Acta Numerica (2005), pp. 363–444
DOI: 10.1017/S096249290400025X

Computational chemistry from the perspective of numerical analysis

Claude Le Bris
CERMICS, École Nationale des Ponts et Chaussées,
6 & 8, Avenue Blaise Pascal, Champs sur Marne,
77455 Marne-La-Vallée Cedex 2, France
and
INRIA Rocquencourt, MICMAC project,
Domaine de Voluceau, B.P. 105, 78153 Le Chesnay Cedex, France
E-mail: `lebris@cermics.enpc.fr`

We present the field of computational chemistry from the standpoint of numerical analysis. We introduce the most commonly used models and comment on their applicability. We briefly outline the results of mathematical analysis and then mostly concentrate on the main issues raised by numerical simulations. A special emphasis is laid on recent results in numerical analysis, recent developments of new methods and challenging open issues.

CONTENTS

1. Outline

The field of computational chemistry is traditionally less well known by applied mathematicians than other fields of the engineering sciences, such as computational mechanics. Nevertheless, it is undoubtedly a rich source of very difficult problems for numerical simulation, some of which are likely to remain among the most challenging simulation tasks for years to come. Examples are the complete and detailed simulation of protein folding, or the description of the long time radiation damage of materials in nuclear power plants.

Many of the difficult problems have already been tackled, with definite success, by experts in computational chemistry. Thanks to their constant effort and their ever-productive ideas, the field has made great progress since its early days. The birth of quantum chemistry is commonly marked by the publication by Heitler and London (1927) on the electronic structure of the hydrogen molecule. That of *computational* quantum chemistry is fixed around 1950 with the first effective computations of molecular systems consisting of a few (say 5 to 20) electrons on the then newly created computers. Fifty years later, contemporary methods and techniques allow for the simulation of a broad spectrum of systems, ranging from molecules of hundreds of electrons modelled by very precise quantum models, up to samples of billions of particles modelled by molecular dynamics equations with force fields parametrized in advance (on the basis of more precise computations of smaller subsystems). These techniques are implemented in a large variety of softwares, freely distributed or not, that have general purposes or are dedicated to specific applications. Thanks to them, theoretical computational chemistry has gained full recognition in the world of chemistry, a domain traditionally more experimentally oriented. The Nobel prize recently awarded to Walter Kohn and John Pople testifies to this success: see Kohn (1999).

In spite of this great success, some challenging issues remain open, mostly related to the simulation of large systems over long times. New techniques must be invented, otherwise it will not be possible to bridge the size and time gaps up to most of the systems of practical interest (*e.g.*, proteins, nanosystems, crystalline materials). Such new ideas will certainly arise among experts of the field. But they are also likely to come from mathematical contributions. In many respects, computational chemistry is still an art, and relies upon a delicate mix of physical intuition, pragmatic cleverness, and practical know-how. Therefore progress is difficult, and slow. For an applied mathematician, such a situation often indicates that the existing discretization techniques and solution procedures suffer from a lack of numerical analysis, and this is indeed the case for computational chemistry. Some results on the numerical analysis have appeared in the past decade, but a lot remains to be done. We conjecture that a better theoretical knowledge of existing techniques will lead to their enhancement, and will therefore improve their applicability, as demonstrated by the history of scientific computing in the engineering sciences.

The purpose of the present article is to overview the numerical difficulties encountered in computational chemistry, to show how they are solved within the current state of the art, and to indicate the needs for further improvements. Of course, whenever they exist, we will indicate the results of numerical analysis that help to give a sound grounding for these techniques. But most often the article will deal with descriptions of techniques rather than with statements of theorems. We hope that this bias will stimulate further works.

The article is organized in a rather narrative way, without any ordering of scientific priority and/or importance. We begin with a description of the models and the discretization techniques for small systems in a static picture. Then, we progressively and (hopefully) pedagogically proceed to the modelling and simulation of more difficult situations: larger systems, systems *in situ*, time-dependent settings. Of course, as the size of the system increases, the models need to be coarse-grained, otherwise they cannot be tackled in practice. Therefore, the article also proceeds from the finest models to the coarsest ones.

The present state-of-the-art survey focuses on issues in numerical analysis for a readership familiar with such questions in other settings. A more detailed description may be found in the book of Le Bris, ed. (2003), and also, to a smaller extent, in the proceedings volume by Defranceschi and Le Bris, eds (2000). For readers with a background in chemistry, we refer to two survey articles, Defranceschi and Le Bris (1997) and Defranceschi and Le Bris (1999), for an introduction to the mathematical and numerical analysis. On the other hand, questions related to the mathematical analysis of models are overviewed in Le Bris and Lions (2005).

2. A short introduction to modelling for molecular simulation

2.1. A hierarchy of models

The domain called *computational chemistry* is traditionally more focused on the accurate simulation of (rather) small systems in their finest details, the term *molecular simulation* covering the other end of the spectrum. As suggested by its title, the present survey is thus more concentrated on small systems. Nevertheless, the current trend is increasingly to account for precise effects even in large-scale simulations. This can be done in one of the following ways.

- **Sequentially** by precomputing the parameters of a coarse model on the basis of quantum simulations of subsystems: typical examples are the computation of force fields for classical molecular dynamics (see Section 5.2), or the fitting of pseudopotentials for large-scale calculations in the solid phase (see Section 4.1).
- **In parallel** by dividing the system under study into pieces that are modelled at different levels, as for quantum mechanics/molecular mechanics (QM/MM) calculations: *e.g.*, the active site of a protein is simulated at the quantum level to account for the change of electronic structure, while the major part of the protein is modelled classically in order to only simulate the changes in the conformation.
- Also **in parallel** by inserting on-the-fly evaluations of interactions by quantum models in classical models, as is done in the *ab initio* molecular dynamics simulations (see Section 5.1).

In any case, computational chemistry irrigates molecular simulation in such an intimate manner, and the two fields are so strongly entangled, that it would not be giving a fair account to overview the former while ignoring the latter. Consequently, some sections of the present survey are aimed at giving at least a rough idea of simulations of very large systems (see Sections 3.7, 5.2 and 5.3). By no means, these sections, of limited size and scope, are intended to give a complete account. They rather aim only to give a flavour of the field.

In computational chemistry, the most accurate approximations are called *ab initio* approximations, for they involve no parameter except the universal constants of physics. They are only tractable for systems of small size. In order to allow for the simulation of systems of larger size, some further approximations are made, and some quantities are neglected or evaluated on the basis of experimental measures. Then the methods are called *semi-empirical.* Just to give one example, a typical quantity that can be inserted in the calculations is an interatomic distance (a quantity that in principle is an *output* of the computation, namely an optimization of the total energy of the system), or the value of an overlap between two electronic orbitals (*i.e.*, the value of some entries of the 'mass matrix' that again in principle should be calculated; see Section 3.2 for the definition of orbitals). The computational task is then reduced, and larger systems can be addressed. Finally, the models can be so much simplified that all the quantum information is aggregated into force fields for classical mechanics, and one reaches the field of molecular simulation, often subdivided into the domains called *molecular mechanics* and *molecular dynamics.* These domains are overwhelmingly those that have percolated efficiently into other fields of sciences related to chemistry, for instance biology and materials science.

Focusing on the *ab initio* models to start with, we notice that in addition, it is natural to focus on the determination of the ground state (that is, the state of minimal energy) of the system under consideration. Indeed, in the natural environment, systems are usually found in their most stable state. Likewise any chemical system A reacts, spontaneously or with a compound X, to give products B, C, … according to a chemical reaction if the variation of energy corresponds to a stabilization of the whole system. The above thermodynamic consideration does not suffice, however, to explain all the observations (kinetics comes into play), but the determination of the ground state and of the ground state energy remains a preliminary calculation needed before turning to other questions in computational chemistry: calculation of excited states, linear or nonlinear response theory, *etc.* The latter questions will not be addressed here and we refer to the bibliography.

Before getting to the heart of the matter, let us recall the orders of magnitude for the objects we will be manipulating henceforth, as they are rather unusual. The typical size of the electronic cloud of an isolated atom is the Angström (10^{-10} m). The size of the nucleus embedded therein is 10^{-15} m. The weight of an atom is of the order of 10^{-26} kg. Regarding the time-scale, the typical vibration period of a molecular bond is the femtosecond (10^{-15} s), while the characteristic relaxation time for an electron is 10^{-18} s. Consequently, computational chemistry concerns the behaviour of very small and very light systems over very short time frames.

An introduction to all the quantum models we will deal with can be read in Levine (1991), for example, while the basics of quantum mechanics are recalled in McWeeny (1992). The main mathematical tools for the standard (linear) analysis with an emphasis on physics are contained in Blanchard and Bruning (1982), Cycon, Froese, Kirsch and Simon (1987), Gustafson and Sigal (2003), Reed and Simon (1975), Schechter (1981), Thirring (1983). In addition, the series of Lipkowitz and Boyd, eds (1995–) periodically publishes state-of-the-art surveys by experts in chemistry. We shall give more specific references later.

2.2. *Standard ab initio models for molecular systems*

In most situations in chemistry, it is legitimate to consider the nuclei as classical objects, and as point-like particles with charges $(z_1, \ldots, z_M)$ at positions $(\bar{x}_1, \ldots, \bar{x}_M)$, while treating the electrons as quantum particles. This is the so-called *Born–Oppenheimer* approximation. In view of this approximation, the determination of the ground state structure of a molecular system consisting of M nuclei and N electrons amounts to solving the following two nested minimization problems:

$$\inf_{(\bar{x}_1,\ldots,\bar{x}_M)\in\mathbb{R}^{3M}} \left\{ W(\bar{x}_1, \ldots, \bar{x}_M) = U(\bar{x}_1, \ldots, \bar{x}_M) + \sum_{1 \leq k < l \leq M} \frac{z_k\, z_l}{|\bar{x}_k - \bar{x}_l|} \right\}, \tag{2.1}$$

where

$$U(\bar{x}_1,\dots,\bar{x}_M)=\inf\bigl\{\langle\psi_e,H_e^{(\bar{x}_1,\dots,\bar{x}_M)}\psi_e\rangle,\quad \psi_e\in\mathcal{H}_e,\quad \|\psi_e\|_{L^2}=1\bigr\}.\quad (2.2)$$

The variational problem (2.2) determines the ground state electronic structure when the nuclei are clamped at the positions $(\bar{x}_1,\dots,\bar{x}_M)$. We concentrate on this problem, and will only briefly address the outer minimization loop (2.1) (that requires techniques of *molecular mechanics*) in Section 3.8 below.

Problem (2.2) consists in finding the lowest eigenvalue of the N-body Hamiltonian $H_e^{(\bar{x}_1,\dots,\bar{x}_M)}$, parametrized by the positions of the nuclei,

$$H_e^{(\bar{x}_1,\dots,\bar{x}_M)}=-\sum_{i=1}^{N}\frac{1}{2}\Delta_{x_i}-\sum_{i=1}^{N}\sum_{k=1}^{M}\frac{z_k}{|x_i-\bar{x}_k|}+\sum_{1\le i<j\le N}\frac{1}{|x_i-x_j|}.\quad (2.3)$$

We easily recognize in (2.3) the kinetic energy of the electrons, the attraction electrostatic energy between the nuclei and the electrons, and the repulsion electrostatic energy between the electrons, respectively.

In order to write $H_e^{(\bar{x}_1,\dots,\bar{x}_M)}$, we have chosen the *atomic unit system*, commonly used in quantum chemistry:

$$m_e=1,\quad e=1,\quad \hbar=1,\quad \frac{1}{4\pi\epsilon_0}=1,$$

where m_e, e, $\hbar$, ϵ_0, respectively, denote the electron mass, the elementary charge, the reduced Planck constant, and the dielectric permittivity of vacuum.

On the other hand, the variational space in (2.2) is set to the following subspace of $L^2(\mathbb{R}^{3N})$, the antisymmetrized tensor product

$$\mathcal{H}_e=\bigwedge_{i=1}^{N}H^1(\mathbb{R}^3),\quad (2.4)$$

in order to ensure that the kinetic energy term is finite.[1] The antisymmetry requirement comes from the Pauli exclusion principle that states that the electronic wavefunction indeed needs to be antisymmetric with respect to any permutation of the electrons.

The Euler–Lagrange equation of the minimization problem (2.2) is the celebrated Schrödinger equation,

$$H_e^{(\bar{x}_1,\dots,\bar{x}_M)}\psi_e=E_e\psi_e,\quad (2.5)$$

---

[1] Here and below, for clarity of exposition, we omit the spin variable, which has of course a huge practical importance. The introduction of the spin in the models and techniques we shall describe in this review is not conceptually difficult, but may give rise to substantial additional technicalities. Again for simplicity, we also assume that the wavefunctions are real-valued.

with E the lowest possible eigenvalue of the self-adjoint operator $H_e^{(\bar{x}_1,\dots,\bar{x}_M)}$ on $\mathcal{H}_e$, in fact equal to $U(\bar{x}_1,\dots,\bar{x}_M)$ given by (2.2).

Unfortunately, for almost all problems of interest, the treatment of the minimization problem (2.2) or alternatively that of equations (2.5) is at the present time essentially impossible, owing to the huge size of the Hilbert space $\mathcal{H}_e$. The only techniques that are indeed tractable at this level are mostly stochastic-like techniques. One class of such methods is called *variational Monte Carlo* and consists in evaluating the multidimensional integrals

$$\langle \psi_e, H_e^{(\bar{x}_1,\dots,\bar{x}_M)} \psi_e \rangle$$

with adequate sampling techniques.[2] The minimization in (2.2) is then performed by standard tools. We refer, for example, to the chapter by W. Lester in Le Bris, ed. (2003). Another approach, not well developed in the world of chemistry[3] but very promising according to Lions (1996) in view of its success in other fields such as financial mathematics, consists in considering the time-dependent parabolic equation

$$\frac{\partial \psi_e}{\partial t} + H_e \psi_e = 0, \tag{2.6}$$

and noticing that, as t goes to infinity,

$$\frac{1}{t}\,\mathrm{Log}\big|\psi_e(t,x)\big| \;=\; \frac{1}{t}\,\mathrm{Log}\big|\mathrm{e}^{-tH_e}\,\psi_e(0,x)\big| \longrightarrow \quad U \quad (\text{defined by (2.2)}). \tag{2.7}$$

Then $\psi_e(t,x)$ is computed using the Feynman–Kac representation formula for the solution to (2.6), which requires efficient sampling techniques.

Apart from these stochastic techniques designed to directly attack problem (2.5), there are the seemingly promising techniques of *sparse tensor products* (also known as *sparse grid methods*) that are only emerging in computational chemistry. Equation (2.5) is a partial differential equation set on a vectorial space of high dimension, and most numerical techniques cannot deal with dimensions larger than 6. Nevertheless, the sparse grid approximations precisely aim at dealing with PDEs in high dimension: see Griebel, Oswald and Schlekefer (1999), Bungartz and Griebel (2004) or Schwab and von Petersdorff (2004). These techniques are definitely successful in many contexts. In their present state, however, they require a high regularity of the solution manipulated, in order to use sparse tensor

---

[2] Regarding deterministic methods, see Bokanowski and Lemou (1998, 2001) for a tentative adaptation (still in its early stage but apparently promising) of the fast multipole method to these multidimensional integrals.

[3] What is however used in chemistry is a simplified version of the approach, known as the *Diffusion Monte Carlo* (DMC) method. We refer to Cancès, Jourdain and Lelièvre (2004*d*) for a first mathematical study of this method.

product spaces without losing any information in comparison to the full tensor product. Now, the functions of chemistry may be singular, notably because of the cusp present in the interaction between electrons (the $\frac{1}{|x_i - x_j|}$ terms in $H_e^{(\bar{x}_1,\dots,\bar{x}_M)}$); we will come back to this point in Section 3.2. Nevertheless, we are allowed to be optimistic, for two reasons. First, in order to deal with cases when there is some lack of regularity, there are works in progress by M. Griebel and colleagues that include the use of *adaptive* sparse tensor products. Second, recent results by Yserentant (2003, 2004*a*, 2004*b*) indicate that the wavefunction solution to the (stationary) Schrödinger equation (2.5) is more regular than expected (and in fact has *almost* the regularity needed for state-of-the-art sparse tensor product techniques). The sparse tensor product approximation *should* therefore work nicely (see Garcke and Griebel (2000) for a first step). On the other hand, it is worth mentioning that dealing with the antisymmetry requirement in the context of sparse tensor products is still an issue (see however Hackbusch (2001) for a possible track).

In addition to these emerging techniques that come from other domains of the engineering sciences, an alternative way has appeared a long time ago in the world of chemistry but is still under practical development. It starts from the observation that the Hamiltonian (2.3) only involves one- and two-electron terms, and therefore that the multidimensional integral $\langle \psi_e, H_e^{(\bar{x}_1,\dots,\bar{x}_M)} \psi_e \rangle$ can be expressed in terms of the second-order reduced matrix

$$\gamma_2(x,y,x',y') = \int_{\mathbb{R}^{3(N-2)}} \psi_e(x,y,x_3,\dots,x_N)\psi_e(x',y',x_3,\dots,x_N)\,\mathrm{d}x_3\cdots\mathrm{d}x_N. \tag{2.8}$$

Next, the minimization problem, possibly under the form of its Euler–Lagrange equation is reformulated, and treated numerically. This is undoubtedly an appealing idea, though still not mature enough (issues both at the theoretical and at the practical levels remain unsolved). Regarding what seems to be a promising track, we refer to Coleman and Yukalov (2000) for the general context (see also many references by the first of these two authors), to Zhao, Braams, Fukuda, Overton and Percus (2004) for an instance of a direct minimization approach, and most of all to the works by D. Mazziotti (see, *e.g.*, Mazziotti (1998*a*, 1998*b*, 1999, 2004)), and C. Valdemoro (see, *e.g.*, Valdemoro, Tel and Perez-Romero (2000)).

At this stage, it seems to us important to emphasize that the main challenge for the future of computational chemistry is to directly attack the N-body problem (2.5), or in a less ambitious manner, increasingly account for the N-body interaction itself (and this begins with $N = 2$). The stochastic approach, the use of sparse tensor products, the reduced density matrix approach described above, are instances of methods that go in this direction.

Likewise, the introduction of many-electron wavefunctions in the basis sets (see Section 3.3) and many very recent approaches emerging in computational chemistry are aimed at addressing this timely question. However, as these methods are not yet mature, we will concentrate in the rest of this state-of-the-art survey on methods that are to some extent better established.

The most commonly used approximations for the minimization problem (2.2) can be filed schematically into two main classes.

- **Wavefunction methods**, exemplified by the famous Hartree–Fock model, aim to find an approximation of the ground state electronic wavefunction, *i.e.*, of the minimizer of (2.2). The variational space $\mathcal{H}_e$ is reduced but the 'exact' form of the energy $\langle \psi_e, H_e^{(\bar{x}_1,\ldots,\bar{x}_M)} \psi_e \rangle$ is kept. Wavefunction methods are preferred by chemists who are interested in the precise simulations of systems of small size, when computational time is not the primary concern. We refer to the treatises of Hehre, Radom, Schleyer and Pople (1986) and Szabo and Ostlund (1982) in the chemistry literature. A famous program implementing Hartree–Fock-type methods is the code GAUSSIAN.
- **Density functional methods** originate from density functional theory. They are based on a reformulation of problem (2.2) in such a way that the unknown function is the electronic density

  $$\rho(x) = N \int_{\mathbb{R}^{3(N-1)}} |\psi_e(x, x_2, \ldots, x_N)|^2 \, \mathrm{d}x_2 \cdots \mathrm{d}x_N$$

  (*i.e.*, a scalar field on $\mathbb{R}^3$) rather than the wavefunction ψ_e (*i.e.*, a scalar field on $\mathbb{R}^{3N}$) as in the original problem (2.2). This is why these methods are widely used by those of the chemists who are interested in large molecular systems (*e.g.*, biological systems) as well as most solid state physicists. The fact that various parameters or even the very form of some terms of the energy functional need to be arbitrarily chosen or tuned for these methods makes the method particularly efficient for some situations but is sometimes seen as a lack of rigour by chemists. Some major references in the chemistry literature are March (1992), Parr and Yang (1989) and Dreizler and Gross (1990).

2.3. Hartree–Fock-type models

The Hartree–Fock (HF) approximation consists in restricting in (2.2) the variational space $\mathcal{H}_e$ to that of functions of variables $(x_1, \ldots, x_N) \in \mathbb{R}^{3N}$ which can be written as a *single* determinant (*i.e.*, an antisymmetrized product) of N functions defined on $\mathbb{R}^3$. Recall that, in the whole generality, an arbitrary element of $\mathcal{H}_e$ is a converging infinite sum of such determinants.

The Hartree–Fock approximation is therefore defined as

$$U^{HF}(\bar{x}_1, \dots, \bar{x}_M) = \inf\big\{\langle \psi_e, H_e \psi_e\rangle : \quad \psi_e \in \mathcal{S}_N\big\}, \tag{2.9}$$

with

$$\mathcal{S}_N = \left\{\psi_e = \frac{1}{\sqrt{N!}} \det(\phi_i(x_j)) : \phi_i \in H^1(\mathbb{R}^3), \int_{\mathbb{R}^3} \phi_i \, \phi_j = \delta_{ij}, \, 1 \le i, j \le N\right\}. \tag{2.10}$$

In quantum chemistry, a function of the form $\frac{1}{\sqrt{N!}} \det(\phi_i(x_j))$ is called a *Slater determinant*, and the ϕ_i are called *molecular orbitals*.

Apart from antisymmetry, the Hartree–Fock approximation heuristically consists in observing that the probability density $|\psi|^2(x_1, \dots, x_N)$ of finding the N electrons at positions $(x_1, \dots, x_N)$ can be approximated by the product $|\phi_1|^2(x_1) \cdots |\phi_N|^2(x_N)$. This is equivalent to considering the positions of the electrons as *independent* variables. This simplification causes a certain loss of *correlation* between the positions of the electrons, and is responsible for some error in the result obtained. Indeed, restricting the minimization to *some* specific forms of functions in (2.9) provides us only with an upper bound on the energy (2.2). On the other hand, the fact that it is an upper bound and not only an approximation of the exact energy is of course a substantial practical advantage of the method, in comparison with other, nonvariational, approximations, such that those coming from density functional theory (see Section 2.4 and below).

Explicitly, the computation of $E^{HF}(\phi_1, \dots, \phi_N) = \langle \psi_e, H_e \psi_e \rangle$ for ψ_e in $\mathcal{S}_N$ leads to

$$\begin{aligned} I_N^{HF} = \inf\Bigg\{ & \sum_{i=1}^{N} \frac{1}{2} \int_{\mathbb{R}^3} |\nabla \phi_i|^2 + \int_{\mathbb{R}^3} \rho \, V + \frac{1}{2} \int_{\mathbb{R}^3} \int_{\mathbb{R}^3} \frac{\rho(x) \, \rho(x')}{|x - x'|} \, \mathrm{d}x \, \mathrm{d}x' \\ & - \frac{1}{2} \int_{\mathbb{R}^3} \int_{\mathbb{R}^3} \frac{|\tau(x, x')|^2}{|x - x'|} \, \mathrm{d}x \, \mathrm{d}x' : \\ & \phi_i \in H^1(\mathbb{R}^3), \quad \int_{\mathbb{R}^3} \phi_i \, \phi_j = \delta_{ij}, \quad 1 \le i, j \le N \Bigg\}, \end{aligned} \tag{2.11}$$

where

$$V(x) = -\sum_{k=1}^{M} \frac{z_k}{|x - \bar{x}_k|}, \tag{2.12}$$

$$\tau(x, x') = \sum_{i=1}^{N} \phi_i(x) \, \phi_i(x'), \tag{2.13}$$

$$\rho(x) = \sum_{i=1}^{N} |\phi_i(x)|^2. \tag{2.14}$$

The functions τ and ρ are respectively called the *density matrix* and the *density* associated to the state ψ_e.

The Euler–Lagrange equations of (2.11) are the *Hartree–Fock equations*

$$\begin{cases} F_\Phi \phi_i & = \lambda_i \, \phi_i, \\ \int_{\mathbb{R}^3} \phi_i \phi_j & = \delta_{ij}, \end{cases} \tag{2.15}$$

where F_Φ is the *Fock operator*

$$F_\Phi = -\frac{1}{2}\Delta - \sum_{k=1}^{M} \frac{z_k}{|x - \bar{x}_k(t)|} + \left(\sum_{j=1}^{N} |\phi_j|^2 \star \frac{1}{|x|} \right) - \sum_{j=1}^{N} \left(\cdot\, \phi_j \star \frac{1}{|x|} \right) \phi_j, \tag{2.16}$$

and the λ_i are the Lagrange multipliers of the orthonormality constraints (owing to an invariance property, obvious on (2.10), of the HF energy functional with respect to orthogonal (unitary) transformations of the ϕ_i, the matrix of Lagrange multipliers may be diagonalized without loss of generality).

The above *Hartree–Fock model* (2.11) has been extensively studied by mathematicians, the two landmark papers being those by Lieb and Simon (1977*a*) and Lions (1987), where the existence of a minimizer is demonstrated under convenient assumptions, and the Euler–Lagrange equations are thoroughly studied.

2.4. Density functional theory models

As announced above, the purpose of density functional theory, abbreviated as DFT, is to replace the minimization problem (2.2) defined in terms of the unknown wavefunction ψ_e by a minimization problem set on the unknown density ρ.

To fulfil this goal, it suffices, for instance, to define

$$\begin{aligned} E(\rho) = \inf \Bigg\{ & \langle \psi_e, \left(-\sum_{i=1}^{N} \frac{1}{2} \Delta_{x_i} + \sum_{1 \le i < j \le N} \frac{1}{|x_i - x_j|} \right) \psi_e \rangle : \\ & \psi_e \in \mathcal{H}_e, \quad \|\psi_e\|_{L^2} = 1, \quad \psi_e \text{ has density } \rho \Bigg\}, \end{aligned} \tag{2.17}$$

on

$$\mathcal{I}_N = \left\{ \rho \ge 0 : \quad \sqrt{\rho} \in H^1(\mathbb{R}^3), \quad \int_{\mathbb{R}^3} \rho = N \right\}, \tag{2.18}$$

so that

$$U(\bar{x}_1, \ldots, \bar{x}_M) = \inf \left\{ E(\rho) - \int \left(\sum_{k=1}^{M} \frac{z_k}{|\cdot - \bar{x}_k|} \right) \rho : \quad \rho \in \mathcal{I}_N \right\}. \tag{2.19}$$

The functional E is the *density functional*. However it is derived (the above manner is one among many, all related to a paper by Hohenberg and Kohn (1964) celebrated in quantum chemistry), finding an explicit expression for E is an open problem. In practice, approximations of the density functional have been developed, that rely on exact or very accurate evaluations of different contributions to the energy for reference systems 'close' to the system under study.

The best option for the approximation of the kinetic energy term is today considered to be the model introduced by Kohn and Sham (1965). Their idea was to take N *non-interacting* electrons as the reference system, and made the DFT approach tractable. Under convenient assumptions, the kinetic energy of such a system reads

$$T_{KS}(\rho) = \inf\left\{ \frac{1}{2}\sum_{i=1}^{N} \int_{\mathbb{R}^3} |\nabla\phi_i|^2 : \quad \phi_i \in H^1(\mathbb{R}^3), \quad \int_{\mathbb{R}^3} \phi_i\phi_j = \delta_{ij}, \quad \sum_{i=1}^{N} |\phi_i|^2 = \rho \right\}. \tag{2.20}$$

This expression is then chosen as an *approximation* of the kinetic energy term for the system of *interacting* electrons under study and added to other terms of electrostatic nature (attraction by the nuclei and inter-electronic repulsion) to form the famous *Kohn–Sham model*

$$I_N^{KS} = \inf\left\{ \frac{1}{2}\sum_{i=1}^{N} \int_{\mathbb{R}^3} |\nabla\phi_i|^2 + \int \rho V + \frac{1}{2}\int_{\mathbb{R}^3}\int_{\mathbb{R}^3} \frac{\rho(x)\rho(y)}{|x-y|}\,\mathrm{d}x\,\mathrm{d}y + E_{xc}(\rho) : \right.$$
$$\left. \phi_i \in H^1(\mathbb{R}^3), \quad \int_{\mathbb{R}^3} \phi_i\phi_j = \delta_{ij} \right\}, \tag{2.21}$$

where ρ is a notation for $\sum_{i=1}^{N} |\phi_i|^2$. The functional $E_{xc}(\rho)$, called the *exchange term*, is a correction term, accounting for the non-independence of the electrons, for which approximations are in turn developed for different situations. One of these approximations consists in using as a reference system a uniform non-interacting electron gas. For such a system, Dirac explicitly computed the exchange energy term

$$E_{xc}(\rho) = -C_D \int_{\mathbb{R}^3} \rho^{4/3}, \tag{2.22}$$

where $C_D = \frac{3}{4}\left(\frac{3}{\pi}\right)^{1/3}$.

This approximation of the exchange term is one occurrence of the *local density approximation* (LDA) for which $E_{xc}(\rho) = \int_{\mathbb{R}^3} F(\rho)$. Other more precise expressions have also been developed.

The Euler–Lagrange equations of the problem (2.21) are the *Kohn–Sham equations*

$$\begin{cases} K(\rho_\Phi)\phi_i &= \lambda_i \phi_i, \\ \int_{\mathbb{R}^3} \phi_i \phi_j &= \delta_{ij}, \end{cases} \tag{2.23}$$

where $\rho_\Phi = \sum_{i=1}^N |\phi_i|^2$,

$$K(\rho_\Phi) = -\frac{1}{2}\Delta - \sum_{k=1}^{M} \frac{z_k}{|\cdot - \bar{x}_k(t)|} + \left(\sum_{i=1}^{N} |\phi_i|^2 \star \frac{1}{|x|} \right) + v_{xc}(\rho_\Phi), \tag{2.24}$$

and $v_{xc} = \frac{\partial E_{xc}(\rho)}{\partial \rho}$.

The comparison of the energy functionals in the Hartree–Fock case (2.11) and in the Kohn–Sham case (2.21) (or that of their respective Euler–Lagrange equations (2.15) and (2.23)) reveals the global similarity between the two approaches from a formal viewpoint. We will therefore concentrate on the Hartree–Fock problem, and also indicate when important the necessary modifications for treating the Kohn–Sham model.

Before we get to this, we would like to mention a variant of the Kohn–Sham model, still in the category of density functional theory: the *orbital-free* models. These models are more or less based upon a rather old idea, indeed an ancestor of the DFT, namely the Thomas–Fermi theory. We mention them here because from the standpoint of the implementation and the algorithmic procedure, they exhibit significant differences to the other approaches.

The idea underlying the TF theory is to use as a reference system the uniform non-interacting electron gas (already mentioned above for the approximation of the exchange term, but this time used *also* for the kinetic energy term). For a uniform non-interacting electron gas, one can indeed compute analytically the kinetic energy

$$T_{TF}(\rho) = C_{TF} \int_{\mathbb{R}^3} \rho(x)^{5/3} \, \mathrm{d}x, \tag{2.25}$$

where $C_{TF} = \frac{10}{3}(3\pi^2)^{2/3}$ denotes the Thomas–Fermi constant. In addition, a correction term, obtained by studying perturbations generated by small heterogeneities of the density, and due to von Weizsäcker, can be expressed in terms of $C_W \int_{\mathbb{R}^3} |\nabla \sqrt{\rho}|^2$ and added to the kinetic energy. The minimization problem obtained is thus of the form

$$\inf \left\{ E(\rho), \quad \rho \geq 0, \quad \sqrt{\rho} \in H^1(\mathbb{R}^3), \quad \int_{\mathbb{R}^3} \rho = N \right\}. \tag{2.26}$$

with

$$E(\rho) = C_W \int_{\mathbb{R}^3} |\nabla\sqrt{\rho}|^2 + C_{TF} \int_{\mathbb{R}^3} \rho^{5/3} + \int_{\mathbb{R}^3} \rho V + \frac{1}{2} \int_{\mathbb{R}^3} \int_{\mathbb{R}^3} \frac{\rho(x)\rho(y)}{|x-y|} \, \mathrm{d}x \, \mathrm{d}y - C_D \int_{\mathbb{R}^3} \rho^{4/3}.$$

In contrast to the Kohn–Sham theory, this model only involves the density ρ. It is attacked by discretizing the density ρ on a grid in $\mathbb{R}^3$, which is an approach completely different to that we describe below for models ultimately involving wavefunctions. Of course, more elaborated energy functionals, still functions of ρ, can be derived, but the spirit remains. After years during which the Thomas–Fermi approach was considered out of date, and definitely superseded by the Kohn–Sham approach, it seems that, for very specific purposes (when at least some vague information on the electronic structure must be inserted in simulations of systems of very large size), this approach is seeing a revival in the form of orbital-free methods. We refer to Carter (2000), for example. A mathematical analysis of a simple form of the method is developed in Blanc and Cancès (2004).

Note that, on the other hand, from the academic (and in particular mathematical) viewpoint, the Thomas–Fermi approach has been a constant subject of interest. Major contributions include those by Lieb and Simon (1977*b*) and review articles on all the aspects of these models include Jones and Gunnarsson (1989), Spruch (1991) and Lieb (1983).

3. Discretization of molecular models

The Galerkin approximation procedure consists in approaching the *infinite-dimensional* HF problem (2.11) by a *finite-dimensional* problem where the HF energy is minimized over the set of molecular orbitals ϕ_i that can be expanded with respect to a given finite basis set $\{\chi_\mu\}_{1\le\mu\le N_b}$:

$$\phi_i = \sum_{\mu=1}^{N_b} C_{\mu i} \chi_\mu.$$

The ith column of the rectangular matrix $C \in \mathcal{M}(N_b, N)$ contains the N_b coefficients in the basis $\{\chi_\mu\}_{1\le\mu\le N_b}$ of each of the N molecular orbitals ϕ_i forming the desired Slater determinant. Letting S be the *overlap* matrix with elements

$$S_{\mu\nu} = \int_{\mathbb{R}_3} \chi_\mu \chi_\nu, \tag{3.1}$$

the constraints $\int_{\mathbb{R}^3} \phi_i \phi_j = \delta_{ij}$ become

$$C^* S C = I_N,$$

where I_N denotes the $N \times N$ identity matrix. We next introduce the notation

$$h_{\mu\nu} = \frac{1}{2}\int_{\mathbb{R}_3} \nabla\chi_\mu \cdot \nabla\chi_\nu + \int_{\mathbb{R}^3} V\chi_\mu\chi_\nu \tag{3.2}$$

for the matrix of the core Hamiltonian $h = -\frac{1}{2}\Delta + V$ with respect to the basis $\{\chi_k\}$, together with

$$J(X)_{\mu\nu} = \sum_{\kappa,\lambda=1}^{N_b} (\mu\nu|\kappa\lambda)X_{\kappa\lambda}, \qquad K(X)_{\mu\nu} = \sum_{\kappa,\lambda=1}^{N_b} (\mu\lambda|\nu\kappa)X_{\kappa\lambda},$$
$$G(X)_{\mu\nu} = J(X)_{\mu\nu} - K(X)_{\mu\nu},$$

where X can be any $N_b \times N_b$ matrix, and

$$(\mu\nu|\kappa\lambda) = \int_{\mathbb{R}^3}\int_{\mathbb{R}^3} \frac{\chi_\mu(x)\chi_\nu(x)\chi_\kappa(x')\chi_\lambda(x')}{|x-x'|}\,\mathrm{d}x\,\mathrm{d}x' \tag{3.3}$$

are the so-called *bi-electronic integrals*. The HF problem then becomes

$$\inf\bigl\{E^{HF}(CC^*): \quad C \in \mathcal{M}(N_b,N), \quad C^*SC = I_N\bigr\}, \tag{3.4}$$

where

$$E^{HF}(CC^*) = \mathrm{Trace}(hCC^*) + \frac{1}{2}\mathrm{Trace}(G(CC^*)CC^*).$$

Alternatively, the HF energy can be written in terms of the symmetric $N_b \times N_b$ *density matrix* $D = CC^*$,

$$\inf\bigl\{E^{HF}(D): \quad D \in \mathcal{P}_N\bigr\}, \tag{3.5}$$

where

$$\mathcal{P}_N = \bigl\{D \in \mathcal{M}(N_b,N_b): \quad DSD = D, \quad \mathrm{Trace}(SD) = N\bigr\}. \tag{3.6}$$

The associated Euler–Lagrange equations therefore read

$$\begin{cases} F(D)C &= SC\Lambda, \\ C^*SC &= I_N, \\ D &= CC^*, \end{cases} \tag{3.7}$$

where

$$F(D) = h + G(D)$$

denotes the Fock operator.

Using, as in the continuous case (2.16), the fact that the HF model (3.4) is invariant with respect to the unitary transform $C \mapsto CU$, the matrix of Lagrange multipliers Λ can be diagonalized. In addition, it must be emphasized at this stage that, for a minimizer of the infinite-dimensional HF problem (2.11), the eigenvalues given by Λ are known to be the lowest N eigenvalues of the Fock operator F_Φ (see Lions (1987) and, for the question of the non-degeneracy of the Nth level, Bach, Lieb, Loss and Solovej (1994)). This property is preserved in the finite-dimensional setting for a minimizer C of (3.4),[4] and it is said that C and $D = CC^*$ satisfy the *Aufbau* principle, which is a principle for placing electrons within shells. This property will be strongly exploited below in the design and the analysis of self-consistent field (SCF) algorithms. Therefore the Euler–Lagrange equations read

$$\begin{cases} F(D)C &= SCE, \qquad E = \mathrm{Diag}(\epsilon_1, \epsilon_2, \dots, \epsilon_N) \\ C^*SC &= I_N \\ D &= CC^*, \end{cases} \tag{3.8}$$

where $\epsilon_1 \leq \epsilon_2 \leq \cdots \leq \epsilon_N$ are the lowest N eigenvalues of the Fock operator $F(D)$. In particular, still denoting by Φ_i the ith column of C,

$$F(D)\Phi_i = \epsilon_i S \Phi_i. \tag{3.9}$$

The examination of equations (3.8) gives us the opportunity to emphasize the following key feature: all the models we deal with in the present article are models at *zero temperature*. This is explicit in the Aufbau principle stated above, as the lowest N eigenstates are occupied, while any higher one is empty. In a picture at *positive temperature*, we introduce occupation numbers $\alpha_i \in [0, 1]$, not necessarily equal to zero or one, along each eigenstate Φ_i, including indices $i \geq N + 1$. The coefficients α_i are simultaneously optimized, accounting for some entropy term. In fact, the *free energy* is then minimized instead of the energy.

The Kohn–Sham models are discretized in a similar way to the HF one:

$$I^{KS} = \inf\big\{E^{KS}(CC^*) : \quad C \in \mathcal{M}(N_b, N), \quad C^*SC = I_N\big\} \tag{3.10}$$

with

$$E^{KS}(D) = \mathrm{Trace}(hD) + \mathrm{Trace}(J(D)D) + E_{xc}(D), \tag{3.11}$$

$E_{xc}(D)$ denoting the exchange-correlation energy. If, for instance, an LDA functional is used,

$$E_{xc}(D) = \int_{\mathbb{R}^3} \rho(x)\, \epsilon_{xc}^{LDA}(\rho(x))\, \mathrm{d}x, \quad \text{with} \ \ \rho(x) = 2\sum_{i=1}^{N_p} D_{\mu\nu}\chi_\mu(x)\chi_\nu(x).$$

---

[4] Actually, different variants of the HF problem exist, owing to the treatment of the spins. We do not want to go into technicalities here and will assume that the property under examination is always satisfied. Even in the absence of a mathematical proof for some variants, the numerical practice shows that it is always true. In the same vein, we shall assume below that this property is also satisfied by the KS problem, while in this latter case it is even unclear at the infinite-dimensional level, however, again, confirmed by experiment.

Likewise, the KS equations read

$$\begin{cases} F^{KS}(D)C &= SCE, \qquad E = \mathrm{Diag}(\epsilon_1, \epsilon_2, \dots, \epsilon_N) \\ C^*SC &= I_{N_p} \\ D &= CC^* \end{cases} \tag{3.12}$$

with $F^{KS}(D) = h + J(D) + \nabla E_{xc}(D)$ and ϵ_i the ith eigenvalue of $F^{KS}(D)$. As announced above, we observe the formal similarity between problems (3.8) and (3.12), which confirms the opportunity to concentrate mainly on the HF problem in the present expository survey.

At this stage, let us also mention that solutions of

$$\begin{cases} FC &= SCE, \qquad E = \mathrm{Diag}(\epsilon_1, \epsilon_2, \dots, \epsilon_N) \\ C^*SC &= I_N \\ D &= CC^* \end{cases} \tag{3.13}$$

(where F is a given matrix) are the same as the solutions in $\mathcal{P}_N$ to the equation

$$[F, D] = 0, \tag{3.14}$$

where $[\cdot,\cdot]$ denotes the 'commutator' defined by $[A, B] = ABS - SBA$. Likewise, the solutions to (3.13) which satisfy in addition the Aufbau principle are the same as the solutions to the problem

$$D = \arg\inf\bigl\{\mathrm{Trace}(FD') : \quad D' \in \mathcal{P}_N\bigr\}. \tag{3.15}$$

If in addition there is a positive gap between the Nth and the $(N+1)$th eigenvalue of F (*i.e.*, if $\epsilon_1 \le \cdots \le \epsilon_N < \epsilon_{N+1} \le \cdots \le \epsilon_{N_b}$), then the Aufbau solutions D to (3.13) are also the solutions to

$$D = \arg\inf\bigl\{\mathrm{Trace}(FD') : \quad D' \in \widetilde{\mathcal{P}}_N\bigr\}, \tag{3.16}$$

where

$$\widetilde{\mathcal{P}}_N = \bigl\{D \in \mathcal{M}(N_b, N_b) : \quad DSD \le D, \quad \mathrm{Trace}(SD) = N\bigr\}. \tag{3.17}$$

This latter property will be briefly justified in Section 3.5 below.

3.1. Anticipating the numerical difficulties

The examination of the discrete form (3.5)–(3.6) of the Hartree–Fock minimization problem suffices to measure the main difficulties experienced in the numerical approach.

The minimization is performed over the manifold of density matrices ($DSD = D$) which is nonconvex (a good way to think of the problem is to think of minimizing a function over a sphere). Whatever the properties of the function to be minimized, the problem is likely to be difficult. It is indeed. At the theoretical level, we of course lose the equivalence between the minimization viewpoint and the Euler–Lagrange viewpoint. A rigorous approach would attack the minimization directly. Unfortunately, on the one hand, the enormous number of critical points that have been observed in practice rule out deterministic gradient algorithms, while on the other hand zero-order methods such as stochastic methods and direct search methods lead to an overwhelming number of function evaluations. Therefore, contrary to rigour, we are obliged to attack the problem by solving the Euler–Lagrange equations.[5] This liberty with rigour will of course plague the numerical analysis of existing approaches, as we will see in Section 3.5. The somewhat surprising fact is that it works in practice, provided a number of precautions are taken, such as a proper choice of an initial guess. Here a point must be made. For a mathematician, trusting a lucky star in order to obtain convergence to the global minimizer is of course both frustrating and crazy, and we by no means pretend otherwise here. But a specificity of computational chemistry comes into the picture. The calculation of a molecular system is rarely done *from scratch*. A computation with a coarser model, or with the same model implemented more coarsely, has often been done before. In some cases as well, the solution procedure is an inner loop of a more global simulation: when the evolution of a molecular system is simulated, the nuclei are moved incrementally through Newton's equation, and for each updated position of the set of nuclei a new calculation of the electronic structure is performed (we shall see such methods in Section 5). Then, the natural initial guess is the output of the previous computation. All this contributes to render the Euler–Lagrange approach successful in practice.

Of course, the chances of success are significantly increased by a design of the solution algorithms for the Euler–Lagrange equations that is, in some way or another, reminiscent of the fact that the solution to be determined is not any critical point, but the global minimizer. And this is where a rigorous numerical analysis reveals itself to be efficient. This is done by at least requiring the Aufbau principle for the solution, but also in a more sophisticated manner, by elaborating algorithmic strategies based upon partial minimizations. We will return to this in Section 3.5.

Having accepted that the Euler–Lagrange approach is the only tractable one, we can adopt either finite difference-type methods or variational methods. The former are far less commonly used, unless for very specific purposes, and we refer to the literature for more details (see, *e.g.*, the review article by Beck (2000) and also the chapters by J. L. Fattebert and J. Chelikowski *et al.* in Le Bris, ed. (2003)). In computational chemistry, finite difference methods are often referred to as *real-space* methods.

---

[5] Obviously, our statement describes the state of the art. New and efficient ideas to attack the problem by minimization are welcome.

Basically, they amount to discretizing the Euler–Lagrange equations on a grid, using high-order schemes (typically order 4 or 6) for the Laplacian operator associated with the kinetic energy term. We will only concentrate on the variational methods. A key issue will be the choice of the variational space. We will again see below some specific features of computational chemistry (mostly related to the approximation of singularities), which often lead to 'problem-dependent' basis sets.

A second point on the Euler–Lagrange approach is to observe the algebraic nature of these equations (3.7): they form a *nonlinear eigenvalue problem.* Heuristically, the price to pay for making the *linear* eigenvalue problem (2.5) tractable numerically is *nonlinearity.* Therefore iterations are required, consisting more or less in freezing the operator and diagonalizing it, before updating it. The computational task is first to assemble the matrix, and next to diagonalize it. Here again, comments are in order.

Let us begin with the assembling step. In the Hartree–Fock setting, the computational effort necessary to build the mean-field Hamiltonian matrix (*i.e.*, the Fock matrix) in a basis containing N_b elements *a priori* scales as N_b^4 because of the calculation of the bielectronic integrals (3.3). For small systems, this quartic scaling constitutes another peculiarity of computational chemistry, because constructing the matrix is there more expensive than diagonalizing it, a fact that must of course be borne in mind for the design of methods. For large systems, however, the scaling is much lower in practice because the overlap of two atomic orbitals attached to two nuclei far away from one another is negligible (we will introduce this particular type of basis functions in Section 3.2, but for the time being it is enough to know that these basis functions are attached to the nuclei, and remark that integrals of type (3.3) are small when χ_μ and χ_ν (resp. χ_κ and χ_λ) have a small overlap). Various algorithms taking benefit of *a priori* estimates of the integrals were developed in the late 1970s and the 1980s (see Gill (1994) and the references therein); it is estimated that the scaling of these algorithms is around $N_b^{2.7}$ in practice. The prefactor mainly depends on the choice of the basis set (in fact of the degree of contraction of the Gaussian atomic orbitals, *i.e.*, of the parameter K in (3.22) below). For very large molecules, a much better scaling ($O(N_b)$) can however be obtained with linear scaling algorithms based on the Fast Multipole Method by Greengard and Rokhlin (1997), adapted to Coulomb and exchange matrix computations by M. Challacombe and coworkers: see Schwegler and Challacombe (1997) and further works.

In the Kohn–Sham model, the third term in (3.11) is evaluated by numerical integration on a grid, a computation that has complexity $O(N_b^3)$. For small molecular systems, the calculation is thus dominated by the computation of the second term in (3.11), and still scales in $O(N_b^4)$ (theoretically). On the other hand, for larger systems when the second term approximately scales in $N_b^{2.7}$, the limiting evaluation is that of the third term, thus in $O(N_b^3)$. Note that linear scaling integration methods have been introduced recently (see Scuseria (1999), Challacombe (2000) and references therein).

Let us turn to the diagonalization step. As mentioned above, it basically scales as N_b^3. It must be emphasized that *stricto sensu* the full diagonalization is not needed as we only search[6] for the *lowest* N eigenvectors and eigenvalues of a matrix of size $N_b \times N_b$ (in view of the Aufbau principle). However, for systems of reasonable size, the most efficient basis sets currently are atomic orbital basis sets for which N_b is typically a few times as large as N, thus the question asked cannot be reduced to finding the first few eigenvectors: the number of these eigenvectors might be half the size of the matrix.[7] The full diagonalization procedure is the most efficient choice, and this is all the more true as it benefits from many rapid implementations developed over the years for various applications of scientific computing. For systems of reasonable size (say a few electrons), the cost of the Hartree–Fock approximation is thus dominated by the N_b^4 cost of the construction of the Fock matrix, while it progressively diminishes to a power of roughly 3 for large systems, where the diagonalization step becomes the limiting process.

The above observation along which no complete diagonalization is *stricto sensu* needed.[8] is at the origin of a class of methods, dedicated to very large systems, and called *alternative to diagonalization methods* They will be overviewed in Section 3.7. Together with a rapid construction of the Fock matrix (by FMM), these methods allow us to bring down the complexity to a linear complexity (or slightly more than that) and make HF calculations of about one thousand atoms feasible on today's available workstations.

Let us mention to end this section that the N_b^4 complexity of the Hartree–Fock method is by no means an upper bound on the complexity of methods in the context of computational chemistry: the so-called post-Hartree–Fock methods, such as configuration interaction methods, MCSCF methods (see Section 3.8) and others have a computational complexity that can reach N_b^8 or more. We now measure the practical limitation of such methods for simulation of large systems, and this is one of the reasons of the success of DFT-based methods for the simulation of such systems, the latter scaling cubically (or less if the linear scaling methods mentioned above are employed). As there is no free lunch, this favourable scaling is obtained at the price of approximations in the model itself. Such approximations are not so rigorously founded, despite huge ongoing efforts, and their impact on the

---

[6] And in fact this statement will be further weakened in the next paragraph.

[7] The statement can be somewhat different for the plane waves basis set, for which the matrix is far larger than the number of eigenvectors needed (say 10 to 100 times larger).

[8] and in fact no diagonalization at all, as will be made clear in Section 3.7.

final result is uneasy to measure. This shows the urgent need for further theoretical contributions in the field.

3.2. Basis sets

We now consider the question of the determination of the $\{\chi_\mu\}$, *i.e.*, that of building an efficient finite-dimensional approximation of the space of wavefunctions to be considered for the determination of the electronic structure of the molecular system under study.

It is natural, in order to figure out the difficulty of the approximation, to look at the qualitative properties that are expected for the wavefunctions or the electronic density. For this purpose, an illuminating step is to consider the hydrogen-like atom, whose Hamiltonian reads

$$H_Z = -\frac{1}{2}\Delta - \frac{Z}{|x|}. \tag{3.18}$$

It is simple to see that the positive ground state of this Hamiltonian is

$$\psi_1^Z(x) = \frac{Z^{3/2}}{\sqrt{\pi}} \mathrm{e}^{-Z\,|x|}, \tag{3.19}$$

and from this, two crucial observations stem. First, the electronic density of the molecular system is expected to have *cusps* at each nucleus of the molecule, *i.e.*, singularities in the first derivatives, as is the case for (3.19). Second, the density is expected to decay exponentially fast at large distance.[9] From these two observations, it can be anticipated that general-purpose basis sets, such as finite elements, will not be very well adapted to the problem. This guess is confirmed by numerics. The singularity around each nucleus typically asks for an extensive refinement of the mesh around these points and the dimension of the discrete variational space correspondingly increases, rendering the approach inefficient.[10] Likewise, large distance effects are difficult to reproduce within such methods. This pleads for dedicated (*i.e.*, *problem-dependent*) basis sets, in the spirit of the *component mode synthesis* or the *reduced basis methods*, advocated by A. Patera, Y. Maday and collaborators in various domains of engineering sciences. We refer to Almroth, Stern and Brogan (1978) and Noor and Peters (1980) for pioneering works some decades ago, and Nguyen, Veroy and Patera (2005)

---

[9] The properties of regularity and decay at infinity of the density of the solution to the original Schrödinger equation (2.5) have been studied in Fournais, Hoffmann-Ostenhof, Hoffmann-Ostenhof and Sorensen (2002*a*, 2002*b*, 2004) and Hoffmann-Ostenhof, Hoffmann-Ostenhof and Sorensen (2001).

[10] Many electronic structure calculations for large systems, and in particular periodic ones, are done with the help of pseudopotentials that, in addition to other purposes, aim to smear out the singularity at each nucleus; then the above discussion no longer holds and basis sets such as plane waves are tractable: see Section 4.1.

for an up-to-date survey and more references. We also refer to Section 5 for a work in progress in the present context. Actually, an ancestor of such methods was introduced as early as the 1930s in computational chemistry. As the molecular system consists of an assembly of atoms, the natural idea then arose to choose as finite-dimensional space for the approximation the vectorial space generated by some particular functions related to the problem, here a finite number of atomic orbitals (AO), *i.e.*, basis functions used to solve the *same* problem but in the *atomic* or hydrogen-like case (only one nucleus). We speak of an *LCAO approximation*, the acronym LCAO standing for *linear combination of atomic orbitals*.

In so doing, we expect that the size of the variational space will be kept reasonably small, contrary to general-purpose basis sets. Atomic orbital basis sets are thus built by associating to each atom A of the molecule a collection $\left\{\xi_\mu^A\right\}_{1\leq\mu\leq n_A}$ of linearly independent functions of $H^1(\mathbb{R}^3)$, and then by collecting all the ξ_μ^A for the different atoms of which the system is composed.

At this stage, we are left with defining a good basis set for each atom of the molecule. Again, it is useful to consider in detail the simple case of the *hydrogen-like* ion, that is, a system modelled by the Hamiltonian (3.18) consisting of a single electron bound by a single nucleus with charge Z. This system indeed serves as a paradigm for the computations of more complicated molecular systems.[11]

Standard general results of spectral theory and explicit calculations give us a very detailed description of not only the ground state (3.19) but also all of the eigenstates of the operator (3.18) that are the functions

$$\psi_{nlm}^Z(r,\theta,\phi) = Q_{nl}(Zr)\mathrm{e}^{-Zr/n}Y_l^m(\theta,\phi), \tag{3.20}$$

for $n \in \mathbb{N}$, $0 \leq l \leq n-1$, $-l \leq m \leq l$, where Q_{nl} denotes a polynomial defined by an induction formula, and where the functions $Y_l^m(\theta,\phi)$ denote the spherical harmonics, in turn defined by the first m derivatives of the Legendre polynomial P_l. Such functions, called *hydrogen-like orbitals* when used to form a basis set for a molecular calculation, provide high accuracy results but through tedious computations. Therefore the idea very early arose to modify them slightly, giving birth to *Slater-type orbitals* (STOs): in (3.20), the polynomial Q_{nl} is replaced by the monomial r^l. These orbitals were introduced in Slater (1930) and widely used in the early days of quantum chemistry. They were in turn superseded by another type of

---

[11] An interesting point to make at this stage is that, since they are primarily based upon a *one-electron* model, the basis sets we will now construct have no reason to be able to adequately represent the *electronic* cusp, *i.e.*, the singularity in the *multielectronic* wavefunction due to the $\frac{1}{|x_i-x_j|}$ singular term in the Hamiltonian. We will return to this in the next section.

basis functions. The reason is the overwhelming computational cost of the bielectronic integrals (3.3)

$$(\mu\nu|\kappa\lambda) = \int_{\mathbb{R}^3}\int_{\mathbb{R}^3} \frac{\chi_\mu(x)\chi_\nu(x)\chi_\kappa(x')\chi_\lambda(x')}{|x-x'|}\,\mathrm{d}x\,\mathrm{d}x'.$$

As there are N_b^4 such integrals, this calculation is a bottleneck for the whole computation. Without any further simplification, it is hopeless to calculate each of these N_b^4 integrals by an integration scheme over $\mathbb{R}^3 \times \mathbb{R}^3$. The computation time required would be prohibitive.

The groundbreaking idea by Boys (1950) that has suddenly changed the whole landscape of quantum chemistry, was to replace, in the role of basis functions, STOs by *Gaussian-type orbitals* (GTOs), which are Gaussian functions or successive derivatives of Gaussian functions:

$$\xi(x,y,z) = C\, x^{n_x} y^{n_y} z^{n_z} \mathrm{e}^{-\alpha r^2}. \tag{3.21}$$

The crucial advantage in considering such functions is that the calculation of the overlap matrix (3.1), of the core Hamiltonian matrix (3.2), and, above all, of the bielectronic integrals (3.3) can then be greatly simplified. Indeed, because of some specific properties of Gaussian functions, the computations of the six-dimensional integrals (3.3) are brought down to the numerical computations of one-dimensional integrals of the form $F(w) = \int_0^1 \mathrm{e}^{-w\,s^2}\,\mathrm{d}s$.

On the other hand, simply using GTOs would not allow for a correct description of the shape of the molecular orbitals both near the nuclei and at infinity, unless a large number of orbitals are employed, which is not desired. The current state of the art of the LCAO approximation is thus to use basis sets made of *contracted Gaussian functions*, which are linear combinations of primitive Gaussian functions,

$$\xi(x,y,z) = \sum_{k=1}^{K} C_k\, x^{n_x^k} y^{n_y^k} z^{n_z^k} \mathrm{e}^{-\alpha_k r^2}, \tag{3.22}$$

in which the C_k are optimized once and for all in order to accurately represent the cusps and the fall-off at infinity. These functions allow both for easy calculation of the bielectronic integrals and for a correct description of the qualitative properties of the wavefunctions. Somehow they constitute the best compromise between STOs and GTOs.

Let us mention for completeness that an alternative to the use of contracted Gaussian functions is that of *fully numerical atomic orbitals*, *i.e.*, basis functions that are solely defined by their numerical values on a grid. They are in general compactly supported in balls centred at the nuclei and whose radii do not exceed a few atomic units. Both the Hamiltonian and the overlap matrix are thus sparse, which is a clear advantage with a view to designing algorithmic approaches of low complexity. However, the use of numerical orbitals makes the computation of integrals of the type

$$\int\int\left(\rho_1 \star \frac{1}{|x|}\right)\rho_2$$

more time-consuming, for they must be carried out by solving a Poisson equation on a large domain, with *ad hoc* boundary conditions, which are not easy to define, and possibly singular functions ρ_1 in the right-hand side (typically think of ρ_1 being a Dirac mass at each nucleus).

However they are derived, atomic orbital basis sets are used in most of the gas or liquid phase calculations, for the determination of the static electronic structure of the molecular system under study. With a surprisingly low number of basis functions, typically a few times the number of electrons (say 2–10), it is then possible to obtain very accurate results.

In some situations, however, the LCAO approximation is not adequate, or at least causes significant problems. Indeed, a drawback of the LCAO approximation lies precisely in the fact that the basis *depends* on the system and is in some sense bound to it. When studying the evolution of a molecular system where the nuclei move, or when studying the interaction of two systems (or also a system embedded in a condensed phase), we are obliged to modify the basis set, either by translating the basis functions according to the motion of the nuclei, or respectively by adding new basis functions to account for the presence of more than one single system (the latter situation gives rise to *basis set superposition error*). In either of these situations, more intrinsic basis sets are preferred. The most commonly used example is that of *plane waves*. Then a much larger number of basis functions is needed, but, as those are fixed, this can still prove to be more efficient than the LCAO in the very particular settings mentioned above. We will come back to them in Section 4.1.

3.3. Evaluation of the quality of the basis set

Let us recall some basics. When a space X_δ of finite dimension is fixed, with a view to approximating the space X, the error between the exact solution Φ_0 of the problem set in infinite dimension and the solution Φ_δ found numerically can be split into two components. One component of this error comes from the fact that the best approximation we can get is not Φ_0, but the function $\pi_\delta\Phi_0$ in X_δ that is as close as possible to Φ_0. The second component is due to the fact that the solution procedure will only provide an approximation Φ_δ of $\pi_\delta\Phi_0$ itself. Therefore we can (formally) estimate the global error as follows:

$$\|\Phi_0 - \Phi_\delta\| \le \|\Phi_0 - \pi_\delta\Phi_0\| + \|\pi_\delta\Phi_0 - \Phi_\delta\|. \tag{3.23}$$

Clearly the first component of the error only depends on the quality of the approximation space X_δ, that is to say, of the basis set of X_δ, while the second component depends on the quality of the solution procedure itself. The latter is said to be optimal if the ratio of the error between the exact solution and the computed solution (second component) by the error between the exact solution and the closest element in the discrete space (first component) does not depend on the size of the basis set.

In the chemistry literature, the theoretical studies on the quality of the basis set are numerous and have all concentrated on the first component of the error, with a view not only to establishing the asymptotic convergence but also to evaluating the rate of convergence of the best approximation $\pi_\delta \Phi_0$ in the given basis to Φ_0, with respect to the size of the basis. Further, in practice, the ratio between the convergence and the complexity of the computations is of greater interest than the rate of convergence itself. Therefore a large body of the chemistry literature has been developed along these lines, particularly in order to enrich the basis sets and improve the convergence rate.

For evaluating the quality of an atomic orbitals basis set, there is no general approach, in contrast to the situation with finite elements or spectral methods such as plane wave basis sets. The choice of an AO basis for solving a given problem mostly relies upon some practical know-how. The lack of rigorous understanding is a pity, because the output of the calculations (typically some molecular property) might be very sensitive to the choice of the basis set. The only available measures of the quality of the basis set are obtained, in the chemistry literature, by choosing test cases, *i.e.*, reference systems, where the solution of the exact Schrödinger equation may be computed, mostly through numerical computations and, when possible, with the help of an analytic calculation.

In the hydrogen-like atom, the system consists of a single electron, and the problem amounts to finding the first eigenvalue and eigenfunction of the Hamiltonian. Klahn and Bingel (1977) were the first in the chemistry literature to investigate the conditions for the convergence to the exact eigenvalue. They established that the basis sets used conventionally[12] were complete for the H^1 topology, thus yielding the asymptotic correctness of the results when the size of the basis goes to infinity. As mentioned above, the critical aspect, as far as the convergence to the exact wavefunction is concerned, is the *representation of the nuclear cusp*. In the chemistry literature, it was shown heuristically by Hill (1985) that a rapid convergence is only possible if the basis set describes correctly the *singularities* of the function to be expanded, a fact that can of course be understood and described on the basis of rigorous, and simple, mathematical arguments.

---

[12] See, however, the comments at the end of the section.

Regarding the convergence rate, Klahn and Morgan, III (1984) have studied the convergence of expansions of the ground state of the H atom in a simplified basis set consisting of Gaussian orbitals, and found that the error of the energy goes as $\sim d^{-3/2}$ if d is the dimension of the basis, which is a very slow convergence. Other studies then aimed at further studying, theoretically (Klopper and Kutzelnigg 1986, Hill 1995) or experimentally (Schmidt and Ruedenberg 1979, Feller and Ruedenberg 1979), this rate of convergence and then improving it by introducing new basis functions.

One important point is that for practical purposes there are many ways to measure the efficiency of a given basis set, depending on the output chosen: *e.g.*, the distance of the expansion to the exact function, the error of the density at the position of the nucleus, the error of the energy value, *etc.* In this direction we cite the series of works by Kutzelnigg (1989, 1994).

In the case of many-electron systems, the question of evaluating the best approximation of the exact ground state wavefunction requires understanding an effect that has been omitted so far in this survey, namely the effect on the convergence of basis expansions of the *correlation cusp*, created by the $\frac{1}{|x_i - x_j|}$ interaction term. Schwartz (1962) was the first to study the rate of convergence of the expansion of correlated wave functions in a one-electron basis. He considered the helium ground state, treating the electron interaction as a perturbation of the one-electron case. More recently Klahn and Morgan, III (1984) and Hill (1985) studied the rate of convergence of variational calculations in a general setting (for a review of this problem see Morgan, III (1984)) while Kutzelnigg and Morgan, III (1992) presented a detailed study of the solution of the Schrödinger equation near $r_{12} = 0$.

It is interesting to note that, with a view to circumventing the difficulty of representing many-electron wavefunctions in terms of one-electron functions, which inevitably lowers the rate of convergence of the expansion, the idea arose to use variational trial wave functions that depend explicitly on the interelectronic distances $|x_i - x_j|$, and allow us to describe the correlation cusp correctly. Hylleraas (1929) initiated the approach with an accurate calculation of the ground state energy of He-like ions using some function $\Psi(x_1, x_2, |x_1 - x_2|)$ with only a small number of parameters. Further works are those of Kinoshita (1957), Pekeris (1958), James and Coolidge (1933), Kolos and Rychlewski (1993), for instance. More recently some progress has been achieved for 3- and 4-electron atoms by Kleindienst and collaborators: see, *e.g.*, Luchow and Kleindienst (1994). The feasibility of the approach for a higher number of electrons is an open issue. Note that, of course, for systems of more than 3 electrons, the coalescence of three particles has to be studied. This is done by the so-called *Fock expansion*: see Fock (1958) and, *e.g.*, Peterson, Wilson, Woon and Dunning, Jr. (1997). It is important to note that these studies certainly need to be complemented on the rigorous mathematical side.

As a conclusion to this section, we would like to point out that atomic orbital basis sets in their contemporary implementation remain the basis sets of choice for electronic structure calculations of small systems. They give an impressive accuracy for a surprisingly small size of the basis. Therefore we believe that the field would definitely benefit from further mathematical studies. One reason is that there is room for improvement in many of the proofs mentioned above, in particular because they sometimes do not apply to the basis sets actually used in practice but rather to an idealized version of them (for instance, exponents in the Gaussian functions are allowed to vary arbitrarily, or contracted Gaussian functions are not addressed). A second reason for this is precisely the incredible efficiency of the atomic orbital basis sets: convergence is obtained long before the asymptotic regime. To some extent, the asymptotic analysis described above is indeed useful for the sake of rigour and as a first step, but not sufficient for shedding light on the practice.

3.4. Convergence analysis

Let us consider now $\pi_\delta \Phi_0$ as being the best fit of Φ_0 by elements of the discrete space X_δ. The question is now to evaluate $\|\pi_\delta \Phi_0 - \Phi_\delta\|$, *i.e.*, the second error term in (3.23). No study in the chemistry literature deals with this question. In the mathematical literature, the question has been addressed by a series of works by Y. Maday and G. Turinici. The following lines are based upon their work.

Above all, some particular precautions have to be taken before evaluating this norm. Owing to the invariance of the HF energy with respect to orthogonal (or unitary) transforms, the error between any two Slater determinants Ψ_1 and Ψ_2 cannot be evaluated naïvely. We need to introduce distances of the type

$$\|\Psi_1 - \Psi_2\| = \inf\{\|U\Psi_1 - \Psi_2\|_{[L^2(\mathbb{R}^3)]^N} : \ U \in \mathcal{U}(N)\},$$

where $\mathcal{U}(N)$ represents the set of all unitary $N \times N$ matrices. In the same spirit, Maday and Turinici (2003) have introduced, for any $\Phi \in [H^1(\mathbb{R}^3)]^N$, the decomposition

$$[H^1(\mathbb{R}^3)]^N = \mathcal{A}_\Phi \oplus \mathcal{S}_\Phi \oplus \Phi^{\perp\perp},$$

where

$$\begin{aligned}
\mathcal{A}_\Phi &= \{C\Phi : \ C \in \mathbb{R}^{N\times N}, C^\star = -C\},\\
\mathcal{S}_\Phi &= \{S\Phi : \ S \in \mathbb{R}^{N\times N}, S^\star = S\},\\
\Phi^{\perp\perp} &= \{\Psi = (\psi_i)_{i=1}^N \in [H^1(\mathbb{R}^3)]^N : \ \langle \psi_i, \phi_j \rangle = 0; i, j = 1, \dots, N\}.
\end{aligned}$$

Applying this to $\Psi - \Phi$, with Φ and Ψ in $[H^1(\mathbb{R}^3)]^N$ satisfying $\langle \phi_i, \phi_j \rangle = \delta_{ij}$,

$\langle \psi_i, \psi_j \rangle = \delta_{ij}$, we thus have the decomposition

$$\Psi = \Phi + C\Phi + S\Phi + W, \quad W \in \Phi^{\perp\perp}. \tag{3.24}$$

Generally, it can be established that, up to an adequate orthogonal transform, C may be set to zero, and that the symmetric part $S\Phi$ is not the main part of the decomposition (when $\Psi - \Phi$ is presumably small) as there exist constants C_1, C_2 depending only on N such that

$$\|S\Phi\|_{[L^2(\mathbb{R}^3)]^N} \leq C_1 \|\Psi - \Phi\|^2_{L^2(\mathbb{R}^3))^N}, \tag{3.25}$$

$$\|S\Phi\|_{[H^1(\mathbb{R}^3)]^N} \leq C_2 \|\Psi - \Phi\|^2_{\mathcal{H}} \|\Phi\|_{[H^1(\mathbb{R}^3)]^N}. \tag{3.26}$$

With the above preparatory work, it is possible to show that in a sufficiently small neighbourhood of Φ_0 (or $\pi_\delta \Phi_0$), there exists a discrete solution Φ_δ of the HF equation (unique in some weakened sense) and such that the error between Φ_0 and Φ_δ is of the same order as $\Phi_0 - \pi_\delta \Phi_0$. Again, it should be emphasized that all these precautions originate from the fact that there is no uniqueness known on the solution to the HF equations, and thus the usual error estimates established in other contexts need to be adapted.

To prove this claim, the following energy functional parametrized by any $\Phi \in [H^1(\mathbb{R}^3)]^N \cap \mathcal{K}$, is introduced:

$$\mathcal{E}^{\Phi}(\psi_1, \dots, \psi_N) = E^{HF}(\psi_1, \dots, \psi_N) + \sum_{i,j=1}^{N} \langle F_\Phi \phi_i, \phi_j \rangle \big(\langle \psi_i, \psi_j \rangle - \delta_{ij} \big), \tag{3.27}$$

where F_Φ denotes the Fock operator. Then, for an arbitrary Ψ decomposed in $\Psi = \pi_\delta(\Phi_0) + S\pi_\delta(\Phi_0) + W$ in view of (3.24), we compute

$$\begin{aligned} E^{HF}(\Psi) - E^{HF}(\pi_\delta(\Phi_0)) &= \frac{1}{2} D^2 \mathcal{E}^{\Phi_0}(W - \Phi_0 + \pi_\delta(\Phi_0), W - \Phi_0 + \pi_\delta(\Phi_0)) \\ &\quad - \frac{1}{2} D^2 \mathcal{E}^{\Phi_0}(\Phi_0 - \pi_\delta(\Phi_0), \Phi_0 - \pi_\delta(\Phi_0)) \\ &\quad + O(\|W\|^3 + \|\Phi_0 - \pi_\delta(\Phi_0)\|^3). \end{aligned}$$

It suffices then to minimize this quantity with respect to W such that Ψ remains in a small neighbourhood of $\pi_\delta(\Phi_0)$, and this yields the correct Φ_δ. It can be shown that such a minimizer is unique (due to the coercivity of the Hessian $D^2 \mathcal{E}^{\Phi_0}$), and that

$$\|W\| \leq c \|\Phi_0 - \pi_\delta \Phi_0\|,$$

thus proving the above claim on the order of the error.

At this stage, we pass from *a priori* considerations (the discrete solution exists and if the discrete space is large enough we obtain an accurate result (even optimal)) to *a posteriori* considerations: in a final stage where one approximate solution has been computed, the need arises to *validate* the result. *A posteriori* analysis and, more precisely, the definition of explicit lower and upper bounds for outputs was introduced in Maday, Patera and Peraire (1999), and first analysed in Maday and Patera (2000).

Let us consider an approximation Φ_δ such that $\|\Phi_0 - \Phi_\delta\|_{[H^1(\mathbb{R}^3)]^N} \leq \varepsilon$, and perform the decomposition $\Phi_0 - \Phi_\delta = S\Phi_\delta + W$, where W belongs to $\Phi_\delta^{\perp\perp}$, $\|W\|_{[H^1(\mathbb{R}^3)]^N} \leq C\varepsilon$ and $\|S\Phi_\delta\|_{[H^1(\mathbb{R}^3)]^N} \leq C\varepsilon^2$. The evaluation of the quality of the approximation is based upon the introduction of the following problem:[13] finding the *reconstructed error* $\hat{W} \in \Phi_\delta^{\perp\perp}$ such that

$$D^2\mathcal{E}^{\Phi_\delta}(\hat{W}, \Psi) + D\mathcal{E}^{\Phi_\delta}(\Psi) = 0, \quad \text{for all } \Psi \in \Phi_\delta^{\perp\perp}, \tag{3.28}$$

a problem that has, owing to some coercivity of $D^2\mathcal{E}^{\Phi_\delta}$, a unique solution. Then,

$$E^{HF}(\Phi_0) = E^{HF}(\Phi_\delta) - \frac{1}{2}D^2\mathcal{E}^{\Phi_\delta}(\hat{W}, \hat{W}) + \frac{1}{2}D^2\mathcal{E}^{\Phi_\delta}(W - \hat{W}, W - \hat{W}) \\ + O(\varepsilon^3)$$

For sufficiently small ε, this yields

$$E^{HF}(\Phi_\delta) \geq E^{HF}(\Phi_0) \geq \mathcal{E}^{HF}(\Phi_\delta) - D^2\mathcal{E}^{\Phi_\delta}(\hat{W}, \hat{W}), \tag{3.29}$$

the left-hand side holding true because a variational approximation always provides a discrete minimum that is larger than the global one. This provides an explicit upper and lower bound on the Hartree–Fock energy. This bound is effective in the sense that it has been proved in Maday and Turinici (2003) that there exists a constant such that

$$\|\hat{W}\|_{[H^1(\mathbb{R}^3)]^N} \leq c\|W\|_{[H^1(\mathbb{R}^3)]^N}, \tag{3.30}$$

so that the width of the bound is small and of the same order as

$$\|E^{HF}(\Phi_\delta) - E^{HF}(\Phi_0)\|_{[H^1(\mathbb{R}^3)]^N}.$$

The estimate (3.29) therefore provides on the solution Φ_δ found numerically an *a posteriori* estimate, both rigorous mathematically and tractable in practice. The estimate can serve as an evaluation of the quality of the basis set employed, and, possibly, indicates the need for an enlargement of this basis set. The procedure was implemented and successfully tested some years ago in an academic code for electronic structure calculations. It seems, however, not to be used today in any widely distributed software in the field.

A corollary of the above technique is the following: $\hat{W}$ can actually be shown to be very close to the actual (main part of) the error W, so that an improvement on the solution Φ_δ can be proposed by setting

$$\tilde{\Phi}_\delta = \Phi_\delta + \hat{S}\Phi_\delta + \hat{W}, \tag{3.31}$$

---

[13] Note that this computation involves a direct problem and not an eigenvalue problem.

where $\hat{S}\Phi_\delta \in S_{\Phi_\delta}$ and $\|\hat{S}\Phi_\delta\| = O(\varepsilon^2)$. This justifies the name *reconstructed error* for $\hat{W}$. Correspondingly, a new evaluation $E^{HF}(\tilde{\Phi}_\delta)$ of the energy can be proposed. Actually, (3.31) can be re-interpreted as follows. It yields the same improvement $\widetilde{\Phi}_\delta$ of Φ_δ as that obtained by performing *one* step of a Newton algorithm on $E^{HF}(e^C\Phi_\delta)$ where C is a matrix subject to some constraints.

3.5. SCF cycles

We now concentrate on the strategy to solve the discretized Hartree–Fock equations (3.8). This solution procedure provides the approximation Φ_δ in (3.23). There lies the third type of numerical analysis involved, after that of Section 3.2 and that of Section 3.3: the speed of convergence of the algorithm toward the solution Φ_δ needs to be evaluated.

The first class of algorithms we report on is that of *self-consistent field* (SCF) algorithms, *i.e.*, iterations of the form

$$\begin{cases} \widetilde{F}_k C_{k+1} &= S C_{k+1} E_{k+1}, \qquad E_{k+1} = \mathrm{Diag}(\epsilon_1^{k+1}, \ldots, \epsilon_N^{k+1}) \\ C_{k+1}^* S C_{k+1} &= I_N \\ D_{k+1} &= C_{k+1} C_{k+1}^*. \end{cases} \tag{3.32}$$

Here, $\epsilon_1^{k+1} \le \epsilon_2^{k+1} \le \cdots \le \epsilon_N^{k+1}$ are the smallest N eigenvalues of the linear generalized eigenvalue problem

$$\widetilde{F}_k \phi = \epsilon\, S\phi,$$

and C_{k+1} contains the corresponding N orthonormal eigenvectors. The expression of the current Fock matrix $\widetilde{F}_k$ characterizes the algorithm. We have, for instance,

$$\widetilde{F}_k = F(D_k)$$

for the simplest algorithm we shall see, but more sophisticated forms will be examined. In spirit, these algorithms are more or less fixed-point iterations. The hope is that C_k, D_k and $F(D_k)$ converge, respectively to C, D and $F(D)$, so that we get from (3.32) a solution to (3.8) in the limit $k \longrightarrow +\infty$.

For years, no mathematical analysis was available for the SCF algorithms, however much used in practice. In the chemistry literature, convergence successes and failures were reported, comparisons of rates of convergence between algorithms were experimentally established, remedies and tricks were given – all without any rigorous understanding. Examples of such contributions are Schlegel and McDouall (1991), Seeger and Pople (1976), Stanton (1981*a*), Starikov (1993), Zerner and Hehenberger (1979), Koutecký and Bonacic (1971), Douady, Ellinger, Subra and Levy (1980), Natiello and

Scuseria (1984), Fischer and Almlöf (1992) and Chaban, Schmidt and Gordon (1997). The first mathematical work appeared some years ago and is due to Auchmuty and Wenyao Jia (1994), who studied the convergence of a prototypical algorithm which is unfortunately not used in practice. The situation recently evolved, both from the standpoint of numerical analysis and from that of the construction of more efficient strategies, with the series of works by Cancès and Le Bris (2000*a*, 2000*b*), Cancès (2000, 2001), Kudin, Scuseria and Cancès (2002) and Cancès, Kudin, Scuseria and Turinici (2003*a*), on which the following lines are based.

Before describing the algorithms and elaborating on their theoretical properties, we need to make a few remarks.

First, the SCF algorithm (3.32) above needs to be well defined. This requires there to be no ambiguity on the choice of C_{k+1} and thus the Nth eigenvalue, counted with multiplicity, should be nondegenerate: $\epsilon_N^{k+1} < \epsilon_{N+1}^{k+1}$ (which is true in the limit $k \to \infty$, in view of a theoretical result mentioned above). Actually, in order to be able to prove convergence, the following slightly stronger property was introduced. An SCF algorithm of the form (3.32) with initial guess D_0 is said to be *uniformly well posed* (UWP) if there exists some positive constant γ such that

$$\text{for all } k \in \mathbb{N}, \qquad \epsilon_{N+1}^{k+1} \geq \epsilon_N^{k+1} + \gamma.$$

This property can be shown to be satisfied automatically at least for one algorithm, namely the level-shifting algorithm we will study below. In practice, it seems to be largely satisfied for the algorithms examined below.

Second, recall that in the present context we look for the minimizer of a nonconvex minimization problem by a solution procedure for the Euler–Lagrange equations. Without uniqueness, the convergence of fixed point-like iterations, and even more the convergence towards a global minimizer, are likely to be impossible to establish. Therefore the notion of convergence has to be weakened, making it more practical, but still interesting, in the present context. In this spirit, an SCF algorithm of the form (3.32) is said to *numerically converge toward a solution to the HF equations* if the sequence (D_k) satisfies

(i) $D_{k+1} - D_k \to 0$,

(ii) $[F(D_k), D_k] \to 0$,

the second condition of course being reminiscent of (3.14). Likewise, we shall say it *numerically converges toward an Aufbau solution to the HF equations* if (i) holds together with a condition stronger than (ii), namely

(iii) $\mathrm{Trace}(F(D_k)D_k) - \inf\big\{\mathrm{Trace}(F(D_k)D) : \quad D \in \mathcal{P}_N\big\} \to 0$.

Of course, in both cases, one should note that the convergence of D_k up to an extraction is not an issue, since the set $\mathcal{P}_N$ defined in (3.6) is compact, because of the finite-dimensional setting.[14]

The simplest fixed point algorithm was introduced by Roothaan (1951). It is now obsolete, but it serves as a basis for more sophisticated algorithms, and as an explanatory example for the numerical analysis. It consists in setting $F_k = F(D_k)$ in (3.32).

It was very early realized that the convergence properties of the Roothaan algorithm are not satisfactory: it sometimes converges towards a solution to the HF equations and frequently oscillates between two states, neither of which are solutions to the HF equations. In addition, the behaviour may depend on the basis set chosen. But anyway, surprisingly, no case other than convergence or oscillation of the above type (say binary oscillations) were observed.

This behaviour can be fully explained by introducing the auxiliary function

$$E(D, D') = \mathrm{Trace}(hD) + \mathrm{Trace}(hD') + \mathrm{Trace}(G(D)\, D'),$$

and noting that the sequence of D_k generated by the Roothaan algorithm is exactly that generated by the relaxation algorithm

$$\begin{aligned} D_{2k+1} &= \arg\inf\bigl\{E(D_{2k}, D), \quad D \in \mathcal{P}_N\bigr\},\\ D_{2k+2} &= \arg\inf\bigl\{E(D, D_{2k+1}), \quad D \in \mathcal{P}_N\bigr\}. \end{aligned}$$

The functional E, which decreases at each iteration of the relaxation procedure, can therefore be interpreted as a Lyapunov functional of the Roothaan algorithm. This basic remark is the foundation of the proof of the following result.

Theorem 1. Let $D_0 \in \mathcal{P}_N$ be such that the Roothaan algorithm with initial guess D_0 is UWP. Then the sequence (D_k^{Rth}) generated by the Roothaan algorithm either numerically converges toward an Aufbau solution to the HF equations, or oscillates between two states, none of them being an Aufbau solution to the HF equations. In the latter case, $(D_{2k}^{\mathrm{Rth}}, D_{2k+1}^{\mathrm{Rth}})$ converges to (D, D'), $D \neq D'$, where

$$\begin{cases} F(D')C &= SCE\\ F(D)C' &= SC'E', \end{cases}$$

together with the other obvious constraints.

---

[14] Actually, we can extend the above definitions, and most of the results and proofs will be given below, to an infinite-dimensional setting. This is useful additional information, particularly when we want to assess the impact of the increase of the basis set on the convergence issues. We refer to the bibliography.

Proof. The proof goes by proving that

$$E(D_{k+1}^{\mathrm{Rth}}, D_{k+2}^{\mathrm{Rth}}) + \frac{\gamma}{2}\|D_{k+2}^{\mathrm{Rth}} - D_k^{\mathrm{Rth}}\|^2 \leq E(D_k^{\mathrm{Rth}}, D_{k+1}^{\mathrm{Rth}}),$$

thus $\sum_{k\in\mathbb{N}} \|D_{k+2}^{\mathrm{Rth}} - D_k^{\mathrm{Rth}}\|^2 < +\infty$, which implies in particular that

$$D_{k+2}^{\mathrm{Rth}} - D_k^{\mathrm{Rth}} \longrightarrow 0.$$

Now, either $D_{k+1}^{\mathrm{Rth}} - D_k^{\mathrm{Rth}}$ converges to zero or it does not. The examination of each case allows us to conclude the alternative stated in the theorem. ☐

A first attempt to stabilize the Roothaan algorithm is the *level-shifting* algorithm due to Saunders and Hillier (1973). It consists in setting

$$\widetilde{F}_k = F(D_k) - bD_k,$$

in (3.32), where b is some sufficiently large positive constant.

Then oscillations disappear, and the algorithm always converges. However, the level-shift parameters b which guarantee convergence are large, so that convergence is very slow, and often the algorithm converges to critical points which do not satisfy the Aufbau principle and are not even local minimizers.

Again, this algorithm can be re-interpreted in a standard way. In view of the analysis of the Roothaan algorithm, it is natural to introduce a simple penalty functional $b\|D - D'\|^2$, where b is a positive constant and where $\|\cdot\|$ denotes the Hilbert–Schmidt norm, in order to enforce $D = D'$ in the limit and thus to obtain a solution of the Euler–Lagrange equation. The relaxation algorithm associated with the minimization problem

$$\inf\bigl\{E^b(D, D'), \quad (D, D') \in \mathcal{P}_N \times \mathcal{P}_N\bigr\},$$

where

$$E^b(D, D') = \mathrm{Trace}(hD) + \mathrm{Trace}(hD') + \mathrm{Trace}(G(D)\,D') + b\,\|D - D'\|^2$$

is exactly the level-shifting algorithm with shift parameter b. Then we have the following.

Theorem 2. For sufficiently large b, the level-shifting algorithm is UWP. The energy $E^{HF}(D_k^b)$ of the kth iterate D_k^b decreases toward some stationary value of E^{HF} and the sequence (D_k^b) numerically converges toward a solution to the HF equations.

Proof. The proof follows the same lines as that of Theorem 1, and relies upon the inequality

$$E^{HF}(D_{k+1}^b) + \frac{b}{2}\,\|D_{k+1}^b - D_k^b\|^2 \leq E^{HF}(D_k^b).$$

See Cancès (2000) for the details. ☐

With a view to both enforcing and accelerating the convergence of the iterations, the *direct inversion in the iterated subspace* (DIIS) algorithm has been introduced by Pulay (1982). It is still commonly used in calculations. The basic idea of the algorithm is to make use of the fact that $[F(D), D] = 0$ is equivalent to the HF equations in order to insert damping into the iterations. This is done by setting

$$\widetilde{F}_k = F(\widetilde{D}_k)$$

in (3.32), where

$$\widetilde{D}_k = \sum_{i=0}^{k} c_i^{\mathrm{opt}} D_i,$$

and

$$\{c_i^{\mathrm{opt}}\} = \arg\inf\left\{ \left\| \sum_{i=0}^{k} c_i [F(D_i), D_i] \right\|^2 : \quad \sum_{i=0}^{k} c_i = 1 \right\}.$$

It turns out that the DIIS algorithm works extremely well: in many cases, it typically converges in a dozen iterations. However, the DIIS algorithm suffers from a qualitative drawback: it is not ensured that the Hartree–Fock energy decreases throughout the iterations. In addition, there exist cases where this algorithm does not converge.

Unfortunately, no numerical analysis on this algorithm is available to date, and thus the convergence failures cannot be satisfactorily explained and remedied. This, at least, has motivated the introduction of other algorithms.

Relaxed constrained algorithms (RCAs) have been introduced in Cancès and Le Bris (2000*b*) and Cancès (2000, 2001). They are based on the following remark: all the local minima of $E^{HF}(D)$ on $\widetilde{\mathcal{P}}_N$ defined in (3.17) indeed belong to $\mathcal{P}_N$ defined by (3.6), which amounts to saying that the constraint $DSD = D$ may be relaxed while keeping the same local minima. Loosely speaking, this is simply due to a property of concavity of the HF energy with respect to the norm of each of the ϕ_i (think again of the minimization of a concave functional on the unit ball and on the unit sphere, respectively). Therefore, without loss of generality, we may transform the HF problem into a minimization problem set on the convex set $\widetilde{\mathcal{P}}_N$, for which many more techniques are available (in particular, and this will be the case here, we can damp the algorithm by using any convex combination of previously computed iterates). Convergence is then easier to establish.

We will focus here on the simplest RCA, called the *optimal damping algorithm* (ODA). It consists in setting $\widetilde{F_k} = F(\widetilde{D}_k)$ where

$$\widetilde{D}_k = \arg\inf\bigl\{E^{HF}(\widetilde{D}) : \quad \widetilde{D} = (1-\lambda)\widetilde{D}_{k-1} + \lambda D_k, \quad \lambda \in [0,1]\bigr\}$$

As E^{HF} is a second-degree polynomial in the density matrix, the computation of $\widetilde{D}_k$ only consists in minimizing a quadratic function of λ in $[0,1]$, which can be done analytically.

In fact, one can again understand the ODA on the basis of a very simple numerical analysis. Because of the Taylor expansion

$$E^{HF}((1-\lambda)\widetilde{D}_{k-1}+\lambda D') = E^{HF}(\widetilde{D}_{k-1}) + \lambda \mathrm{Trace}(F(\widetilde{D}_{k-1})\cdot(D'-\widetilde{D}_{k-1})) + \frac{\lambda^2}{2}\mathrm{Trace}\big(G(D'-\widetilde{D}_{k-1})\cdot(D'-\widetilde{D}_{k-1})\big),$$

for any $\lambda \in [0,1]$, the direction D_k selected by the Aufbau principle, namely

$$D_k = \arg\inf\big\{\mathrm{Trace}(F(\widetilde{D}_{k-1})D') : \ D' \in \mathcal{P}_N\big\},$$

can be interpreted as the steepest descent direction, while the choice of the damping parameter λ in the ODA is the optimal step along this direction. Therefore the ODA is a representative of a standard descent algorithm in this context.[15,16] This observation underlies the following theorem.

Theorem 3. Let us consider an initial guess $D_0 \in \mathcal{P}_N$ such that the optimal damping algorithm is UWP. Then,

(1) the sequence $E^{HF}(\widetilde{D}_k)$ of energies of the intermediate matrices $\widetilde{D}_k$ decreases toward a stationary value of the HF energy;
(2) the sequence (D_k) numerically converges toward an Aufbau solution to the HF equations.

Proof. One may show that

$$E^{HF}(\widetilde{D}_{k+1}) \leq E^{HF}(\widetilde{D}_k) - \alpha\|D_{k+1}-\widetilde{D}_k\|^2$$

for some $\alpha > 0$, which implies that

$$D_{k+1} - \widetilde{D}_k \longrightarrow 0. \tag{3.33}$$

As $\widetilde{D}_{k+1} \in [\widetilde{D}_k, D_{k+1}]$, it follows that $\widetilde{D}_{k+1} - \widetilde{D}_k \longrightarrow 0$, and then that $D_{k+1} - D_k \longrightarrow 0$. The proof is then easy to complete. ☐

---

[15] In fact, pursuing the analogy, the algorithm known in computational chemistry as the *mixing algorithm*, where $\widetilde{F}_k = F(\widetilde{D}_k)$ with $\widetilde{D}_k = (1-\alpha)\widetilde{D}_{k-1} + \alpha D_k$ and α is a fixed damping parameter, can be recast as a steepest descent procedure with a fixed step, which, naturally, performs rather poorly.

[16] Then the following question arises: Since in other fields of optimization it is well known that the gradient direction is not the best direction to take, why not take a more efficient one? A practical answer to this question is that the big advantage of this direction is that it is 'easy' to calculate, since it is that obtained by diagonalization, and quantum chemistry codes use optimized diagonalization routines.

Numerical tests show that

- the solution obtained by the ODA is always the same whatever the initial guess chosen in the list of commonly used initial guesses (this robustness is a very important property),
- the energy of the solution obtained by the ODA is always lower than or equal to that of the solution obtained by any other method,
- the ODA always converges,
- the ODA is less demanding in terms of memory than, *e.g.*, DIIS,
- however, the ODA, like any RCA available today, does not converge as fast as the DIIS algorithm when the latter does converge, and proves to be rather slow in the latest steps of the convergence.

The latter observation motivated the introduction by Kudin *et al.* (2002) of the *energy direct inversion in the iterative subspace* (EDIIS) algorithm as an improvement of the ODA for the latest steps. For the damping step, the HF energy is, in the spirit of DIIS, minimized on the convex set generated by all (or some of) the density matrices computed at the previous iterations:

$$\widetilde{D}_k = \arg\inf\left\{ E^{HF}(\widetilde{D}) : \qquad \widetilde{D} = \sum_{i=0}^{k} c_i D_i, \quad 0 \leq c_i \leq 1, \quad \sum_{i=0}^{k} c_i = 1 \right\}.$$

Since this is exactly the HF energy which is minimized, and not

$$\left\| \sum_{i=0}^{k} c_i [F(D_i), D_i] \right\|^2,$$

the damping step does force convergence.

Let us mention that, for the KS problem, the same algorithms (Roothaan, level-shifting, DIIS, RCA, ODA, EDIIS) can be applied. The main two differences are, first, that there is no proof of convergence, and, second, that relaxing the constraints $DSD = D$ in the KS model modifies the model itself and leads to the *extended* Kohn–Sham model. We refer the reader to Cancès (2001).

3.6. Second-order methods

The SCF iterations are basically first-order methods, as shown by their interpretation given above. In order to accelerate their convergence in the latest steps, one can insert damping, as in the DIIS, ODA, or EDIIS algorithms, or, and this is the purpose of the present section, one may resort to second-order algorithms.

The first Newton-like algorithm for computing HF ground states is due to Bacskay (1961). The basic idea is to make a change of variable in order to remove the constraints and use a standard Newton algorithm for *unconstrained* optimization. The convenient parametrization of the manifold $\mathcal{P}_N$ used by Bacskay is the following: for any $C \in \mathcal{M}(N_b, N_b)$ such that $C^* SC = I_{N_b}$,

$$\begin{aligned}\mathcal{P}_N = \bigg\{ C \exp(A) D_0 \exp(-A) C^* : \quad D_0 = \begin{bmatrix} I_N & 0 \\ 0 & 0 \end{bmatrix}, \\ A = \begin{bmatrix} 0 & -A_{vo}^* \\ A_{vo} & 0 \end{bmatrix}, \quad A_{vo} \in \mathcal{M}(N_b - N, N) \bigg\},\end{aligned}$$

where, in the language of chemistry, the subscript vo denotes the 'virtually occupied' off-diagonal block of the matrix A. Let us now write

$$E^C(A_{vo}) = E^{HF}(C \exp(A) D_0 \exp(-A) C^*).$$

The problem now reads as the minimization of $E^C(A_{vo})$. Starting from some reference matrix C, the *Bacskay QC algorithm* (QC standing for *quadratically convergent*) consists in applying to this unconstrained minimization problem, *one* Newton step starting from $A_{vo} = 0$, and next to update C. It thus reads:

$$\begin{cases} \text{compute the solution } \ A_{vo}^k \\ \text{of the Newton equation } \ \nabla^2 E^{C_k}(0) \cdot A_{vo} + \nabla E^{C_k}(0) = 0, \\ \text{set } \ C_{k+1} = C_k \exp(A_k) \ \text{ with } \ A_k = \left[\begin{smallmatrix} 0 & -A_{vo}^{k*} \\ A_{vo}^k & 0 \end{smallmatrix} \right]. \end{cases}$$

A natural alternative to Bacskay QC is to use a Newton-like algorithm for *constrained* optimization. We write down the optimality equations for problem (3.8) and then solve them by Newton iterations. Unfortunately, owing to the unitary invariance of the HF energy, the system of equations obtained is not well posed, and some technical modifications are in order. This gives rise to a variety of Newton-type algorithms. We refer to the literature and in particular to Shepard (1993).

The computational costs of the various Newton-type algorithms are particularly high in the present context. Indeed, the construction of many Fock matrices per step is needed, and we have noticed that this construction is especially costly. In order to lower the computational cost, various attempts have been made to build quasi-Newton versions of the Bacskay QC algorithm (see, for instance, Fischer and Almlöf (1992), Chaban *et al.* (1997)), but we are not aware of any work on quasi-Newton methods for solving the constrained optimization problem (3.4).

To conclude this section, we would like to mention that one of the most recent and efficient combinations of a first-order algorithm in the earliest steps of SCF iterations with a second-order algorithm in the latest step is that proposed by Cancès *et al.* (2003*a*). The setting is that of a KS-type model: the initial value D_0 of the second-order algorithm is the density matrix output of the EDIIS algorithm. In the spirit of the Bacskay QC algorithm, the manifold of density matrices is parametrized by

$$D = \Omega \begin{pmatrix} I_N & 0 & 0 \\ 0 & \Lambda & 0 \\ 0 & 0 & 0 \end{pmatrix} \Omega^*$$

with some matrices Ω and Λ that are updated at each iteration through $\Omega_{k+1} = \Omega_k \exp A_k$ and $\Lambda_{k+1} = \Lambda_k + M_k$. The matrix A_k, of particular form, and the matrix Ω_k are determined by performing one step of the Newton algorithm for the minimization of

$$E^{KS} \left(\Omega_k \exp A \begin{pmatrix} I_N & 0 & 0 \\ 0 & \Lambda_k + M & 0 \\ 0 & 0 & 0 \end{pmatrix} \exp(-A)\, \Omega_k^* \right).$$

We refer to Cancès *et al.* (2003*a*) for the details. More generally, we also refer to Areshkin, Shenderova, Schall and Brenner (2003) for a recent survey of SCF methods and techniques for their acceleration.

3.7. Diagonalization procedure: small and large size systems

In the previous section, we focused on the SCF cycles, *i.e.*, the iterations on the nonlinearity. At each cycle, the current mean-field Hamiltonian $\widetilde{F}_k$ is used to build a new density matrix on the basis of the Aufbau principle. This in principle amounts to solving the minimization problem (3.15), that is,

$$\inf\left\{ \mathrm{Trace}(FD), \quad DSD = D, \quad \mathrm{Trace}(SD) = N \right\}, \tag{3.34}$$

where F is frozen at the value $\widetilde{F}_k$. It has already been said that, typically, for atomic orbitals basis sets, N_b is of the order of $2N$ to $10N$ (the matrix F then being sparse owing to the localization of atomic orbitals), while for plane wave basis sets, which will be mentioned in Section 4.1, N_b can be one hundred times as large as N, and the matrix is dense.[17]

The direct approach to solving these problems is to diagonalize F. The algorithms in use are standard algorithms, no specificity of computational chemistry arising at this level. Nevertheless, this procedure has complexity N^3 (see, *e.g.*, Demmel (1997)), and cannot be applied to systems of large size. The limitation is all the more of concern as the diagonalization is the inner loop of the SCF procedure, which may itself be one step of an outer

---

[17] Notice, therefore, that when we speak of linear scaling algorithms below, it might be quite different *at the practical level* to consider an algorithmic complexity w.r.t. N or w.r.t. N_b in the case of plane waves basis sets, even if *in the asymptotic regime* the two complexities are the same.

loop. This is the case for calculations in the solid phase (when there are as many equations as points in the reciprocal lattice – see Section 4.1), or for geometry optimization routines (when the problem is parametrized by the positions of nuclei – see Section 3.8), or for time-dependent simulations by *ab initio* molecular dynamics (see Section 5.1).

The paradigm of *linear scaling* calculations has therefore arisen in the past decade, with a view to designing procedures that would scale linearly with respect to the size of the system. Linear scaling methods are founded on the following simple remark: in fact, the solution of (3.34) requires the projector onto the subspace generated by the eigenstates associated to the lowest N eigenvalues, and not the eigenstates themselves. Diagonalization can thus be avoided in principle, hence the name *alternative to diagonalization* for such methods, which can significantly reduce the algorithmic complexity, basically from N^3 to N, at least in some cases. From the physical standpoint, some assumptions justify linear scaling methods, the most important being *locality of interactions*: two regions of a large molecular system that are very far away from one another only slightly interact.

The linear scaling methods can be schematically divided into three categories:

- decomposition methods,
- penalization approaches,
- non-variational approaches.

The decomposition methods rely on the *divide and conquer* paradigm. Loosely speaking, the idea is to partition the molecular system into subsystems, and solve iteratively the subproblems by fine schemes in parallel, and the global problem by a coarse solver. Surprisingly, it seems that there is no mature version of such methods in the context of computational chemistry as there is in other fields of scientific computing. Note that we have in mind decomposition domain methods at the discrete level, but also to a smaller extent methods at the pure algebraic level, in the vein of Schur complement techniques. Even if, in the latter case, it could be possible to apply generic methods, it seems that they have not percolated very much in computational chemistry either. The state of the art in chemistry seems to be at best a one-shot algorithm: computing the ‘partial’ density matrices, and merging adequately the submatrices to build the global density matrix. More sophisticated algorithms are currently being tested in Barrault, Cancès, Hager and Le Bris (2004*c*).

Therefore we refer to the bibliography for the divide and conquer approach and prefer now to concentrate on the last two categories. For the description of the main representative methods in each category, we let the overlap matrix S be the Identity, for simplicity, understanding that algorithms can be adapted if this were not the case.

In order to make alternatives to diagonalization practical, the problem (3.34) is reformulated in such a way that the constraint $DSD = D$ disappears,[18] and next an algorithm is constructed, which might scale cubically in the whole generality, but scales linearly when F is sparse and when the density matrix D to be determined is assumed to be sparse.[19] This favourable scaling is obtained because the algorithm is deliberately constructed in such a way that only a limited number of products of sparse matrices are performed. Of course, in order to define the sparsity, some cut-off parameters have to be adequately tuned, on the basis of physical assumptions such as that of locality, alluded to above.

The *penalization methods* consist in eliminating the constraint of idempotency by constructing an *exact penalized functional* (any local minimizer to the constrained problem is a minimizer to the unconstrained one). Then a standard algorithm of unconstrained numerical minimization, such as the nonlinear conjugate gradient algorithm for instance, is performed on the latter problem.

For this purpose, one idea is to penalize the constraint $D^2 = D$ in (3.34) by using functionals of the type

$$\mathrm{Trace}(FD) + \mathrm{Trace}(Fg(D)) \tag{3.35}$$

for some convenient function g. The simplest choice is $g(D) = 3D^2 - 2D^3 - D$, hence the *Density Matrix Minimization* method, due to Li, Nunes and Vanderbilt (1993):

$$\inf\big\{\mathrm{Trace}\big((F - \varepsilon_F\,\mathrm{Id})(3D^2 - 2D^3)\big) : \quad D \in \mathcal{M}_S(N_b)\big\}. \tag{3.36}$$

It can be shown that this problem has a unique local minimizer, although the infimum is $-\infty$. The solution of (3.34) is obtained by solving (3.36) with a nonlinear conjugated gradient algorithm. For this purpose, it is necessary that the initial guess of the conjugated gradient is in the 'attraction basin' of the local minimum. Despite the definitely 'risky' nature of this numerical approach, it performs well in practice.

An alternative to the above techniques is provided by *non-variational approximations*. They consist in approaching the solution D to the problem (3.34) as the implicit function

$$D = \mathcal{H}(\varepsilon_F\,\mathrm{Id} - F),$$

where $\mathcal{H}$ denotes the Heaviside function (all states of energy lower than ε_F are occupied, the other ones above ε_F being empty).

---

[18] The constraint $\mathrm{Trace}(SD) = N$ fixing the number of electrons is easy to deal with since it can be associated with *one scalar* Lagrange multiplier ε_F, called the *Fermi level*, determined iteratively by an outer loop; we therefore treat ε_F as known.

[19] The latter assumption is in some sense an *a posteriori* assumption, and not easy to analyse.

A first option is to resort to the *Fermi operator expansion* (FOE), which consists in approaching the Heaviside function $\mathcal{H}$ by a Chebyshev polynomial approximation. Up to a renormalization, we may assume that the Fermi level ε_F is zero and that the eigenvalues of F all lie in the range $[-1, 1]$, so that the minimizer D of (3.34) satisfies $D = \mathcal{H}(-F)$. Decomposing $\mathcal{H}$ on the range $[-1, 1]$ into

$$\mathcal{H}(-x) = \sum_{j=0}^{+\infty} c_j T_j(x),$$

where T_j is the jth Chebyshev polynomial and $(c_j)_{0\le j\le +\infty}$ are the Chebyshev coefficients, we obtain

$$D = \sum_{j=0}^{+\infty} c_j T_j(F).$$

The FOE method consists in truncating the above expansion to a given order k which depends both on the spectral gap and on the required accuracy (see Goedecker (1999), and Liang *et al.* (2003) for a recent improvement). Note that the truncation is a very delicate issue, for which no analysis is known, and that has a crucial impact on the quality of the result.

Note also that the computation of the truncated expansion

$$D_k = \sum_{j=0}^{k} c_j T_j(F)$$

is done by taking advantage of the recursion formula

$$T_{j+1}(F) = 2FT_j(F) - T_{j-1}(F), \quad T_0(F) = I_{N_b}, \quad T_1(F) = F,$$

which allows us to compute *independently* each column of the matrix and makes the method easily parallelizable.

A second instance of a nonvariational approximation technique is provided by the method of *purification of the density matrix*. This method was introduced by Palser and Manopoulos (1998) following the earlier work by McWeeny (1992). The idea is to remark that for $x_0 \in]-1/2, 3/2[$ and $f(x) = 3x^2 - 2x^3$, the algorithm defined by the induction formula $x_{k+1} = f(x_k)$ converges to $\mathcal{H}(1/2 - x_0)$. Now, again up to a renormalization of F, the minimizer D of (3.34) satisfies

$$D = \mathcal{H}(1/2 - F),$$

and thus the sequence defined by

$$D_0 = F, \qquad D_{k+1} = f(D_k) = 3D_k^2 - 2D_k^3$$

converges toward D. This algorithm can be interpreted as the approximation of the Heaviside function by a polynomial, namely that defined by the nth iteration of the function f (which is called the *McWeeny purification function*).

For more details and other linear scaling methods, we refer to the articles of Ordejon, Drabold and Martin (1995), Clementi and Davis (1966), Jay, Kim, Saad and Chelikowski (1999), Kohn (1996), Scuseria (1999), Shepard (1993), Shao, Saravan, Head-Gordon and White (2003) and Head-Gordon, Shao, Saravan and White (2003), and also to the survey articles of Daniels and Scuseria (1999), Galli (2000), Goedecker (1999), Bowler *et al.* (1997), Bowler and Gillan (1999) and Bowler, Miyazaki and Gillan (2002).

Let us, however, conclude this section with a necessarily schematic state of the art for these linear scaling methods. Essentially, one may say that, when employed with localized basis sets of limited size per atom, these methods are remarkably efficient for the modelling of insulators, a physical situation that corresponds to a large enough gap $\epsilon_{N+1} - \epsilon_N = \gamma > 0$ between the Nth eigenvalue of F and the following one (recall that such an assumption also plays a role in the convergence of SCF iterations, as manifested by the UWP property stated above). On the other hand, they experience the worst difficulties when dealing with metallic systems ($\gamma \simeq 0$). For the latter, they are clearly in a nonsatisfactory state and need to be further developed and adapted. From the numerical standpoint, the difficulty of metallic systems is twofold. First, the problem of finding the eigenvalues is ill-conditioned in the sense that the eigenvalues for the Hamiltonian of such systems are very close to one another. Second, the density matrix D for the ground state is dense. The two difficulties together are an overwhelming task for the current algorithms. Note an attempt by Barrault, Bencteux, Cancès and Duwig (2004*d*) to develop deflation techniques in this setting in order to artificially enlarge the gap γ and consequently enhance the efficiency of the methods. However, definite conclusions about the efficiency of the approach are yet to be obtained.

It is to be emphasized that the numerical analysis of the linear scaling methods overviewed above that would account for cut-off rules and locality assumptions, is not yet available. The efficiency of the different methods has therefore only been investigated on a few benchmark calculations which are far from reproducing all the situations met in practice. In addition, even at the formal level, the interaction between linear scaling procedures for the linear subproblems and the SCF iterations has not been investigated yet.

3.8. Additional issues

We conclude our survey of the methods for molecular systems by addressing here a few additional topics.

Beyond Hartree–Fock

Many post-Hartree–Fock methods exist in the chemical literature. As the Hartree–Fock approximation is a variational approximation of (2.2), that is, an approximation constructed by restricting the variational space to a smaller one, most of its improvements consist in enlarging the variational space.

The *multiconfiguration self-consistent field method* (MCSCF) aims to recover more generality on the wavefunction ψ_e by minimizing on *sums* of determinants:

$$E_N^K = \inf\left\{ \langle \psi_e, H_e\psi_e\rangle : \quad \psi_e = \sum_{I=\{i_1,\dots,i_N\}\subset\{1,\dots,K\}} c_I \frac{1}{\sqrt{N!}} \det(\phi_{i_1},\dots,\phi_{i_N}), \right.$$
$$\left. \phi_i \in H^1(\mathbb{R}^3), \quad \int_{\mathbb{R}^3} \phi_i\phi_j = \delta_{ij}, \quad \sum_I c_I^2 = 1 \right\}, \tag{3.37}$$

where $K \geq N$ is some fixed integer.

The mathematical knowledge on the MCSCF model is now at the level of that on the HF model, owing to a recent work by Lewin (2004), following prior works by Le Bris (1994) and Friesecke (2003).

The numerical practice consists, as in the Hartree–Fock case for which (3.8) is attacked, in solving the Euler–Lagrange equations for (3.37), the *MCSCF equations*, which take the form of the following system:

$$\begin{cases} \left(\left(-\frac{\Delta}{2} + V\right)\Gamma + 2\,W_\Phi\right)\cdot\Phi + \Lambda\,\Phi = 0, \\ H_\Phi \cdot c = \beta \cdot c. \end{cases} \tag{3.38}$$

In (3.38), the first line translates the optimality of the wavefunctions Φ_i and is in fact a system of K nonlinear PDEs involving the Lagrange multipliers matrix Λ to account for the orthonormality constraints. The matrix Γ is easily computed from the coefficients c_I of the expansion appearing in (3.37) while V is defined by (2.12) and W_Φ denotes the interelectronic interaction term, also easily obtained from the c_I. On the other hand, the second line translates the optimality of the coefficients c_I, with the Lagrange multipliers β to account for the normalization. The matrix H_Φ is the $\binom{K}{N}\times\binom{K}{N}$ matrix with general term $\langle H_N\Phi_I, \Phi_J\rangle$ with $\Phi_I = \frac{1}{\sqrt{N!}}\det(\phi_{i_1},\dots,\phi_{i_N})$ in the notation of (3.37).

The recent work by Cancès, Galicher and Lewin (2004*a*) aims to solve (3.38), particularly in order to rigorously define and efficiently compute excited states in the MCSCF setting.

Relativistic models

In the case when the molecular system under study involves one or many heavy atoms, the relativistic effects need to be accounted for, otherwise erroneous conclusions, even at the qualitative level,[20] can be drawn from the computations.

---

[20] such as, gold is *not* yellow

The huge difference in the relativistic modelling is that the Laplacian operator appearing in the Hamiltonian (2.3) has to be replaced by the *Dirac Hamiltonian*,

$$H_c = -i\alpha_1 \frac{\partial}{\partial x_1} - i\alpha_2 \frac{\partial}{\partial x_2} - i\alpha_3 \frac{\partial}{\partial x_3} + c^2\beta, \tag{3.39}$$

where c is the speed of light, while α_k, $k = 1, 2, 3$, and β are 4×4 matrices depending on the Pauli matrices. The introduction of this Hamiltonian, by Dirac, is motivated by the fact that H_c^2 needs to be equal to the operator $-c^2\Delta + c^4$ which is the quantum analogue of the Hamiltonian of classical relativity $p^2c^2 + c^4$ (where p is the momentum operator). The Dirac Hamiltonian H_c acts on 4-spinors, *i.e.*, wavefunctions valued in $\mathbb{C}^4$. The crucial point is that its spectrum $\sigma(H_c) =]-\infty, -c^2] \cup [c^2, +\infty[$, contrary to that of the Laplacian $[0, +\infty[$, is not bounded from below. When inserted in the modelling of an hydrogen-like atom, it therefore leads to a minimization problem that is not well posed, and a good definition of the ground state has to be introduced. Basically, the minimization has to be replaced by adequate saddle-point methods. Some new minimax characterizations have been established by Esteban and Séré (2002), Dolbeault, Esteban and Séré (2000*a*), Desclaux *et al.* (2003), and have given rise to new algorithmic techniques to compute the eigenfunctions and eigenvalues of the Dirac operator in molecules: see Dolbeault, Esteban, Séré and Vanbreugel (2000*b*), Dolbeault, Esteban and Séré (2003). Likewise, in the many-electron case where models such as the Dirac–Fock model, introduced in Swirles (1935, 1936), play the role of the Hartree–Fock model, adequate definitions of the ground state need to be derived. Again, from the numerical viewpoint, an adequate treatment has to be developed. After years of rather brutal techniques, the situation has recently evolved toward more rigour, and also efficiency, with the series of works by the authors cited above.

Molecular mechanics

As mentioned above, the search for the electronic ground state for a fixed set of positions of nuclei might only be an *inner* calculation. The outer loop consists in solving the minimization problem (2.1)

$$\inf_{(\bar{x}_1,\ldots,\bar{x}_M)\in\mathbb{R}^{3M}} \left\{ W(\bar{x}_1, \ldots, \bar{x}_M) = U(\bar{x}_1, \ldots, \bar{x}_M) + \sum_{1\le k<l\le M} \frac{z_k\, z_l}{|\bar{x}_k - \bar{x}_l|} \right\}.$$

that is a purely classical optimization problem in dimension $3N$, up to trivial invariance properties (translation and rigid rotation at least). Of course, the potential $U(\bar{x}_1, \ldots, \bar{x}_M)$ can be parametrized on the basis of precomputations performed with the *ab initio* models we have seen above, and this gives rise to the field called *molecular mechanics*. This field is prominent in biology, say, where, for instance, stable conformations of protein must be determined. From the computational viewpoint, the problem is that of minimizing a parametrized function in a space of very high dimension, for which billions of local minimizers are likely to exist. The relevant theory is numerical optimization, or even combinatorial optimization, since in practice substructures are first optimized and then assembled combinatorially to find (at least a good guess for) the most stable global structure.

Here we would like to concentrate on a somewhat different problem, that of finding the optimal configuration of nuclei when the number of nuclei is not so large but when the potential $U(\bar{x}_1, \ldots, \bar{x}_M)$ is indeed that obtained by some of the computations above, *i.e.*, approximations of (2.2).

In most situations, except those when gradient-free (or direct search) algorithms are utilized, the optimization algorithm, in order to be efficient, needs to account for derivatives of $U(\bar{x}_1, \ldots, \bar{x}_M)$ with respect to the $\bar{x}_k$.

The key point is that determining the gradient $\frac{\partial U}{\partial \bar{x}_k}$ (or further derivatives) only requires a small additional computational time. This is not the case in other settings, where the computation of the derivative is generically considered as many times more costly than the function evaluation itself.

To illustrate the situation, let us write (2.1)–(2.2) in the abstract form

$$\inf\big\{W(x): \quad x \in \Omega\big\}, \qquad W(x) = \inf\big\{E(x,\phi): \quad \phi \in \mathcal{H}, \quad g(x,\phi) = 0\big\}. \tag{3.40}$$

In this formal setting it is indeed easy to recognize x as the collection of coordinates of the nuclei, ϕ as the electronic wavefunction, $\mathcal{H}$ as the variational space, $E(x,\phi)$ as the energy functional depending both on the nuclear coordinates and the electronic wavefunction, and $g(x,\phi)$ as the orthonormality conditions on the molecular orbitals. We make the latter depend explicitly on x as it is the case when problem (3.40) is considered at the discrete level and when AO basis sets are used. When $\phi(x)$ denotes the ground state for x (here assumed to be unique for simplicity), we may write formally

$$\frac{\partial W}{\partial x_i}(x) = \frac{\partial}{\partial x_i} E(x,\phi(x)) = \frac{\partial E}{\partial x_i}(x,\phi(x)) + \left\langle \nabla_\phi E(x,\phi(x)), \frac{\partial \phi}{\partial x_i}(x) \right\rangle, \tag{3.41}$$

by the chain rule. Next, as $\phi(x)$ is a minimizer, it satisfies

$$\nabla_\phi E(x,\phi(x)) = d_\phi g(x,\phi(x))^T \cdot \lambda(x)$$

for some Lagrange multiplier $\lambda(x)$. On the other hand, by differentiation of the constraint $g(x,\phi(x)) = 0$, we have

$$\frac{\partial g}{\partial x_i}(x,\phi(x)) + d_\phi g(x,\phi(x)) \cdot \frac{\partial \phi}{\partial x_i}(x) = 0.$$

Thus (3.41) yields

$$\frac{\partial W}{\partial x_i}(x) = \frac{\partial E}{\partial x_i}(x) - \left\langle \lambda(x), \frac{\partial g}{\partial x_i}(x, \phi(x)) \right\rangle.$$

The crucial point is that $\frac{\partial \phi}{\partial x_i}(x)$ has been eliminated. Therefore, the gradient of W can be directly computed from $(x, \phi(x), \lambda(x))$ (that is to say, the set of positions of nuclei considered, the electronic ground state, and the Lagrange multipliers, *i.e.*, the monoelectronic energies) without any further calculations. This property, referred to as *analytical derivatives*, is also used in the context of *ab initio* molecular dynamics in Section 5.1.

For the sake of completeness, let us mention that the existence of the global minimizer of (2.1) has been theoretically investigated in a series of works: Catto and Lions (1992, 1993*a*, 1993*b*, 1993*c*). While the existence is theoretically proved in most academic cases, it is to be emphasized that in the Hartree–Fock case it is still an open question, even for the simplest diatomic molecular systems.

4. The condensed phase

4.1. The solid phase

In the case of a crystalline solid, the formal Hartree–Fock equations are derived through Bloch's theorem (see Ashcroft and Mermin (1976), Kittel (1996)): all sums over j involved in the definitions (2.13)–(2.14) of τ and ρ are replaced by sums over j and integrals over the Brillouin zone BZ, *i.e.*, the Wigner–Seitz cell of the lattice $\mathcal{R}^\star$ reciprocal to the physical lattice $\mathcal{R}$. The wave functions and energies, that are here in infinite (uncountable) number, are labelled by $j \in \mathbb{N}^*$ as in the molecular case, *and* by $k \in BZ$, a specificity of the crystalline solid phase. More precisely, setting

$$\tau(x, x') = \sum_{j \in \mathbf{N}} \int_{BZ} \phi_j^k(x) \phi_j^{k^*}(x') (\varepsilon_F - \varepsilon_j^k)_+ \, \mathrm{d}k, \tag{4.1}$$

where the term $(\varepsilon_F - \varepsilon_j^k)_+$ selects only the states with energy lower than the Fermi energy ε_F, and defining V_{tot} to be the solution to

$$\begin{cases} -\Delta V_{\text{tot}} = -4\pi \big(\sum_{T \in \mathcal{R}} m(\cdot + T) - \rho \big), \\ V_{\text{tot}} \quad \mathcal{R}\text{-periodic}, \end{cases} \tag{4.2}$$

where $\rho(x) = \tau(x, x)$ and m is the measure defining the nuclei in the primitive unit cell, we may write down the Fock operator

$$F\phi = -\frac{1}{2}\Delta\phi + V_{\text{tot}}\phi - \int_{\mathbb{R}^3} \frac{\tau(x, x')}{|x - x'|} \phi(x') \, \mathrm{d}x'. \tag{4.3}$$

The Hartree–Fock wavefunctions ϕ_j^k are then defined to be the solutions of

$$\begin{cases} F\phi_j^k = \varepsilon_j^k\,\phi_j^k, \\ \text{for all } j \in \mathbb{N} \text{ and } k \in BZ, \quad \mathrm{e}^{-ikx}\phi_j^k(x) \quad \mathcal{R}\text{-periodic}, \\ \int_Q \phi_j^k(x)\,\phi_{j'}^{k'}(x)^*\,\mathrm{d}x = \delta(k-k')\delta_{jj'}. \end{cases} \tag{4.4}$$

For a study of the rigorous foundation of this model, we refer to a series of works initiated in Catto, Le Bris and Lions (1998) and more particularly to Catto, Le Bris and Lions (2001).

For the Kohn–Sham model, the equations read

$$\begin{cases} -\frac{1}{2}\Delta\phi_j^k + V_{\text{eff}}\phi_j^k = \varepsilon_j^k\phi_j^k, \quad \text{for all } j,k, \\ V_{\text{eff}} = V_{\text{tot}}(\rho) + v_{xc}(\rho), \\ \rho = \sum_j \int_{BZ} |\phi_j^k|^2(\varepsilon_F - \varepsilon_j^k)_+\,\mathrm{d}k, \end{cases} \tag{4.5}$$

and are treated analogously to the Hartree–Fock case.

In principle, we need to solve an infinite number of Hartree–Fock equations, for system (4.4) is indeed an infinite collection of molecular-like Hartree–Fock-type systems

$$F\phi_j^k = \varepsilon_j^k\phi_j^k$$

indexed by the points k of the Brillouin zone. In practice, it turns out that, fortunately, a limited number of points k is generally enough to obtain accurate results. The general trend is that for metals many points (say hundreds of points) are needed, while for insulators a few (or even one) k-points yield realistic values: see Blanc (2000) for an introduction, and, *e.g.*, Dovesi *et al.* (2000) for specific details. Regarding software, we may cite the code CRYSTAL, based on Hartree–Fock-type models, while the code ABINIT is based upon models from density functional theory.

Regarding the basis set used for developing the wavefunctions ϕ_j^k, a peculiarity of the solid phase setting comes into play. Contrary to the molecular case where, as explained above, GTO basis sets are the method of choice (except for very specific applications), the periodicity of the solid phase makes the choice of plane wave (PW) basis sets natural and simple.[21] Notably, they make the kinetic operator diagonal and FFT algorithms can be systematically adopted. The disadvantage of using PWs is that the fine oscillations of some of the orbitals (in fact the valence orbitals) near the nuclei require a huge number of PWs to be described accurately. The latter difficulty is in turn mostly circumvented by the introduction of a *pseudo-potential.*

---

[21] Note that a combination of GTO and PW functions to form a basis set presenting the best compromise is also an option.

The technique consists in

- eliminating the explicit consideration of the core states (*i.e.*, in a classic picture those corresponding to electrons orbiting close to the nucleus) by freezing them and aggregating them with the nuclei, while treating their effect upon the valence electrons almost exactly (those orbiting far away),
- replacing the wavefunctions of the valence electrons by pseudowavefunctions (indeed generated by the diagonalization of an operator with pseudopotential) that are less oscillating and more regular, so that the size of the PW basis set needed for accuracy can be reduced.

Over the years, numerous pseudopotentials of increasingly better quality have appeared and are now widely spread: see, *e.g.*, Troullier and Martins (1990) and Vanderbilt (1990). One point is that there is no rigorous foundation, and no mathematical or formal understanding of the derivation of a pseudopotential. Therefore the method lacks a theoretical foundation, a lack that translates into a problem of crucial practical interest, that of *transferability* (a pseudopotential is definitely useful when it can be used for different atomic arrangements). Current efforts in the mathematics community are directed toward giving a sound base to the concept of pseudopotential. In the chemistry literature, the reference that is the most accessible to a mathematical audience, and that is the best attempt to introduce a rigorous formalism in the development of pseudopotentials, is Blöchl (1994).

4.2. The liquid phase

Most of the physical and chemical phenomena of interest in chemistry and biology take place in the liquid phase (see Allen and Tildesley (1987) for an introduction to the modelling issues) and it is well known from experimental evidences that solvent effects play a crucial role in these processes. Accounting for such effects is thus a main concern.

A natural idea is that of building a 'supermolecule' consisting of the solvated molecule under study plus several neighbouring solvent molecules. It seems that the additional work needed to treat the latter ones makes the approach inefficient in most[22] cases of practical interest. In addition it may be remarked that long-range effects of the solute–solvent interaction are not included in such an approach. Coupling a quantum model for the solvated molecule with a solvation continuum model provides an economical, and

---

[22] Not *all* cases: when the solvated molecule is already very large, and thus coarsely modelled, the solvent molecules that need to be added are not so numerous, in comparison.

actually more accurate, alternative. This consists in locating the solute molecule under study inside a cavity Ω, modelling a solvent excluding volume, surrounded by a continuous medium modelling the solvent.

In the standard model, the continuous medium behaves as a homogeneous isotropic dielectric of relative permittivity ϵ_s ($\epsilon_s > 1$). The electrostatic interactions between the charge distributions which compose the solute (point nuclei and electronic cloud) are affected by the presence of the solvent: the standard Coulomb potential $\frac{1}{|x-y|}$, which is the Green kernel $G(x-y)$ of $-\frac{1}{4\pi}\Delta$ in $\mathbb{R}^3$ must be replaced by that of the operator $-\frac{1}{4\pi}\mathrm{div}\,(\epsilon\nabla\cdot)$, with $\epsilon(x) = 1$ inside the cavity Ω and $\epsilon(x) = \epsilon_s$ outside. Correspondingly, a charge ρ creates a potential V solution to[23]

$$-\mathrm{div}\,(\epsilon(x)\nabla V(x)) = 4\pi\rho(x). \tag{4.6}$$

The various terms of the Hartree–Fock (respectively KS) energy functional are changed correspondingly. Note, however, that in practice (with a view to keeping the efficiency of the computations of bielectronic integrals in vacuum) the exchange term is often left unchanged.

When the solvent is an ionic solution, equation (4.6) is replaced by the *linearized Poisson–Boltzmann equation*

$$-\mathrm{div}(\epsilon(x)\nabla V(x)) + \epsilon(x)\kappa^2(x)V(x) = 4\pi\rho(x) \tag{4.7}$$

(with $\epsilon(x) = 1$ and $\kappa(x) = 0$ inside the cavity Ω and $\epsilon(x) = \epsilon_s > 1$ and $\kappa(x) = \kappa_s > 0$ outside), while for a liquid crystal, it keeps the form (4.6) but the dielectric constant $\epsilon(x)$ is no longer a scalar but a 3×3 anisotropic symmetric tensor $\underline{\underline{\epsilon}}(x)$.

In practice, equation (4.6) is most often solved by an integral equation method. The equation is posed on the surface of Ω, called the *molecular surface*. The approach necessitates efficient meshing techniques for this molecular surface. We refer to Cancès, Le Bris, Mennucci and Tomasi (1999) and Le Bris, ed. (2003) for details and extensions.

5. Time-dependent problems

Ideally, the determination of the evolution of a molecular system requires the solution of the time-dependent Schrödinger equation,

$$i\,\frac{\partial}{\partial t}\Psi \,=\, H\,\Psi, \tag{5.1}$$

---

[23] Notice the analogy with the case of solids where the Coulomb potential is indeed replaced by the Green kernel of the Laplacian, but with periodic boundary condition on the unit cell, see (4.2). This gives a unified setting to all the models addressed here.

where the wavefunction describes the state of the complete system (electrons plus nuclei) and the Hamiltonian is also the complete one,

$$
\begin{aligned}
H = &-\sum_{k=1}^{M} \frac{1}{2\,m_k} \Delta_{\bar{x}_k} - \sum_{i=1}^{N} \frac{1}{2} \Delta_{x_i} - \sum_{i=1}^{N} \sum_{k=1}^{M} \frac{z_k}{|x_i - \bar{x}_k|} \\
&+ \sum_{1 \le i < j \le N} \frac{1}{|x_i - x_j|} + \sum_{1 \le k < l \le M} \frac{z_k\, z_l}{|\bar{x}_k - \bar{x}_l|}.
\end{aligned}
\tag{5.2}
$$

Even when inserting in the above description the approximation that the wavefunction is *a product* of the wavefunction of the electronic degrees of freedom times that of the nuclear ones, this equation remains intractable for any system consisting of more than a few particles. Indeed, equation (5.1) is a time-dependent partial differential equation set on a vectorial space of high dimension. Here again, the use of sparse grid techniques, already mentioned in the static setting in Section 2.2, can be envisioned. Nevertheless, there is again an issue about the regularity of the function manipulated. For time-dependent equations, such a regularity is typically obtained by supplying the equation with regular data (initial and/or boundary conditions), or by using regularization properties of the equation itself, as is the case for parabolic equations. Now, as mentioned above, the functions of chemistry may be singular, and the mixed parabolic/hyperbolic nature of the Schrödinger equation makes the regularization properties very peculiar and different from those of parabolic equations. Therefore it seems that further efforts are needed to apply such techniques to the case of the Schrödinger equation, at least as efficiently as in the parabolic case.

Fortunately, the solution of (5.1), which considers the nuclei as quantum objects, is not needed in most applications, apart from very particular ones issued from fundamental physics. An example of the latter is provided by the emerging domain of laser control of molecular evolutions where light-matter interactions are to be modelled in the most precise way. An introduction to the physical modelling, as well as the mathematical and numerical challenges of this field, has appeared in the recent books of Le Bris, ed. (2003) and Bandrauk, Delfour and Le Bris, eds (2004). Other instances of applications where the nuclei need to be modelled by quantum mechanics, along with numerical approaches for this purpose, can be read in Worth and Robb (2002).

For almost all of the applications in chemistry and biology, the nuclei can be, as in the time-independent setting, treated as classical objects, and the Schrödinger equation above thus simplifies into a system coupling the Newton equation of motion for the positions $\bar{x}_k(t) \in \mathbb{R}^3$ of the nuclei and the Schrödinger equation for the electronic structure.

In turn, as is the case for the stationary problem, the Schrödinger equation ruling the evolution of the electrons cannot be treated without further approximations. One of them is the time-dependent Hartree–Fock approximation, which is obtained by forcing the wave function ψ_e to evolve on the manifold

$$\mathcal{A} = \left\{ \psi_e(x_1, \ldots, x_n) = \frac{1}{\sqrt{N!}} \det(\phi_i(x_j)) : \quad \phi_i \in H^1(\mathbb{R}^3), \int_{\mathbb{R}^3} \phi_i \cdot \phi_j = \delta_{ij} \right\}$$

of $\mathcal{H}_e$ and in replacing the time-dependent Schrödinger equation for the evolution of the electronic structure by the stationarity condition for the action

$$\int_0^T \langle \psi_e(t), (i\partial_t \psi_e(t) - H_e(t)\psi_e(t)) \rangle \, \mathrm{d}t.$$

In so doing, we obtain the following mixed *quantum/classical* system ruling the evolution of the complete molecular system (nuclei and electrons),

$$\begin{cases} m_k \frac{\mathrm{d}^2 \bar{x}_k}{\mathrm{d}t^2}(t) & = -\nabla_{\bar{x}_k} W(t; \bar{x}_1(t), \ldots, \bar{x}_M(t)), \\ W(t; \bar{x}_1, \ldots, \bar{x}_M) & = -\sum_{k=1}^M \sum_{i=1}^N z_k \int \frac{|\phi_i(t,x)|^2}{|x - \bar{x}_k|} \, \mathrm{d}x + \sum_{1 \le k < l \le M} \frac{z_k \, z_l}{|\bar{x}_k - \bar{x}_l|}, \\ i \frac{\partial \phi_i}{\partial t} & = -\frac{1}{2}\Delta\phi_i - \sum_{k=1}^M \frac{z_k}{|\cdot - \bar{x}_k(t)|}\phi_i + \left(\sum_{j=1}^N |\phi_j|^2 \star \frac{1}{|x|} \right)\phi_i \\ & \quad - \sum_{j=1}^N \left(\phi_j^* \phi_i \star \frac{1}{|x|} \right) \phi_j, \end{cases} \tag{5.3}$$

supplied with the initial condition $\bar{x}_k(0) = \bar{x}_k^0$, $\frac{\mathrm{d}\bar{x}_k}{\mathrm{d}t}(0) = \bar{v}_k^0$, $\phi_i(0) = \phi_i^0$. The above system is a prototypical example of a *non-adiabatic simulation.* It was proved to be well posed in Cancès and Le Bris (1999), a work that very much relies on the previous important study by Chadam and Glassey (1975) in a slightly different (uncoupled) setting. The simulation of this system is still a demanding task, necessary in some situations such as collisions of molecular systems. The practical bottleneck consists in the discrepancy between the time-scale of the electronic motion (typically 10^{-18} s) and that of the nuclear motion (typically 10^{-15} s).

Recent works developing numerical algorithms for the solution of quantum dynamics equations as in the above systems are those of Jahnke and Lubich (2003) and Jahnke (2003, 2004). Regarding the specific simulation of the TDHF equations themselves, we refer to the new ideas related to variational integrators developed in Lubich (2004) that deal with the time-dependent multiconfiguration Hartree (not Hartree–*Fock*) equations, in the vein of Section 3.8.

5.1. Ab initio molecular dynamics

Again, for most applications, the above setting can be further simplified. Indeed, it can be considered, within a good level of approximation, that the electrons stay in a well-defined energy surface. This surface, called the *Born–Oppenheimer energy surface*, is parametrized by the set of positions of the nuclei, and is often the ground-state energy surface (and we shall suppose it is henceforth). The system under consideration then reads

$$\begin{cases} m_k \frac{\mathrm{d}^2 \bar{x}_k}{\mathrm{d}t^2}(t) & = -\nabla_{\bar{x}_k} W(\bar{x}_1(t), \ldots, \bar{x}_M(t)), \\ W(\bar{x}_1, \ldots, \bar{x}_M) & = U(\bar{x}_1, \ldots, \bar{x}_M) + \sum_{1 \le k < l \le M} \frac{z_k \, z_l}{|\bar{x}_k - \bar{x}_l|}, \\ U(\bar{x}_1, \ldots, \bar{x}_M) & \text{energy of the electronic degrees of freedom} \\ & \text{evaluated in a given static model.} \end{cases} \tag{5.4}$$

The main advantage of this setting is that the time-step for numerical integration of the dynamics can now be chosen of the same order of magnitude as the characteristic evolution time of the *nuclei* rather than that of the *electrons*. But, as will be seen shortly, each time-step is likely to be more costly.

This approximation mainly relies on physical arguments: the characteristic relaxation time of the electrons is so small with respect to that of the nuclei that it can be considered that the electronic wavefunction reacts *adiabatically* to a change in the position of the nuclei.

As far as applications are concerned, the adiabatic approximation turns out to be valid for the simulation of *physical* properties (phase diagrams, surface reconstruction, diffusion in alloys), as well as for the simulation of most chemical reactions. Both theoretically and practically, however, huge difficulties arise when the energy surfaces happen to cross each other for a given particular set of positions of nuclei (see Hagedorn (1996), Teufel (2003) for related mathematical works).

In practice, the potential U in (5.4) has to be approximated, as in the pure time-independent case, by one of the standard (Hartree–Fock- or DFT-type) methods. If the model is the Hartree–Fock approximation, we need to find at each time-step the Hartree–Fock ground state, which in practice (following the discussion of the previous sections) amounts to solving the SCF equations. Thus the system to be simulated reads

$$\begin{cases} m_k \frac{\mathrm{d}^2 \bar{x}_k}{\mathrm{d}t^2}(t) & = -\nabla_{\bar{x}_k} W(\bar{x}_1(t), \ldots, \bar{x}_M(t)), \\ W(\bar{x}_1, \ldots, \bar{x}_M) & = U(\bar{x}_1, \ldots, \bar{x}_M) + \sum_{1 \le k < l \le M} \frac{z_k \, z_l}{|\bar{x}_k - \bar{x}_l|}, \\ U(\bar{x}_1, \ldots, \bar{x}_M) & = E^{HF}(\phi_1, \ldots, \phi_N) \\ \begin{cases} F_\Phi^{\bar{x}_1, \ldots, \bar{x}_M} \phi_i & = \lambda_i \, \phi_i, \\ \int_{\mathbb{R}^3} \phi_i \phi_j & = \delta_{ij} \end{cases} & \end{cases} \tag{5.5}$$

where we recall that $F_\Phi^{\bar{x}_1, \ldots, \bar{x}_M}$ is the Fock operator (2.16) that depends parametrically on the positions $\bar{x}_k$ of the nuclei and the ϕ_j are the lowest N eigenfunctions of F_Φ.

Likewise, if the static model is, *e.g.*, a Kohn–Sham model, then the last two lines of (5.5) are replaced by the equations (2.23), and thus

$$\begin{cases} m_k \frac{\mathrm{d}^2 \bar{x}_k}{\mathrm{d}t^2}(t) & = -\nabla_{\bar{x}_k} W(\bar{x}_1(t), \ldots, \bar{x}_M(t)), \\ W(\bar{x}_1, \ldots, \bar{x}_M) & = U(\bar{x}_1, \ldots, \bar{x}_M) + \sum_{1 \le k < l \le M} \frac{z_k \, z_l}{|\bar{x}_k - \bar{x}_l|}, \\ U(\bar{x}_1, \ldots, \bar{x}_M) & = E^{KS}(\phi_1, \ldots, \phi_N) \\ \begin{cases} K^{\bar{x}_1, \ldots, \bar{x}_M}(\rho_\Phi)\phi_i = \lambda_i \phi_i, \\ \int_{\mathbb{R}^3} \phi_i \phi_j = \delta_{ij} \end{cases} & \end{cases} \tag{5.6}$$

Even within the above approximation, the coupled problem (5.4) remains very time-consuming since a minimization problem (*i.e.*, a nonlinear eigenvalue problem) has to be solved on the fly for each time-step. The solution procedure of the static electronic problem is thus the *inner loop* of the dynamics. Therefore, from a numerical viewpoint, the task for simulating an adiabatic-type model is a sequence of 3-step iterations on the time variable:

(i) determine the electronic state by solving the nonlinear eigenvalue problem (SCF problem),

(ii) compute the gradient of the interaction potential W, using the techniques of analytical derivatives described in Section 3.8,

(iii) integrate in time the Newtonian dynamics.

With a view to circumventing the difficulty of solving a nonlinear eigenvalue problem at each time-step, Car and Parrinello (1985) introduced the idea of replacing the last two lines of (5.6) by a *virtual* time evolution, thus:

$$\begin{cases} m_k \frac{\mathrm{d}^2 \bar{x}_k}{\mathrm{d}t^2}(t) & = -\nabla_{\bar{x}_k} W(\bar{x}_1(t), \ldots, \bar{x}_M(t), t), \\ W(\bar{x}_1, \ldots, \bar{x}_M, t) & = E^{KS}_{\bar{x}_1, \ldots, \bar{x}_M}(\phi_1(t), \ldots, \phi_N(t)) + \sum_{1 \le k < l \le M} \frac{z_k \, z_l}{|\bar{x}_k - \bar{x}_l|}, \\ \mu \frac{\partial^2 \phi_i}{\partial t^2}(t) & = -K^{\bar{x}_1, \ldots, \bar{x}_M}(\rho_{\Phi(t)})\phi_i(t) + \sum_{j=1}^N \Lambda_{ij}(t)\phi_j(t), \\ \Lambda_{ij}(t) & = \langle \phi_j(t), K^{\bar{x}_1, \ldots, \bar{x}_M}(\rho_{\Phi(t)})\phi_j(t) \rangle \; - \; \mu \int_{\mathbb{R}^3} \frac{\partial \phi_j}{\partial t}(t) \frac{\partial \phi_i(t)}{\partial t}(t), \end{cases} \tag{5.7}$$

where μ is a fictitious mass (the limit $\mu \longrightarrow 0$ formally yields the adiabatic approximation (5.6)). The time-step used needs to be smaller than that used for the adiabatic simulation, but the Car–Parrinello method is usually more efficient because no minimization is required. The method is thus extremely popular and very successful, and is thus widely used in a broad spectrum of contexts. It has allowed for the treatment of definitely larger systems, which is huge progress. However, for our main focus here, regarding numerical analysis, the practical difficulty of the method lies in the proper tuning of the parameter μ, for which no theoretical grounding is known.

The only mathematical work on the approach is due to Bornemann and Schütte (1998). Notice that in practice, the forces $\nabla_{\bar{x}_k} W$ are determined, as in the case of (5.4), by the technique of analytical derivatives, this time apparently without any rigorous foundation.

For the sake of completeness, let us mention another track that is currently investigated in the applied mathematics community. It consists in keeping the minimization problem as such (and not modifying it as in the Car–Parrinello approach), but treating it in a rather approximate way, through the paradigm of reduced basis techniques. As the minimization is parametrized by the positions of the nuclei, it is natural to envision a method where the solution is indeed developed on an adequate problem-dependent basis made of the solutions of the same problem for reference positions of the nuclei. Ideas in this direction, still in their infancy, are described in Cancès, Le Bris, Maday and Turinici (2002), Barrault, Maday, Nguyen and Patera (2004*a*) and Barrault *et al.* (2004*b*). The issues under investigation in particular embody issues regarding reduced basis techniques for eigenvalue problems, for vectorial problems, and for nonlinear problems in general, along with the development of adequate error estimators to certify the results.

5.2. Classical molecular dynamics

We concentrate in this section on the numerical simulation of Newtonian dynamics, which is a part of any of the above coupled simulations: the non-adiabatic one (5.3), the adiabatic one (5.4), and even the Car–Parrinello simulation (5.7). We again emphasize, as we did in the Introduction, that the present section does not pretend to be a comprehensive exposition of the state of the art of molecular dynamics, but rather a rapid guided tour of the challenging issues in the domain. Nor will we go into a description of all the applications of molecular dynamics, which is indeed the most popular and commonly used field of molecular simulation. This would require a whole encyclopaedia.

The literature is rich. On the one hand, we refer to the classical monographs of Hairer, Nørsett and Wanner (1993), Hairer and Wanner (1996) and Sanz-Serna and Calvo (1994) for the numerical analysis of methods for ordinary differential equations and Hamiltonian systems. The reference Griebel, Knapek, Zumbusch and Caglar (2004) is dedicated to molecular dynamics, and also more algorithmically oriented. On the other hand, from the application viewpoint, the treatises by Allen and Tildesley (1987), Frenkel and Smit (2001), Schlick (2002), Haile (1992) and Rapaport (1995) are useful references in the field. In the chemistry literature, there are regular surveys by experts in the field, and we would like to mention Neumaier (1997), Tuckerman and Martyna (2000) and Tuckerman (2002). Finally, proceedings books such as Deuflhard *et al.*, eds (1999) or Nielaba, Mareschal and Ciccotti, eds (2002) collect various contributions and show how lively the field is.

For simplicity we restrict ourselves to the case of the Newtonian equations contained in (5.4) that are autonomous (no explicit dependence of the Hamiltonian with respect to time). For extensions to the non-autonomous case, we refer to the literature. The focus is therefore on the simulation of

$$m_k \frac{\mathrm{d}^2 \bar{x}_k}{\mathrm{d}t^2}(t) = -\nabla_{\bar{x}_k} W(\bar{x}_1(t), \ldots, \bar{x}_M(t)), \tag{5.8}$$

supplied with initial conditions on the positions and the velocities. The system may be recognized as a *Hamiltonian system*:

$$\begin{cases} \frac{\mathrm{d}q_k}{\mathrm{d}t} = \frac{\partial H}{\partial p_k}(q_1, p_1, \ldots, q_M, p_M), & k = 1, \ldots, M, \\ \frac{\mathrm{d}p_k}{\mathrm{d}t} = -\frac{\partial H}{\partial q_k}(q_1, p_1, \ldots, q_M, p_M), & k = 1, \ldots, M, \end{cases} \tag{5.9}$$

where we have introduced the *Hamiltonian*

$$H(q_1, p_1, \ldots, q_M, p_M) = \frac{1}{2} \sum_{k=1}^{M} \frac{p_k^2}{m_k} + W(q_1, \ldots, q_M). \tag{5.10}$$

In classical molecular dynamics, the potential W is typically a parametrized potential which gives rise to force fields ∇W that are representable in terms of simple mathematical forms, say, *e.g.*, as explicit functions of the bond lengths, and the dihedral angles, *etc.*, in the molecular system. The analytic form of the functions and the parameters in such potentials are often least-square fitted with *ab initio* computations performed off-line on smaller systems. Two of the most famous force fields are those of the codes AMBER and CHARMM. Parametrized potentials are of course unable to simulate the changes of electronic structure in the molecule (thus in particular chemical reactions) contrary to the coupled quantum/classical simulations (5.4) and, above all, systems such as (5.3).[24]

For such potentials, the computational price of (5.8) is only due to the number of interacting particles: it is only when millions of atoms are simulated that calculating the interactions is a serious task, which can for instance be done with rapid methods such as FMM, and/or multiple timestep methods. For a smaller number of particles it is an easy task. On the other hand, when the potential is of quantum nature and is calculated on the fly, the computational cost of each evaluation of the potential is itself

---

[24] Note, however, the existence of rough approximations, such as the *variable charge molecular dynamics*, that aim to account for changes in the electronic structures while using parametrized potentials.

costly, even for a small system. The state of the art of the technology[25] is as follows: with parametrized force fields, millions of atoms can be simulated over a time frame of 10^{-8} s, while for quantum forces, only a few hundreds atoms can be simulated on 10^{-11} s.

The major point to bear in mind when addressing the construction and numerical analysis of integration schemes for molecular dynamics is that the question asked is *not* to simulate the particular evolution of a single system, starting from a precise initial configuration. Of course, such a task exists, in particular when simulating chemical reactions: details of the dynamics will then be 'observed' that are mostly not accessible to experiment (unless emerging and still difficult techniques such as those of femtochemistry are employed). But the main purpose of molecular dynamics is to simulate the evolution of *a set* of systems, in order to compute *statistical ensemble averages*, with a view to evaluating thermodynamic properties, which is of primary interest because again some of these properties cannot be provided by experiment. This latter objective has its theoretical roots in the (claimed) ergodicity of the system under study. Typically, the average value $\langle A\rangle$ of some observable A on a system of M particles reads as the following integral over the phase space of the position/impulsion of the M particles:

$$\langle A\rangle = \int_{\mathbb{R}^{6M}} A(q_1,p_1,\dots,q_M,p_M)\, f(q_1,p_1,\dots,q_M,p_M)\,\mathrm{d}q_1\,\mathrm{d}p_1\cdots\mathrm{d}q_M\,\mathrm{d}p_M, \tag{5.11}$$

where f is the distribution function in the phase space. It can be evaluated through a Monte Carlo sampling method, but it is often more efficient to obtain it by

$$\langle A\rangle = \lim_{T\longrightarrow+\infty}\frac{1}{T}\int_0^T A(q_1(t),p_1(t),\dots,q_M(t),p_M(t))\,\mathrm{d}t \tag{5.12}$$

along a trajectory of the system obeying to the dynamics

$$\begin{cases} \frac{\mathrm{d}q_i}{\mathrm{d}t} = p_i, & i=1,\dots,M,\\ \frac{\mathrm{d}p_i}{\mathrm{d}t} = F(q_j,p_j), & i=1,\dots,M, \end{cases} \tag{5.13}$$

where F is some force field, so that the measure

$$f(q_1,p_1,\dots,q_M,p_M)\,\mathrm{d}q_1\,\mathrm{d}p_1\cdots\mathrm{d}q_M\,\mathrm{d}p_M$$

is precisely the invariant measure of the dynamics. In the simplest case, the statistical ensemble to sample is the microcanonical ensemble (N,V,E)

---

[25] We provide here a hopefully representative statement, on figures that of course are highly sensitive to the computing facilities at hand.

and the dynamics to be considered is the Hamiltonian dynamics (5.9). We mostly concentrate on this case.

The numerical challenge can be gauged on (5.12). There is no free lunch, and transforming the difficult sampling of the phase space in order to evaluate (5.11) into the dynamics (5.13) results in the fact that it is only in the long-time limit that the average is obtained. Some comments are then in order.

First, ergodicity is not easy to establish. For most systems it can be at best conjectured, but is rarely proved (see Walters (1982) or Gutzwiller (1990) for the mathematical background). The case of Hamiltonian systems has been examined in Markus and Meyer (1974): they are *generically not* ergodic. In addition, ergodicity may stem from various phenomena: the ergodic nature that integrable Hamiltonian systems might have is very peculiar, and, *e.g.*, different from that of 'chaotic' systems.[26] In fact, the lack of a satisfactory theoretical understanding of ergodicity is not a limitation for the numerical practice. What is indeed a bottleneck is the evaluation of the time T on which the system can reasonably be considered to have visited its whole space phase. For the rare systems for which this time can be evaluated, T can be as large as many times the age of the universe, which makes the ergodicity property useless in practice. One way or another, it must be understood how to circumvent the largeness of T in (5.12). This will be the purpose of some acceleration techniques for molecular dynamics that we will introduce in Section 5.3.

Second, the difficulty is enhanced by the fact that, by nature, the molecular dynamics is a multiscale phenomenon. Recall that, in its simplest occurrence, the evolution of bond lengths, dihedral angles, *etc.*, are simulated. Typically, there are in this set of variables rapidly changing degrees of freedom, oscillating over time periods of the order of $10^{-15}\,$s, and also slower ones, and we wish to simulate all of them over a time frame of a few fractions of a second, to say the least. Therefore, even for accessible times T, there are still challenging issues due to the highly oscillatory character of the system.

Third, as we have mentioned above, it is not a question of simulating the evolution for a precise initial configuration. This clearly advocates a geometric viewpoint, where flows, rather than individual trajectories, are the objects of interest. This is therefore the domain of geometric integration (see Hairer, Lubich and Wanner (2002), or Leimkuhler and Reich (2005)), and as the system often has a Hamiltonian structure, the field of symplectic integration is concerned. In order to reproduce the qualitative properties of the evolution at the continuous level, namely the symplectic nature and pos-

---

[26] The systems of molecular dynamics seem to be equally far from either of these two categories.

sibly the reversibility, integration schemes that conserve these properties are utilized. However, there is no simple way to go beyond this. Schematically, one could say that, from the standpoint of numerical analysis,

- it is well understood how to depart from the question of accuracy for short times and rather turn one's interest to stability and conservation issues in the long time, which is the purpose of geometric and symplectic integration,
- it is still an open question to go further than that in the spirit of the computation of averages: to a certain extent there is no better way in order to compute averages than to follow individual trajectories as precisely as possible (in the sense of the first item above).

Fourth, even when using up-to-date techniques for treating oscillatory systems together with the dedicated tools of geometric integration, the time T that can be reached for systems of practical interest is still often too small to get correct ensemble properties (and this is true even in the simplest versions of molecular dynamics). Therefore, classical molecular dynamics is not enough, and we resort to more efficient techniques. Such techniques basically all rely on stochastic simulations. As the main object is the phase space (a fact already exploited by the geometric viewpoint above), we definitely focus on the energy landscape, and designs techniques, more general than 'simply' following trajectories, that aim at exploring this landscape. This allows us to reach simulation times that are, eventually, of practical interest. The next section is devoted to such techniques for the acceleration of simulations in order to bridge the time gap.

In the rest of this section, we overview some of the most commonly used techniques for integration of the equations of motion over reasonably long times and for the treatment of oscillatory terms.

We begin with the long-time integration. From the numerical viewpoint, the purpose is, as usual, to build algorithms that reproduce the theoretical mathematical properties of the system to be simulated. The main property is *symplecticity* (and also possibly *reversibility in time* when the Hamiltonian is autonomous as in (5.9)).

We simply recall here that symplecticity always implies that the flow keeps the volume constant in phase space, which conservation is indeed related to the conservation of energy. In fact, it can be shown, by *backward analysis*, that algorithms enjoying symplecticity at the discrete level have the following property: their *numerical flow* Φ_n is close to the exact flow $\tilde{\Phi}$ of a Hamiltonian system (in fact approximately of order $\mathrm{e}^{-1/\Delta t}$ if Δt denotes the discretization time-step). This latter system is not the original system, but its energy $\tilde{H}$ is close to the energy H of the original system (in fact approximately of order $(\Delta t)^p$ if the numerical scheme is of order p).

The flow $\tilde{\Phi}$, being the exact flow of a Hamiltonian system, preserves its energy $\tilde{H}$. Consequently, $\tilde{\Phi}$ almost preserves H. Finally, Φ_n, being close to $\tilde{\Phi}$, behaves accordingly, and indeed nearly conserves the energy at order $(\Delta t)^p$ over time intervals of length $\mathrm{e}^{1/\Delta t}$. The symplecticity is thus the key property for the simulation of Hamiltonian systems on large times.

An interesting application of backward error analysis in this framework is performed in the recent works of Cancès *et al.* (2004*b*, 2004*c*) that study the speed of convergence of the discretized version of (5.12) toward the average value (5.11) when a symplectic scheme is used.[27] It is proved there that, in the long time limit, the fact that the numerical trajectory generated is the exact trajectory of a modified Hamiltonian allows us to evaluate averages over an isosurface of the Hamiltonian, with a speed of convergence that is $O\left(\frac{1}{T}\right)$. More precisely, one can show that

$$\left|\left(\frac{1}{T}\int_0^T A(q(t),p(t))\,\mathrm{d}t\right)_{\substack{\text{numerical}\\\text{approximation}}} - \langle A\rangle\right| = O\left(\frac{1}{T}\right) + O\left(\Delta t^r\right) \qquad (5.14)$$

where r is the order of the symplectic scheme, and the prefactor in $O\left(\frac{1}{T}\right)$ indeed depends on the largest oscillations in the system. This estimate can be rigorously established in the (somewhat academic) case of integrable systems (then the average $\langle A\rangle$ of course denotes the average for given values of the invariants of the system), and then extended by KAM theory to the case of near-integrable ones (loosely speaking, such systems that are perturbations of integrable systems behave like integrable systems over periods of time exponentially long w.r.t. the perturbation size). Despite this extension, the result unfortunately covers only a tiny subset of the set of Hamiltonians (see again Markus and Meyer (1974)). Estimate (5.14) in turn leads to an acceleration technique for the computation for averages by (5.12), the acceleration being based on the use of signal filtering techniques and ending up in a convergence at the rate $O\left(\frac{1}{T^k}\right) + O(\Delta t^r)$, k arbitrarily large, in (5.14). The technique yields promising results for test cases, but its adaptation to real cases of interest, where Hamiltonians are not near-integrable, is still unclear. It is of course to be emphasized that the technique aims at accelerating the $O\left(\frac{1}{T}\right)$ convergence *only* when it holds. On the other hand, when, *e.g.*, the convergence only holds at the rate $O\left(\frac{1}{\sqrt{T}}\right)$, which is the case for many systems of practical interest, then the method does not succeed in improving the rate of convergence. More details can be found in the above references. Despite the limitation of these works, they are among the rare

---

[27] Actually, the use of a *symmetric* scheme for a *reversible integrable* or a *reversible near-integrable* Hamiltonian would allow for the same conclusions (see Hairer *et al.* (2002, Chapter 11)).

ones that, in some weak sense at least, try to assess the accuracy of molecular dynamics simulations on the basis of the output they are primarily used to provide, namely averages. Some related issues are addressed by Tupper (2005).

The prototypical example of an algorithm that is symplectic and reversible and that is commonly used for molecular simulation is the following *leap-frog algorithm*, known in the chemistry literature as the *Verlet algorithm* for it was introduced there by Verlet (1967). It is an explicit algorithm that, for system (5.9) (for $M = 1$), becomes

$$\begin{cases} q_{n+1} &= q_n + \delta t\, p_{n+1/2}, \\ p_{n+1/2} &= p_{n-1/2} + (\delta t)\, \frac{\partial H}{\partial q}(q_n), \end{cases} \tag{5.15}$$

or equivalently

$$\begin{cases} q_{n+1} &= q_n + \delta t\, p_n + \frac{(\delta t)^2}{2}\, \frac{\partial H}{\partial q}(q_n), \\ p_{n+1} &= p_n + \frac{\delta t}{2}\left(\frac{\partial H}{\partial q}(q_{n+1}) + \frac{\partial H}{\partial q}(q_n)\right), \end{cases} \tag{5.16}$$

the latter version being called *velocity Verlet*.

This algorithm works remarkably well in the context of molecular dynamics. Higher-order schemes, still symplectic and reversible, are used when accuracy is required. For their expression, as well as for their numerical analysis, we refer to the treatises mentioned before. We also refer to Hairer, Lubich and Wanner (2003) for a pedagogic presentation of the Verlet algorithm.

The situation described above is the case when a Hamiltonian dynamics in the (microcanonical) (N, V, E) ensemble must be generated. But in fact, computing ensemble averages in this ensemble is of little interest[28] in comparison to the (canonical) (N, V, T) ensemble. Of course, in the limit of an infinite number of particles, or in an infinite volume, the two averages coincide (at least for local observables A), but this is not the case in practice.[29] Therefore, there is the need to sample the (N, V, T) ensemble and this can be performed by *ad hoc* trajectories. For this purpose, a method in chemistry is that of thermostats. The idea has been developed in Nosé (1984), Hoover (1985) and Nosé (1986). For the purpose of illustration, we only mention the method in its simplest case, namely for one particle in 1D.

---

[28] Note that we do not claim that simulating (N, V, E) trajectories is also of little interest, as it can help in sampling ensembles different from (N, V, E).

[29] Works in progress by Olla aim at evaluating the speed of convergence of one average to the other when the volume of the system goes to infinity.

The dynamics then reads

$$\begin{cases} \frac{\mathrm{d}q}{\mathrm{d}t} &= \frac{p}{m}, \\ \frac{\mathrm{d}p}{\mathrm{d}t} &= F - \frac{p_\xi}{Q}\, p, \\ \frac{\mathrm{d}\xi}{\mathrm{d}t} &= \frac{p_\xi}{Q}, \\ \frac{\mathrm{d}p_\xi}{\mathrm{d}t} &= \frac{1}{m}\, p^2 - k_B\, T, \end{cases} \tag{5.17}$$

where Q is a coupling constant and T denotes the temperature that needs to be fixed (k_B is the Boltzmann constant). The evolution of the additional pair of variables (ξ, p_ξ) aims to measure to what extent the constraint on the temperature is obeyed. This form is in fact only a trivial case of a general form of the so-called *Nosé–Hoover chain*, where more than one additional pair of variables is used. The method is widely used, but there are still open questions on its validity. First, on the very theoretical level, there is no justification of the method, even in the simplest occurrence described above.[30] Second, in practice, some observations are puzzling: for instance the efficiency of the method is highly sensitive to the number of thermostats used, and there is no convincing explanation of this fact. This twofold statement justifies at least the use of alternatives methods. One of them is based upon the Langevin equation. Simply stated, it consists in replacing the Hamiltonian dynamics,

$$\begin{cases} \frac{\mathrm{d}q}{\mathrm{d}t} &= p, \\ \frac{\mathrm{d}p}{\mathrm{d}t} &= -\nabla V(q), \end{cases} \tag{5.18}$$

by the stochastic dynamics,

$$\begin{cases} \mathrm{d}q &= p\,\mathrm{d}t, \\ \mathrm{d}p &= -\big(\gamma\, p + \nabla V(q)\big)\,\mathrm{d}t + \sigma\,\mathrm{d}W_t, \end{cases} \tag{5.19}$$

where $\mathrm{d}W_t$ is a Brownian motion, σ depends on the temperature, and $\gamma \neq 0$ is a constant. Here, there exists a theoretical foundation for the computation of the average of an observable using the evaluation along the trajectory. In other words, ergodicity need not be assumed: it is *proved*. There is convergence in law in the long time to the invariant measure for the (N, V, T) ensemble, and this convergence occurs exponentially fast, which is good news for the computational cost.[31] However, in practice, the need to

---

[30] It is only known that, if ergodicity is assumed, then the Nosé–Hoover dynamics does sample the correct ensemble (see Nosé (1984), and also Bond, Leimkuhler and Laird (1999) for a study devoted to the Nosé–Hoover dynamics).

[31] However, nothing is known mathematically on the variation of the speed of convergence with respect to the number of particles N (here taken to one for simplicity), while it is expected that the convergence is more rapid as N grows to infinity.

compute the empirical mean, which requires averaging over Brownian trajectories, counterbalances this gain. In comparison to other approaches, the method can be costly, but the fact that it has a sound theoretical ground is undoubtedly appealing. We refer to Mattingly, Stuart and Higham (2002) for a related mathematical study.

Let us turn to the treatment of oscillatory terms. In this respect, molecular mechanics is a domain very close to domains such as structural mechanics, robotics, chemical engineering, and other domains where systems of ODEs with different time-scales must be handled. Note that the difference in time-scales for the various variables can come from the characteristic time itself (a rapid oscillation of a bond), or also from a viewpoint mixing time-scales and distance-scales (the long-distance potential created by an atom that is far away needs not be updated so frequently). Heuristically, the treatment of the system can be based upon

- a dedicated treatment of the full system by multiple time-step methods,
- an elimination of the rapidly oscillating degrees of freedom using an algebraic constraint,
- the addition of a stochastic modelling, possibly ending in a friction term, in order to damp the rapid oscillations,

all options with a view to adopting a time-step in the simulation limited by the slow degrees of freedom and far larger than that of the rapid degrees. Whichever option is followed, one key issue is the way the information provided by the rapid degrees of freedom is inserted into the dynamics of the slow degrees of freedom, because at some point, some averaging or homogenization technique is required. This issue is indeed intimately related to renormalization techniques.

The toy model is that of the following system:

$$\begin{cases} \frac{\mathrm{d}y}{\mathrm{d}t} & = f(y,z), \\ \varepsilon\,\frac{\mathrm{d}z}{\mathrm{d}t} & = g(y,z), \end{cases} \tag{5.20}$$

where y stands for the slow degrees of freedom and z for the rapid ones, ε denoting the discrepancy between the timescales. The direct treatment of the above system leads to operator splitting methods, where possibly the effect of the rapid variable z onto the slow one y is obtained by homogenization. We refer to the literature. On the other hand, ε can be considered as so small that the second equation of (5.20) is replaced by $0 = g(y,z)$, thus leading to the algebraic-differential system

$$\begin{cases} \frac{\mathrm{d}y}{\mathrm{d}t} & = f(y,z), \\ 0 & = g(y,z). \end{cases} \tag{5.21}$$

In the present context, a prototypical situation is the dynamics for the following Hamiltonian:

$$H(q,p) = \frac{p^2}{2} + V(q) + \frac{1}{\varepsilon} W(q), \tag{5.22}$$

namely

$$\begin{cases} \frac{\mathrm{d}q}{\mathrm{d}t} & = p, \\ \varepsilon \, \frac{\mathrm{d}p}{\mathrm{d}t} & = -\varepsilon \, \frac{\mathrm{d}V}{\mathrm{d}q}(q) - \frac{\mathrm{d}W}{\mathrm{d}q}(q), \end{cases} \tag{5.23}$$

which is approximated by

$$\begin{cases} \frac{\mathrm{d}q}{\mathrm{d}t} & = p, \\ 0 & = \frac{\mathrm{d}W}{\mathrm{d}q}(q), \end{cases} \tag{5.24}$$

The numerical simulation of a system like (5.21) resorts to the well-known techniques of constrained dynamics. The situation crucially depends on whether the constraint is holonomic or not, *i.e.*, depends only on the position of the system (which is the case in (5.24)), or also on the velocity. For holonomic constraints (think, for instance, of a bond length that is fixed in the molecular dynamics), algorithms such as SHAKE, introduced by Ryckaert, Giccotti and Berendsen (1977), and its improvement RATTLE due to Andersen (1983), are employed. Basically, they consist in running the first line of (5.21) regardless of the constraint, while next imposing the constraint by projection at each time-step. Higher-order variants of these algorithms have been introduced and developed by Jay (1994, 1996).

Regarding the alternative techniques based on an adequate stochastic damping of the rapid degrees of freedom, which is kind of a compromise between the true simulation of the complete system, and the constrained dynamics, the literature is very rich. We refer, *e.g.*, to the works by Schütte, Walter, Hartmann and Huisinga (2004) and Vanden-Eijnden (2003).

Before we get to the next section, we would like to mention a general-purpose technique that can be applied in particular to the molecular dynamics trajectories, in order to improve the applicability of all the above techniques. The technique we allude to is a domain decomposition technique *in time*, called the *parareal method*. It is well known that in scientific computing there have been many attempts to adapt the domain decomposition method, successfully applied to the space variables, in order to apply it to the time variable. The parareal method is the most recent attempt to date in this direction, and seems to be a breakthrough. It is originally due to Lions, Maday and Turinici (2001) and was further developed in a series of works by Maday, Turinici and collaborators. The method is dedicated to PDEs, while other previous attempts were focused on ODEs: see, *e.g.*, Bellen and Zennaro (1989) or Chartier and Philippe (1993). As in the spatial case, the paradigm is based upon adequate iterations between a local solver (fine time-step Δt) and a global, or coarse, solver. The originality of the method resides in the way the iterations are done. Its efficiency heavily relies upon the definition of the coarse solver. It can of course be the same solver as the local one, but with a larger time-step $\Delta T \gg \Delta t$, a choice that does work for parabolic equations and some hyperbolic equations. However, for many hyperbolic equations it is of crucial importance to design the coarse solver adequately, *e.g.*, by solving with the fine time-step Δt a coarse-grained model, otherwise the method is not interesting. An example of a successful application of the method to the present context is discussed in Baffico *et al.* (2002).

We devote the next section to our last point, the acceleration techniques.

5.3. Methods for bridging the time-scale gap

Basically, the dynamics of a molecular system consists of a succession of long periods of time where the system oscillates around local minimizers of the energy inside a given basin, and rapid transitions between two nearby basins, usually following a path that goes through a saddle-point. The direct simulation of a dynamics in this context requires long integration times that are mostly uninteresting, but that cannot be skipped without running the risk of missing the *rare events*, that is, escape from the current basin followed by transition to another.

Unfortunately, in many if not all cases, these rare events occur after a time that is not accessible to a direct simulation. Thus alternative techniques have to be developed. As briefly mentioned above, the techniques that have recently appeared in the literature and that aim to enlarge the applicability of molecular dynamics, focus on the energy landscape rather than on the dynamics itself. This has the twofold interest of making possible long time dynamics and identifying the relevant objects (saddle-points = transition states, and local minimizers = metastable states) for the system under study.

Schematically, one can say that the dynamics starting from an energy basin denoted by A can be decomposed in the following steps:

(a) find the list of basins B that are accessible from A,
(b) determine the pathway from A to each B,
(c) (randomly) choose one B in the list,

then set $A{=}B$ and continue. We now rapidly examine some issues related to each of the above steps.

The first difficulty to overcome when starting a dynamics from a point in a given energy basin is to find an appropriate escape path more quickly than in reality. More or less, the idea is to modify the probability of an escape. As the depth of the basin is indeed responsible for the long time needed to escape, a possibility is to ‘modify’ this depth.

First, we may notice that implicitly the depth that is seen by the system depends on the temperature: in a simplified picture, the transition state theory relates the energy barrier ΔE to overcome in order to escape the basin with the rate of escape r, at a given temperature θ, through

$$r = (\text{Const.}) \times \exp\left(-\frac{\Delta E}{k_B \theta}\right). \tag{5.25}$$

Therefore heating the system amounts to raising the probability of escaping from energy minimizers. This is the bottom line of the *temperature accelerated dynamics* introduced by Sorensen and Voter (2000) (see also Montalenti and Voter (2002)). Then we need to correct the output of the method, as of course some escapes that are almost impossible in practice will indeed be observed at virtual high temperatures: should the need arise, the dynamics is reflected back in the basin if the transition is inconvenient. Note that, from the practical viewpoint, it is an issue to know whether the upper boundary of the basin has been attained by the dynamics or not. One way to proceed is to perform a descent method, periodically along the dynamics, in order to check whether we get back to the starting basin A, or to another one $B \neq A$, the latter case indicating the transition. Another option is to monitor the lowest eigenvalue of the Hessian. As the *relative* rates of escape are correct but not the rates themselves (see (5.25)), we extrapolate from the virtual time of escape the real time of escape at the real temperature using formula (5.25). Impressive boosting factors of the dynamics can be observed (up to 10^7 in convenient cases) but some practical issues remain, and the method is not applicable to all situations.

Many alternative methods can be quoted, similar in spirit to the temperature accelerated dynamics. They modify the shape of the energy surface in order also to escape more easily. One is the *hyperdynamics method*, again due to Voter (1997), predating the temperature-accelerated method. It designs a biased potential surface with a potential $\tilde{V}$ modified from the original potential V, that ensures that the saddle-points of V and $\tilde{V}$ are the same, but that the basins of $\tilde{V}$ are less deep. We refer to Sanz-Navarro and Smith (2001) for an application. Another method is that introduced by Laio and Parrinello (2002), where a non-Markovian coarse-grained dynamics is performed. The idea is to modify on the fly the potential surface in order not to visit again zones that have already been explored, which amounts to filling in progressively each basin of the energy surface. A related idea is that introduced by Barth, Laird and Leimkuhler (2003), who also modify the energy landscape by generating a modified ensemble dynamics, which amounts to reducing the depths of the basins (in a slightly different way from above, since the method leaves the bottoms of the basins unchanged). Still another idea is explored in Darve, Wilson and Pohorille (2002).

A somewhat different paradigm can be used to deal with item (a) (together indeed with (b) and (c)): there is the possibility of running many trajectories (and this can be done on the original energy surface, or a modified one as above) in order to make the rare event more frequent in terms of wall-clock time. This is the essence of the *method of replicas* introduced in Voter (1998) (see also Voter and Sorensen (1999) for a review). With this method, the general spirit of most acceleration methods for molecular dynamics becomes obvious: the fundamental idea is to replace a long trajectory (that required by (5.12)) by a set of smaller ones, plus some post-treatment of the result. With the help of such methods, we are then able to reach longer times of virtual simulation, only performing simulation on small times. It must of course be understood that 'small' means small in comparison with the time T appearing in (5.12), but 'as large as possible' in view of the current state of the art for the best trajectory simulation algorithms available. In some sense, the dynamics simulation is seen as an inner calculation, inserted in a second step in a method based upon another paradigm.

For the sake of illustration, let us present a schematic description of the method of replicas. Several trajectories are simulated in parallel, and the transition time is modelled by an exponential law. When the first transition is observed in the list of all dynamics generated in parallel, the corresponding wall-clock time is set to the sum of all the individual times of each of the trajectories. In so doing, we obtain correct transition times, and may detect transitions to other basins more easily. The rates of transitions obtained may be used in a second step in a kinetic Monte Carlo simulation, a technique we will come back to below.

Let us turn specifically to step (b) and suppose that we have at hand two basins, respectively called A and B. We now need to discover the correct transition pathway from A to B, which in chemistry is called the *reaction pathway*, the curve abscissa along the pathway being called the *reaction coordinate*. Think typically of an angle in a molecule that modifies in order to oscillate between two enantiomers (stable configurations).

Techniques used at this stage essentially reduce to generating moves in the space of all trajectories linking A and B along the energy surface, with a view to determining the realistic one. Often it is one that goes through the saddle-point(s) separating the basin of A from that of B. The move in the trajectory space can be deterministic, and then it is based on the properties of the first and second derivatives near a saddle-point (following gradient information along the current trajectory to locate the saddle-point), or more stochastic, and not necessarily relying on a saddle-point information. Techniques in this vein are the *nudge elastic band* method by Henkelman and Jonsson (2000), the *string* method by E, Ren and Vanden-Eijnden (2002) (see also E, Ren and Vanden-Eijnden (2004*b*), the *dimer* method by Henkelman and Jonsson (1999), and also E, Ren and Vanden-Eijnden (2004*a*), the method by Garrahan and Chandler (2002), that by Zuckerman and Woolf (1999), by Ayala and Schlegel (1997), and so on. We also refer to the survey, with a self-explanatory title, by Bolhuis, Chandler, Dellago and Geissler (2002), and to the introductory text by Chandler (1998).

To perform step (c), a method already used in (a) to escape the basin may of course be used, but a new paradigm can be adopted. When minimizers and transition pathways are located,[32] the rate of escapes from each basin can be evaluated (by transition state theory) and a purely stochastic method can be performed, called *kinetic Monte Carlo*, based on the same paradigm as that mentioned above for the method of replicas: independent transition rates following exponential laws are employed. This time, no dynamical trajectory is explicitly used, and the long time dynamics of the system boils down to a sequence of random numbers, monitoring in fact the transitions and non-escapes in a follow-up of basins. An instance of an alternative approach for item (c) is introduced in Mousseau and Barkema (2004).

What about the mathematical understanding of all the above methods? Actually, depending on the viewpoint, it can be considered as either sufficient or poor. As the output of most methods is a simple Monte Carlo simulation, and since this method has long been the method of choice for studies in probability theory because of the wide range of its applications, there is not much to say. On the other hand, the global strategy definitely needs some understanding and mathematical foundation. A series of works with a solid mathematical ground is that by Huisinga and Schütte (2003), which also gives rise at the algorithmic level to reportedly efficient methods for the above problem: see Deuflhard, Huisinga, Fischer and Schütte (2000), Schütte, Fischer, Huisinga and Deuflhard (1999), and other works by the same authors. The formalization is as follows. The dynamics over a time frame of width τ is seen as a transition operator T_τ that associates the initial point to the final one. If the configuration space is discretized, the examination of the spectrum and spectral projector of this transition operator reveals the metastable zones of the configuration space (in brief, the zones where it is mostly likely that over the time τ any trajectory starting from a point in the zone will end up in another point in the same zone) and the transition rates from one metastable state to the other.

We wish to emphasize that, clearly, the above list of methods is by no means comprehensive. For instance, we have not even approached the techniques based upon the renormalization paradigm, where a coarse-grained

---

[32] In fact there is no hope of locating all of them, but the above means that, at some stage, it is considered that a sufficient knowledge of the topology of the energy surface has been reached, at least at the vicinity of the configuration of the system under study, so that one may proceed to the next step.

model featuring only a limited number of degrees of freedom is derived. Because of this limited size, classical approaches such as those of the previous section are efficient. Typically a set of mesoscale (*i.e.*, intermediate scale) particles is simulated that interact through an adequate potential (the determination of which is the key issue). We refer, *e.g.*, to Forrest and Suter (1995) and to the so-called dissipative particle dynamics technique.

The field of acceleration methods for molecular dynamics is under construction, and we are convinced it will witness huge efforts in view of the importance of the applications.

6. Current and future trends

The domain of computational chemistry is now a well-established domain both from the downstream standpoint, that of applications, and from the upstream standpoint, that of theory, modelling and, increasingly, numerical analysis. To some extent, the publication of the present article in *Acta Numerica* testifies to the latter.

The relevance of computational chemistry does not only concern traditional fields such as chemistry, and its companion field biology. Because the size of technological devices is ever shrinking, once irrelevant phenomena at the microscopic level are now considered relevant. At the other end of the spectrum, for macroscopic compounds or devices, understanding of microscopic behaviour is becoming a key issue, in order to reach maximum efficiency. Let us quote two instances of this trend.

In biology, dynamics of proteins, possibly with chemical reactions at some sites, involves the coupled simulation of quantum degrees of freedom with classical ones: see Monard and Mertz, Jr. (1999) for a review of applications in biochemistry.

In materials science, multiscale methods in computational mechanics are growing in importance. There, computational chemistry is involved in the simulation of the microscopic degrees of freedom, and coupled to more usual techniques of the engineering sciences, such as finite element methods for computational continuum mechanics. The simulation of dislocations, fractures, *etc.*, with a view to further understanding, *e.g.*, fatigue phenomena cannot be studied without a pinch of computational chemistry. For instances of works and challenges in this direction, we refer to the books by Barth, Chan and Haimes, eds (2002), Bulatov *et al.* (1999), Deák, Frauenheim and Pederson, eds (2000), Kirchner, Kubin and Pontikis, eds (1996), Kitagawa *et al.*, eds (1998), Raabe (1998), the special issue by Liu *et al.*, eds (2004), and to the emerging techniques coupling the atomistic level to the continuum description such as Tadmor, Smith, Bernstein and Kaxiras (1999), Shenoy *et al.* (1998), Miller, Tadmor, Phillips and Ortiz (1998), Tadmor, Phillips and Ortiz (1996), Tadmor, Ortiz and Phillips (1996) and Shenoy *et al.* (1999).

All this makes computational chemistry an important field for the future. From the numerical analysis viewpoint, however, the field is not completely explored. It can be considered that some challenging issues, such as the convergence of SCF algorithms, have been treated in a satisfactory way, but many well-established techniques still require mathematical understanding. It is of course even clearer for the new techniques that appear almost every day, and that aim to treat problems of outstanding difficulty: linear scaling methods for the static description of large size systems, evolution PDEs in high dimensions, acceleration methods for dynamics over long times, and so on.

Obviously, the competences required are varied: optimization, linear and nonlinear programming, approximations of PDEs, of ODEs, stochastic processes, to name a few.

Acknowledgements

I have benefited from enlightening interactions with a number of colleagues. Some of them also made a careful reading of a draft version of this article, suggested many improvements, or pointed out references that are included in the present version. I would like to thank all of them: X. Blanc, E. Cancès, F. Castella, Ph. Chartier, M. Esteban, E. Faou, M. Griebel, F. Legoll, T. Lelièvre, M. Lewin, C. Lubich, S. Olla, A. Patera, E. Séré, P. Tupper, G. Turinici and G. Zérah. It is also my pleasure to thank my co-authors for the book Cancès, Defranceschi, Kutzelnigg, Le Bris and Maday (2003*b*). Some sections of the present paper draw much of their inspiration from this earlier work.

REFERENCES

M. P. Allen and D. J. Tildesley (1987), *Computer Simulation of Liquids*, Oxford Science Publications.

B. O. Almroth, P. Stern and F. A. Brogan (1978), 'Automatic choice of global shape functions in structural analysis', *AIAA Journal* **16**, 525–528.

H. C. Andersen (1983), 'Rattle: A "velocity" version of the Shake algorithm for molecular dynamics calculations', *J. Comput. Phys.* **52**, 24–34.

D. A. Areshkin, O. A. Shenderova, J. D. Schall and D. W. Brenner (2003), 'Convergence acceleration scheme for self consistent orthogonal basis set electronic structure methods', *Molecular Simulation* **29**, 269–286.

N. W. Ashcroft and N. D. Mermin (1976), *Solid-State Physics*, Saunders College Publishing.

G. Auchmuty and Wenyao Jia (1994), 'Convergent iterative methods for the Hartree eigenproblem', *Math. Model. Numer. Anal.* **28**, 575–610.

P. Y. Ayala and P. B. Schlegel (1997), 'A combined method for determining reaction paths, minima and transition state geometries', *J. Chem. Phys.* **107**, 375–384.

V. Bach (1992), 'Error bound for the Hartree–Fock energy of atoms and molecules', *Comm. Math. Phys.* **147**, 527–548.

V. Bach, E. H. Lieb, M. Loss and J. P. Solovej (1994), 'There are no unfilled shells in unrestricted Hartree–Fock theory', *Phys. Rev. Lett.* **72**, 2981–2983.

G. B. Bacskay (1961), 'A quadratically convergent Hartree–Fock (QC-SCF) method: Application to closed shell systems', *Chem. Phys.* **61** 385–404.

L. Baffico, S. Benard, Y. Maday, G. Turinici and G. Zerah (2002), 'Parallel in time molecular dynamics simulations', *Phys. Rev. E* **66**, 057701.

A. Bandrauk, M. Delfour and C. Le Bris, eds (2004), *Quantum Control: Mathematical and Numerical Challenges*, AMS, CRM proceedings series.

M. Barrault, Y. Maday, N. C. Nguyen and A. Patera (2004*a*), 'An "empirical interpolation" method: Application to efficient reduced-basis discretization of PDEs', *CR Acad. Sci., Paris, Série I, Math.* **339**, 667–672.

M. Barrault, E. Cancès, C. Le Bris, Y. Maday, N. C. Nguyen, A. Patera and G. Turinici (2004*b*), in preparation.

M. Barrault, E. Cancès, W. Hager and C. Le Bris (2004*c*), 'Multilevel domain decomposition method for electronic structure calculations', in preparation.

M. Barrault, G. Bencteux, E. Cancès and V. Duwig (2004*d*) Toward a linear scaling for ill-conditioned eigenvalue problems in quantum chemistry. Technical report.

E. J. Barth, B. B. Laird and B. J. Leimkuhler (2003), 'Generating generalized distributions from dynamical simulation', *J. Chem. Phys.* **118** 5759.

T. J. Barth, T. Chan and R. Haimes, eds (2002), *Multiscale and Multiresolution Methods: Theory and Applications*, Vol. 20 of *Lecture Notes in Computational Science and Engineering*, Springer.

T. L. Beck (2000), 'Real-space mesh techniques in density-functional theory', *Rev. Modern Phys.* **72**, 1041–1080.

A. Bellen and M. Zennaro (1989), 'Parallel algorithms for initial-value problems for difference and differential equations', *J. Comput. Appl. Math.* **25**, 341–350.

X. Blanc (2000), A mathematical insight into ab initio simulations of solid phase, in *Mathematical Models and Methods for ab initio Quantum Chemistry* (M. Defranceschi and C. Le Bris, eds), Vol. 74 of *Lecture Notes in Chemistry*, Springer, pp. 133–158.

X. Blanc and E. Cancès (2004), Nonlinear instability of density-independent orbital-free kinetic energy functionals, *J. Chem. Phys.*, submitted.

P. Blanchard and E. Bruning (1982), *Variational Methods in Mathematical Physics*, Springer.

P. E. Blöchl (1994), 'Projector augmented-wave method', *Phys. Rev. B* **50**, 17953–17979.

O. M. Bokanowski and M. Lemou (1998), 'Fast multipole method for multidimensional integrals', *CR Acad. Sci., Paris, Série I, Math.* **326** 105–110.

O. M. Bokanowski and M. Lemou (2001), 'Fast multipole method for multi-variable integrals', Laboratoire MIP, Toulouse, preprint.

P. G. Bolhuis, D. Chandler, C. Dellago and P. Geissler (2002), 'Transition paths sampling: Throwing ropes over rough mountain passes, in the dark', *Annu. Rev. Phys. Chem.* **53**, 291–318.

S. D. Bond, B. J. Leimkuhler and B. B. Laird (1999), 'The Nosé–Poincaré method for constant temperature molecular dynamics', *J. Comput. Phys.* **151** 114–134.

F. A. Bornemann (1998), *Homogenization in Time of Singularly Perturbed Mechanical Systems*, Vol. 1697 of *Lecture Notes in Mathematics*, Springer.

F. A. Bornemann and C. Schütte (1998), 'A mathematical investigation of the Car–Parrinello method', *Numer. Math.* **78**, 359–376.

F. A. Bornemann, P. Nettesheim and C. Schütte (1996), 'Quantum-classical molecular dynamics as an approximation to full quantum dynamics', *J. Chem. Phys.* **105**, 1074–1083.

D. Bowler and M. Gillan (1999), 'Density matrices in $O(N)$ electronic structure calculations', *Comput. Phys. Comm.* **120**, 95–108.

D. Bowler *et al.* (1997), 'A comparison of linear scaling tight-binding methods', *Model. Simul. Mater. Sci. Eng.* **5**, 199–202.

D. Bowler, T. Miyazaki and M. Gillan (2002), 'Recent progress in linear scaling *ab initio* electronic structure theories', *J. Phys. Condens. Matter* **14**, 2781–2798.

S. F. Boys (1950), 'Electronic wavefunctions I: A general method of calculation for the stationary states of any molecular system', *Proc. Roy. Soc. A* **200**, 542–554.

V. V. Bulatov *et coll.* (1999), *Multiscale Modelling of Materials*, MRS.

H. J. Bungartz and M. Griebel (2004), 'Sparse grids', in *Acta Numerica*, Vol. 13, Cambridge University Press, pp. 147–269.

E. Cancès (2000), SCF algorithms for Hartree–Fock electronic calculations, in *Mathematical Models and Methods for ab initio Quantum Chemistry* (M. Defranceschi and C. Le Bris, eds), Vol. 74 of *Lecture Notes in Chemistry*, Springer, pp. 17–43.

E. Cancès (2001), 'SCF algorithms for Kohn–Sham models with fractional occupation numbers', *J. Chem. Phys.* **114**, 10616–10623.

E. Cancès and C. Le Bris (1998), 'On the perturbation method for some nonlinear Quantum Chemistry models', *Math. Models Methods Appl. Sci.* **8**, 55–94.

E. Cancès and C. Le Bris (1999), 'On the time-dependent electronic Hartree–Fock equations coupled with a classical nuclear dynamics', *Math. Models Methods Appl. Sci.* **9**, 963–990.

E. Cancès and C. Le Bris (2000*a*), 'On the convergence of SCF algorithms for the Hartree–Fock equations', *Math. Model. Numer. Anal.* **34**, 749–774.

E. Cancès and C. Le Bris (2000*b*), 'Can we outperform the DIIS approach for electronic structure calculations', *Int. J. Quantum Chem.* **79**, 82–90.

E. Cancès, C. Le Bris, B. Mennucci and J. Tomasi (1999), 'Integral equation methods for molecular scale calculations in the liquid phase', *Math. Models Methods Appl. Sci.* **9**, 35–44.

E. Cancès, C. Le Bris, Y. Maday and G. Turinici (2002), 'Towards reduced basis approaches in *ab initio* electronic computations', *J. Sci. Comput.*, **17**, 461–469.

E. Cancès, K. Kudin, G. Scuseria and G. Turinici (2003*a*), 'Quadratically convergent algorithm for fractional occupation numbers in density functional theory', *J. Chem. Phys.* **118**, 5364–5368.

E. Cancès, M. Defranceschi, W. Kutzelnigg, C. Le Bris and Y. Maday (2003*b*), Computational chemistry: A primer, in *Handbook of Numerical Analysis*, Vol. X, *Computational Chemistry* (C. Le Bris, ed.), North-Holland, pp. 3–270.

E. Cancès, H. Galicher and M. Lewin, (2004*a*), 'Computing electronic structures: A new multiconfiguration approach for excited states', *J. Comput. Phys.*, submitted.

E. Cancès, F. Castella, P. Chartier, E. Faou, C. Le Bris, F. Legoll and G. Turinici (2004*b*), 'High-order averaging schemes with error bounds for thermodynamical properties calculations by MD simulations', *J. Chem. Phys.* **121** 10346–10355.

E. Cancès, F. Castella, P. Chartier, E. Faou, C. Le Bris, F. Legoll and G. Turinici (2004*c*), 'Long-time averaging for integrable Hamiltonian dynamics', *Numer. Math.*, to appear.

E. Cancès, B. Jourdain and T. Lelièvre (2004*d*), 'Quantum Monte-Carlo simulations of fermions: A mathematical analysis of the fixed-node approximation', *Math. Models Methods Appl. Sci.*, submitted.

R. Car and M. Parrinello (1985), 'Unified approach for molecular dynamics and density functional theory', *Phys. Rev. Lett.* **55**, 2471–2474.

E. Carter and Y. A. Wang (2000), Orbital-free kinetic energy density functional theory, in *Theoretical Methods in Condensed Phase Chemistry* (S. D. Schwartz, ed.), Progress in Theoretical Chemistry and Physics, Kluwer, pp. 117–84.

I. Catto and P.-L. Lions (1992), 'Binding of atoms and stability of molecules in Hartree and Thomas–Fermi type theories I: A necessary and sufficient condition for the stability of general molecular systems', *Comm. Part. Diff. Equ.* **17**, 1051–1110.

I. Catto and P.-L. Lions (1993*a*), 'Binding of atoms and stability of molecules in Hartree and Thomas–Fermi type theories 2: Stability is equivalent to the binding of neutral subsystems', *Comm. Part. Diff. Equ.* **18**, 305–354.

I. Catto and P.-L. Lions (1993*b*), 'Binding of atoms and stability of molecules in Hartree and Thomas–Fermi type theories 3: Binding of neutral subsystems', *Comm. Part. Diff. Equ.* **18**, 381–429.

I. Catto and P.-L. Lions (1993*c*), 'Binding of atoms and stability of molecules in Hartree and Thomas–Fermi type theories 4: Binding of neutral systems for the Hartree model', *Comm. Part. Diff. Equ.* **18**, 1149–1159.

I. Catto, C. Le Bris and P.-L. Lions (1998), *Mathematical Theory of Thermodynamic Limits: Thomas–Fermi Type Models*, Oxford University Press.

I. Catto, C. Le Bris and P.-L. Lions (2001), 'On the thermodynamic limit for Hartree–Fock type models', *Ann. Inst. Henri Poincaré Anal. non linéaire* **18**, 687–760.

I. Catto, C. Le Bris and P.-L. Lions (2002), 'On some periodic Hartree-type models for crystals', *Ann. Inst. Henri Poincaré Anal. non linéaire* **19**, 143–190.

G. Chaban, M. W. Schmidt and M. S. Gordon (1997), 'Approximate second order method for orbital optimization of SCF and MCSCF wavefunctions', *Theor. Chem. Acc.* **97**, 88–95.

J. M. Chadam and R. T. Glassey (1975), 'Global existence of solutions to the Cauchy problem for time-dependent Hartree equations', *J. Math. Phys.* **16**, 1122–1230.

M. Challacombe (2000), 'Linear scaling computation of the Fock matrix V: Hierarchical cubature for numerical integration of the exchange-correlation matrix', *J. Chem. Phys.* **113**, 10037–10043

D. Chandler (1998), Barrier crossings: Classical theory of rare but important events, in *Classical and Quantum Dynamics in Condensed Phase Simulations*, (Berne *et al.*, eds), World Scientific, p. 3.

P. Chartier and B. Philippe (1993), 'A parallel shooting technique for solving dissipative ODEs', *Computing*, **51** (3–4).

E. Clementi and D. R. Davis (1966), 'Electronic structure of large molecular systems', *J. Comput. Phys.* **1**, 223–244.

A. J. Coleman and V. I. Yukalov (2000), *Reduced Density Matrices*, Vol. 72 of *Lecture Notes in Chemistry*, Springer.

H. L. Cycon, R. G. Froese, W. Kirsch and B. Simon (1987), *Schrödinger Operators with Applications to Quantum Mechanics and Global Geometry*, Springer.

A. Daniels and G. Scuseria (1999), 'What is the best alternative to diagonalization of the Hamiltonian in large scale semiempirical calculations?', *J. Chem. Phys.* **110**, 1321–1328.

E. Darve, M. Wilson and A. Pohorille (2002), 'Calculating free energies using scaled-force molecular dynamics algorithm', *Molecular Simulation* **28**, 113.

P. Deák, T. Frauenheim and M. R. Pederson, eds (2000), *Computer Simulation of Materials at Atomic Level*, Wiley, 2000.

M. Defranceschi and P. Fischer (1998), 'Numerical solution of the Schrödinger equation in a wavelet basis for hydrogen-like atoms', *SIAM J. Numer. Anal.* **35**, 1–12.

M. Defranceschi and C. Le Bris (1997), 'Computing a molecule: A mathematical viewpoint', *J. Math. Chem.* **21**, 1–30.

M. Defranceschi and C. Le Bris (1999), 'Computing a molecule in its environment: A mathematical viewpoint', *Int. J. Quantum Chem.* **71**, 257–250.

M. Defranceschi and C. Le Bris, eds (2000), *Mathematical Models and Methods for ab initio Quantum Chemistry*, Vol. 74 of *Lecture Notes in Chemistry*, Springer.

J. W. Demmel (1997), *Applied Numerical Linear Algebra*, SIAM.

J. P. Desclaux, J. Dolbeault, P. Indelicato, M. J. Esteban and E. Séré, (2003), Computational approaches of relativistic models in quantum chemistry, in *Handbook of Numerical Analysis* (P. G. Ciarlet, series ed.), Vol. X, *Computational Chemistry* (C. Le Bris, ed.), North-Holland.

P. Deuflhard *et al.*, eds (1999), *Computational Molecular Dynamics: Challenges, Methods, Ideas*, *Lecture Notes in Computational Science and Engineering*, Springer.

P. Deuflhard, W. Huisinga, A. Fischer and C. Schütte (2000), 'Identification of almost invariant aggregates in reversible nearly uncoupled Markov chains', *Linear Algebra Appl.* **315**, 39–59.

J. Dolbeault, M. J. Esteban and E. Séré (2000*a*), Variational methods in relativistic quantum mechanics: New approach to the computation of Dirac eigenvalues, in *Mathematical Models and Methods for ab initio Quantum Chemistry* (C. Le Bris and M. Defranceschi, eds), Vol. 74 of *Lecture Notes in Chemistry*, Springer.

J. Dolbeault, M. J. Esteban, E. Séré and M. Vanbreugel (2000*b*), 'Minimization methods for the one-particle Dirac equation', *Phys. Rev. Lett.* **85**, 4020–4023

J. Dolbeault, M. J. Esteban and E. Séré (2003), 'A variational method for relativistic computations in atomic and molecular physics', *Int. J. Quantum Chem.* **93**, 149–155.

J. Douady, Y. Ellinger, R. Subra and B. Levy (1980), 'Exponential transformation of molecular orbitals: A quadratically convergent SCF procedure I: General formulation and application to closed-shell ground states', *J. Chem. Phys.* **72**, 1452–1462.

R. Dovesi, R. Orlando, C. Roetti, C. Pisani and V. R. Saunders (2000), 'The periodic Hartree–Fock method and its implementation in the Crystal code', *Phys. Stat. Sol.* (b) **217**, 63–88.

R. M. Dreizler and E. K. U. Gross (1990), *Density Functional Theory*, Springer.

W. E, W. Ren and E. Vanden-Eijnden (2002), 'String method for the study of rare events', *Phys. Rev. B* **66**, 052301.

W. E, W. Ren and E. Vanden-Eijnden (2004*a*), 'Minimum action method for the study of rare events', *Comm. Pure Appl. Math.* **LVII**, 1–20.

W. E, W. Ren and E. Vanden-Eijnden (2004*b*), 'Finite temperature string method for the study of rare events', preprint.

M. J. Esteban and E. Séré (2002), 'An overview on linear and nonlinear Dirac equations', *Discrete Contin. Dyn. Syst.* **8** (2), 381–397.

D. F. Feller and K. Ruedenberg (1979), 'Systematic approach to extended even-tempered orbital bases for atomic and molecular calculations', *Theoret. Chim. Acta* **52**, 231–251.

T. H. Fischer and J. Almlöf (1992), 'General methods for geometry and wave function optimization', *J. Phys. Chem.* **96**, 9768–9774.

V. Fock (1958), 'On Schrödinger equation for the helium atom', *K. Norske Vidensk. Selsk. Forhandl.* **31**, 138–152.

B. M. Forrest and U. W. Suter(1995), 'Accelerated equilibration of polymer metals by time coarse graining', *J. Chem. Phys.* **18**, 7256–7266.

S. Fournais, M. Hoffmann-Ostenhof, T. Hoffmann-Ostenhof and T. Sorensen (2002*a*), On the regularity of the density of electronic wavefunctions, in *Mathematical Results in Quantum Mechanics: Taxco 2001*, Vol. 307 of *Contemp. Math.*, AMS, Providence, RI, pp. 143–148.

S. Fournais, M. Hoffmann-Ostenhof, T. Hoffmann-Ostenhof and T. Sorensen (2002*b*), 'The electron density is smooth away from the nuclei', *Comm. Math. Phys.* **228**, 401–415.

S. Fournais, M. Hoffmann-Ostenhof, T. Hoffmann-Ostenhof and T. Sorensen (2004), 'Analyticity of the density of electronic wavefunctions', *Ark. Mat.* **42**, 87–106.

D. Frenkel and B. Smit (2001), *Understanding Molecular Simulation*, 2nd edn, Academic Press.

G. Friesecke (2003), 'The multiconfiguration equations for atoms and molecules: Charge quantization and existence of solutions', *Arch. Rat. Mech. Anal.* **169**, 35–71.

G. Galli (2000), 'Large scale electronic structure calculations using linear scaling methods', *Phys. Stat. Sol.* (b) **217**, 231–249.

J. Garcke and M. Griebel (2000), 'On the computation of the eigenproblems of hydrogen and helium in strong magnetic and electric fields with the sparse grid combination technique', *J. Comput. Phys.* **165**, 694–716.

J. P. Garrahan and D. Chandler (2002), 'Geometrical explanation and scaling of dynamical heterogeneities in glass forming systems', *Phys. Rev. Lett.* **89** (3), 035704–035707.

P. M. W. Gill (1994), Molecular integrals over Gaussian basis functions, in *Advances in Quantum Chemistry* (P.-O. Löwdin, J. R. Sabin and M. C. Zerner, eds), Vol. 25, Academic Press, pp. 141–205.

S. Goedecker (1999), 'Linear scaling electronic structure methods', *Rev. Modern Phys.* **71**, 1085–1123.

R. Greengard and V. Rokhlin (1997), A new version of the fast multipole method for the Laplace equation in three dimensions, in *Acta Numerica*, Vol. 6, Cambridge University Press, pp. 229–269.

M. Griebel, P. Oswald and T. Schlekefer (1999), 'Sparse grids for boundary integral equations', *Numer. Math.* **83** (2), 279–312.

M. Griebel, S. Knapek, G. Zumbusch and A. Caglar (2004), *Numerische Simulation in der Moleküldynamik: Numerik, Algorithmen, Parallelisierung, Anwendungen*, Springer.

S. J. Gustafson and I. M. Sigal (2003), *Mathematical Concepts of Quantum Mechanics*, Universitext, Springer.

M. C. Gutzwiller (1990), *Chaos in Classical and Quantum Mechanics*, Vol. 1 of *Interdisciplinary Applied Mathematics*, Springer.

W. Hackbusch (2001), 'The efficient computation of certain determinants arising in the treatment of Schrödinger's equations', *Computing* **67**, 35–56.

G. A. Hagedorn (1996), 'Crossing the interface between chemistry and mathematics', *Notices Amer. Math. Soc.*, March 1996, 297–299.

J. M. Haile (1992), *Molecular Dynamics Simulations*, Wiley.

E. Hairer and G. Wanner (1996), *Solving Ordinary Differential Equations II*, 2nd edn, Springer.

E. Hairer, S. P. Nørsett and G. Wanner (1993), *Solving Ordinary Differential Equations I*, 2nd edn, Springer.

E. Hairer, C. Lubich and G. Wanner (2002), *Geometric Numerical Integration: Structure-Preserving Algorithms for Ordinary Differential Equations*, Springer.

E. Hairer, C. Lubich and G. Wanner (2003), Geometric numerical integration illustrated by the Störmer–Verlet method, in *Acta Numerica*, Vol. 12, Cambridge University Press, pp. 399–450.

M. Head-Gordon, Y. Shao, C. Saravan and C. White (2003), 'Curvy steps for density matrix based energy minimization: Tensor formulation and toy applications', *Mol. Phys.* **101** (1–2), 37–43.

W. J. Hehre, L. Radom, P. v. R. Schleyer and J. A. Pople (1986), *Ab initio Molecular Orbital Theory*, Wiley.

W. Heitler and F. London (1927), 'Wechselwirkung neutraler Atome und homöopolare Bindung nach der Quantenmechanik', *Z. Phys.* **44**, 455–472.

G. Henkelman and H. Jonsson (1999), 'A dimer method for finding saddle points on high dimensional potential surfaces using only first derivatives', *J. Chem. Phys.* **111** (15), 7010–7022.

G. Henkelman and H. Jonsson (2000), 'Improved tangent estimates in the nudged elastic band method for finding minimum energy paths and saddle points', *J. Chem. Phys.* **113** (22), 9978–9985.

S. C. Hill (1985), 'Rates of convergence and error estimation formulas for the Rayleigh–Ritz variational method', *J. Chem. Phys.* **83**, 1173–1196.

R. N. Hill (1995), 'Dependence of the rate of convergence of the Rayleigh–Ritz method on a nonlinear parameter', *Phys. Rev. B* **51**, 4433–4471.

P. Hohenberg and W. Kohn (1964), 'Inhomogeneous electron gas', *Phys. Rev. B* **136**, 864–871.

M. Hoffmann-Ostenhof, T. Hoffmann-Ostenhof and T. Sorensen (2001), 'Electron wavefunctions and densities for atoms', *Ann. Henri Poincaré* **2**, 77–100.

W. H. Hoover (1986), 'Canonical dynamics: Equilibrium phase-space distributions', *Phys. Rev. A* **31**, 1695–1697.

W. Huisinga and C. Schütte (2003), Biomolecular conformations can be identified as metastable sets of molecular dynamics, in *Handbook of Numerical Analysis*, Vol. X, *Computational Chemistry* (C. Le Bris, ed.), North-Holland.

E. A. Hylleraas (1929), 'Neue Berechnung der Energie des Heliums im Grundzustande, sowie des tiefsten Terms von Ortho-Helium', *Z. Phys.* **54**, 347–366.

T. Jahnke (2003), Numerische Verfahren für fast adiabatische Quantendynamik, PhD Dissertation, Universität Tübingen.

T. Jahnke (2004), 'Long-time-step integrators for almost adiabatic quantum dynamics', *SIAM J. Sci. Comput.* **25**, 2145–2164.

T. Jahnke and C. Lubich (2003), 'Numerical integrators for quantum dynamics close to the adiabatic limit', *Numer. Math.* **94** (2), 289–314.

H. M. James and A. S. Coolidge (1933), 'The ground state of the hydrogen molecule', *J. Chem. Phys.* **1**, 825–835.

L. O. Jay (1994), Runge–Kutta type methods for index three differential-algebraic equations with applications to Hamiltonian systems, PhD thesis, Department of Mathematics, University of Geneva.

L. O. Jay (1996), 'Symplectic partitioned Runge–Kutta methods for constrained Hamiltonian systems', *SIAM J. Numer. Anal.* **33**, 368–387.

L. O. Jay, H. Kim, Y. Saad and J. R. Chelikowski (1999), 'Electronic structure calculations for plane wave codes without diagonalization', *Comput. Phys. Comm.* **118**, 21–30.

R. O. Jones and O. Gunnarsson, 'The density functional formalism, its applications and prospects', *Rev. Modern Phys.* **61**, 689–746.

T. Kinoshita (1957), 'Ground state of the helium atom', *Phys. Rev.* **105**, 1490–1502.

O. Kirchner, L. P. Kubin and V. Pontikis, eds (1996), *Computer Simulation in Materials Science*, Kluwer.

H. Kitagawa *et al.*, eds (1998), *Mesoscopic Dynamics of Fracture*, *Advances in Materials Research*, Springer.

C. Kittel (1996), *Introduction to Solid State Physics*, 7th edn, Wiley.

B. Klahn and W. A. Bingel (1977), 'The convergence of the Rayleigh–Ritz method in quantum chemistry', *Theoret. Chim. Acta* **44**, 26–43.

B. Klahn and J. D. Morgan, III (1984), 'Rates of convergence of variational calculations of expectation values', *J. Chem. Phys.* **81**, 410–433.

W. Klopper and W. Kutzelnigg (1986), 'Gaussian basis sets and the nuclear cusp problem', *J. Mol. Struct. Theochem.* **135**, 339–356.

W. Kohn (1996), 'Density functional and density matrix method scaling linearly with the number of atoms', *Phys. Rev. Lett.* **76**, 3168–3171.

W. Kohn (1999), 'Nobel Lecture: Electronic structure of matter-wave functions and density functionals', *Rev. Modern Phys.* **71**, 1253–1266.

W. Kohn and L. J. Sham, (1965), 'Self-consistent equations including exchange and correlation effects', *Phys. Rev. A* **140**, 1133–1138.

W. Kolos and J. Rychlewski (1993), 'Improved theoretical dissociation energy and ionization potential for the ground-state of the hydrogen molecule', *J. Chem. Phys.* **98**, 3960–3967.

J. Koutecký and V. Bonacic (1971), 'On convergence difficulties in the iterative Hartree–Fock procedure', *J. Chem. Phys.* **55**, 2408–2413.

K. Kudin and G. E. Scuseria (1998), 'A fast multipole algorithm for the efficient treatment of the Coulomb problem in electronic structure calculations of periodic systems with Gaussian orbitals', *Chem. Phys. Lett.* **289**, 611–616.

K. Kudin, G. E. Scuseria and E. Cancès (2002), 'A black-box self-consistent field convergence algorithm: One step closer', *J. Chem. Phys.* **116**, 8255–8261.

W. Kutzelnigg (1989), Convergence expansions in Gaussian basis' in *Strategies and Applications in Quantum Chemistry: A Tribute to G. Berthier* (M. Defranceschi and Y. Ellinger, eds), Kluwer, Dordrecht, pp. 79–102.

W. Kutzelnigg (1994), 'Theory of the expansion of wave functions in a Gaussian basis', *Int. J. Quantum Chem.* **51**, 447–463.

W. Kutzelnigg and J. D. Morgan III (1992), 'Rate of convergence of the partial-wave expansions of atomic correlation energies', *J. Chem. Phys.* **96**, 4484–4508.

A. Laio and M. Parrinello (2002), 'Escaping free-energy minima', *Proc. Nat. Acad. Sci.* **99**, 20.

C. Le Bris (1994), 'A general approach for multiconfiguration methods in quantum molecular chemistry', *Ann. Inst. Henri Poincaré Anal. non linéaire* **11**, 441–484.

C. Le Bris, ed. (2003), *Handbook of Numerical Analysis*, Vol. X, *Computational Chemistry*, North-Holland.

C. Le Bris and P.-L. Lions (2005), 'From atoms to crystals: A mathematical journey', *Bull. Amer. Math. Soc.*, in press.

B. Leimkuhler and S. Reich (2005), *Simulating Hamiltonian Mechanics*, Cambridge Monographs on Applied and Computational Mathematics, Cambridge University Press, to appear.

I. N. Levine (1991), *Quantum Chemistry*, 4th edn, Prentice-Hall.

M. Lewin (2004), 'Solutions of the multiconfiguration equations in quantum chemistry', *Arch. Rat. Mech. Anal.* **171** (1), 83–114.

X. P. Li, R. W. Nunes and D. Vanderbilt (1993), 'Density matrix electronic structure method with linear system-size scaling', *Phys. Rev B* **47**, 10891–10894.

W. Liang, C. Saravan, Y. Shao, R. Baer, A. T. Bell and M. Head-Gordon (2003), 'Improved Fermi operator expansion methods for fast electronic structure calculations', *J. Chem. Phys.* **119** (8), 4117–4125.

E. H. Lieb (1981), 'Thomas–Fermi and related theories of atoms and molecules', *Rev. Modern Phys.* **53**, 603–641.

E. H. Lieb (1983), 'Density functionals for Coulomb systems', *Int. J. Quantum Chem.* **24**, 243–277.

E. H. Lieb (1985), Density functionals for Coulomb systems, in *Density Functional Methods in Physics* (R. M. Dreizler and J. da Providencia, eds), Plenum, New York, pp. 31–80.

E. H. Lieb and B. Simon (1977*a*), 'The Hartree–Fock theory for Coulomb systems', *Comm. Math. Phys.* **53**, 185–194.

E. H. Lieb and B. Simon (1977*b*), 'The Thomas–Fermi theory of atoms, molecules and solids', *Adv. Math.* **23**, 22–116.

J.-L. Lions, Y. Maday and G. Turinici (2001), 'Résolution d'EDP par un schéma en temps "pararéel"' (A 'parareal' in time discretization of PDE's), *CR Acad. Sci., Paris, Série I, Math.* **332** (7), 661–668.

P.-L. Lions (1985), Hartree–Fock and related equations, in *Nonlinear Partial Differential Equations and their Applications*, *Lect. Coll. de France Semin.*, Vol. IX, *Pitman Res. Notes Math. Ser.*, Vol. 181, pp. 304–333.

P.-L. Lions (1987), 'Solutions of Hartree–Fock equations for Coulomb systems', *Comm. Math. Phys.* **109**, 33–97.

P.-L. Lions (1996), Remarks on mathematical modelling in quantum chemistry, in *Computational Methods in Applied Sciences*, Wiley, pp. 22–23.

K. B. Lipkowitz and D. B. Boyd, eds (1995–) *Reviews in Computational Chemistry*, 18 volumes to date, Wiley.

W. K. Liu *et al.*, eds (2004), Special issue on multiple scale methods for nanoscale mechanics and materials, *Comput. Methods Appl. Mech. Eng.* **193** (17–20).

C. Lubich (2004), 'A variational splitting integrator for quantum molecular dynamics', *Appl. Numer. Math.* **48**, 355–368.

A. Lüchow and H. Kleindienst (1994), 'Accurate upper and lower bounds to the ^{2}S states of the lithium atom', *Int. J. Quantum Chem.* **51**, 211–224.

R. McWeeny (1992), *Methods of Molecular Quantum Mechanics*, 2nd edn, Academic Press.

Y. Maday and A. T. Patera (2000), 'Numerical analysis of *a posteriori* finite element bounds for linear functional outputs', *Math. Models Methods Appl. Sci.* **10** (5), 785–799.

Y. Maday and G. Turinici (2003), 'Error bars and quadratically convergent methods for the numerical simulation of the Hartree–Fock equations', *Numer. Math.* **94**, 739–770.

Y. Maday, A. T. Patera and J. Peraire (1999), 'A general formulation for *a posteriori* bounds for output functionals of partial differential equations: Application to the eigenvalue problem', *CR Acad. Sci., Paris, Série I, Math.* **328** (9), 823–828.

N. H. March (1992), *Electron Density Theory of Atoms and Molecules*, Academic Press.

L. Markus and K. R. Meyer (1974), 'Generic Hamiltonian dynamical systems are neither integrable nor ergodic', *Mem. Amer. Math Soc.* **144**.

J. C. Mattingly, A. M. Stuart and D. J. Higham (2002), 'Ergodicity for SDEs and approximations: Locally Lipschitz vector fields and degenerate noise', *Stochastic Process. Appl.* **101** (2), 185–232.

D. Mazziotti (1998*a*), '$3,5$-contracted Schrödinger equation: Determining quantum energies and reduced density matrices without wave functions', *Int. J. Quantum Chem.* **70**, 557–570.

D. Mazziotti (1998*b*), 'Contracted Schrödinger equation: Determining quantum energies and two-particle density matrices without wave functions', *Phys. Rev. A* **57**, 4219–4234.

D. Mazziotti (1999), 'Comparison of contracted Schrödinger and coupled-cluster theories', *Phys. Rev. A* **60**, 4396–4408.

D. Mazziotti (2004), 'Realization of quantum chemistry wave functions through first-order semidefinite programming', *Phys. Rev. Lett.* **93**, 21.

R. Miller, E. B. Tadmor, R. Phillips and M. Ortiz (1998), 'Quasicontinuum simulation of fracture at the atomic scale', *Model. Simul. Mater. Sci. Eng.* **6**.

G. Monard and K. Mertz, Jr. (1999), 'Combined quantum mechanical/molecular mechanical methodologies applied to biomolecular systems', *Acc. Chem. Res.* **32**, 904–911.

F. Montalenti and A. F. Voter (2002), 'Exploiting past visits or minimum-barrier knowledge to gain further boost in the temperature-accelerated dynamics', *J. Chem. Phys.* **116** (12), 4819–4828.

J. D. Morgan, III (1984), in *Numerical Determination of the Electronic Structure of Atoms, Diatomic and Polyatomic Molecules* (M. Defranceschi and J. Delhalle, eds), Kluwer, Dordrecht, pp. 49–84

J. D. Morgan, III (1986), 'Convergence properties of Fock's expansions for s-state eigenfunctions of the helium atom', *Theoret. Chim. Acta* **69**, 181–224.

J. D. Morgan, III and W. Kutzelnigg (1993), 'Hund's rules, the alternating rule, and symmetry holes', *J. Phys. Chem.* **97**, 2425–2434.

N. Mousseau and G. T. Barkema (2004), 'Efficient sampling in complex materials at finite temperature: The thermodynamically-weighted activation-relaxation method', submitted.

M. A. Natiello and G. E. Scuseria (1984), 'Convergence properties of Hartree–Fock SCF molecular calculations', *Int. J. Quantum Chem.* **24**, 1039–1049.

A. Neumaier (1997), 'Molecular modeling of proteins and mathematical prediction of protein structure', *SIAM Rev.* **39**, 407–460.

N. C. Nguyen, K. Veroy and A. T. Patera (2005), Certified real-time solution of parametrized PDEs, in *Handbook of Materials Modeling* (R. Catlow, H. Shercliff and S. Yip, eds), Kluwer/Springer, pp. 1523–1558.

P. Nielaba, M. Mareschal and G. Ciccotti, eds (2002), *Bridging the Time Scales: Molecular Simulations for the Next Decade*, Vol. 605 of *Lecture Notes in Physics*, Springer.

A. K. Noor and J. M. Peters (1980), 'Reduced-basis technique for non-linear analysis of structures', *AIAA Journal* **18**, 455–462.

S. Nosé (1984), 'A molecular dynamics method for simulation in the canonical ensemble', *Mol. Phys.* **52**, 255–268.

S. Nosé (1986), 'An extension of the canonical ensemble molecular dynamics method', *Mol. Phys.* **57**, 187–191.

S. Olla, private communication: for an analogous study on canonical and grand-canonical ensembles, see works by N. Cancrini and co-workers.

P. Ordejon, D. A. Drabold and R. M. Martin (1995), 'Linear system-size scaling methods for electronic structure calculations', *Phys. Rev. B* **51**, 1456–1476.

A. Palser and D. Manopoulos (1998), 'Canonical purification of the density matrix in electronic structure calculations', *Phys. Rev. B* **58**, 12704–12711.

R. G. Parr and W. Yang (1989), *Density Functional Theory of Atoms and Molecules*, Oxford University Press.

C. L. Pekeris (1958), 'Ground state of two-electron atoms', *Phys. Rev.* **112**, 1649–1658.

K. A. Peterson, A. K. Wilson, D. E. Woon and T. H. Dunning, Jr. (1997), 'Benchmark calculations with correlated molecular wave functions 12: Core correlation effects on the homonuclear diatomic molecules B_2, F_2', *Theoret. Chim. Acta* **97**, 251–259.

P. Pulay (1982), 'Improved SCF convergence acceleration', *J. Comput. Chem.* **3**, 556–560.

D. Raabe (1998), *Computational Materials Science*, Wiley.

D. C. Rapaport (1995), *The Art of Molecular Dynamics Simulation*, Cambridge University Press.

M. Reed and B. Simon (1975–1980), *Methods of Modern Mathematical Physics*, in 4 volumes, Academic Press.

C. C. J. Roothaan (1951), 'New developments in molecular orbital theory', *Rev. Modern Phys.* **23**, 69–89.

J.-P. Ryckaert, G. Giccotti and H. J. C. Berendsen (1977), 'Numerical integration of the Cartesian equations of motion of a system with constraints: Molecular dynamics of n-alkanes', *J. Comput Phys.* **23**, 327–341.

C. F. Sanz-Navarro and R. Smith (2001), 'Numerical calculations using the hyper-molecular dynamics simulation method', *Comput. Phys. Comm.* **137**, 206.

J. M. Sanz-Serna and M. P. Calvo (1994), *Numerical Hamiltonian Problems*, Chapman and Hall.

V. R. Saunders and I. H. Hillier (1973), 'A "level-shifting" method for converging closed shell Hartree–Fock wavefunctions', *Int. J. Quantum Chem.* **7**, 699–705.

M. Schechter (1981), *Operator Methods in Quantum Mechanics*, North-Holland.

H. B. Schlegel and J. J. W. McDouall (1991), Do you have SCF stability and convergence problems?, in *Computational Advances in Organic Chemistry*, Kluwer Academic, pp. 167–185.

T. Schlick (2002), *Molecular Modeling and Simulation*, Springer.

M. W. Schmidt and K. Ruedenberg (1979), 'Effective convergence to complete orbital bases and to the atomic Hartree–Fock limit through systematic sequences of Gaussian primitives', *J. Chem. Phys.* **71**, 3951–3962.

C. Schütte, A. Fischer, W. Huisinga and P. Deuflhard (1999), 'A direct approach to conformational dynamics based on hybrid Monte Carlo', *J. Comput. Phys.* **151**, 146–168.

C. Schütte, J. Walter, C. Hartmann and W. Huisinga (2004), 'An averaging principle for fast degrees of freedom exhibiting long-term correlations', *SIAM Multiscale Model. Simul.* **2**, 501–526.

C. Schwab and T. von Petersdorff (2004), 'Numerical solution of parabolic equations in high dimensions', *M2AN: Math. Model. Numer. Anal.* **38**, 93–127.

C. Schwartz (1962), 'Importance of angular correlation between atomic electrons', *Phys. Rev.* **126**, 1015–1019.

E. Schwegler and M. Challacombe (1997), 'Linear scaling computation of the Fock matrix', *J. Chem. Phys.* **106**, 5526–5536.

G. E. Scuseria (1999), 'Linear scaling density functional calculations with Gaussian orbitals', *J. Phys. Chem. A* **103**, 4782–4790.

R. Seeger and J. A. Pople (1976), 'Self-consistent molecular orbital methods XVI: Numerically stable direct energy minimization procedures for solution of Hartree–Fock equations', *J. Chem. Phys.* **65**, 265–271.

Y. Shao, C. Saravan, M. Head-Gordon and C. White (2003), 'Curvy steps for density matrix based energy minimization: Application to large-scale self-consistent-field calculations', *J. Chem. Phys.* **118** (14), 6144–6151.

V. B. Shenoy, R. Miller, E. B. Tadmor, R. Phillips and M. Ortiz, (1998), 'Quasicontinuum models of interfacial structure and deformation', *Phys. Rev. Lett.* **80** (4), 742.

V. B. Shenoy, R. Miller, E. B. Tadmor, D. Rodney, R. Phillips and M. Ortiz, (1999), 'An adaptative finite element approach to atomic-scale mechanics: The QuasiContinuum method', *J. Mech. Phys. Solids* **47**, 611.

R. Shepard (1993), 'Elimination of the diagonalization bottleneck in parallel direct-SCF methods', *Theoret. Chim. Acta* **84**, 343–351.

J. C. Slater (1930), 'Atomic shielding constants', *Phys. Rev.* **36**, 57–64.

M. R. Sorensen and A. F. Voter (2000), 'Temperature-accelerated dynamics for simulation of rare events', *J. Chem. Phys.* **112** (21), 9599–9606.

L. Spruch (1991), 'Pedagogic notes on Thomas–Fermi theory (and on some improvements): Atoms, stars and the stability of bulk matter', *Rev. Modern Phys.* **63**, 151–209.

R. E. Stanton (1981*a*), 'The existence and cure of intrinsic divergence in closed shell SCF calculations', *J. Chem. Phys.* **75**, 3426–3432.

R. E. Stanton (1981*b*), 'Intrinsic convergence in closed-shell SCF calculations: A general criterion', *J. Chem. Phys.* **75**, 5416–5422.

E. B. Starikov (1993), 'On the convergence of the Hartree–Fock selfconsistency procedure', *Mol. Phys.* **78**, 285–305.

B. Swirless (1935), 'The relativistic self-consistent field', *Proc. Roy. Soc. A* **152**, 625–649.

B. Swirless (1936), 'The relativistic interaction of two electrons in the self-consistent field method', *Proc. Roy. Soc. A* **157**, 680–696.

A. Szabo and N. S. Ostlund (1982), *Modern Quantum Chemistry: An Introduction to Advanced Electronic Structure Theory*, MacMillan.

E. B. Tadmor, R. Phillips and M. Ortiz (1996), Mixed atomistic and continuum models of deformation in solids, *Langmuir* **12**, 4529–4534.

E. B. Tadmor, M. Ortiz and R. Phillips (1996), 'Quasicontinuum analysis of defects in solids', *Phil. Mag. A* **73**, 1529–1563.

E. B. Tadmor, G. S. Smith, N. Bernstein and E. Kaxiras, (1999), 'Mixed finite element and atomistic formulation for complex crystals', *Phys. Rev. B* **59** (1), 235.

S. Teufel (2003), *Adiabatic Perturbation Theory in Quantum Dynamics*, Vol. 1821 of *Lecture Notes in Mathematics*, Springer.

W. Thirring (1983), *A Course in Mathematical Physics*, in 4 volumes, Springer.

N. Troullier and J. L. Martins (1990), 'A straightforward method for generating soft transferable pseudopotentials', *Solid State Comm.* **74**, 613–616.

M. E. Tuckerman (2002), '*Ab initio* molecular dynamics: Basic concepts, current trends and novel applications', *J. Phys. Condens. Matter* **14**, R1297–R1355.

M. E. Tuckerman and G. J. Martyna (2000), 'Understanding modern molecular dynamics: Techniques and applications', *J. Phys. Chem.* **104**, 159–178.

P. Tupper (2005), 'Ergodicity and the numerical simulation of Hamiltonian systems', *SIAM J. Appl. Dyn. Syst.*, to appear.

C. Valdemoro (1992), 'Approximating the second-order reduced density matrix in terms of the first-order one', *Phys. Rev. A* **45**, 4462–4467.

C. Valdemoro, L. M. Tel and E. Perez-Romero (2000), 'N-representability problem within the framework of the contracted Schrödinger equation', *Phys. Rev. A* **61**, 032507–032700.

E. Vanden-Eijnden (2003), 'Numerical techniques for multi-scale dynamical system with stochastic effects', *Comm. Math. Sci.*, **1** (2), 385–391.

D. Vanderbilt (1990), 'Soft self-consistent pseudopotentials in a generalized eigenvalue formalism', *Phys. Rev. B* **41**, 7892–7895.

L. Verlet (1967), 'Computer "experiments" on classical fluids I: Thermodynamical properties of Lennard–Jones molecules', *Phys. Rev.* **159**, 98–103.

A. F. Voter (1997), 'Hyperdynamics: Accelerated molecular dynamics of infrequent events', *Phys. Rev. Lett.* **78**, 3908.

A. F. Voter (1998), 'Parallel replica method for dynamics of infrequent events', *Phys. Rev. B*, *Rapid Comm.* **57** (22), 57–60.

A. F. Voter and M. R. Sorensen, (1999), 'Accelerating atomistic simulations of defect dynamics: Hyperdynamics, parallel replica dynamics and temperature-accelerated dynamics', *Mat. Res. Soc. Symp. Proc.* **538**, 427–439.

P. Walters (1982), *An Introduction to Ergodic Theory*, Vol. 79 of *Graduate Texts in Mathematics*, Springer.

G. A. Worth and M. A. Robb (2002), 'Applying direct molecular dynamics to non-adiabatic systems', *Adv. Chem. Phys.* **124**, 355–431.

H. Yserentant (2003), On the electronic Schrödinger equation, Lecture Notes, Universität Tübingen.

H. Yserentant (2004*a*), 'On the regularity of the electronic Schrödinger equation in Hilbert spaces of mixed derivatives', *Numer. Math.* **98**, 731–759.

H. Yserentant (2004*b*), 'Sparse grid spaces for the numerical solution of the electronic Schrödinger equation', *Numer. Math.*, submitted.

M. C. Zerner and M. Hehenberger (1979), 'A dynamical damping scheme for converging molecular SCF calculations', *Chem. Phys. Lett.* **62**, 550–554.

Z. Zhao, B. J. Braams, M. Fukuda, M. L. Overton and J. K. Percus (2004), 'The reduced density matrix method for electronic structure calculations and the role of three-index representability conditions', *J. Chem. Phys.* **120** (5), 2095–2104.

D. Zuckerman and T. Woolf (1999), 'Dynamic reaction paths and rates through importance-sampled stochastic dynamics', *J. Chem. Phys.* **111** (21), 9475–9484.