in our code, so a Linux script was written to generate the appropriate Q-Chem input files in this case.

Previously, in Chapter 2 we introduced a nomenclature for classifying fragmentation scheme. According to this nomenclature, the calculations presented here employ a user-defined fragmentation method at the $n = 2$ many-body truncation level, a capping method equivalent to that used in the systematic molecular fragmentation method, and no embedding method. All energies are computed at the MP2/6-311++G(d,p) level.

Four systems are investigated here, and these are depicted in Fig. 1 along with group assignments for each. (Cartesian coordinates for these systems are available in Ref. [56].) These systems include one polyatomic example, C$_{11}$H$_{18}$, where fragmentation across covalent bonds is necessary, plus three different non-covalent clusters: (CH$_2$O)$_7$, (H$_2$O)$_6$F$^-$, and Gly·(H$_2$O)$_{10}$. The (H$_2$O)$_6$F$^-$ cluster, in particular, was selected because previous work by our group suggests that fluoride–water clusters are challenging test cases for monomer-based methods. Since (H$_2$O)$_6$F$^-$ represents the first test of the MOBE for ionic systems, we have also included for comparison the charge-neutral Gly·(H$_2$O)$_{10}$ system, where glycine (Gly) exists in its zwitterionic tautomer, $^{\text{+}}$NH$_3$CH$_2$CO$_2^-$. 

In the interest of fairness, it should be noted that the MOBE has previously been applied only to macromolecular systems, not clusters, using a chemically-motivated fragmentation scheme based on the covalent-bond topology of the macromolecule. Nevertheless, the MOBE does lend itself to a set-theoretical presentation, and a
Table 2: Unsigned errors in two-body expansions, relative to supersystem MP2/6-311++G(d,p) calculations.

<table>
<thead>
<tr>
<th>System</th>
<th>Group labels</th>
<th>Error/kcal mol⁻¹</th>
<th>GMBE</th>
<th>MOBE</th>
</tr>
</thead>
<tbody>
<tr>
<td>(CH₂O)₇</td>
<td>Fig. 1ᵃ</td>
<td>0.03</td>
<td>&lt;0.01</td>
<td></td>
</tr>
<tr>
<td>C₁₁H₁₈</td>
<td>Fig. 1ᵃ</td>
<td>&lt;0.01</td>
<td>0.23</td>
<td></td>
</tr>
<tr>
<td>Gly·(H₂O)₁₀</td>
<td>1 ↔ 3ᵇ</td>
<td>0.11</td>
<td>0.18</td>
<td></td>
</tr>
<tr>
<td>Gly·(H₂O)₁₀</td>
<td>1 ↔ 4ᵇ</td>
<td>0.11</td>
<td>0.85</td>
<td></td>
</tr>
<tr>
<td>Gly·(H₂O)₁₀</td>
<td>1 ↔ 7ᵇ</td>
<td>0.11</td>
<td>0.54</td>
<td></td>
</tr>
<tr>
<td>Gly·(H₂O)₁₀</td>
<td>2 ↔ 7ᵇ</td>
<td>0.14</td>
<td>0.52</td>
<td></td>
</tr>
<tr>
<td>Gly·(H₂O)₁₀</td>
<td>5 ↔ 7ᵇ</td>
<td>0.15</td>
<td>0.14</td>
<td></td>
</tr>
<tr>
<td>Gly·(H₂O)₁₀</td>
<td>6 ↔ 7ᵇ</td>
<td>0.02</td>
<td>0.48</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>Fig. 1ᵃ</td>
<td>0.12</td>
<td>0.17</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>1 ↔ 3ᵇ</td>
<td>0.13</td>
<td>2.64</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>1 ↔ 4ᵇ</td>
<td>0.13</td>
<td>2.47</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>1 ↔ 7ᵇ</td>
<td>0.12</td>
<td>1.93</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>2 ↔ 7ᵇ</td>
<td>0.47</td>
<td>0.71</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>5 ↔ 7ᵇ</td>
<td>0.22</td>
<td>0.26</td>
<td></td>
</tr>
<tr>
<td>(H₂O)₆F⁻</td>
<td>6 ↔ 7ᵇ</td>
<td>0.17</td>
<td>0.42</td>
<td></td>
</tr>
</tbody>
</table>

ᵃPartitioned as shown in Fig. 1.
ᵇSwapping two group labels, relative to Fig. 1.

direct comparison of this approach to the deeply set-theoretical GMBE proves to be informative.

### 3.2.2 Comparison of GMBE and MOBE

Unsigned errors for the two-body GMBE and MOBE methods, relative to the corresponding supersystem calculation, are listed in Table 2 for each of the systems examined here. Before analyzing these results, it bears pointing out that these are
somewhat contrived fragmentation calculations, not least because each of the three
dimers common to both the GMBE and the MOBE are one group shy of being the en-
tire system. Nevertheless, some significant differences between these two approaches
will be noted below.

Of the three systems considered here, one might expect [(H\(_2\)O)\(_6\)]\(^{-}\) clusters to ex-
hibit a relatively large contribution from the “triple intersection” term in Eq. (3.7),
owing to three-body polarization effects. Our analysis will therefore focus on [(H\(_2\)O)\(_6\)]\(^{-}\).
Using the group assignment for [(H\(_2\)O)\(_6\)]\(^{-}\) that is depicted in Fig. 1, both the two-
body GMBE and the two-body MOBE exhibit similar errors of 0.1–0.2 kcal/mol,
seemingly suggesting that the three-fragment intersection is not important or is ade-
quately approximated by Eq. (3.8). Careful examination of Fig. 1, however, reveals
that the term in question—the intersection of groups 3, 4, and 7—involves three
water molecules but not the fluoride ion. For this reason, we also consider several
alternative partitions in which we simply relabel which group is defined as group 7.
In particular, we swap group label 7 with that of group 1, 2, 5, or 6. (Swapping 3 \(\leftrightarrow\) 7
or 4 \(\leftrightarrow\) 7 does not change the original calculation.) Results for these alternative num-
bering schemes are also listed in Table 2, and we find one case (1 \(\leftrightarrow\) 7) for which the
two-body MOBE exhibits an error of almost 2 kcal/mol while the GMBE is accurate
to \(\approx 0.1\) kcal/mol. Further swapping of group labels identified two other cases (1 \(\leftrightarrow\) 3
and 1 \(\leftrightarrow\) 4) for which the two-body MOBE exhibits errors \(\gtrsim 2.5\) kcal/mol. These are
huge errors for a system where one expects these methods to be nearly exact, in view
of the fact that dimers encompass nearly the entire system. In contrast, none of the
Table 3: Energy decomposition analysis of $E_{\text{GMBE}}^{(2)}$ for $(\text{H}_2\text{O})_6\text{F}^-$, with groups 1 ↔ 7 exchanged relative to Fig. 1.

<table>
<thead>
<tr>
<th>Interaction</th>
<th>Energy/hartree</th>
</tr>
</thead>
<tbody>
<tr>
<td>$E_{347}^{(1)}$</td>
<td>$-252.356265$</td>
</tr>
<tr>
<td>$E_3^{(1)}$</td>
<td>$-76.2938278$</td>
</tr>
<tr>
<td>$E_4^{(1)}$</td>
<td>$-76.2937145$</td>
</tr>
<tr>
<td>$E_7^{(1)}$</td>
<td>$-99.6975948$</td>
</tr>
<tr>
<td>$\Delta E_{34}^{(1)}$</td>
<td>$0.001223$</td>
</tr>
<tr>
<td>$\Delta E_{37}^{(1)}$</td>
<td>$-0.036402$</td>
</tr>
<tr>
<td>$\Delta E_{47}^{(1)}$</td>
<td>$-0.039012$</td>
</tr>
<tr>
<td>$\Delta E_{347}^{(1)}$</td>
<td>$-0.0030632$</td>
</tr>
</tbody>
</table>

Group labeling schemes result in a two-body GMBE error larger than 0.5 kcal/mol.

Focusing on the case where the group labels differ by 1 ↔ 7 interchange relative to Fig. 1, we can understand the large difference between $E_{\text{MOBE}}^{(2)}$ and $E_{\text{GMBE}}^{(2)}$ based on the fact that, for this particular case, the 3–4–7 triple intersection includes the F$^-$ ion, so polarization effects are expected to be quite important for this term. Table 3 decomposes the 3–4–7 intersection in the GMBE in terms of all of the interactions that go into it. As discussed in Section 3.1.1, the two-body MOBE properly accounts for both single groups and pairwise group interactions appearing in the Hamiltonian. Subtracting these contributions from the interaction energy for the 3–4–7 intersection, we conclude that the three-group interaction energy is $-0.0030632$ hartree or 1.92 kcal/mol, which is essentially identical to the error in the two-body MOBE for this particular partition of $(\text{H}_2\text{O})_6\text{F}^-$.  

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Of the four “n ↔ 7” cases in Table 2, the 1 ↔ 7 interchange is unique in that it results in the fluoride ion appearing in two fragments rather than three. The 1 ↔ 3 and 1 ↔ 4 interchanges, which also lead to large errors in the two-body MOBE, have the fluoride ion appearing in the 3–4–7 intersection but not in all three of these monomers. That the GMBE is largely insensitive to this imbalance in the fragmentation patterns bodes well for its use with automated, “black box” fragmentation schemes based on distance thresholds rather than covalent bond connectivity. Such approaches are presently being pursued in our group.

The MOBE’s sensitivity with respect to the choice of fragments can be seen in the Gly·(H₂O)₁₀ results as well, where we performed the same swaps amongst fragment labels as in the case of (H₂O)₆F⁻. For Gly·(H₂O)₁₀, errors in the two-body MOBE range from 0.13–0.85 kcal/mol (see Table 2), which is not as large as the variations seen in the case of (H₂O)₆F⁻, perhaps because the water–glycine interaction energy is smaller than that of water–fluoride. Nevertheless, errors for the two-body GMBE are ≤ 0.15 kcal/mol for each Gly·(H₂O)₁₀ fragmentation scheme.

3.2.3 Timings and accuracy for a larger system

In the calculations reported above, we considered only small systems in order to make an incisive, term-by-term comparison of the MOBE and the GMBE. Ultimately, fragment-based methods are intended for larger systems, so in this section we present some results for (H₂O)₅₇ clusters. The accuracy of various GMBE-based methods, relative to supersystem calculations performed at the Hartree-Fock (HF)/6-31G(d) and B3LYP/6-31+G(d) level are shown in Table 4. As in the previous chapter, we use
Table 4: Mean absolute errors per H$_2$O monomer in the energies of five different isomers of (H$_2$O)$_{57}$, relative to supersystem calculations performed at the HF/6-31G(d) or B3LYP/6-31+G(d) level.

<table>
<thead>
<tr>
<th>Method</th>
<th>MAE/kcal mol$^{-1}$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>HF</td>
</tr>
<tr>
<td>SMF(2)</td>
<td>4.87</td>
</tr>
<tr>
<td>EE-SMF(2)</td>
<td>0.45</td>
</tr>
<tr>
<td>GEBF(1)</td>
<td>3.80</td>
</tr>
<tr>
<td>EE-GEBF(1)</td>
<td>0.22</td>
</tr>
<tr>
<td>GEBF(2)$^a$</td>
<td>2.69</td>
</tr>
<tr>
<td>EE-GEBF(2)$^a$</td>
<td>0.13</td>
</tr>
<tr>
<td>GEBF(2)$^b$</td>
<td>0.02</td>
</tr>
<tr>
<td>EE-GEBF(2)$^b$</td>
<td>0.04</td>
</tr>
</tbody>
</table>

$^a$Limited to dimers formed from intersecting fragments; from Ref. [54].

$^b$Full GEBF(2) results.

the notation “XYZ($n$)” to denote an $n$-body truncation of the GMBE (where $n = 1$ or 2 here), in combination with fragmentation method XYZ. The notation “EE-XYZ($n$)” denotes the use of a point-charge electrostatic embedding. The two fragmentation methods examined in Table 4 are the systematic molecular fragmentation (SMF) method of Deev and Collins,$^{23}$ which is based on bond connectivity and for these calculations amounts to one H$_2$O monomer per fragment, and the generalized energy-based fragmentation (GEBF) method of Li et al.,$^{27}$ which is based on a 3 Å distance threshold, which in (H$_2$O)$_{57}$ amounts to 3–4 monomers per fragment. Five isomers of (H$_2$O)$_{57}$ were considered in Ref. [54], structures and additional details can be found there.

Initially when running calculations on (H$_2$O)$_{57}$, we were forced to resort to highly
restrictive cutoffs for forming dimers of fragments, due to limitations in our fragmentation algorithm. In Table 4 we report calculations in which this restriction has been lifted, owing to improvements in our algorithm for computing intersections. It is useful to compare these “full” GEBF(2) results to the previous ones because it reveals that the restriction to “overlapping dimers” is a serious one, at least in the absence of electrostatic embedding. The discrepancies are less pronounced when electrostatic embedding is employed, presumably because the point charges mimic the polarization effects of distant water molecules, which are the sorts of dimers that were neglected in previous GEBF(2) calculations on \((\text{H}_2\text{O})_{57}\). This observation may ultimately prove useful to reduce the number of independent electronic structure calculations that are required at the GEBF(2) level, based on some kind of distance- or intersection-based thresholding criteria. In any case, we observe that GEBF(2) calculations—either with or without electrostatic embedding—reproduce supersystem energies to an accuracy of \(\leq 0.04\) kcal/mol per H\(_2\)O monomer.

The next reasonable question is, “at what cost?” To answer this, timings for the three most accurate methods, averaged over five isomers of \((\text{H}_2\text{O})_{57}\), are presented in Table 5. Although the individual electronic structure calculations required for GEBF(2) are small (\(\leq 8\) H\(_2\)O molecules in this example), the number of such calculations is quite large in the case of a full GEBF(2) calculation, and the total wall time required for GEBF(2) actually significantly exceeds that required for a supersystem calculation. Several points are worth noting, however. First, had we chosen a correlated wave function method scaling as \(O(N^5)\) or worse, or had we employed a
Table 5: CPU time required\textsuperscript{a} for a single-point energy calculation on (H\textsubscript{2}O\textsubscript{57} at the HF/6-31G(d) or B3LYP/6-31+G(d) level.

<table>
<thead>
<tr>
<th>Method</th>
<th>CPU time/sec</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>HF</td>
</tr>
<tr>
<td>Supersystem</td>
<td>397</td>
</tr>
<tr>
<td>EE-GEBF(2)\textsuperscript{b}</td>
<td>326</td>
</tr>
<tr>
<td>GEBF(2)\textsuperscript{c}</td>
<td>10,241</td>
</tr>
<tr>
<td>EE-GEBF(2)\textsuperscript{c}</td>
<td>10,250</td>
</tr>
</tbody>
</table>

\textsuperscript{a}Calculations performed using Q-Chem\textsuperscript{55} running on a single 2.5 GHz Opteron processor.

\textsuperscript{b}Limited to dimers formed from intersecting fragments.

\textsuperscript{c}Full GEBF(2) results.

significantly larger basis set that might be beset by numerical linear dependencies in a large system, then the supersystem calculation might not even be feasible. Second, the real advantage of GMBE-based methods lies in their “embarrassingly parallel” nature. Assuming, as a rough estimate, that the use of \( p \) processors would reduce the total wall time for GEBF calculations by a factor of \( p \), then we can guess that only \( p \approx 26 \) processors [HF/6-31G(d) level] or \( p \approx 14 \) processors [B3LYP/6-31+G(d) level] are required in order to render the fragment-based calculation faster (in terms of wall time) than the supersystem calculation, at least when the latter is run in serial mode. This is a fairly modest level of parallelism.

Finally, the timings in Table 5 highlight the importance of dimer cutoffs, based on overlap criteria, which can avoid the factorial growth in the number of independent electronic structure calculations required for GMBE(2) calculations.\textsuperscript{54} EE-GEBF(2)
calculations in which all nonintersecting dimers are discarded reproduce supersystem energies to within $\approx 0.3$ kcal/mol (Table 4), yet are faster than the corresponding supersystem calculations even when no parallelism is exploited at all. For the MP2/6-311++G(d,p) calculations on Gly·(H₂O)₁₀ that were reported in Section 3.2.2, the total CPU time for the MOBE calculations is only about 5% more than that required for the corresponding GMBE calculation, hence these comments regarding timings should carry over to MOBE calculations as well.

### 3.3 Conclusions

Two generalizations of the many-body expansion to the case of intersecting (overlapping) fragments have been examined here. Of the two, only the method that we call the GMBE counts all interactions appearing in the supersystem Hamiltonian exactly once. This result, which was proved in the last chapter, lends theoretical justification to existing fragment-based methods\(^{23,27,30}\) that are based on either an exact or an approximate one-body energy formula with overlapping fragments. In contrast, the GMBE is extended here to include two-body terms, yielding very high accuracy. As an alternative to the GMBE, the MOBE energy expression,\(^{53}\) when truncated at the $n$-body level, does not directly evaluate the energy of subsystems constructed from the intersection of $n$ fragments formed from intersections of $n$ monomers, whereas such terms are included explicitly in the GMBE.

Numerical calculations on (H₂O)$_₆$F⁻ and Gly·(H₂O)$_{10}$ clusters demonstrate that both the two-body GMBE and the two-body MOBE exhibit good accuracy for certain
fragmentation schemes, but omission of “triple intersection” terms \(F_1^{(1)} \cap F_2^{(1)} \cap F_3^{(1)}\) in the MOBE sometimes lead to large errors (\(\gtrsim 2\) kcal/mol) for certain fragmentation patterns. This suggests that greater care is needed when selecting fragments for ionic systems. GMBE results, on the other hand, are much more robust with respect to the choice of fragments. This feature makes the GMBE a promising approach for use with “black box” fragmentation schemes that do not require user oversight and are not based on covalent bond topology, as well as for application to macromolecular systems with ionic functional groups. Applications to \((\text{H}_2\text{O})_{57}\) demonstrate that excellent accuracy (< 0.1 kcal/mol) is maintained in this larger system. Significant speed-up, without significant loss of accuracy, is possible by placing thresholds on dimer formation, which is an aspect that we plan to explore systematically in future work.
CHAPTER 4

Many-body expansion versus the generalized many-body expansion

As a means of elucidating the similarities and differences between the many-body expansion (MBE) and the generalized MBE (GMBE), in this chapter we will consider numerical applications of both expansions to \((\text{H}_2\text{O})_N\) and \(\text{F}^-\text{(H}_2\text{O})_{10}\) clusters. \((\text{H}_2\text{O})_N\), with \(3 \leq N \leq 10\), structures have been obtained from Bates, Smith, and Tschumper,\(^5^9\) whereas \((\text{H}_2\text{O})_N\) structures with \(N = 57\) and the 10 \(\text{F}^-\text{(H}_2\text{O})_{10}\) isomers were generated by means of molecular dynamics simulations with the amoeba force field.\(^6^0\) The merits of the MBE and GMBE will be decided by comparison to the full supersystem energy, as well as relative energetics.

Here we do not consider the one-body methods SMF(1) or EE-SMF(1), because the fragments in these cases are limited to a single \(\text{H}_2\text{O}\) molecule or \(\text{F}^-\) ion, and thus these methods are nearly devoid of intermolecular interactions. The GEBF(1) method also truncates the GMBE at the one-body level, but employs larger fragments (a couple molecules per fragment) and is therefore worth considering. Because the SMF fragmentation method creates disjoint fragments for the systems considered here, the SMF(2) and EE-SMF(2) expansions are equivalent to normal MBEs, which
have been considered previously for water clusters.\textsuperscript{17} The calculations in Ref. [17] provide a useful point of comparison for MBE results, whereas the results by Li \textit{et al}\textsuperscript{27} provide closely related GEBF(1) results.

Tables 6 and 7 list the mean signed errors and the mean signed errors per monomer, respectively, for the systems just described. They serve as a useful companion to the forthcoming discussion.

\section*{4.1 \((H_2O)_N\) Results}

\subsection*{4.1.1 Absolute Energetics}

Figure 2 plots the unsigned errors resulting from six different fragment based approaches. For the least accurate methods, the errors emerge in a hierarchical manner so that we can make a general statement that the accuracy increases in the order \textit{SMF(2)} \textless \textit{GEBF(1)} \textless \textit{EE-SMF(2)}. Each of the other three methods—\textit{GEBF(2)}, EE-GEBF(1), and EE-GEBF(2)—exhibits errors not substantially larger than 1 kcal/mol.

The relative accuracy of certain methods is readily explained in terms of fragment size. The \textit{SMF(1)} fragments consist of an individual water molecule, and it follows that the fragments in \textit{SMF(2)} are water dimers. In fact, for these particular systems, \textit{SMF(2)} is equivalent to a traditional two-body cluster expansion. We anticipate large many-body polarization effects in \((H_2O)_N\) clusters (\textit{e.g.}, 9–13 kcal/mol in the hexamer\textsuperscript{61}), and indeed many of the \textit{SMF(2)} errors are larger than 10 kcal/mol. The GEBF(1) fragmentation approach, on the other hand, leads to fragments consisting
Table 6: Mean signed error (MSE) and mean absolute errors (MAE), both in kcal/mol, as obtained using various fragment methods.

<table>
<thead>
<tr>
<th>System</th>
<th>Method</th>
<th>Type of error</th>
<th>No embedding</th>
<th>Mulliken embedding&lt;sup&gt;a&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>SMF1(2)</td>
<td>GEBF(1)</td>
</tr>
<tr>
<td>Absolute</td>
<td>HF</td>
<td>MSE</td>
<td>17.83</td>
<td>4.39</td>
</tr>
<tr>
<td>energies,</td>
<td>HF</td>
<td>MAE</td>
<td>17.83</td>
<td>5.59</td>
</tr>
<tr>
<td>(H₂O)&lt;sub&gt;N&lt;/sub&gt;</td>
<td>B3LYP</td>
<td>MSE</td>
<td>12.12</td>
<td>3.56</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MAE</td>
<td>12.12</td>
<td>4.06</td>
</tr>
<tr>
<td>Relative</td>
<td>HF</td>
<td>MSE</td>
<td>-0.12</td>
<td>6.27</td>
</tr>
<tr>
<td>energies,</td>
<td>HF</td>
<td>MAE</td>
<td>1.47</td>
<td>6.65</td>
</tr>
<tr>
<td>(H₂O)&lt;sub&gt;N&lt;/sub&gt;</td>
<td>B3LYP</td>
<td>MSE</td>
<td>-0.70</td>
<td>4.97</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MAE</td>
<td>1.23</td>
<td>5.88</td>
</tr>
<tr>
<td>Relative</td>
<td>HF</td>
<td>MSE</td>
<td>-0.22</td>
<td>-2.36</td>
</tr>
<tr>
<td>energies,</td>
<td>HF</td>
<td>MAE</td>
<td>1.46</td>
<td>6.84</td>
</tr>
<tr>
<td>F&lt;sup&gt;-&lt;/sup&gt;(H₂O)&lt;sub&gt;10&lt;/sub&gt;</td>
<td>B3LYP</td>
<td>MSE</td>
<td>-0.70</td>
<td>4.97</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MAE</td>
<td>2.51</td>
<td>6.36</td>
</tr>
</tbody>
</table>

<sup>a</sup>EE-MB-b embedding<sup>17</sup> using gas-phase Mulliken charges.
Table 7: Summary of errors in absolute energies per monomer (in kcal/mol), using various fragment methods.

<table>
<thead>
<tr>
<th>System</th>
<th>Method</th>
<th>Type of error</th>
<th>No embedding</th>
<th>Mulliken embedding&lt;sup&gt;a&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>SMF1(2)</td>
<td>GEBF(1) GEBF(2)</td>
</tr>
<tr>
<td>Absolute energies, (H_2O)_N</td>
<td>HF</td>
<td>MSE</td>
<td>2.04</td>
<td>0.49 0.00</td>
</tr>
<tr>
<td></td>
<td>HF</td>
<td>MAE</td>
<td>2.04</td>
<td>0.58 0.00</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MSE</td>
<td>1.75</td>
<td>0.50 0.03</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MAE</td>
<td>1.75</td>
<td>0.56 0.06</td>
</tr>
<tr>
<td>Absolute energies, F^- (H_2O)_{10}</td>
<td>HF</td>
<td>MSE</td>
<td>-1.45</td>
<td>0.59 0.04</td>
</tr>
<tr>
<td></td>
<td>HF</td>
<td>MAE</td>
<td>1.45</td>
<td>0.74 0.05</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MSE</td>
<td>-2.21</td>
<td>0.56 0.08</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MAE</td>
<td>2.21</td>
<td>0.71 0.08</td>
</tr>
<tr>
<td>Absolute energies, (H_2O)_{57}</td>
<td>HF</td>
<td>MSE</td>
<td>4.87</td>
<td>3.80 2.69</td>
</tr>
<tr>
<td></td>
<td>HF</td>
<td>MAE</td>
<td>4.87</td>
<td>3.80 2.69</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MSE</td>
<td>3.74</td>
<td>2.95 2.07</td>
</tr>
<tr>
<td></td>
<td>B3LYP</td>
<td>MAE</td>
<td>3.74</td>
<td>2.95 2.07</td>
</tr>
</tbody>
</table>

<sup>a</sup>EE-MB-b embedding<sup>17</sup> using gas-phase Mulliken charges.
Figure 2: Total unsigned errors (plotted on a logarithmic scale) in fragment-based calculations for $(\text{H}_2\text{O})_N$ clusters at (a) the HF/6-31G(d) and (b) the B3LYP/6-31+G(d,2p) level.
Table 1: Total unsigned errors per monomer, plotted on a logarithmic scale, in fragment-based calculations for $(\text{H}_2\text{O})_N$ clusters at (a) the HF/6-31G(d) and (b) the B3LYP/6-31+G(d,2p) level.

<table>
<thead>
<tr>
<th>$N$</th>
<th>SMF1(2)</th>
<th>GEBF(1)</th>
<th>GEBF(2)</th>
<th>EE-SMF1(2)</th>
<th>EE-GEBF(1)</th>
<th>EE-GEBF(2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>6</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>7</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>8</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>9</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
<tr>
<td>10</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
<td>0.01</td>
<td>0.1</td>
<td>1</td>
</tr>
</tbody>
</table>

Figure 3: Total unsigned errors per monomer, plotted on a logarithmic scale, in fragment-based calculations for $(\text{H}_2\text{O})_N$ clusters at (a) the HF/6-31G(d) and (b) the B3LYP/6-31+G(d,2p) level.
of three or four water molecules, whose intermolecular interactions are therefore incorporated even at the one-body level, and errors are reduced to the 1–10 kcal/mol range for GEBF(1) calculations. We note that GEBF(1) is not equivalent to MBE(3) or MBE(4), where the fragments are trimers and tetramers, respectively, because the GEBF(1) method omits three- and four-body interactions between water molecules more distant than $\xi = 3.0$ Å. These would be included in MBE(3) and MBE(4) calculations.

We find that the EE-SMF(2) is actually more accurate than GEBF(1), despite the fact that the former approach does not include any explicit three-body interactions at all. Three-body and higher-order effects are included in EE-SMF(2) implicitly (and approximately), via the embedding charges, whereas GEBF(1) neglects all many-body effects beyond those that arise explicitly from the presence of three or four H$_2$O molecules per fragment. These observations are especially noteworthy in view of the reduced fragment size in EE-SMF(2) relative to GEBF(1).

In order to make contact with previous literature, we point out that the SMF(2) method, as applied to water clusters, is equivalent to standard two-body application of the MBE; Dahlke and Truhlar$^{17}$ have termed this the many-body pairwise additive (MB-PA) approach. EE-SMF(2) calculations for (H$_2$O)$_N$, with the embedding scheme used here, are equivalent to the EE-MB-PA method of Ref. [17]. We should also note that our implementation of GEBF(1) differs slightly from the method originally implemented by Li et al.$^{27}$ insofar as we use fixed, gas-phase Mulliken charges for the electrostatic embedding, whereas in Ref. [27] the charges were obtained from natural
population analysis\textsuperscript{43} and were iterated toward self-consistency. Interestingly, for the \((\text{H}_3\text{O}^+)_5(\text{HO}^-)_5(\text{H}_2\text{O})_{22}\) system considered in Ref. [27], self-consistent iteration modifies the embedding charges by only \(\sim 0.01e\), so for the rather simple test systems examined in this chapter, the lack of self-consistency may not be a major concern.

In contrast, the GEBF(2) and EE-GEBF(2) methods have only been considered by our group, which would not have been possible except for the formulation of the GMBE in Chapter 2 that extends the MBE to intersecting monomers. These are the first two-body calculations to exploit intersecting monomers\textsuperscript{*} and it is apparent from Fig. 2 that extending the GEBF method to dimers has the desired result. Comparing GEBF(1) and GEBF(2), we see an increase in accuracy of one or two orders of magnitude when the dimer terms are included. A similar increase in accuracy is observed in comparing EE-GEBF(1) to EE-GEBF(2) and indeed we will see that the intersecting-dimer approaches generally outperform the intersecting-monomer approaches.

As pointed out by Beran,\textsuperscript{62} for non-covalent clusters one expects that the total error to be an extensive quantity in fragment-based calculations. The absolute errors per monomer, which are intensive, are plotted in Fig. 3 and the corresponding error statistics are listed in Table 7. For the SMF(2) and EE-SMF(2) methods, we obtain MAEs of about 2 kcal/mol/\text{H}_2\text{O} and 0.2 kcal/mol/\text{H}_2\text{O}, respectively. (As a check of our implementation, we note that these values are in good agreement with the statistical errors reported by Dahlke and Truhlar for the same systems, using the equivalent

\textsuperscript{*From a certain point of view, intersecting dimers were considered in the SMF calculations of Ref. [23], insofar as pairs of groups that were not covalently bonded were explicitly incorporated into the set of fragments. The important distinction is that these were pairs of \textit{groups}, not pairs of \textit{monomers}, and thus they constitute additional fragments rather than dimers.}
MB-PA and EE-MB-PA methods.\textsuperscript{17} The GEBF(2) and EE-GEBF(2) methods prove to be much more accurate, with MAEs and MSEs of \(< 0.01 \text{ kcal/mol/H}_2\text{O}\). We should note that data points with errors less than 0.1 kcal/mol are not shown in either Fig. 2 or Fig. 3, since the range of the data is such that it would be awkward to plot all of them on a single set of axes, even using a logarithmic scale. The absence of a data point for a particular method thus indicates that the error is basically negligible.

4.1.2 Relative energetics

The error statistics for absolute energies (which translate directly into errors in the cluster binding energies) are quite promising, but it is important to consider relative conformational energies as well. For the purpose of this comparison, we set \(E = 0\) for each cluster size based on whichever structure is lowest in energy for the supersystem calculation, meaning that the fragment methods may afford negative relative energies if the lowest-energy isomer is predicted incorrectly. The isomer whose energy is set to zero is not included in computing error statistics.

Figure 4 plots the relative energy as predicted by the fragment methods against the correct (\textit{i.e.}, supersystem) relative energy. The GEBF(1) results are quite poor, with errors that approach 20 kcal/mol in some cases. [In fact, several GEBF(1) data points lie outside of the range plotted in Fig. 4, but to avoid further compressing the more interesting data, these points are omitted]. This observation is particularly interesting because it means that SMF(2) performs \textit{better} than GEBF(1) for relative energies, despite performing \textit{worse} for absolute energies. The explanation lies in the fact that all of the SMF(2) absolute energy errors have the same sign (as can be
Figure 4: Relative energies for $(\text{H}_2\text{O})_N$ clusters predicted by fragment-based methods, as compared exact (supersystem) results, at (a) the HF/6-31G(d) level and (b) the B3LYP/6-31+G(d,2p) level. The oblique solid line corresponds to exact agreement with a supersystem calculation.
inferred from the fact that the MAE and the MSE in Table 6 are identical), whereas GEBF(1) exhibits both positive and negative errors in the absolute energies. The GEBF(1) errors lie erratically around the supersystem result, leading to larger errors in relative energies.

The water decamer provides an illustrative example. In this case, GEBF(1) over-stabilizes the minimum-energy isomer by about 3 kcal/mol at the HF/6-31G(d) level but under-stabilizes the so-called “PP2” isomer\textsuperscript{59} by 15 kcal/mol, for a total MAE of 18 kcal/mol. The SMF1(2) approach understabilizes both structures by about 25 kcal/mol, so that the error in the absolute electronic energy is significantly larger for either isomer, as compared to GEBF(1) results, but the SMF1(2) error in the relative energies is $< 1$ kcal/mol.

Much of the literature on fragment-based quantum chemistry methods has focused on errors in absolute energies with respect to supersystem calculations, with water clusters being a popular test system. Relative conformational energies have been considered far less frequently, leaving us with little precedent as to the magnitudes of errors that we might expect. Tschumper and co-workers\textsuperscript{63} have considered a series of water clusters with the intent of benchmarking how well an ONIOM-like “QM:QM” approach reproduces high-level \textit{ab initio} results. The QM:QM approach is equivalent to a “level two” MIM expansion,\textsuperscript{64} in which a lower level of theory (MP2/cc-pVTZ in this case) is applied to the full system and corrected by means of a three-body expansion at a higher level of theory [CCSD(T)/aug-cc-pVTZ]. Amongst the calculations presented in Ref. [63], of particular interest are a series of five (H\textsubscript{2}O)\textsubscript{16} isomers, for
which a MAE of 0.1 kcal/mol is reported for the relative isomer energies. This is in good agreement with results presented here for two-body methods.

Pruitt et al. have considered the relative energies of various isomers of the open-shell OH(H₂O)₅ cluster within the fragment molecular orbital (FMO) approach, which merits some explanation. The FMO method employs user-defined fragments and frozen-orbital caps whenever covalent bonds are severed, and both a two-body truncation of the MBE (“FMO2”) and a three-body truncation (“FMO3”) have been introduced. For clusters such as (H₂O)₅ or OH(H₂O)₅, FMO calculations have typically employed single-molecule fragments, in which case FMO2 is the same as EE-SMF1(2), except that FMO2 uses self-consistent (albeit non-variational) Mulliken embedding charges, whereas our EE-SMF1(2) charges are fixed at gas-phase values.

FMO2 calculations for six different isomers of OH(H₂O)₅, with fragment calculations performed at the ROMP2/aug-cc-pVTZ level, are found to afford a MAE of 1.7 kcal/mol in the relative isomer energies. This may be compared to the MAEs of 0.4–0.6 kcal/mol reported in Table 6 for EE-SMF1(2) calculations (H₂O)₅ relative energies at the HF and B3LYP levels. One should not read too much into this comparison, given that the systems in question are different, yet the significantly smaller errors observed in the EE-SMF1(2) calculations suggest that the lack of self-consistency in the EE-SMF1(2) embedding charges is perhaps not the largest source of error in these calculations. Rather, the two-body truncation, and the use of single-molecule fragments seem to be more important than the intimate details of the charge-embedding scheme. This supposition is supported, to some extent, by the fact
that three-body FMO3 calculations reduce the MAE in the OH(H₂O)₅ relative energies to 0.3 kcal/mol. In view of this, it is promising that EE-GEBF(2) calculations for (H₂O)ₕ clusters exhibit MAEs of only 0.05 kcal/mol.

**Larger water clusters**

The GEBF(2) and EE-GEBF(2) results presented above seem quite promising, but one might object that because the GEBF(2) fragmentation algorithm results in 3–4 H₂O molecules per fragment, some of the fragments constitute a significant fraction of the total cluster size, which might make the results appear more favorable than they would be in larger systems. To investigate this possibility, we next consider a (H₂O)₅₇ cluster, in order to ascertain whether GEBF(2) and EE-GEBF(2) remain the most accurate approaches when the resulting dimers no longer compose a majority of the molecule.

In order to reduce the number of dimers that we need to consider, for this particular system we have employed two cutoffs. For SMF1(2) calculations we consider only those pairs of monomers that are within 3.0 Å of each other. Because the GEBF(1) monomers are larger, we reduced this cutoff to 1.0 Å for GEBF(1) calculations, which has the effect that dimers are created only from monomers that intersect. Admittedly, these cutoffs are considerably more restrictive than what has been used in the literature to date, e.g., Dahlke and Truhlar¹⁸ utilize a 5–6 Å cutoff for water clusters. We justify our choice by the simple fact that it affords reasonable accuracy. In future work, the convergence with respect to the dimer cutoff distance should be investigated.
Table 7 lists the MSEs and MAEs for these clusters on a per-molecule basis, and the trends mirror what we observe in smaller clusters. Of the non-embedded approaches, GEBF(2) performs the best and is about 1 kcal/mol more accurate than GEBF(1), and 2 kcal/mol more accurate than SMF1(2). Electrostatic embedding increases the accuracy by about an order of magnitude, and EE-GEBF(2) is the most accurate embedded method. Relative to the results in smaller water clusters, we do observe a notable increase in the error per monomer at both the GEBF(1) and GEBF(2) levels, with or without electrostatic embedding, although the errors remain small (≤ 0.4 kcal/mol, with embedding). The important point is that for \((\text{H}_2\text{O})_{57}\), the GEBF(2) dimers no longer encompass the majority of the cluster and we expect these results to be more typical of the errors that one can expect when using GEBF(2) in large clusters, i.e., we are probing the intrinsic accuracy of the method in these calculations.

To place this level of error in context, we note that FMO2 results reported for a single isomer of \((\text{H}_2\text{O})_{64}\), performed using B3LYP/6-31+G* and B3LYP/6-31++G**, with two \(\text{H}_2\text{O}\) molecules per fragment, were larger than 0.7 kcal/mol/\(\text{H}_2\text{O}\). At the FMO3 level, the same setup results in errors less than 0.1 kcal/mol/\(\text{H}_2\text{O}\). In a recent study, the accuracy of the SMF and FMO methods was compared for water clusters, defining water molecules within 2.3 Å of one another to be “bonded” for the purposes of applying the SMF3 fragmentation method. Proceeding in this way, the accuracy of SMF3 and FMO3 was found to be similar.
4.2 Fluoride–water clusters

As compared to neat water clusters, hydrated ions may represent more challenging systems due to the greater degree of polarization and the large ion–water interaction. Indeed, FMO calculations on large Na$^+(\text{H}_2\text{O})_N$ clusters have shown that two-body (FMO2) calculations yield very poor approximations to the total energy, with errors greater than 65 kcal/mol even with as many as 31 H$_2$O molecules included in the same fragment as the cation, and $\sim$ 100 kcal/mol when only six water molecules are included with Na$^+$. Superscript 67 (FMO3 calculations perform much better, although errors remain on the order of 2–6 kcal/mol, even with a very large central fragment. Superscript 67)

Hydrated anions are likely to be even more challenging owing to the greater extent of charge delocalization associated with the ion, and here we perform tests on a set of F$^-(\text{H}_2\text{O})_{10}$ using one- and two-body GMBE methods.

4.2.1 Fixed-charge embedding

Figure 5 plots errors in the total energy per monomer for a set of ten F$^-(\text{H}_2\text{O})_{10}$ isomers, using the same fixed-charge embedding procedure that was used for the water clusters. For the most part, the trends that we observe are the same as those observed for water clusters: SMF1(2) performs the worst and EE-GEBF(2) performs the best, electrostatic embedding generally improves the accuracy of the results, and the use of intersecting monomers generally improves the accuracy as well.

One anomaly stands out, however. For neutral water clusters, EE-GEBF(1) was a significant (factor of ten) improvement over GEBF(1), yet for these fluoride–water
Figure 5: Unsigned error in the total electronic energy per water monomer (plotted on a logarithmic scale) for a set of ten $\text{F}^-(\text{H}_2\text{O})_{10}$ cluster isomers. Calculations were performed at (a) the HF/6-31+G(d) and (b) the B3LYP/6-31+G(d,2p) levels of theory.
Figure 6: Relative energies for isomers of $\text{F}^-(\text{H}_2\text{O})_{10}$ as predicted by various fragment methods at (a) the HF/6-31+G(d) and (b) the B3LYP/6-31+G(d,2p) level of theory. The oblique solid line indicates exact agreement with the supersystem calculation.
clusters both methods exhibit comparable accuracies of $\sim 1$ kcal/mol. This may be due to over-polarization brought about by using intersecting monomers. Suppose that water molecule $A$ belongs to the same monomer as the fluoride ion. In such a case, one would expect $A$'s electron density to be significantly distorted relative to what it would be when $A$ appears in another, charge-neutral fragment. As a result of this asymmetry, the embedding point charges are averages over two very different electronic environments. In principle, the same error is present in EE-GEBF(2) calculations, though perhaps less pronounced owing to increased dimer size, and in fact EE-GEBF(2) is significantly more accurate for $F^-(H_2O)_{10}$ relative energies, as compared to the other methods considered here. Nevertheless, these observations point to the need to explore alternative ways to compute embedding charges in the case of intersecting monomers.

Relative energies of the fluoride–water clusters are plotted versus supersystem results in Fig. 6. Again we see that GEBF(1) is the least accurate method for relative energies, whereas EE-GEBF(2) is the most accurate. The main point of interest for these figures is that the errors obtained using EE-GEBF(1) and EE-GEBF(2) are an order of magnitude larger that what was observed in application of the same methods to $(H_2O)_N$ clusters. We suspect that this is once again a deficiency of the embedding charges, and points to the need to explore alternate, self-consistent embedding schemes.
4.2.2 Self-consistent XPol embedding

As a preliminary example of one such self-consistent charge embedding, we consider the use of XPol/ChElPG embedding charges. As noted in Chapter 2, a naïve implementation of self-consistency will cause the total energy to be non-variational. This can be avoided by the use of XPol embedding charges, as was recently suggested in the context of the MBE.\(^{68}\)

As a simple example to illustrate the procedure, consider a conventional two-body approximation to the energy of the trimer \(IJK\), where \(I\), \(J\), and \(K\) are non-intersecting fragments. Following Eqs. (2.3) and (2.4), let us write this approximation in the following way:

\[
E_{IJK} \approx E^{(1)}_{ijk} + E^{(1)}_{iJk} + E^{(1)}_{ijK} + \Delta E^{(2)}_{IJk} + \Delta E^{(2)}_{ijK} + \Delta E^{(2)}_{iJK}. \tag{4.1}
\]

Capitalized indices in this expression imply that the indexed fragment is treated at the SCF level, while fragments with lower-case indices are represented by embedding charges. All three one-body terms can be extracted from a single XPol calculation on \(IJK\), whereas each two-body calculation requires a separate XPol calculation in which one of the fragments is a dimer. For example, the \(\Delta E^{(2)}_{iJK}\) term would be computed using an XPol calculation involving two fragments: \(IJ\) and \(K\). In that particular calculation, SCF equations on \(K\) must be iterated to convergence even though it is ultimately only \(IJ\)’s energy that is extracted from the calculation, which introduces additional computational complexity as compared to the more naïve self-consistent procedures discussed above, but the number of additional iterations is
minimal. (Even when starting from isolated, gas-phase initial-guess wavefunctions, the XPol procedure typically converges in $\leq 4$ loops over monomers.)

Error statistics for the GEBF(1) and GEBF(2) methods with XPol embedding, as applied to $F^-(H_2O)_{10}$, are listed Table 8. For comparison, we also tabulate the statistical errors using fixed, gas-phase ChElPG embedding charges (analogous to the “EE-MB-b” embedding used above but with ChElPG charges replacing Mulliken charges). For the GEBF(1) method, XPol embedding does afford an increase in accuracy for both absolute and relative energies as compared to earlier results using fixed, fragment-averaged embedding charges, and the same is true if we obtain these fixed charges using ChElPG. This suggests that at least part of the problem with the earlier EE-GEBF(1) results is indeed related to erratic polarization caused by the fragmented-averaged charges. On the other hand, the EE-GEBF(2)/ChElPG results for relative isomer energies are significantly worse when the charges are iterated to self-consistency (cf. the last two columns in Table 8).

For the calculations reported in Table 8, we used a fairly coarse ChElPG grid spacing of 1.0 Å, as this was sufficient to provide reasonable results in previous XPol/ChElPG calculations,\textsuperscript{46} as compared to earlier results using $\Delta x = 0.3$ Å.\textsuperscript{45} [It is also sufficient to provide very accurate GEBF(2) results when gas-phase ChElPG embedding charges are used, as the results in Table 8 will attest.] However, the coarser grid engenders a fairly serious loss of rotational invariance, which went unnoticed in our previous work, probably because the weighted least-squares procedure that we use to compute the ChElPG charges\textsuperscript{46} ensures that the charges are smooth functions of the
Table 8: Statistical errors in EE-GEBF($n$) calculations for $F^-(H_2O)_{10}$ isomers using ChElPG embedding charges, in units of kcal/mol/H$_2$O. Results are compared for fixed gas-phase ChElPG embedding charges and for charges that are converged self-consistently using the XPol procedure. All ChElPG calculations use a grid spacing $\Delta x = 1.0$ Å.

| Method | Type of error | Absolute energies | | | Relative energies | | |
|--------|---------------|-------------------|-------------------|-------------------|-------------------|-------------------|
|        |               | GEBF(1)           | GEBF(2)           | GEBF(1)           | GEBF(2)           | GEBF(1)           | GEBF(2)           |
|        | Fixed         |                   |                   |                   |                   |                   |                   |
| HF     | MSE           | -0.76             | -0.34             | 0.01              | 0.00              | -2.45             | -2.10             |
| HF     | MAE           | 0.76              | 0.34              | 0.01              | 0.06              | 2.82              | 1.86              |
| B3LYP  | MSE           | -0.46             | -0.03             | 0.10              | 0.08              | -1.55             | -1.30             |
| B3LYP  | MAE           | 0.46              | 0.12              | 0.10              | 0.12              | 2.29              | 1.60              |
nuclear coordinates. Provided that one works only in the molecule-fixed coordinate frame, the lack of rotational invariance may therefore go completely unnoticed. In the present context, however, simply re-ordering the fragments in the Q-Chem input file (which amounts to rotating the molecule-fixed frame with respect to the laboratory frame) may change the energy by \( \sim 10^{-4} \) Hartree.

To examine this issue further, we have performed EE-SMF1(2) calculations using a finer grid \( (\Delta x = 0.3 \text{ Å}) \), and Table 9 compares these results to those obtained using \( \Delta x = 1.0 \text{ Å} \). The fine grid reduces the errors in absolute energies only slightly (by about 0.2 kcal/mol/H\(_2\)O), but significantly reduces the errors in the relative energies (by about a factor of two for the MAEs and a factor of ten for the MSEs). However, the fine grid also significantly increases the cost of these calculations, to the point that we have not attempted GEBF\((n)\) calculations with the finer grid, as the number of electronic structure calculations is much larger for these methods.

One puzzling aspect of the data in Table 9 is the fact that results obtained using gas-phase ChElPG embedding charges remain more accurate than the self-consistent, XPol-embedded results. This is especially true for absolute energies, where the fixed-charge results exhibit errors of \( \leq 0.1 \) kcal/mol/H\(_2\)O, even when the coarse grid is used, whereas XPol-embedded results with the fine grid exhibit errors of 0.7–0.8 kcal/mol/H\(_2\)O. For relative energies, the XPol-embedded results are only slightly worse than those obtained using gas-phase embedding charges, which makes us wonder whether the problem may once again stem from lack of rotational invariance. We are currently working to implement ChElPG charges using sparse, atom-centered
Table 9: Statistical errors in EE-SMF1(2) calculations for $F^{-}(H_{2}O)_{10}$ isomers using ChElPG embedding charges, in units of kcal/mol/H$_{2}$O. Results are compared for fixed gas-phase ChElPG embedding charges and for charges that are converged self-consistently using the XPol procedure.

<table>
<thead>
<tr>
<th>Method</th>
<th>Type of error</th>
<th>Absolute energies</th>
<th>Relative energies</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Fixed charges$^{a}$</td>
<td>XPol charges</td>
</tr>
<tr>
<td></td>
<td></td>
<td>coarse grid$^{a}$</td>
<td>fine grid$^{b}$</td>
</tr>
<tr>
<td>HF</td>
<td>MSE</td>
<td>0.10</td>
<td>0.83</td>
</tr>
<tr>
<td>HF</td>
<td>MAE</td>
<td>0.10</td>
<td>0.83</td>
</tr>
<tr>
<td>B3LYP</td>
<td>MSE</td>
<td>0.00</td>
<td>0.99</td>
</tr>
<tr>
<td>B3LYP</td>
<td>MAE</td>
<td>0.03</td>
<td>0.99</td>
</tr>
</tbody>
</table>

$^{a}$Grid spacing $\Delta x = 1.0$ Å. $^{b}$Grid spacing $\Delta x = 0.3$ Å.
grids, which will significantly reduce the computational overhead such that more systematic tests can be performed. This approach should also reduce the magnitude of the rotational invariance errors.\textsuperscript{69,70}

## 4.3 Conclusions

We have introduced a generalized many-body expansion (GMBE) for fragment-based quantum chemistry, which extends the traditional MBE to the case where fragments may share some nuclei in common. Application of the GMBE, truncated at some \( n \)-body level of approximation, provides a systematic means to approach the exact supersystem energy, analogous to how the MBE is applied in the case of non-intersecting fragments. The GMBE, which reduces to the traditional MBE in the case of non-intersecting fragments, provides a universal energy expression for fragment-based methods, which are therefore differentiated by their fragmentation, capping, and embedding procedures, but not by the formula that is used to compute the energy.

This formulation provides a unified view of several fragment-based methods that have been proposed previously, and suggests that it is possible to create a number of novel fragment-based methods simply by combining elements from existing approaches in new ways. One of these new ways, namely, a two-body extension of the previously-reported GEBF method\textsuperscript{27–29} (which, in fact, is based on the same energy expression as the CG-MTA approach\textsuperscript{30,71,72}) is reported here for the first time, and appears to be quite promising.
Numerical results for \((\text{H}_2\text{O})_N\) and \(\text{F}^-\text{(H}_2\text{O})_{10}\) clusters indicate that methods based on intersecting fragments are more accurate, for both absolute and relative energies, than are methods that utilize non-intersecting fragments, when the GMBE is truncated at the two-body level. Notably, this remains true even in large clusters such as \((\text{H}_2\text{O})_{57}\), where all of the fragments are small as compared to the size of the overall system. Although electrostatic embedding in most cases significantly improves the accuracy of results based on the GMBE (as seen in many previous studies using the traditional MBE), for the \(\text{F}^-\text{(H}_2\text{O})_{10}\) we find that this need not be the case. The reason probably lies in the use of fixed embedding charges, which was done here in order to make contact with previous methods in the literature, and points to the need to develop self-consistent charge embedding schemes for use with the GMBE.

At present, the primary drawback that limits applications of the GMBE is the steep cost of computing all possible mutual intersections between different fragments, which is necessary once the fragments are allowed to intersect. Efforts to reduce this cost by means of thresholding procedures are currently underway in our group, and we expect that improved fragmentation algorithms will facilitate systematic tests of GMBE-based fragment methods, in the near future.
CHAPTER 5

High accuracy many-body expansions

Up until this point our many-body expansion (MBE) calculations have focused on proof of concept results and we have made no attempt to replicate experimental results or high-accuracy \textit{ab initio} benchmarks. In this chapter we show that the MBE is capable of replicating CCSD(T)/CBS results to within chemical accuracy. In order to do this though it becomes necessary to account for basis-set superposition error (BSSE) in a computationally affordable way. In order to do this we must first introduce the concept of BSSE.

5.1 BSSE

The concept of BSSE is often introduced via the canonical example of calculating the binding energy (BE) of a dimer. In such an electronic structure calculation, it is well known that naïve attempts to use the formula

\begin{equation}
\text{BE} = E_{AB} - E_A - E_B
\end{equation}

usually result in significant overestimation of the $A \cdots B$ binding energy, owing to BSSE, which disappears only very slowly as the monomer basis sets approach completeness. This BSSE is a manifestation of the fact that Eq. (5.1) is an unbalanced
approximation in the sense that $E_{AB}$ is computed using a more flexible basis set than
is used to compute the monomer energies. Heuristically, this can be corrected for by
utilizing the widely-used Boys-Bernardi counterpoise (CP) procedure\textsuperscript{73} which corrects
this imbalance by computing all three energies using the dimer ($AB$) basis set. The
obvious generalization of this CP correction to $N_F$-body clusters is\textsuperscript{74–76}
\begin{equation}
\text{BE} = E_{IJK\ldots} - \sum_{i=I,J,K\ldots}^{N_F} E_{i}^{IJK\ldots},
\end{equation}
where $E_{i}^{IJK\ldots}$ denotes the energy of monomer $i$ computed using a basis set with
functions on monomers $I,J,K\ldots$. Operationally, this means placing “ghost atoms”
(atoms that have the same basis functions as the atom they are replacing, but no
electrons or nuclear charge) on all monomers $J \neq i$.

Although the generalized CP correction in Eq. (5.2) has sometimes been criticized
for neglecting “basis-set extension” effects,\textsuperscript{77} which are further discussed below, we
will show that this approach correctly reproduces known complete basis-set (CBS) ener-
geretics, if the individual energies are evaluated in large basis sets and extrapolated
to the CBS limit. We will furthermore demonstrate how the cost of such calcula-
tions can be dramatically reduced, without substantial loss of accuracy, by consistent
application of a truncated many-body expansion (MBE) to each of the energies in
Eq. (5.2). We thereby aim to reproduce the whole sequence of CP-corrected MP2/
aug-cc-pVXZ energies (abbreviated MP2/aXZ, for $X = D$, T, or Q), and thereby
perform MP2/CBS extrapolations in a small fraction of the computer time that is
required for traditional calculations. Finally, we will show that a triples correction
\begin{equation}
\delta_{\text{CCSD}(T)} = E_{\text{CCSD}(T)} - E_{\text{MP2}}
\end{equation}
can also be accurately approximated by means of truncated MBEs. Together, these techniques extend well-established techniques for estimating CCSD(T)/CBS-quality energetics to clusters that are far larger than what was previously possible.

5.2 BSSE background

Equation (5.2) nominally requires \( N_F + 1 \) calculations in the full \( N_F \)-body cluster basis set. Our strategy is to replace each individual energy in this equation with a MBE, then apply a consistent truncation of each. For the cluster energy \( E_{IJK\ldots} \), this looks like a traditional MBE,

\[
E_{IJK\ldots} = \sum_{i=1}^{N_F} E_i + \sum_{i=1}^{N_F} \sum_{j>i} \Delta E_{ij} + \sum_{i=1}^{N_F} \sum_{j>i} \sum_{k>j} \Delta E_{ijk} + \cdots ,
\]

where

\[
\Delta E_{ij} = E_{ij} - E_i - E_j
\]

(5.5a)

\[
\Delta E_{ijk} = E_{ijk} - E_{ij} - E_{ik} - E_{jk} + E_i + E_j + E_k .
\]

(5.5b)

For the monomer energies \( E_{IJK\ldots}^I \), however, some of the “bodies” \( I, J, K, \ldots \) are simply ghost atoms, and the energy of any term in the MBE that contains only ghost atoms is zero. The non-vanishing terms can be written

\[
E_{IJK\ldots}^I = E_I^I + \Delta E_I^{(2)} + \Delta E_I^{(3)} + \cdots
\]

(5.6)

where \( \Delta E_I^{(2)} \) and \( \Delta E_I^{(3)} \) represent the non-vanishing two- and three-body terms in the MBE of \( E_{IJK\ldots}^{I} \). After rearranging some terms, one obtains the following explicit
\[
\Delta E_{AB} = E(\begin{array}{ccc}
A & B & C \\
D & & \\
\end{array}) - E(\begin{array}{ccc}
A & B & C \\
D & & \\
\end{array}) - E(\begin{array}{ccc}
A & B & C \\
D & & \\
\end{array})
\]

\[
\Delta E_A^{(2)} = -3E(\begin{array}{ccc}
A & & \\
& & \\
\end{array}) + E(\begin{array}{ccc}
A & & \\
& & \\
\end{array})
\]

\[
\Delta E_A^{(3)} = +E(\begin{array}{ccc}
A & & \\
& & \\
\end{array}) + E(\begin{array}{ccc}
A & & \\
& & \\
\end{array})
\]

Figure 7: Illustration of one particular two-body term \(\Delta E_{IJ}\) that contributes to the binding energy of cluster \(IJKL\), and also a two-body term \(\Delta E_I^{(2)}\) that appears in the monomer energy \(E_I^{IJKL}\) [Eq. (5.7a)]. Monomers labeled with letters are actual molecules containing electrons, whereas unlabeled monomers are comprised of ghost atoms. Monomers shaded red are included in the calculation whereas monomers shaded gray are not.

Formulas for these corrections:

\[
\Delta E_I^{(2)} = -(N_F - 1)E_I^I + \sum_{J \neq I}^{N_F} E_I^{IJ} \tag{5.7a}
\]

\[
\Delta E_I^{(3)} = \frac{1}{2}(N_F - 1)(N_F - 2)E_I^I - (N_F - 2) \sum_{J \neq I}^{N_F} E_I^{IJ} + \sum_{J \neq I}^{N_F} \sum_{K > J}^{N_F} E_I^{IJK}. \tag{5.7b}
\]

Here, \(E_I^{IJK\cdots}\) denotes the energy of monomer \(I\), computed in the \(IJK\cdots\) basis, which therefore contains ghost atoms in place of monomers \(J, K, \ldots\).

The basic idea of this many-body counterpoise correction is illustrated in Fig. 7, which provides a pictorial representation of some two-body contributions to the binding energy of a cluster \(IJKL\). The term \(\Delta E_{IJ}\) is a traditional two-body energy correction, where dimer \(IJ\) is computed using the \(IJ\) basis set, and an estimate of
the binding energy is obtained by subtracting the monomer energies, computed using
their respective monomer basis sets. The term $\Delta E^{(2)}_I$ in the lower portion of Fig. 7
represents a two-body correction for the energy of monomer $I$ computed in the $IJKL$
basis. This term consists of three calculations involving a dimer basis with one ghost
monomer, along with a one-body calculation in a one-body basis set.

An $n$-body, CP-corrected approximation to the binding energy is obtained as the
difference between the cluster energy [Eq. (5.4)] and the monomer energies $E^{IJK\cdots}_I$
[Eq. (5.6)], each truncated at the $n$-body level. We refer to this procedure as an
nth-order many-body CP correction, MBCP($n$), and its aim is to reproduce the CP-
corrected binding energy in Eq. (5.2), albeit at significantly reduced cost. As such,
extrapolation is still required in order to obtain CBS-quality energetics, but this
can be accomplished by traditional means insofar as a high-quality approximation to
Eq. (5.2) can be obtained for a whole sequence of correlation-consistent basis sets.
It is worth noting that alternative fragment-based approaches such as the fragment
molecular orbital (FMO) method$^{32}$ appear to work best in small basis sets,$^{78}$ and
therefore cannot be exploited for what we aim to accomplish here.

The CP correction that is embodied by Eq. (5.2) has been criticized$^{77}$ for for
neglecting so-called “basis set extension” effects, which are best defined in the context
of the projection-operator formalism of the chemical Hamiltonian approach,$^{79}$ but
which should disappear in the CBS limit. An alternative CP correction that directly
addresses basis-set extension effects has been proposed by Valiron and Mayer,$^{77}$ but
the number of independent electronic structure calculations required for this Valiron-Mayer function counterpoise (VMFC) approach grows factorially with the number of monomers. Truncated two- and three-body versions, which we will call VMFC(2) and VMFC(3), were introduced later.\textsuperscript{80,81}

In fact, VMFC(2) is completely equivalent to MBCP(2), though the two approaches differ starting at \( n = 3 \). For \( n \geq 3 \), our MBCP(\( n \)) approach requires fewer independent electronic structure calculations; at the \( n = 3 \) level, for example, MBCP(3) requires only monomer calculations in the trimer basis set, whereas VMFC(3) requires both monomer and dimer calculations in the trimer basis. For a cluster with \( N = 11 \) monomer units, as in some of the numerical examples that follow, the VMFC(2)/MBCP(2) method requires 110 distinct electronic structure calculations whereas three-body approaches require an additional 990 calculations for VMFC(3) but only half that number for MBCP(3).

**Computational Methods**

For \((\text{H}_2\text{O})_6\), we use the MP2/haTZ geometries from Ref. [82], whereas Gly(\( \text{H}_2\text{O})_{10} \) and \((\text{H}_2\text{O})_{10}\text{F}^-\) structures are taken from our own simulations, using the \textsc{amoeba} force field,\textsuperscript{83} and were not relaxed. Only valence electrons were correlated in MP2 and CCSD(T) calculations, and MP2 calculations for Gly(\( \text{H}_2\text{O})_{10} \) and \((\text{H}_2\text{O})_{10}\text{F}^-\) employed the resolution-of-identity (RI) approximation, in conjunction with standard auxiliary basis sets.\textsuperscript{84} For CBS extrapolations, we first extrapolate the Hartree-Fock energy using a three-point (D, T, Q) exponential \textit{ansatz},\textsuperscript{85} then use a two-point
Figure 8: Comparison of two- and three-body counterpoise corrections, with and without electrostatic embedding (EE), for MP2/aDZ calculations on two different systems. Errors are reported with respect to a calculation performed on the entire cluster, for which the CP-corrected binding energy is defined by Eq. (5.2). To better resemble the self-consistent charge-embedding used in the original VMFC\((n)\) calculations, embedding charges are computed using the self-consistent XPol-ChElPG procedure.

\((T, Q)\) extrapolation of the MP2 correlation energy, using an \(X^{-3}\) ansatz.\(^{86}\) All electronic structure calculations were performed using Q-CHEM.\(^{55, 87}\) A home-built code, FRAGMECT (as described in Refs. [54] and [56]) was used as a driver.

### 5.3 VMFC\((n)\) compared to MBCP\((n)\)

Before considering CBS extrapolations, which is the main topic of this chapter, we first consider a numerical comparison of the VMFC\((n)\) and MBCP\((n)\) schemes. Fig. 8 shows the binding energy errors for various two- and three-body methods applied to two different systems: \((H_2O)_{10}F^-\) and Gly\((H_2O)_{10}\), where “Gly” denotes the zwitterionic tautomer of glycine. (These are challenging test cases owing to large many-body
polarization effects, and we have previously used them to test a variety of fragment-based approaches.\textsuperscript{46,54,56,57,88,89} Ten different isomers of both systems were used to generate error statistics, and “error” is defined in this chapter as deviation from the binding energy computed using Eq. (5.2).

Some of the monomer-based methods considered in Fig. 8 utilize electrostatic embedding (EE) for the \(n\)-body (dimer and trimer) electronic structure calculations, and in the VMFC\((n)\) calculations originally reported in Ref. \[81\], this was done in a sophisticated way based on charges and point dipoles that were iterated to self-consistency. In the interest of making a fair comparison, the EE results in Fig. 8 also employ self-consistent embedding charges, determined using our ChElPG-based version\textsuperscript{45,46} of the “explicit polarization” (XPol) procedure.\textsuperscript{44}

Examining the MP2/aDZ results in Fig. 8, we see that the two-body method is simply unacceptable unless electrostatic embedding is employed, consistent with the results of MBEs in which no attempt at CP correction is made.\textsuperscript{17} The difference here is that CP-corrected MP2/aDZ is an acceptable (if qualitative) level of theory for clusters, whereas small-basis MP2 calculations with no correction for BSSE whatsoever should not be trusted. The fact that fragment-based methods can accurately approximate supersystem energies in clusters is largely meaningless unless BSSE is addressed, by means of large basis sets and/or CP corrections.

The VMFC\((3)\) method, with or without electrostatic embedding, exhibits larger errors for the very challenging (H\(_2\)O)\(_{10}\)F\(^-\) system, as compared to MBCP\((3)\), and the EE-MBCP\((3)\) method appears quite promising. For this reason, our primary
focus will be on extending EE-MBCP\((n)\) methods to larger basis sets and evaluating their performance in CBS extrapolations, although a few additional results using the VMFC\((n)\) approach will be considered below, for comparative purposes.

Electrostatically-embedded MBEs are often remarkably insensitive to the details of the embedding scheme,\(^9\) at least for clusters composed of small, polar monomers, and in view of this observation the remaining calculations presented herein employ a very simple embedding in which those monomer units that are not included in the electronic structure calculation are replaced with gas-phase Mulliken charges computed at the B3LYP/6-31G* level. (Ghost atoms do not contribute embedding charges.) This approach is admittedly more simplistic than a self-consistent embedding procedure, and it is possible that a more sophisticated embedding might improve the EE-VMFC\((n)\) results. In view of the favorable performance of EE-MBCP\((n)\) with this simple embedding, however, we have not considered such alternatives.

5.4 Convergence to the CBS limit

Fig. 9 shows the convergence towards the basis-set limit of MP2/aXZ binding energies for the “bag” isomer of \((\text{H}_2\text{O})_6\). (Analogous plots for seven other isomers can be found in Appendix A, but the behavior of the methods discussed here is very similar in each case.) Extrapolating to the CBS limit using standard techniques (see Sec 5.2 for details), we obtain the same binding energy, to four significant digits, that was previously reported\(^8\) as the MP2/CBS limit, based on MP2-R12 calculations in a very large basis (modified aug-cc-pV5Z). CBS extrapolation using aug-cc-pVXZ through X
Figure 9: Convergence to the CBS limit for the “bag” isomer of \((\text{H}_2\text{O})_6\). CP-MP2 denotes traditional counterpoise-corrected MP2 [Eq. (5.2)], whereas EE-MBCP(3) is a three-body approximation to CP-MP2. The EE-MB(3) method is a three-body approximation to the uncorrected MP2 energy. The shaded region delineates ±1 kcal/mol of the MP2/CBS binding energy.

\(= 5\) agrees with these results as well,\(^{91}\) which gives us confidence that the MP2/CBS binding energy has been accurately determined for this system. Results in Fig. 9 demonstrate that we can accurately approximate this limit via a low-order MBE, provided that CP corrections are included.

When attempting to compute cluster binding energies in the CBS limit, it is commonly assumed that the CP-corrected and uncorrected results place error bars on the value that would be obtained in the CBS limit.\(^{91,92}\) For this \((\text{H}_2\text{O})_6\) example, we do obtain usable error bars, but even at the quadruple-\(\zeta\) level these bounds are no better than ±1 kcal/mol. On the other hand, the average of the CP-corrected and uncorrected binding energies affords a quite accurate estimate of the CBS limit.
at the triple-ζ level ($< 0.04$ kcal/mol error). The same cannot be said at the double-ζ level, where even this average is in error by 1.4 kcal/mol. This is important to consider in the context of fragment-based electronic structure methods, which have often\textsuperscript{17–19,21,81,93} (though not always\textsuperscript{59,62,63,94–97}) been performed using double-ζ basis sets.

Here, we observe monotonic convergence of the many-body approximations to the binding energy, as a function of $X (= D, T, Q)$. The EE-MBCP(3) method affords a very accurate approximation to the CP-corrected MP2 binding energy in each basis set (errors $< 0.3$ kcal/mol, and improving with basis size), and can be used on its own to obtain the MP2/CBS result (error = 0.12 kcal/mol). Better still, having done that calculation, one has all the information required for a more traditional three-body approximation \textit{without} CP correction. This method, which we call EE-MB(3), affords a highly accurate approximation to the \textit{uncorrected} MP2 binding energy (except at the double-ζ level, where the error is 0.8 kcal/mol). Together, the EE-MBCP(3) and EE-MB(3) methods can be used to bracket the CBS limit in the usual way, but without the need for any electronic structure calculations on systems larger than trimers.

5.5 Timings

Moreover, this approach requires only a fraction of the computer time that is required for traditional supersystem calculations. Considering only the MP2 calculations required for the BSSE corrections, Fig. 10 shows the total aggregate computer time
Figure 10: Timing data for RI-MP2/aXZ single-point calculations on $(\text{H}_2\text{O})_{10}\text{F}^-$. The total aggregate wall time required for a CP-MP2 calculation is shown on the logarithmic scale at right, whereas the linear axis on the left shows the ratio of the MBCP(2) or MBCP(3) time to the CP-MP2 time, which indicates the speed-up for the fragment-based calculations. All calculations were run in serial on a single 2.5 GHz Opteron processor, meaning that we have not taken advantage of the embarrassingly-parallel nature of the MBCP($n$) methods.

required to perform CP-corrected MP2/aXZ calculations for the $\text{F}^-(\text{H}_2\text{O})_{10}$ system, for $X = D$, $T$, and $Q$. For $X = Q$, the 12 different calculations required by Eq. (5.2) consume a total of 87 days of wall time. Setting aside, for the moment, the fact that the MBCP($n$) calculations are embarrassingly parallelizable, and instead simply focusing simply on the total wall time required for all of the individual calculations, we find that the MBCP(3) approach reduces the total time for $X = Q$ by more than 70%,
and MBCP(2) reduces it by more than 98%! Moreover, no single electronic structure calculation is more expensive than 1737 sec [MBCP(2)] or 8510 sec [MBCP(3)], so the total waiting time can be made as short as that, given a sufficient number of processors. (For \( N = 11 \) monomers, that “sufficient number” is 445, which nowadays does not even constitute “massively parallel”.)

### 5.6 \( \delta_{\text{CCSD(T)}} \) corrections

Furthermore, these MP2/CBS binding energies can be extended to CCSD(T)/CBS quality by means of a MBE applied to the difference \( E_{\text{CCSD(T)}} - E_{\text{MP2}} \), Eq. (5.3). This difference converges more rapidly with respect to basis expansion than do either of the individual energies,\(^{98-101} \) and basis sets of triple-\( \zeta \) quality are sufficient to converge this correction term. In the case of (H\(_2\)O\(_6\)), the haTZ basis set (aTZ without diffuse functions on hydrogen) has been used for this purpose, and values of \( \delta_{\text{CCSD(T)}} \) for eight different isomers are reported in Ref. [82].

Fig. 10 compares these benchmark values to corrections obtained based on a two- or a three-body approximation to \( \delta_{\text{CCSD(T)}} \). Both approximations prove to be quite accurate, with mean unsigned errors (MUEs) of only 0.09 kcal/mol for the EE-MB(2) approximation and < 0.01 kcal/mol for the EE-MB(3) approximation, with respect to an exact calculation of \( \delta_{\text{CCSD(T)}} \) requiring CCSD(T)/haTZ calculations on the full hexamer. In terms of accuracy, the EE-MBCP(3) method, applied to approximate the sequence of MP2/aXZ energies and thereby to extrapolate the MP2/CBS limit, augmented with a two-body CCSD(T) approximation, affords results that differ by
Table 10: Triples corrections, $\delta_{\text{CCSD(T)}}$, for isomers of (H$_2$O)$_6$ and errors engendered by low-order many-body approximations to $\delta_{\text{CCSD(T)}}$.

<table>
<thead>
<tr>
<th>isomer</th>
<th>$\delta_{\text{CCSD(T)}}^{a,b}$</th>
<th>error$^{a,c}$</th>
<th>EE-MB(2)</th>
<th>EE-MB(3)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bag</td>
<td>0.33</td>
<td>$-0.08$</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>Boat1</td>
<td>0.53</td>
<td>0.04</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>Boat2</td>
<td>0.51</td>
<td>0.04</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>Book1</td>
<td>0.33</td>
<td>$-0.04$</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>Book2</td>
<td>0.33</td>
<td>$-0.04$</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>Cage</td>
<td>0.13</td>
<td>$-0.20$</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>Cyclic</td>
<td>0.53</td>
<td>0.05</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>Prism</td>
<td>$-0.06$</td>
<td>$-0.20$</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>MUE$^d$</td>
<td>—</td>
<td>0.09</td>
<td>0.00</td>
<td></td>
</tr>
</tbody>
</table>

$^a$All values in kcal/mol. $^b$Values obtained from CCSD(T)/haTZ calculations in Ref. [82]. $^c$Errors engendered by two- and three-body CCSD(T)/haTZ calculations. $^d$Mean unsigned error for all eight isomers.

< 0.1 kcal/mol as compared to the best existing estimates of the CCSD(T)/CBS binding energy for (H$_2$O)$_6$.

It is certainly true that the triples correction for (H$_2$O)$_6$ is small relative to values obtained for some dispersion-dominated systems. An example of the latter is the benzene dimer, for which $\delta_{\text{CCSD(T)}} \approx 2.0\text{--}2.5$ kcal/mol.$^{102}$ On the other hand, three-body effects are no larger than 0.33 kcal/mol for any isomer of benzene trimer,$^{103}$ and are more often an order-of-magnitude smaller than that.$^{103,104}$ In acetylene clusters, the triples correction is not much larger than it is for the water hexamer.$^{96,105}$ In view of the general success of two-body approximations to the correlation energy,$^{18,62,95,106}$
we expect the combination of fragment-based and CP-corrected MP2/CBS extrapolations, in conjunction with a two-body CCSD(T) correction, to be a robust and accurate approach.

5.7 Analysis of BSSE corrected results

To test the robustness of these procedures, we examine errors (with respect to MP2/CBS benchmarks) for eight isomers of (H$_2$O)$_6$. Figure 11(a) shows error statistics obtained using a variety of MBE-based methods to approximate the MP2/aXZ energies, which are then extrapolated to the CBS limit and compared to the benchmarks to determine the error. (Several of these methods represent “control experiments” designed to understand the limits of the methodology, rather than practical procedures intended for production calculations, as will become clear in the discussion below.)

Consistent with the results for the bag isomer in 9, where extrapolation of uncorrected MP2 binding energies does not afford the correct MP2/CBS limit, we observe MUEs $> 0.4$ kcal/mol for the EE-MB(2) and EE-MB(3) methods that do not employ CP correction. In fact, the three-body approximation actually affords the larger error, owing to fortuitous error cancellation in the two-body case. Specifically, three-body effects contribute $\sim 10$ kcal/mol to the binding energy of (H$_2$O)$_6$, so a two-body approximation would underbind by about this much except that BSSE overstabilizes the cluster by approximately the same amount. This error cancellation is also the reason why CP correction slightly increases the mean error at the two-body level, but when
the important three-body interactions are included, CP correction serves to significantly decrease the mean error. Together, these results demonstrate the importance of CP correction even when CBS extrapolation is employed, as is also seen in the basis-set convergence behavior shown in 9, which is smoother for the CP-corrected results than for the uncorrected ones.

As another experiment, we use an $n$-body $[\text{EE-MB}(n)]$ approximation to the cluster energy and subtract from this a "full" CP correction, in which each monomer energy is computed using the entire cluster basis set. (In other words, we use an $n$-body approximation for $E_{IJK...}$ in Eq. (5.2) but not for $E_{i}^{IJK...}$.) We consider this to be an unbalanced approximation, and one that is rather expensive as compared to EE-MBCP($n$), but we include it here simply to demonstrate that such a correction cannot rescue the $n = 2$ calculations from errors $> 0.4$ kcal/mol. On the other hand, a balanced, two-body approximation to Eq. (5.2), i.e., the EE-MBCP(2) method, actually affords slightly larger errors as compared to this unbalanced "full CP" correction.

To achieve an accuracy of $\lesssim 0.1$ kcal/mol, three-body terms are evidently required, as has been found in previous studies where CP-corrected two- and three-body terms have been used in a MBE.\textsuperscript{9,107,108} For EE-MBCP(3) method, the MUE is an acceptable 0.1 kcal/mol. A "full" CP correction reduces this MUE only very slightly (and not in all cases, as shown below), and does not justify the greatly increases cost of adding a cluster’s worth of extra virtual orbitals to each monomer calculation.

In 11(b) we consider a larger and more challenging test case, namely, ten isomers
of \((\text{H}_2\text{O})_{10}\text{F}^-\), where binding energies for our unrelaxed structures are on the order of \(-115\) kcal/mol and span a range of 10 kcal/mol. Here, the performance of EE-MBCP(3) exceeds even that of EE-MB(3) with a full CP correction—possibly owing to the unbalanced nature of the latter approach—and affords a MUE of 0.18 kcal/mol with respect to CP-corrected MP2/CBS benchmarks. The EE-VMFC(3) approach affords a MUE that is only slightly larger, 0.28 kcal/mol, demonstrating that any “basis extension” effects\textsuperscript{77,79} still present in the CP-corrected binding energy defined by Eq. (5.2) must be quite small. The MUE for the relative isomer energies, computed at the EE-MBCP(3) level, is 0.24 kcal/mol, which demonstrates that not only total binding energies but also relative conformational energies are predicted accurately by this low-cost approximation.

5.8 Summary

In summary, we have shown that the EE-MBCP(3) method, which incorporates counterpoise corrections in a simple way and requires electronic structure calculations on subsystems no larger than trimers, can be used to approximate the sequence of CP-corrected MP2/aug-cc-pVXZ calculations \(X = \text{D, T, Q}\). The MP2/CBS limit can thus be obtained (via traditional extrapolation techniques) at low cost, even in challenging systems such as \((\text{H}_2\text{O})_{10}\text{F}^-\). This many-body counterpoise correction may also be useful in studies of non-covalent interactions in even larger systems, where no attempt may be made to extrapolate to the CBS limit, but where CP correction is nevertheless useful for avoiding large artifacts in potential energy surfaces that are...
caused by BSSE.\textsuperscript{109–113}

Total computational time is dramatically reduced by our EE-MBCP(3) procedure, even if no parallelism is exploited at all. Owing to the embarrassingly-parallel nature of the truncated MBE, wall times can be reduced even further by farming out the subsystem calculations to a large number of processors. For rough screening of the energy landscape at a slightly lower level of accuracy, two-body EE-MBCP(2) calculations can be performed at a total cost that is dramatically reduced even in comparison to the three-body method.

In conjunction with \textit{two}-body CCSD(T) calculations in a triple-\(\zeta\) basis set, binding energies within \(\lesssim 0.2\) kcal/mol of CCSD(T)/CBS benchmarks are obtained for hydrogen-bonded clusters whose total binding energies exceed 40 kcal/mol, which represents an error of \(< 0.5\%\). Previous work at much lower levels of theory (\textit{e.g.}, B3LYP/double-\(\zeta\)) has shown that we can reproduce lower-level binding energy benchmarks quite accurately in systems as large as \((\text{H}_2\text{O})_{57}\);\textsuperscript{54,56,88} which makes us optimistic about our ability to scale up the techniques presented here, to significantly larger cluster sizes. This paves the way to obtaining CCSD(T)/CBS-quality energetics in clusters of hitherto unthinkable size, as well as to geometry optimizations on BSSE-free potential energy surfaces.
Figure 11: Mean unsigned errors with respect to MP2/CBS binding energies for (a) eight isomers of \((\text{H}_2\text{O})_6\) and (b) ten isomers of \((\text{H}_2\text{O})_{10}\text{F}^–\), computed by basis-set extrapolation using an assortment of low-cost many-body methods to approximate the MP2/aXZ energies \((X = D, T, Q)\). The “full CP” correction means that the entire cluster basis set is used to compute the monomer energies.
CHAPTER 6

Thorough comparison of many-body counterpoise corrections

In the previous chapter, Chapter 5, we saw the importance of correcting for BSSE when high accuracy is the desired goal. We also briefly mentioned another many-body BSSE correction method designed for this purpose, known as VMFC($n$). The purpose of this chapter is to study both of these BSSE corrections in more detail, particularly to see if we can discern scenarios in which the more costly VMFC($n$) is to be preferred over the less costly MBCP($n$). Ultimately, it will be concluded that no such discernment can be made for the systems considered here, causing us to recommend the use of MBCP($n$).

6.1 Introduction

Ab initio calculations are routinely used to predict various chemical properties. Two factors control the accuracy of such calculations: the level of theory used to describe electron correlation, and the size of the one-particle basis set. Convergence with respect to the latter, which is the topic of the present work, is generally not an option and one must resort to extrapolation procedures to estimate the complete
basis-set (CBS) limit. The fact that the basis set is not complete implies that the finite-basis solution to Schrödinger’s equation lacks sufficient flexibility to model the true wave function, leading to *basis-set incompleteness error* (BSIE). It is worth noting that BSIE can sometimes compensate for inadequacies in the treatment of electron correlation; to unmask such errors, it is important to be able to perform CBS extrapolations for the systems of interest.

An additional complication arises for energy differences, namely, the presence of *basis-set superposition error* (BSSE). Consider the canonical case of computing a dimer (*A*···*B*) binding energy. Here, the dimer (*AB*) basis set is larger and more flexible than either monomer basis set, hence a naïve calculation of the binding energy according to the equation

\[ \Delta E = E_{AB} - E_A - E_B , \]  

in any finite basis set, represents an unbalanced approximation. BSSE is a reflection of this fact. The familiar Boys-Bernardi counterpoise (CP) correction\(^\text{73}\) amounts to adding extra basis functions in calculating *E*\(_A\) and *E*\(_B\), in such a way as to correct for the unbalanced nature of the binding energy in Eq. (6.1).

BSSE and BSIE are intimately related,\(^\text{114,115}\) which makes it difficult to disentangle them or quantitatively define either one.\(^\text{75}\) Whereas Eq. (6.1) suggests that BSSE is solely an intermolecular phenomenon, *intramolecular* BSSE may exist as well, especially in larger molecules, and may affect the relative energies of, *e.g.*, a compact versus an extended structure of a polypeptide.\(^\text{109–113,116}\)
Unfortunately, the separation between inter- and intramolecular BSSE is somewhat arbitrary in a macromolecule, depending upon the semantics of defining boundaries between “molecular” units that sever covalent bonds, although intramolecular CP corrections along these lines have been proposed. The present study sidesteps this issue by focusing on clusters of small molecules that should thus contain little intramolecular BSSE. We therefore make no attempt to correct for intramolecular BSSE except via extrapolation to the CBS limit.

The Boys-Bernardi CP correction and its many-body generalizations, which are discussed in Section 5.2, provide a means to account for finite-basis inadequacies. Many of these corrections, however, rely on a series of calculations in the full (supersystem) basis set, which can become burdensome for large clusters of molecules, or where a high level of theory is employed. For sufficiently large clusters, even non-BSSE-corrected calculations become intractable, and in such cases a popular avenue is fragment-based quantum chemistry. (See Ref. [5] for a recent review and Ref. [54] for additional discussion of how some of these methods are related to one another.) Fragment-based methods assume that supersystem properties are obtainable from isolated subsystem properties, allowing for a host of smaller calculations, that are embarrassingly parallelizable and can be combined to given an approximate value for the supersystem quantity of interest.

In the interest of obtaining high-level benchmarks using fragment-based methods, we wish to explore their use with correlated wave functions and large, correlation-consistent basis sets. To this end, two different BSSE corrections have been introduced
that are compatible with a truncated (at order \( n \)) many-body expansion: the many-body counterpoise correction, MBCP(\( n \)),\textsuperscript{118} and the Valiron-Mayer function counterpoise correction, VMFC(\( n \)).\textsuperscript{81} A preliminary comparison of these two approaches was presented in Chapter 5, and the present study provides a more complete follow-up, with particular emphasis on extrapolation to the CBS limit.

At the outset, we note that several previous studies\textsuperscript{63,89,118} have demonstrated that a two- or three-body expansion in a triple-\( \zeta \) basis set is sufficient to obtain a high accuracy “triples” correction,

\[
\Delta E^{\text{CCSD(T)}} = E^{\text{CCSD(T)}} - E^{\text{MP2}}. \tag{6.2}
\]

Thus, by understanding how errors from a truncated \( n \)-body expansion (with or without CP corrections) compare to MP2/CBS results, we learn how such errors affect CCSD(T)/CBS results.

### 6.2 “Exact” and approximate BSSE corrections

In the previous chapter, we provided some background on BSSE corrections, appropriate for our purposes there. Here, however, we provide a more thorough background so that the forthcoming analyses are on firmer grounds.

#### 6.2.1 “Exact” BSSE corrections

In the spirit of Boys-Bernardi CP correction, many-body BSSE corrections will involve “ghost atom” basis functions on some monomers. We will use a notation with subscripts refer to monomer indices, as we have till this point, but we now introduce
superscript indices to indicate which monomers contribute basis functions to a given term. For example, \( E_I^{IJ} \) represents the energy of the “real” monomer \( I \) computed in the basis of dimer \( IJ \), and \( E_{IJ}^{IJK} \) denotes the energy of the dimer \( IJ \) computed in the basis of the trimer \( IJK \).

**Boys-Bernardi counterpoise correction**

The most popular BSSE correction method, the Boys-Bernardi CP correction, uses the full cluster basis set for each monomer calculation. The CP-corrected binding energy, \( E_{\text{B.E.}} \), is therefore given by

\[
E_{\text{B.E.}} = E_{IJK\cdots N_F} - \sum_I E_{I}^{IJK\cdots N_F} .
\] (6.3)

This formula represents the natural \( N_F \)-body generalization of the method introduced by Boys and Bernardi for dimers, and we will refer to it simply as the CP correction. Equation (6.3) has also been called the “site-site function CP method”.

It is convenient to add and subtract the energy of each monomer, in its own basis set, to arrive at an additive correction, \( \mathcal{E}^{\text{CP}} \), to the uncorrected energy:

\[
E_{\text{B.E.}} = E_{\text{uncorrected}} + \mathcal{E}^{\text{CP}} .
\] (6.4)

The uncorrected binding energy is computed by generalizing the naïve formula of Eq. (6.1),

\[
E_{\text{uncorrected}}^{\text{B.E.}} = E_{IJK\cdots N_F} - \sum_I E_{I}^{IJK\cdots N_F} ,
\] (6.5)

and therefore the CP correction is

\[
\mathcal{E}^{\text{CP}} = \sum_I (E_{I}^{I} - E_{I}^{IJK\cdots N_F}) .
\] (6.6)
The convenience of this additive correction is that it facilitates a correction for intramolecular BSSE by fragmenting a molecule across covalent bonds. 117

**Valiron-Mayer function counterpoise correction**

In the literature concerning BSSE, there is a prevalent belief that the CP scheme, in one fashion or another, does not properly account for BSSE, though many of these early claims were later refuted. 75 Perhaps the most familiar criticism of the Boys-Bernardi scheme is that it neglects “higher-order” BSSE effects. 77 Valiron and Mayer suggest that for a cluster of \( N_F \) monomers, the proper way to remove all BSSE is to remove BSSE from all pairs of monomers, from all trimers of monomers, and so on. Using this reasoning, it is straightforward to arrive at a BSSE-corrected binding energy of the form 77

\[
E_{\text{B.E.}} = E_{\text{B.E.}}^{\text{uncorrected}} + \sum_i \left( E_i' - E_i^{IJK\cdots N_F} \right) + \sum_{i<j} \left( \Delta E_{ij}' - \Delta E_{ij}^{IJK\cdots N_F} \right) + \sum_{i<j<k} \left( \Delta E_{ijk}' - \Delta E_{ijk}^{IJK\cdots N_F} \right) + \cdots
\]

Of particular importance here is the fact that the first correction to the binding energy is a term equal to the standard Boys-Bernardi CP correction, which lends support to the claim that the latter procedure neglects higher-order BSSE effects. The BSSE correction \( E^{\text{VMFC}} \) that is suggested by Eq. (6.7) is known as the Valiron-Mayer function counterpoise (VMFC) correction.
CP versus VMFC

The VMFC method has seen little practical use because its cost grows rapidly with the number of monomers. This is easily seen by considering the number of individual calculations each method requires. For an $N_F$ monomer cluster, the VMFC correction requires $2^N - 1$ calculations in the supersystem basis set, whereas the Boys-Bernardi CP correction requires only $N_F$. Furthermore, various studies have shown that the differences in VMFC and CP binding energies is typically less than 1.0 kcal/mol.\textsuperscript{80,81,120} A literature search reveals only one exception, namely, (H$_2$O)$_6$ binding energies computed at the MP2/cc-pVDZ level of theory, for which a difference of about 4 kcal/mol is obtained.\textsuperscript{81} However, this sizable difference is reduced to only 0.3 kcal/mol by the addition of diffuse basis functions.\textsuperscript{81}

The claim that CP is negligible naturally poses the question of which BSSE method is best. Currently this question is unanswered and it seems likely that debate will continue for some time because any attempt to resolve this issue must contend with the fact that the difference between the CBS result and any truncated basis set result is equal to the sum of BSIE and BSSE. Without an explicit formula for either it is impossible to determine whether CP, VMFC, or some other correction best eliminates the “true” BSSE. Here, we focus instead on each method’s ability to replicate benchmark results.
Table 11: Total number of distinct electronic structure calculations required in order to evaluate various BSSE corrections.

<table>
<thead>
<tr>
<th>Name</th>
<th>Full basis\textsuperscript{a}</th>
<th>m-mer basis\textsuperscript{b}</th>
<th>Total\textsuperscript{c}</th>
</tr>
</thead>
<tbody>
<tr>
<td>CP</td>
<td>(N_F)</td>
<td>0</td>
<td>(N_F)</td>
</tr>
<tr>
<td>VMFC</td>
<td>(2N_F - 2)(\sum_{i=2}^{2m - 2} N C_i)</td>
<td>((2^m - 2)N C_m)</td>
<td>(N_F\sum_{i=2}^{2m - 2} N C_i)</td>
</tr>
<tr>
<td>VMFC((n))</td>
<td>0</td>
<td>((2^m - 2)N C_m)</td>
<td>(N_F\sum_{i=2}^{2m - 2} N C_i)</td>
</tr>
<tr>
<td>MBCP((n))</td>
<td>0</td>
<td>(N_F N_{F-1} C_{m-1})</td>
<td>(N_F\sum_{i=2}^{n} N_{F-1} C_{i-1})</td>
</tr>
</tbody>
</table>

\textsuperscript{a}Number of calculations involving the supersystem basis
\textsuperscript{b}Number of calculations involving a subsystem basis with functions on \(m\) monomers (\(m < N_F\))
\textsuperscript{c}Total number of distinct electronic structure calculations

### 6.2.2 Approximate BSSE corrections

The number of terms required to apply the BSSE corrections discussed above is given in Table 11. For VMFC, the number of calculations in the supersystem basis set grows exponentially with \(N_F\). That fact, combined with an unwieldily number of smaller calculations as well, means that the VMFC approach is feasible only for very small clusters. The CP approach is more tractable but also becomes expensive for large systems, particularly those likely to be investigated using fragment-based methods.

To apply these two BSSE corrections to larger systems, approximate versions based on \(n\)-body truncation have been proposed\textsuperscript{81,118}. We next discuss these approximate methods.

**MBCP\((n)\)**

Our group recently proposed an approximate form of the Boys-Bernardi CP correction that we called the *many-body counterpoise correction*,\textsuperscript{118} abbreviated as MBCP\((n)\)
when the MBE is truncated at order \( n \). The idea behind MBCP(\( n \)) is that each one of the \( E^{IJK}_{\cdots N_F} \) terms in the normal CP correction [Eq. (6.3)] can be fragmented using a MBE. This gives a hierarchy of methods, each corresponding to a particular value of \( n \). Here, we focus on the cases \( n = 2 \) and \( n = 3 \), for which the MBCP(\( n \)) corrections are

\[
E^{\text{MBCP}(2)} = \sum_I \sum_{J \neq I} (E^{IJ}_I - E^{I}_I) 
\]

(6.8a)

\[
E^{\text{MBCP}(3)} = \sum_I \sum_{J \neq I} \sum_{K > J} \sum_{K \neq I} [E^{IJK}_I - (E^{IJ}_I - E^{I}_I) \nonumber \\
- (E^{IK}_I - E^{I}_I) - E^{I}_I] 
\]

(6.8b)

The many-body nature of these equations is immediately apparent when compared to Eq. (2.4) and Eq. (2.5). The final BSSE-corrected binding energy, at the MBCP(3) level for example, would be written

\[
E^{\text{MBCP}(3)}_{\text{B.E.}} = E^{\text{uncorrected}}_{\text{B.E.}} + \sum_I E^I_I 
+ \mathcal{E}^{\text{MBCP}(2)} + \mathcal{E}^{\text{MBCP}(3)} 
\]

(6.9)

There are several points worth making at this time. For MBCP(\( n \)) with \( n < N_F \), there will be no supersystem basis set calculations, in fact it is readily seen that the largest basis set needed is that of \( n \) monomers at a time. Furthermore, no calculation needed for MBCP(\( n \)) will have more than one “real” monomer at a time, e.g., \( E^{IJK}_I \) in Eq. (6.8b) consists of one real monomer and two ghost monomers. Finally, because each term in the correction is independent of the other terms, the MBCP(\( n \)) procedure is highly parallelizable.
VMFC($n$)

Kamiya et al.\textsuperscript{81} have proposed an approximate form of the VMFC that we will call VMFC($n$). This approach is motivated by the realization that Eq. (6.7) has terms involving monomer basis sets, dimer basis sets, and so on up to the full supersystem basis set. Neglecting all terms in Eq. (6.7) that involve basis functions on more than $n$ monomers affords

$$E_{\text{B.E.}} = E_{\text{B.E.}}^{\text{uncorrected}} + \sum_{I=1}^{N_F} E_I^I + \sum_{I<J}^{N_F C_2} \Delta E_{I,J}^{I,J}$$

(6.10)

+ \sum_{I<J<K}^{N_F C_3} \Delta E_{I,J,K}^{I,J,K} + \cdots + \sum_{I<J<K<\cdots<n}^{N_F C_n} \Delta E_{I,J,K<\cdots<n}^{I,J,K<\cdots<n}.

Upon relabeling the terms, we can rewrite this equation as

$$E_{\text{B.E.}} = E_{\text{B.E.}}^{\text{uncorrected}} + \sum_{I=1}^{N_F} E_I^I + \mathcal{E}^{\text{VMFC}(2)}$$

(6.11)

+ \mathcal{E}^{\text{VMFC}(3)} + \cdots + \mathcal{E}^{\text{VMFC}(n)},$$

which defines the various $n$-body BSSE corrections, $\mathcal{E}^{\text{VMFC}(n)}$.

For a given truncation order, $n$, VMFC($n$) includes all the terms that MBCP($n$) does, as well as terms arising from dimers in the $n$-body basis, trimers in the $n$-body basis, and so on, up to $(n-1)$-mers in the $n$-body basis. As such, VMFC($n$) is far more expensive than MBCP($n$), except for $n = 2$, where the two methods are equivalent. It is reasonable to ask at this point if these “extra” terms afford additional accuracy, but as discussed in Section 6.2.1, the answer is complicated by BSIE, as well as by the error in truncating the MBEs that give rise to VMFC($n$) and MBCP($n$). These errors are difficult to disentangle. The results presented below, along with
previous studies, \cite{80,81,120} seem to suggest that these terms are not worth the increased computational time.

6.3 Computational details

In previous tests of our MBCP($n$) method, \cite{118} we used eight isomers of (H$_2$O)$_6$ for which binding energies computed at the MP2-R12/K2-- level of theory, \cite{121,122,123} along with MP2/haTZ geometries, are available in Ref. [82]. The K2-- basis set is a modified version of aug-cc-pV5Z and due to the rapid convergence of the MP2-R12 energy with respect to basis expansion, these energies are expected to be converged to the CBS result without the need for extrapolation. \cite{82} This makes them ideal benchmarks for comparing MBCP($n$) and VMFC($n$).

We also consider a set of ten (H$_2$O)$_{10}$F$^-$ clusters, using unrelaxed structures from a molecular dynamics simulation as reported in Ref. [54]. Energetics were computed at the resolution-of-identity (RI) MP2 level, \cite{124} using standard auxiliary basis sets. \cite{84}

CBS-quality results were obtained via separate extrapolations for the Hartree-Fock (HF) energy and the correlation energy by means of standard extrapolation procedures. For the HF energies a three-point fit was used, \cite{85}

$$E_{\zeta}^{HF} = E_{CBS}^{HF} + ae^{-b\zeta}$$ (6.12)

where $a$ and $b$ are fitting parameters and $\zeta = 2, 3, 4$ for the aug-cc-pVDZ, aug-cc-pVTZ, aug-cc-pVQZ basis sets. (We will refer to these as the aug-cc-pV$\zeta$Z sequence of basis sets, or “a$\zeta$Z” for short.) For the correlation energy we used a two-point fit,
where $c$ is a fitting parameter. When the highest basis set used is of aug-cc-pV($\zeta+1$)Z quality, both of these extrapolation schemes have been shown to be capable of replicating benchmark results of at least aug-cc-pV($\zeta+1$)Z quality. This means that our current CBS extrapolation procedure should adequately replicate the quintuple-$\zeta$ benchmarks.

Binding energies are reported with respect to relaxed monomers. This adds an additional complication from a BSSE correction standpoint, because BSSE corrections are performed at the supersystem geometry. It therefore becomes necessary to account for the relaxation via an additive correction, $E_{\text{relax}}$. The form of the relaxation energy,

$$E_{\text{relax}} = \sum_{I=1}^{N_F} (E_I^I - E_{I}^{\text{opt}}) ,$$

is independent of the type of BSSE correction. Here, $E_I^I$ denotes monomer $I$’s energy computed in its own basis at the supersystem geometry, and $E_{I}^{\text{opt}}$ is the same quantity computed at the minimum-energy monomer geometry.

All electronic structure calculations were performed using Q-Chem. Creation of Q-Chem inputs for the MBE calculations was carried out using our program FRAGME\textsc{nT}, which creates the appropriate input files when the user inputs the desired fragmentation, embedding, and capping method. (In the present study, each fragment consists of either a single H$_2$O molecule or F$^-$ ion, so no capping is necessary.) FRAGME\textsc{nT} also handles the creation of all input files required to compute the
BSSE corrections. The MBE is truncated at either \( n = 2 \) or \( n = 3 \); we refer to these two methods as “2B” and “3B”, respectively. The EE-2B and EE-3B methods are the corresponding electrostatically-embedded (EE) methods. We use a point-charge embedding along the lines of that used by Dahlke and Truhlar,\(^{17,18,93}\) in which Mulliken charges (computed at the B3LYP/6-31G* level) are used to represent those atoms not included in a monomer, dimer, or trimer electronic structure calculation. The monomer geometries used to compute these point charges are those appropriate for the cluster geometry.

### 6.4 Results

#### 6.4.1 CBS extrapolation

We are using nonlinear fits to extrapolate a sum of energy components, so the order of the summation does not commute with the extrapolation and results are sensitive to whether various components of the binding energy are added before or after extrapolation. In an attempt to ensure that our forthcoming results are not biased unfairly towards one BSSE correction or another, we briefly consider the impact of several different ways of calculating the binding energy. The relaxed binding energy, \( \tilde{E}_{\text{B.E.}}^X \), where the tilde indicates that the relaxation energy is included and \( X \) indicates a particular flavor of BSSE correction, \( e.g., \ X = \text{CP} \), can be extrapolated in eight
unique ways:

\[ E_{\text{B.E.}} \cdot X = (E_{\text{uncorrected}} + E_{\text{relax}}) + (\mathcal{E}^X) \]  
(6.15a)

\[ E_{\text{B.E.}} \cdot X^n = (E_{\text{uncorrected}}) + (E_{\text{relax}} + \mathcal{E}^X) \]  
(6.15b)

\[ E_{\text{B.E.}} \cdot X^n = (E_{\text{uncorrected}}) + (E_{\text{relax}} + \mathcal{E}^X) \]  
(6.15c)

\[ E_{\text{B.E.}} \cdot X^n = \left( E_{(\text{H}_2\text{O})_6} + E_{\text{relax}} + \mathcal{E}^{X*} \right) \]  
(6.15d)

\[ E_{\text{B.E.}} \cdot X^n = \left( E_{(\text{H}_2\text{O})_6} + E_{\text{relax}} \right) + (\mathcal{E}^{X*}) \]  
(6.15e)

\[ E_{\text{B.E.}} \cdot X^n = \left( E_{(\text{H}_2\text{O})_6} + \mathcal{E}^{X*} \right) + (E_{\text{relax}}) \]  
(6.15f)

\[ E_{\text{B.E.}} \cdot X^n = \left( E_{(\text{H}_2\text{O})_6} \right) + (E_{\text{relax}} + \mathcal{E}^{X*}) \]  
(6.15g)

\[ E_{\text{B.E.}} \cdot X^n = \left( E_{(\text{H}_2\text{O})_6} \right) + (E_{\text{relax}} + \mathcal{E}^{X*}) \]  
(6.15h)

In each of these equations, the terms grouped in parenthesis are added together prior to extrapolation, so that in Eq. (6.15d), for example, only a single extrapolation is performed, whereas in Eq. (6.15h) all three components of the binding energy are extrapolated separately. As will become evident shortly, \((E_{\text{B.E.}} + E_{\text{relax}} + \mathcal{E}^X)\) is equivalent to Eq. (6.15d) and \((E_{\text{B.E.}} + \mathcal{E}^X) + (E_{\text{relax}})\) is equivalent to Eq. (6.15f) so the equations above represent all unique permutations.

For convenience, the various energetic components in these equations are defined in Table 12, but we call attention to two components in particular. For a particular BSSE correction method, \(X\), we can define

\[ \mathcal{E}^X = E_{\text{B.E.}}^X - E_{\text{B.E.}}^{\text{uncorrected}} \]  
(6.16)

and a formula for \(\mathcal{E}^X\) can be worked out from Eq. (6.4), Eq. (6.9), or Eq. (6.11) for \(X = \text{CP}, \text{MBCP}(n), \text{and VMFC}(n)\) respectively. The definition of \(\mathcal{E}^{X*}\) is best given
Table 12: Energetic quantities used in the CBS extrapolations in Eq. (6.15).

<table>
<thead>
<tr>
<th>Quantity</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \tilde{E}_{\text{X}B} )</td>
<td>Total relaxed, BSSE-corrected binding energy using BSSE correction method X</td>
</tr>
<tr>
<td>( E_{\text{X}B} )</td>
<td>BSSE-corrected binding energy using correction method X</td>
</tr>
<tr>
<td>( E_{\text{X}B}^{\text{uncorrected}} )</td>
<td>BSSE-corrected binding energy using correction method X</td>
</tr>
<tr>
<td>( E_{\text{relax}}^{\text{uncorrected}} )</td>
<td>The energy of the ((\text{H}_2\text{O})_6) supersystem</td>
</tr>
<tr>
<td>( E_{\text{relax}} )</td>
<td>Sum of the individual monomer relaxation energies</td>
</tr>
<tr>
<td>( E_{\text{X}} )</td>
<td>BSSE correction for BSSE method X</td>
</tr>
<tr>
<td>( E_{\text{X}^{*}} )</td>
<td>Same as ( E_{\text{X}} ) except that the ( \sum_j E_j ) terms in ( E_{\text{X}} ) and ( E_{\text{X}^{*}} ) have been cancelled</td>
</tr>
<tr>
<td>( E_{\text{relax}} )</td>
<td>Sum of the individual monomer relaxation energies</td>
</tr>
</tbody>
</table>

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Table 13: Errors (relative to MP2/CBS benchmark results in MP2/CBS binding energies of \((\text{H}_2\text{O})_6\) obtained by extrapolating results from five different BSSE correction schemes using the eight different extrapolation methods in Eq. (6.15).

<table>
<thead>
<tr>
<th></th>
<th>(6.15a)</th>
<th>(6.15b)</th>
<th>(6.15c)</th>
<th>(6.15d)</th>
<th>(6.15e)</th>
<th>(6.15f)</th>
<th>(6.15g)</th>
<th>(6.15h)</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>1.60</td>
<td>1.65</td>
<td>1.60</td>
<td>0.73</td>
<td>0.75</td>
<td>1.07</td>
<td>0.75</td>
<td>1.11</td>
</tr>
<tr>
<td>CP</td>
<td>0.88</td>
<td>0.13</td>
<td>0.88</td>
<td>0.09</td>
<td>0.02</td>
<td>0.09</td>
<td>0.02</td>
<td>0.38</td>
</tr>
<tr>
<td>MBCP(2)</td>
<td>0.67</td>
<td>0.10</td>
<td>0.67</td>
<td>0.33</td>
<td>0.19</td>
<td>0.32</td>
<td>0.19</td>
<td>0.17</td>
</tr>
<tr>
<td>MBCP(3)</td>
<td>0.89</td>
<td>0.16</td>
<td>0.89</td>
<td>0.10</td>
<td>0.04</td>
<td>0.10</td>
<td>0.04</td>
<td>0.40</td>
</tr>
<tr>
<td>VMFC(3)</td>
<td>0.90</td>
<td>0.12</td>
<td>0.90</td>
<td>0.09</td>
<td>0.05</td>
<td>0.09</td>
<td>0.05</td>
<td>0.41</td>
</tr>
</tbody>
</table>

mathematically:

\[ \mathcal{E}^{X^*} = \mathcal{E}^X - \sum_{I=1}^{N_I} E^I_f. \]  

(6.17)

For the eight \((\text{H}_2\text{O})_6\) clusters, we have computed the MP2/CBS value of \(\tilde{E}_{\text{B.E.}}^X\) for each of the five BSSE correction methods, \(X\), that are considered in this work (including no BSSE correction at all), using each of the eight extrapolations suggested in Eq. (6.15). Mean unsigned errors (MUEs) for each data set, relative to the benchmark results in Ref. [82], are listed in Table 13. It is immediately apparent that the eight schemes do not predict results of equal quality.

In light of the results in Table 13, we will use Eq. (6.15e) to compute CBS binding energies for the rest of the manuscript. Aside from being the most accurate partitioning scheme [alongside Eq. (6.15g)], Eq. (6.15e) has the added benefit that the terms in the first set of parenthesis only depend on how the supersystem’s energy is computed and the second set contains all of the dependence on the particular choice of BSSE.
correction. Consequentially, error considerations in the rest of the paper will be fa-
cilitated by allowing us to break the final error into contributions from fragmenting
the supersystem and those from approximate BSSE corrections. Because the BSSE
corrections are additive, the errors will be as well.

6.4.2 \((\text{H}_2\text{O})_6\) clusters

Extrapolation without counterpoise correction

Historically, fragment methods have been used as an approximation to a particular
level of theory, and their merit has been judged by their ability to reproduce supersys-
tem properties computed at the same level of theory. Here, we repeat this exercise for
the relaxed binding energies of the water hexamers. The mean signed errors (MSEs),
where

\[
\text{error} = E_{X/a\zeta Z} - E_{\text{MP2}/a\zeta Z},
\]

(6.18)

for \(X = 3B, \text{EE-2B}, \text{EE-3B}\). (Recall that \(a\zeta Z \equiv \text{aug-cc-pV}\zeta Z\)) are shown in
Fig. 12. Based on previous work by Dahlke and Truhlar,\textsuperscript{17,18,93} albeit in a more
limited selection of basis sets, it is possible to give an empirical accuracy ordering of

\[2B < 3B \approx \text{EE-2B} < \text{EE-3B}\]

for the fragment methods considered here. To a large extent, the data in Fig. 12 are in
agreement with this trend. (MSEs for 2B/a\zeta Z are not shown in Fig. 12, but are on the
order of 10 kcal/mol.) We do note a tendency for the fragment methods to underbind
the cluster, and we suggest that this arises from a neglect of stabilizing higher-order
interactions; similar underbinding has been seen by other researchers.\textsuperscript{17,18,81,93}
Figure 12: Mean signed error (MSE) in the uncorrected MP2/a\(\zeta\) binding energies for eight isomers of \((\text{H}_2\text{O})_6\) computed at the MP2/a\(\zeta\) level. The MSE is computed with respect to supersystem MP2 results in the same basis set. The “a∞\(\zeta\)” values represent CBS extrapolations.

The ability for fragment methods to accurately reproduce a given level of theory is a nice result, but perhaps the more interesting result from Fig. 12 is that the errors generally decrease as \(\zeta\) increases, with the sole exception being the fortuitously-accurate EE-2B/aDZ results. The latter method thus represents a “Pauling point”, in the sense that both addition of three-body terms (EE-3B/aDZ) and/or extension of the basis set (EE-2B/aTZ or EE-3B/aTZ) have deleterious effects on the agreement with supersystem benchmarks. In view of the popularity of double-\(\zeta\) basis sets in fragment-based approaches, often at the MP2 level, this error cancellation should be borne carefully in mind. In fact, there has been little systematic analysis of the errors in fragment-based methods as a function of basis size. In the few studies where a sequence of aug-cc-pV\(\zeta\)Z basis sets has been used, the conclusions are mixed. Often (but not always), the results improve as \(\zeta\) increases.
but the fragment molecular orbital (FMO) method, as applied to (H$_2$O)$_{16}$, exhibits errors that clearly grow larger as a function of $\zeta$.\textsuperscript{78}

At some level, the error statistics in Fig. 12 serves to reiterate the conclusions of Dahlke and Truhlar,\textsuperscript{17,18,93} namely, that two- and three-body expansions offer reasonable accuracy for clusters of polar molecules if (and only if) electrostatic embedding is used. For (H$_2$O)$_6$, all such methods afford errors < 0.6 kcal/mol, whereas non-embedded three-body results err by > 1.2 kcal/mol. However, we are interested in pushing the limits of such approaches in terms of their ability to reproduce high-level benchmarks, and to this end we have recomputed the MSEs for (H$_2$O)$_6$, except that now we use MP2/CBS values\textsuperscript{82} as the benchmark for all fragment-based methods, regardless of basis set. In other words, we replace $E_{\text{MP2/a}\zeta Z}$ in Eq. (6.18) by $E_{\text{MP2/CBS}}$ in order to define the error. These results are plotted in Fig. 13.
It is important to note that most previous benchmark studies of fragment-based methods have not examined errors with respect to large- or complete-basis results. As such, Fig. 13 reveals an important point that is perhaps worth stating explicitly: being within chemical accuracy of a poor level of theory is not desirable. Interestingly, of the various methods examined in Fig. 13, the full (supersystem) MP2 results are less accurate, as compared to MP2/CBS benchmarks, than the truncated MBEs. (The exception is the two-body method without electrostatic embedding, which exhibits MSEs of $\sim 10$ kcal/mol that are not shown in Fig. 13.) As such, the more faithfully that a fragment method reproduces MP2/a$\zeta$Z results, the larger its MSE with respect to MP2/CBS results. Of course, the difference in the MP2/a$\zeta$Z and MP2/CBS binding energies is equal to the sum of the BSSE and BSIE and so Fig. 13 is really proving that neither of these errors is negligible. Moreover, we have noted previously\textsuperscript{118} that extrapolation of non-BSSE-corrected MP2/a$\zeta$Z energies for (H$_2$O)$_6$ fails to reproduce the consensus value\textsuperscript{82,91,118} of the MP2/CBS limit (at least when basis sets no larger than aQZ are employed), and this is evident in Fig. 13. In contrast, extrapolation of CP-corrected energies through MP2/aQZ does obtain the correct limit.\textsuperscript{118} The BSSE will be dealt with below.

In chemistry we are often interested in relative energies rather than total binding energies, and if two conformations are of approximately the same shape and size, then it is possible that the two might exhibit comparable BSSE, such that a BSSE correction would not be necessary in order to predict the relative energy. To this end, we have calculated the relative stabilities of the eight (H$_2$O)$_6$ isomers and compared
Figure 14: Convergence (to the CBS limit) of the relative energies of (H$_2$O)$_6$ isomers. The mean signed errors (MSEs) are computed with respect to MP2/CBS benchmarks. MSEs obtained from this analysis are plotted as a function of basis set size in Fig. 14.

Unlike the total binding energies, which fail to converge to the CBS limit even following extrapolation, owing to residual BSSE even in the aQZ basis set, the relative energies computed using supersystem MP2 calculations do converge to the correct limit, and are within 0.2 kcal/mol of that limit already at the MP2/aTZ level. This supports our hypothesis that the BSSE for these systems is similar and cancel for relative energy calculations. Further confirmation is obtained by computing the CP corrections to these relative energies. For the aDZ, aTZ, and aQZ basis sets, these CP corrections are 0.5, 0.3, 0.1 kcal/mol, respectively, and < 0.1 kcal/mol for the CBS-extrapolated result. Comparing Figs. 13 and 14, where the benchmark is MP2/CBS in both cases, we see that BSSE cancellation leads to relative energies that are significantly more accurate as compared to total binding energies, and various
truncated MBEs achieve an accuracy of \(< 1 \text{ kcal/mol}\) with respect to relative energies computed at the MP2/CBS level.

That said, the success of this cancellation hinges on the various isomers being of approximately the same size and shape, and cannot hold globally across the potential energy surface. For example, an energy calculation on six sufficiently well-separated water monomers will afford zero BSSE, and from this point of view, a calculation of the total binding energy is just an extreme example of a relative energy calculation. Moreover, compact \((\text{H}_2\text{O})_6\) structures are smaller than the radial extent of the most diffuse atomic orbitals in the aTZ and aQZ basis sets, suggesting that all isomers may exhibit roughly comparable BSSE. Calculations performed on a linear (chain) isomer of \((\text{H}_2\text{O})_6\) afford CP corrections that are 3.6, 1.8, and 0.83 kcal/mol different from those obtained for the prism isomer, in the aDZ, aTZ, and aQZ basis sets, respectively, and 0.24 kcal/mol different for the CBS-extrapolated result. These values are considerably larger than the average CP corrections quoted above for the compact \((\text{H}_2\text{O})_6\) structures, reflecting the difference in cluster shape. This underscores the importance of CP corrections in exploring the \textit{global} potential energy surface, where the BSSE may not cancel from one basin to the next.

In fact, even for stable, hydrogen-bonded cluster isomers, different regions of the potential surface may be affected differently by BSSE, which can be seen by examining larger clusters where a greater variety of hydrogen-bonding morphologies is available. As an example, we have computed dual-basis\textsuperscript{130} RIMP2/CBS energetics (based on a two-point cc-pVTZ and cc-pVQZ extrapolation) for 80 different isomers.
Figure 15: Relative energies of twenty isomers from each of four structural motifs of (H$_2$O)$_{20}$. Energies were computed at the dual-basis RIMP2/cc-pVXZ level (for X = T and Q), either with or without CP correction, and then extrapolated to the complete-basis limit using an X$^{-3}$ extrapolation formula. For three of the four motifs, CP correction alters the relative energies by no more than 0.2 kcal/mol. For the dodecahedral isomers, however, the CP-corrected and uncorrected results differ by $\approx$ 1 kcal/mol.
of \((\text{H}_2\text{O})_{20}\), corresponding to the 20 lowest-energy structures from each of four families of isomers, as determined by extensive basin-hopping Monte Carlo simulations\(^\text{131}\) on the TIP4P\(^\text{132}\) potential surface\(^*\). Examples of these structural motifs are depicted in Fig. 15, where we also plot the relative energies of all 80 isomers. Both CP-corrected and uncorrected results are shown, and the difference between the two is uniformly small \((\lesssim 0.2 \text{ kcal/mol})\) for three of the four classes of isomers. Apparently, the BSSE is approximately the same for all 60 of these isomers. For the dodecahedral isomers, however, the CP correction shifts the energies by about 1 kcal/mol relative to the energies of the other three families of isomers, meaning that the BSSE must be about 1 kcal/mol different in the dodecahedral regions of the potential surface.

**BSSE-corrected results**

We next discuss the use of truncated MBEs in conjunction with BSSE corrections. As discussed above, BSSE and BSIE are intimately intertwined, nevertheless it must be the case that the differences between the BSSE-free MP2/CBS benchmarks in Ref. [82] and the uncorrected MP2 energy computed in any finite basis set is equal to the total basis set error (BSE), that is

\[
\text{BSE} = \text{BSSE} + \text{BSIE}.
\] (6.19)

BSSE can be reduced (if not eliminated) by means of the CP- and VMFC-type corrections discussed in Section 5.2, while BSIE is eliminated only by extrapolation to the CBS limit.

\(^*\)TIP4P geometries for the \((\text{H}_2\text{O})_{20}\) clusters (from Ref. [131]) were downloaded from the Cambridge Cluster Database (http://www-wales.ch.cam.ac.uk/CCD.html).
Figure 16: MSEs in MP2/a\(\zeta\)Z binding energies for isomers of \((H_2O)_6\) using four different BSSE corrections in various basis sets. The error, computed with respect to MP2/CBS benchmarks, may be identified as the residual basis set error (BSSE + BSIE).

Figure 16 plots the MSEs for BSSE-corrected, MP2/a\(\zeta\)Z binding energies of \((H_2O)_6\) isomers, with respect to MP2/CBS benchmarks. We identify the difference between the MP2/a\(\zeta\)Z and the MP2/CBS result as the BSE, which is well-defined once the CBS limit is established. On the other hand, we do not consider that any of the BSSE corrections discussed in Section 5.2 rigorously defines BSSE, hence only the sum BSSE + BSIE is well-defined. On the other hand, the BSIE is independent of the BSSE correction that is used, so its net effect is then to shift each one of the errors by some amount. Thus, the relative difference between errors in Fig. 16 evaluated for the same basis set, but for different BSSE corrections is indicative of the error inherent to a given BSSE correction. These relative differences are quite small compared to the total residual BSE, so we cannot say conclusively, based on this one system, which BSSE correction is the most accurate. However, the MBCP(2)
[≡ VMFC(2)] method is likely the least accurate, as it provides results that are significantly different from the other three BSSE corrections, and upon extrapolation, misses the established MP2/CBS benchmark by almost 0.2 kcal/mol, whereas the other three BSSE corrections predict the correct limit to within 0.05 kcal/mol.

For a given fragmentation method, basis set, and BSSE correction method, the final error is then the sum of the error incurred by using a truncated MBE (Fig. 12), which is usually positive (indicative of underbinding), plus the residual BSE (Fig. 16), which is also positive. Figure 13 shows us that in general all of these methods overbind, when BSSE is not accounted for, and so error cancellation occurs, particularly between the BSSE and the fragment approximation making the uncorrected fragment calculations better estimates of the benchmark value than the full supersystem calculation. Similar error cancellation was observed in an earlier study of the VMFC(n) method.81

6.4.3 (H$_2$O)$_{10}$F$^-\text{ clusters}$

In the previous section, we examined various contributions to the error in a truncated many-body approximation to the binding energy of (H$_2$O)$_6$, both with and without corrections for BSSE. Here, we examine a larger and more strongly-bound system, namely, isomers of (H$_2$O)$_{10}$F$^-$ that we have previously shown to be much more challenging for fragment-based quantum chemistry, as compared to water clusters.46,54,56–58 As will be evident from the timing data presented below, computing CP-corrected MP2/CBS binding energies using traditional supersystem methods is quite challenging for systems of this size, and we cannot push the benchmarks too
Figure 17: Convergence of uncorrected RIMP2/aζZ binding energies to the CBS limit, as measured by the mean signed error (MSE) for ten (H₂O)$_{10}$F$^-$ cluster isomers. The MSE is measured relative to the supersystem RIMP2 in the same basis set.

much larger without considerable effort. In particular, we again use Eq. (6.15e) to extrapolate to the CBS limit, but for (H₂O)$_{10}$F$^-$ large-basis MP2-R12 calculations are not available, and (RI-)MP2/aQZ is the highest level of theory that is feasible on the hardware available to us, so we have no independent means to validate the MP2/CBS extrapolations for this system.

The most straightforward error is that associated with truncation of the MBE, which we can assess in the same way that we did for the (H₂O)$_6$ clusters, namely, by comparing the uncorrected supersystem RIMP2/aζZ binding energy to that obtained using a truncated MBE at the same level of theory. The MSEs for the 3B and EE-3B methods are shown in Fig. 17. As with the (H₂O)$_6$ clusters we again see a decrease in error as a function of ζ, in contrast to FMO results for (H₂O)$_{16}$ using cc-pVζZ basis sets.$^{78}$ Our (H₂O)$_{10}$F$^-$ system is closer in size to (H₂O)$_{10}$, as
compared to the water hexamers examined above, which suggests that system size
does not explain the deterioration in the FMO results with increasing basis size.
The authors of Ref. [78] suggest that the smaller polarization function exponents in
the larger correlation-consistent basis sets are a problem for the FMO method, per-
haps due to (unspecified) problems with the self-consistent embedding scheme when
basis functions centered on one monomer strongly overlap another monomer. Our
own (unpublished) experience with self-consistent “XPol” embedding\(^{46}\) suggests that
larger basis sets can be a problem when proper monomer densities, as opposed to
point charges, are used to compute the intermonomer Coulomb interactions in a self-
consistent embedding scheme. In any case, the present results show that this is not
a problem for the point-charge embedding used here, which is stable with respect to
expansion of the basis set, even in the presence of diffuse functions.

Further analysis requires some estimate of the benchmark quantity. To this end,
we assume that the CBS-extrapolated, CP-corrected RIMP2 binding energies lie
closer to the true RIMP2/CBS value as compared to extrapolation without BSSE
correction, which is the case for all eight of the \((\text{H}_2\text{O})_6\) isomers.\(^{118}\) We furthermore assume that the CP-corrected RIMP2 binding energies converge to the CBS
limit from above and that the uncorrected results converge from below, which is
again true of all the \((\text{H}_2\text{O})_6\) isomers\(^{118}\) as well as other systems that we have stud-
ied, such as tryptamine–water.\(^{92}\) Indeed, it is this empirical observation that has
led to the average of CP-corrected and uncorrected results, each extrapolated to the
basis-set limit, being used as an estimate of the true CBS result.\(^{91,92}\) For \((\text{H}_2\text{O})_6\)
Figure 18: Convergence of the uncorrected RIMP2/αζ binding energies to the CBS limit, for ten (H₂O)₁₀F⁻ clusters. Convergence is measured using the mean signed error (MSE) with respect to an RIMP2/CBS benchmark computed as a weighted average of CP-corrected and uncorrected RIMP2 results, each extrapolated to the CBS limit, as described in the text.

, extrapolation of the CP-corrected MP2 results affords very good agreement with an independently-verifiable MP2/CBS limit, but for (H₂O)₁₀F⁻ we have no such independent benchmark, and extrapolation using only aDZ, aTZ, and aQZ results may or may not achieve the true CBS limit. As such, we will use a 3:1 weighted average of the CP-corrected and uncorrected extrapolations as a benchmark for the MP2/CBS limit. (Thus, the chosen benchmark lies closer to the CP-corrected extrapolation.) Error bars on this MP2/CBS result will be established by assuming that the unweighted (1:1) average of the extrapolated CP-RIMP2/CBS and RIMP2/CBS results is a lower bound to the true MP2/CBS result, and that the CP-RIMP2/CBS extrapolation provides an upper bound. Based on these assumptions, we conclude that our RIMP2/CBS benchmarks should be accurate to within about 0.4 kcal/mol.
Figure 19: Convergence of the relative energies of \((\text{H}_2\text{O})_{10}\text{F}^–\) cluster isomers to the CBS limit. MSEs are measured relative to the RIMP2/CBS benchmark that is discussed in the text.

Figure 18 plots MSEs in the uncorrected RIMP2/\(a\zeta\)Z binding energies as a function of basis size, using the weighted average just described as the RIMP2/CBS benchmark. Based on Fig. 18, it is apparent that a cancellation of errors (with BSSE compensating for truncation of the MBE) is again at work, as EE-3B/\(a\zeta\)Z results lie closer to the benchmark as compared to RIMP2/\(a\zeta\)Z results. (As a result, reproducing the full RIMP2/\(a\zeta\)Z result in a given basis set is not the best measure of how well a given fragment method reproduces the binding energy in the CBS limit.) This shows that the approximate cancellation between BSSE and higher-order many-body effects continues to hold in clusters larger than \((\text{H}_2\text{O})_6\); the magnitude of both is increasing with system size.

As in the case of the water hexamer, aQZ results—possibly in conjunction with CBS extrapolation—is required to get within \(\sim 1\) kcal/mol of the benchmark CBS
Figure 20: Residual basis set error for ten isomers of (H₂O)₁₀F⁻, computed at the RIMP2 level using various basis sets. The MSE is evaluated with respect to the RIMP2/CBS benchmark that is discussed in the text.

value of the total binding energy. Accurate prediction of relative energies is less demanding, as shown in Fig. 19. Errors in EE-3B/aζZ results are < 0.6 kcal/mol in magnitude, as compared to RIMP2/CBS benchmarks, even in the aDZ basis set, and with a triple-ζ basis the error is < 0.2 kcal/mol. As in the case of (H₂O)₆ clusters, calculation of the BSSE corrections for each (H₂O)₁₀F⁻ isomer confirms that they are of similar magnitude and therefore cancel in the evaluation of relative energies. Somewhat surprisingly, these corrections are similar in magnitude to the values obtained for (H₂O)₆ isomers, despite the increased system size.

We next apply the BSSE corrections, and in Fig. 20 we plot the residual BSE across the aug-cc-pVζZ sequence of basis sets, using several different BSSE corrections. The difference in accuracy between the MBCP(3) and VMFC(3) methods is about 0.2 kcal/mol, smaller than the ≈ 0.4 kcal/mol error bar that was established above for
the benchmark values. [Recall, however, that the MBCP(3) method is less expensive.] Combined with the similar results for the \((\text{H}_2\text{O})_6\) systems, this suggests that both the VMFC\((n)\) and the MBCP\((n)\) corrections converge rapidly and to nearly the same value. This implies that basis-set extension effects, which are absent in the MBCP\((n)\) approach, are negligible.

Given the very similar performance of VMFC(3) and MBCP(3), we prefer the latter for reasons of cost, as the MBCP(3) approach requires only a proper subset of the electronic structure calculations that are required for VMFC(3). Timing data for a \((\text{H}_2\text{O})_{10}\text{F}^-\) cluster are shown in Fig. 21. These timings represent the total, aggregate wall time require to compute the CP-corrected [Eq. (6.3)] RIMP2/\(a\zeta Z\) binding energy in each aug-cc-pV\(\zeta Z\) basis set, along with the relative speed-up engendered.
by using the MBCP(2), MBCP(3), or VMFC(3) correction. For the purposes of this comparison, all calculations are run in serial, meaning that the “embarrassingly parallelizable” nature of the fragment-based corrections is not exploited. Wall times for the fragment-based calculations could therefore be trivially and dramatically reduced by running individual jobs on separate processors; already, however, the MBCP(3) method reduces the cost by $\sim 70\%$, without significant loss of accuracy.

6.5 Summary

The present chapter had two aims. First and foremost, we continue our efforts\textsuperscript{54, 56, 118} to understand the strengths and weaknesses of fragment-based methods, particularly for high-accuracy calculations. Considering that a large number of previous studies using fragment-based quantum chemistry have focused on results obtained using double-$\zeta$ basis sets, we have explored the ability of truncated many-body expansions to replicate MP2/CBS results rather than, say, MP2/aug-cc-pVDZ results. Accuracy of $< 1$ kcal/mol in total binding energies (with respect to MP2/CBS) is obtainable by means of electrostatically-embedded three-body expansions, but requires the use of quadruple-$\zeta$ basis sets and/or CBS extrapolation. We also find that the three-body result in a given, finite basis set, often lies closer to the MP2/CBS benchmark as compared to full (supersystem) MP2 in the same basis set. This is ultimately fortuitous, resulting from a cancellation of errors wherein BSSE partially offsets errors engendered by neglecting higher-order many-body effects, it is worth noting all the same, as it implies that evaluating the accuracy of fragment-based methods in small
basis sets may not provide a full picture of how such methods perform in the basis-set limit.

A second focus of this work is on the effects of low-cost BSSE corrections based on low-order many-body expansions, including the MBCP\(n\) method of Ref. [118] and the VMFC\(n\) method of Ref. [81]. The intertwined nature of BSSE and basis incompleteness makes it difficult to ascertain which approach is most accurate, but at the \(n = 3\) level the difference between the two is comparable to, or smaller than, the intrinsic error in establishing the CBS limit. On the one hand, this implies that so-called “basis-set extension” effects, which are not corrected by the MBCP\(n\) approach, must be quite small, at least for the \((\text{H}_2\text{O})_6\) and \((\text{H}_2\text{O})_{10}\text{F}^-\) examples considered here. At the same time, it means that there is no reason not to use the lower-cost MBCP\(n\) approach, which results in significant computational savings and enables smooth extrapolation of MP2/aug-cc-pV\(\zeta\)\(Z\) results \((\zeta = D, T, Q)\) to the MP2/CBS limit, by means of electronic structure calculations on systems no larger than trimers.
APPENDIX A

BSSE convergence of water hexamers

Included in this appendix are figures analogous to Fig. 9 in Chapter 5, but for each of the eight isomers of \((\text{H}_2\text{O})_6\) that are considered in Ref. [82]. These are Figs. 22–29 below. In Table 14, we provide the numerical data used to produce Fig. 8 in Chapter 5.
Table 14: Numerical data for Fig. 8 in the paper.

<table>
<thead>
<tr>
<th>Method</th>
<th>Gly(H₂O)₁₀</th>
<th>F⁻(H₂O)₁₀</th>
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<tbody>
<tr>
<td>MBCP(2)</td>
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<td>14.41</td>
</tr>
<tr>
<td>VMFC(3)</td>
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<td>EE-VMFC(3)</td>
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<tr>
<td>EE-MBCP(3)</td>
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<td>0.73</td>
</tr>
</tbody>
</table>

Figure 22: Convergence to the CBS limit for the “Bag” isomer of (H₂O)₆. CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 23: Convergence to the CBS limit for the “Boat1” isomer of \((\text{H}_2\text{O})_6\). CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 24: Convergence to the CBS limit for the “Boat2” isomer of (H₂O)₆. CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 25: Convergence to the CBS limit for the “Book1” isomer of $\left(\text{H}_2\text{O}\right)_6$. CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 26: Convergence to the CBS limit for the “Book2” isomer of (H₂O)₆. CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 27: Convergence to the CBS limit for the “Cage” isomer of (H₂O)₆. CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MB(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 28: Convergence to the CBS limit for the “Cyclic” isomer of \((\text{H}_2\text{O})_6\). CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
Figure 29: Convergence to the CBS limit for the “prism” isomer of \((\text{H}_2\text{O})_6\). CP-MP2 denotes traditional counterpoise-corrected MP2, EE-MBCP(3) is a three-body approximation to the binding energy defined by Eq. (3) from the main text and EE-MB(3) represents a three-body approximation to the cluster energy, following which the binding energy is computed with no attempt at counterpoise correction. The horizontal line is the benchmark MP2/CBS value.
BIBLIOGRAPHY


