From Benchmarking to Periodic Fock Exchange in the Auxiliary Density Matrix Method via k-Point Sampling with Gaussian Basis Sets

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Abstract

While Gaussian basis sets have been successfully used in various electronic structure codes for elucidation of structures and processes in computational chemistry, they are not nearly as popular in solid state physics. There are various reasons for this, one of them being that in comparison to the plane wave approach there is no single numerical parameter like the cutoff energy, which can be used to systematically increase the accuracy of the calculation. Furthermore do basis sets depend either on a specific method, or can only be used together with matching pseudopotentials in the case of valence basis sets. Finally, in contrast to a molecular setting are electrons in periodic systems often not localised and therefore many optimisations used with atom-centred Gaussian basis sets do not work as efficiently. The number of codes targeting the intersection of computational chemistry and solid efficiently state physics is therefore small, as is the availability of universally applicable basis set families.

In this thesis we are evaluating the recently revised MOLOPT basis set with pseudopotentials and all-electron calculations in both molecular and condensed matter settings, for three different functionals in Density Functional Theory, each on a different rung on "Jacob's Ladder". Once again, we demonstrate the outstanding performance of the MOLOPT basis sets for molecular systems and show that [Gaussian-type Orbital](#page-12-0) codes perform reasonably well for solids, and that this can also be achieved with a universal basis set family.

We further investigate the required framework for running and analysing such large benchmark calculations to pave the way for fully automated benchmarking and iterative development of Gaussian basis sets and pseudopotentials. The implementation of the of the actual benchmarks with three different approaches leads to the development of Python-based parser and input generation libraries and utilities for CP2K, as well as contributions and extensions to the Automated Interactive Infrastructure and Database (AiiDA).

To extend the support for periodic systems further within CP2K, we then progress to implement **k**-point sampling in CP2K's [Hartree-Fock Exchange,](#page-12-1) required to run calculations with Hybrid functionals. And to be able to make this usable on realistic systems, we extend the Auxiliary Density Matrix Method to **k**-point sampling as well. Together, this novel implementation can be used as a reference implementation and stepping stone for the development of more efficient algorithms for the [Hartree-Fock](#page-12-2) approximation and Hybrid functionals in [Density Functional Theory](#page-12-3) with CP2K.

Kurzzusammenfassung

Während Gaußsche Basissätze erfolgreich in verschiedenen Elektronenstrukturprogrammen zur Aufklärung von Strukturen und Prozessen in der rechnergestützten Chemie eingesetzt werden, sind sie in der Festkörperphysik weniger verbreitet. Dafür gibt es mehrere Gründe, einer davon ist, dass es im Vergleich zum ebenen Wellen Ansatz keine einzelne numerische Grösse wie die Grenzwert Energie gibt, welche dazu benutzt werden kann um systematisch die Genauigkeit der Rechnung zu erhöhen. Im Weiteren hängen die Basissätze entweder von einer spezifischen Methode ab, oder können im Fall von Valenz Basis Sätzen nur mit passenden Pseudopotentialen verwendet werden. Schließlich sind die Elektronen in periodischen Systemen im Gegensatz zu molekularen Systemen oft nicht lokalisiert, so dass viele Optimierungen, die mit atomzentrierten Gaußschen Basissätzen verwendet werden, nicht so effizient funktionieren. Die Anzahl der Softwareprogramme welche auf die Schnittstelle zwischen rechnergestützten Chemie und Festkörperphysik abzielen ist demzufolge klein, sowie die Verfügbarkeit von universell einsetzbaren Basissatzfamilien.

In dieser Arbeit evaluieren wir die kürzlich revidierte MOLOPT Basissatzfamilie mit Pseudopotentialen und Gesamtelektronenberechnungen für molekulare Systeme als auch für Systeme der kondensierten Matterie, für drei verschiedene Funktionale der Dichtefunktionaltheorie, jede auf einer anderen Sprosse der "Jacob's Ladder". Damit demonstrieren wir einmal mehr die hervorragende Leistung der MOLOPT-Basissätze für molekulare Systeme und zeigen, dass Codes welche Orbitale vom Gauß-Typ für Festkörper gut funktionieren, und dass dies auch mit einer universellen Basissatzfamilie erreicht werden kann.

Darüber hinaus untersuchen wir den erforderlichen Rahmen für die Durchführung und Analyse solch großer Benchmark-Berechnungen um den Weg für ein vollautomatisches Benchmarking und die iterative Entwicklung von Gaußschen Basissätzen und Pseudopotentialen zu ebnen. Die Implementierung der aktuellen Benchmarks mit drei verschiedenen Ansätzen führt zur Entwicklung von Python-basierten Parser- und Eingabegenerierungsbibliotheken und Dienstprogrammen für CP2K, sowie Beiträge und Erweiterungen zur Automated Interactive Infrastructure and Database (AiiDA).

Um die Unterstützung für periodische Systeme in CP2K weiter auszubauen, implementieren wir **k**-Punkt Abtastung in CP2Ks Hartree-Fock Austausch, die für Berechnungen mit Hybridfunktionalen erforderlich ist. Und um dies für realistische Systeme nutzbar zu machen, erweitern wir die Auxiliary Density Matrix Method (ADMM) ebenfalls auf **k**-Punkt Abtastung. Zusammengenommen kann diese neuartige Implementierung als Referenzimplementation und Sprungbrett für die Entwicklung von effizienteren Algorithmen für die Hartree-Fock-Näherung und Hybridfunktionale in der Dichtefunktionaltheorie mit CP2K verwendet werden.

Academic Record

- ▶ Thomas D. Kühne, Marcella Iannuzzi, Mauro Del Ben, Vladimir V. Rybkin, Patrick Seewald, Frederick Stein, Teodoro Laino, Rustam Z. Khaliullin, Ole Schütt, Florian Schiffmann, Dorothea Golze, Jan Wilhelm, Sergey Chulkov, Mohammad Hossein Bani-Hashemian, Valéry Weber, Urban Borštnik, Mathieu Taillefumier, Alice Shoshana Jakobovits, Alfio Lazzaro, Hans Pabst, Tiziano Müller, Robert Schade, Manuel Guidon, Samuel Andermatt, Nico Holmberg, Gregory K. Schenter, Anna Hehn, Augustin Bussy, Fabian Belleflamme, Gloria Tabacchi, Andreas Glöß, Michael Lass, Iain Bethune, Christopher J. Mundy, Christian Plessl, Matt Watkins, Joost VandeVondele, Matthias Krack, and Jürg Hutter. "CP2K: An Electronic Structure and Molecular Dynamics Software Package - Quickstep: Efficient and Accurate Electronic Structure Calculations." In: *J. Chem. Phys.* 152.19 (May 21, 2020)
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	- Migration from Subversion to Git, general tooling improvements (*XV.F*)
- ▶ Sebastiaan P. Huber, Spyros Zoupanos, Martin Uhrin, Leopold Talirz, Leonid Kahle, Rico Häuselmann, Dominik Gresch, Tiziano Müller, Aliaksandr V. Yakutovich, Casper W. Andersen, Francisco F. Ramirez, Carl S. Adorf, Fernando Gargiulo, Snehal Kumbhar, Elsa Passaro, Conrad Johnston, Andrius Merkys, Andrea Cepellotti, Nicolas Mounet, Nicola Marzari, Boris Kozinsky, and Giovanni Pizzi. "AiiDA 1.0, a Scalable Computational Infrastructure for Automated Reproducible Workflows and Data Provenance." In: *Sci Data* 7.1 (1 Sept. 8, 2020)
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	- Development of practical taxonomy, classification.

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Contents

Acronyms

ADMM Auxiliary Density Matrix Method. [2,](#page-1-0) [22](#page-35-0), [24–](#page-37-0)[26](#page-39-0), [60,](#page-73-2) [61](#page-74-1), [67](#page-80-1)[–70](#page-83-1), [72,](#page-85-0) [74](#page-87-0)–[76](#page-89-0), [78,](#page-91-2) [79](#page-92-2), [81,](#page-94-1) [83](#page-96-0) **AE** All-Electron. [1,](#page-0-0) [2](#page-1-0), [16,](#page-29-0) [17](#page-30-0), [27,](#page-40-2) [47](#page-60-2), [61](#page-74-1) **API** Application Programming Interface. [31,](#page-44-0) [45](#page-58-0)

BSSE basis set superposition error. [17](#page-30-0) **BvK** Born-von Kármán. [18,](#page-31-1) [19](#page-32-0) **BZ** Brillouin Zone. [18](#page-31-1)

CO Crystalline Orbital. [19](#page-32-0)

DFT Density Functional Theory. [i](#page-2-1), [1,](#page-0-0) [8,](#page-21-1) [13](#page-26-1), [14,](#page-27-0) [16](#page-29-0), [17,](#page-30-0) [20](#page-33-1), [25](#page-38-1)[–27](#page-40-2), [67](#page-80-1) **DIIS** Direct Inversion of the Iterative Subspace. [68](#page-81-0), [75](#page-88-1)

ERI Electron Repulsion Integral. [2](#page-1-0), [13,](#page-26-1) [14](#page-27-0), [17,](#page-30-0) [20](#page-33-1), [21,](#page-34-1) [25](#page-38-1), [26,](#page-39-0) [67](#page-80-1)–[69](#page-82-2), [73,](#page-86-1) [75](#page-88-1), [76,](#page-89-0) [79](#page-92-2)

FAM Fabric-attached memory. [76](#page-89-0) **FFT** Fast-Fourier Transformation. [14](#page-27-0) **FP-LAPW** Full-Potential Linearized Augmented Plane Wave method. [2](#page-1-0), [15,](#page-28-0) [16](#page-29-0), [51,](#page-64-2) [56](#page-69-1), [77](#page-90-2)

GAPW Gaussian and Augmented Planewave. [1](#page-0-0), [2](#page-1-0), [16,](#page-29-0) [28](#page-41-1), [49,](#page-62-0) [50](#page-63-1), [53,](#page-66-1) [59](#page-72-1), [60,](#page-73-2) [69](#page-82-2), [77](#page-90-2) **GGA** Generalized Gradient Approximation. [2,](#page-1-0) [10](#page-23-1), [12,](#page-25-0) [25](#page-38-1), [28](#page-41-1) **GPW** Gaussian and Plane Waves Method. [1](#page-0-0), [2,](#page-1-0) [14](#page-27-0), [16,](#page-29-0) [19](#page-32-0), [49,](#page-62-0) [50](#page-63-1), [55,](#page-68-1) [60](#page-73-2), [76,](#page-89-0) [85](#page-98-1) **GTO** Gaussian-type Orbital. [i](#page-2-1), [1,](#page-0-0) [15](#page-28-0), [16,](#page-29-0) [26](#page-39-0), [27,](#page-40-2) [68](#page-81-0), [77–](#page-90-2)[79](#page-92-2)

h-BN Hexagonal boron nitride. [69–](#page-82-2)[75](#page-88-1) **HF** Hartree-Fock. [i,](#page-2-1) [13](#page-26-1), [19,](#page-32-0) [68](#page-81-0) **HFX** Hartree-Fock Exchange. [i,](#page-2-1) [2,](#page-1-0) [7](#page-20-0), [8,](#page-21-1) [17](#page-30-0), [20,](#page-33-1) [25](#page-38-1), [26,](#page-39-0) [67](#page-80-1)[–70,](#page-83-1) [72](#page-85-0), [73,](#page-86-1) [75](#page-88-1), [76,](#page-89-0) [78](#page-91-2), [79](#page-92-2) **HFXk** Hartree-Fock Exchange with **k**-point. [2](#page-1-0), [69](#page-82-2) **HPC** High-performance computing. [v](#page-6-1), [32,](#page-45-1) [80](#page-93-0)

ISDF interpolative separable density fitting. [68](#page-81-0), [69](#page-82-2)

JSON JavaScript Object Notation. [30](#page-43-1), [31,](#page-44-0) [35](#page-48-1), [37](#page-50-0)

LCAO linear combination of atomic orbitals. [19](#page-32-0), [22](#page-35-0) **LDA** Local Density Approximation. [25](#page-38-1) **LiH** Lithiumhydrid. [69](#page-82-2)–[71,](#page-84-0) [75](#page-88-1)

MD molecular dynamics. [17](#page-30-0), [20,](#page-33-1) [41](#page-54-1) **MO** Molecular Orbital. [6](#page-19-0), [13,](#page-26-1) [14](#page-27-0), [16,](#page-29-0) [19](#page-32-0), [20,](#page-33-1) [22](#page-35-0), [23,](#page-36-0) [25](#page-38-1), [68](#page-81-0)

occ-RI-K occupied orbital [Resolution of Identity \(RI\)](#page-12-6)-K. [68](#page-81-0)

PAW Projector Augmented-Wave method. [16](#page-29-0) **PGF** primitive Gaussian function. [21](#page-34-1) **PP** pseudopotential. [1](#page-0-0), [2,](#page-1-0) [14](#page-27-0)[–16,](#page-29-0) [27](#page-40-2), [78,](#page-91-2) [79](#page-92-2), [81,](#page-94-1) [85](#page-98-1), [105](#page-118-0) **PW** plane wave. [1,](#page-0-0) [2,](#page-1-0) [14](#page-27-0)–[16](#page-29-0), [19,](#page-32-0) [77](#page-90-2), [79](#page-92-2)

REST Representational state transfer. [30,](#page-43-1) [31](#page-44-0) **RI** Resolution of Identity. [xi,](#page-12-7) [68](#page-81-0), [76,](#page-89-0) [79](#page-92-2)

SCF self-consistent field. [20,](#page-33-1) [26](#page-39-0), [41,](#page-54-1) [74](#page-87-0), [75,](#page-88-1) [79](#page-92-2) **SIE** self-interaction error. [8,](#page-21-1) [12](#page-25-0)

xii Acronyms

SMDB Small Molecules Database. [28,](#page-41-1) [32](#page-45-1), [48,](#page-61-1) [60,](#page-73-2) [78](#page-91-2), [81–](#page-94-1)[83](#page-96-0)

TC Truncated Coulomb. [75](#page-88-1) **TTS** time to solution. [73](#page-86-1)

XC Exchange-Correlation. [14,](#page-27-0) [16](#page-29-0)

Introduction

Mankind's development has historically been driven by the discovery of elements and materials, starting from copper up to the current age of silicon. However, since the first predictions in the periodic table of elements by Mendeleev, this has started to change. Nowadays experimental discoveries in the materials sciences are not only elucidated by accompanying computational simulations, but guided by them. To do so, one has to solve the famous Schrödinger equation, describing the behaviour of quantum particles such as the electrons. There exist many possible ways to do so, each with their own strengths and weaknesses. While [plane wave \(PW\)](#page-12-8) approaches cater more to the needs of the solid state community, approaches using [Gaussian-type Orbital \(GTO\)](#page-12-0) orbitals permit direct insight into the chemistry involved, such as chemical bonds. As one of the few codes making use of a combined [GTO](#page-12-0) and [PW](#page-12-8) basis approach in what is called the [Gaussian and Plane Waves Method \(GPW\)](#page-12-9), the CP2K software package can excellently target the intersection of both fields. While [GTO](#page-12-0) based codes have been used successfully at least since the 60's in computational chemistry, they have generated a Zoo of different basis sets optimised for various levels of theory, methods and use cases. And although generating a basis set family – a series of increasingly larger number of basis functions – for a specific case is not difficult anymore (and has been a common task), developing one which is robust enough such that it can be used for a wide range of tasks is not trivial. Unlike with [PW](#page-12-8), there is also no rigorous way to proof that extending a [GTO](#page-12-0) basis set will improve the result, other than by computation. But as the possibilities for computation have grown – quantum chemistry and classical molecular dynamics make up for 4̃0% of all high-performance computation time –, so have the use cases. Meaning that a basis set family nowadays should ideally cover the full periodic table, as well as various functionals of [Density Functional Theory \(DFT\)](#page-12-3). Finally, running a benchmark on such a large basis set family has its own challenges, requiring a large number calculations on different systems to cover all of the above.

This dissertation thus encompasses three distinct areas of computation.

In the first section, we concentrate on the fundamental components needed to run a large amount of calculations for evaluating basis sets and pseudopotentials for various systems and functionals, and how they can be executed effectively and dependably. This involves the development of a minimal domain-specific workflow manager, along with required foundation libraries for automated input configuration generation, output data parsing, as well as data transport and load distribution. By using a proper component-based software architecture we can then integrate the tools in the much more general AiiDA workflow management system to improve the integration of CP2K.

We then progress to applying the developed tools to run two different benchmarks to evaluate the recently revised MOLOPT valence basis sets alongside their also revised Gödecker-Teter-Hutter [pseudopotential \(PP\)](#page-12-10) with the [GPW](#page-12-9) method, and the newly added [All-Electron \(AE\)](#page-12-11) MOLOPT basis set using the[Gaussian and Augmented Planewave \(GAPW\)](#page-12-12) method. First, a database of small molecules will be used to compare the performance of CP2K in a molecular setting, with reference calculations obtained using the G16 software package. This benchmark is performed for three different functionals on different rungs of *Jacob's Ladder of Density Functional Approximations*: [Generalized Gradient Approximation \(GGA\),](#page-12-13) meta-[GGA](#page-12-13) and Hybrid functionals, using PBE, TPSS and PBE0. For the Hybrid functional PBE0 also the effect of using [Auxiliary Density Matrix](#page-12-14) [Method \(ADMM\)](#page-12-14) is investigated. This allows us to draw a complete picture of the performance of the complete MOLOPT basis set in a molecular setting, as well as investigate the transferability of basis set and pseudopotential within a rung. Additionally, we identify important requirements for running such benchmarks in an automated fashion.

The second benchmark is then geared towards the solid state use case by using the Δ-test metric and comparing against published high-precision results. Given the larger number of calculations, it makes full use of our own workflow manager, as well as AiiDA together with custom extensions. Since this benchmark is aimed at determining accuracy between different codes or methods and consists only of elemental crystals, it draws its significance even more from single-point comparisons with reference values than the previous benchmark. To extend this benchmarks towards covering different functionals, we therefore devise and implement a strategy to generate all data starting from the high-accuracy [Full-Potential Linearized Augmented Plane Wave method \(FP-LAPW\)](#page-12-15) method (available via the integration of SIRIUS) to [AE](#page-12-11) [GAPW](#page-12-12) calculations to [PP](#page-12-10) calculations with [PW](#page-12-8) (again via SIRIUS) and [GPW](#page-12-9). This reference is obtained with the PBE functional and we validate the approach with the closely related PBEsol.

The third and final part of this thesis covers the enabling of the previously mentioned solid state benchmarks to be run with CP2K using Hybrid functionals such as PBE0. While [Hartree-Fock Exchange \(HFX\)](#page-12-1) has been implemented in CP2K since quiet some time, it only covers the periodic case without **k**-point sampling. A supercell approach could be employed to sample the Brillouin zone instead, but this supercell must become very large to reach the same **k**-point density as with direct **k**-point sampling, rendering such calculations prohibitively expensive. The rate limiting step in this calculation is the number of [Electron Repulsion Integral \(ERI\)](#page-12-16) which have to be calculated for the [HFX,](#page-12-1) which depends highly on both size and type of the basis set. Within a [Hartree-Fock Exchange with](#page-12-17) **k**[point \(HFX](#page-12-17)**k**) calculation this becomes even more pronounced as some of the techniques employed previously – namely the caching of summed-up four-centre [ERI](#page-12-16) – can not be applied anymore due to the sheer amount of such [ERIs](#page-12-16) and their associated storage requirement. And since the goal is to calculate solid state – including metallic – systems, screening on the density matrix to reduce the number of quartets to calculate becomes ineffective. Which is why we have not only added **k**-point-support to [HFX](#page-12-1), but also extended the [ADMM](#page-12-14) to support **k**-point calculations. By employing a smaller (and less diffuse) auxiliary basis set, it is possible to significantly lower the number of primitive basis functions, making such calculations feasible.

Theory 2.

In this chapter, we are reviewing the required theory for the Density Functional Theory (DFT) and the Hartree-Fock approximation when solving the Schrödinger equation of electronic structure theory. We will furthermore look into the Auxiliary Density Matrix Method to reduce the computational effort and – more importantly – its extension to periodic **k**-point Hartree-Fock theory, permitting the use of ADMM for condensed matter systems. Additionally, a short recapitulation of Gaussiantype orbitals in electronic structure theory in the form of the Gaussian and plane-waves (GPW) method will be presented, together with the mentioning of pseudopotentials and basis sets since these have been under investigation as part of this thesis.

A more stringent introduction into the matter can be found in the usual textbooks[[6–](#page-122-0)[11\]](#page-122-1)

2.1. Hartree-Fock Theory

To calculate the electronic structure of molecules and solids we are trying to solve the time-independent Schrödinger equation in the Born-Oppenheimer (BO) approximation of fixed atomic nuclei, which is

$$
\mathcal{H}\psi = E\psi \tag{2.1}
$$

and where the (non-relativistic) electronic Hamilton operator in atomic units[[7\]](#page-122-2) is written as

$$
\mathcal{H} = -\sum_{i=1}^{N} \frac{1}{2} \nabla_i^2 - \sum_{i=1}^{N} \sum_{A=1}^{M} \frac{Z_A}{r_{iA}} + \sum_{i=1}^{N} \sum_{j>i}^{N} \frac{1}{r_{ij}}.
$$
 (2.2)

The terms of the Hamiltonian are in the order of appearance: the kinetic energy of the electrons, the Coulomb terms of the attraction between electrons and nuclei and the electron-electron interaction, with r_{ii} and r_{iA} the distance between the *i*-th and *j*-th electron, respectively the *i*-th electron and the A -th nucleus, and N and M the number of electrons and nuclei.

As part of the BO approximation, we can neglect the contribution of the kinetic energy of the nuclei as the electrons can be assumed to adjust themselves immediately compared to the time frame in which the nuclei change position. Given that the proton-electron mass ratio is $\mu = \frac{m_{\mu}}{r}$ $\frac{m_p}{m_e} \approx$ 1836 the inverse effect can also be neglected. Since the Coulomb term of the nucleus-nucleus interaction can also be assumed to be constant, it has been omitted as well as it would only add a constant shift to the energy.

The general form of ψ is a many-body 4N-dimensional wavefunction $\psi(\mathbf{x}_1, \mathbf{x}_2, ..., \mathbf{x}_N)$ with each \mathbf{x}_i consisting of three real space components and one spin component $\mathbf{x}_i = \{\mathbf{r}_i, \omega_i\}$. Since this is not solvable in useful

time for non-trivial systems we need a different ansatz. Quantum mechanics demands that for Fermionic particles (electrons in our case) the wavefunction must be totally antisymmetric

$$
\psi(\mathbf{x}_1, ..., \mathbf{x}_i, ..., \mathbf{x}_j, ..., \mathbf{x}_N) = -\psi(\mathbf{x}_1, ..., \mathbf{x}_j, ..., \mathbf{x}_i, ..., \mathbf{x}_N),
$$
 (2.3)

which means that the simple Hartree product ansatz of

$$
\psi(\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N) = \chi_1(\mathbf{x}_1) \chi_2(\mathbf{x}_2) \cdots \chi_N(\mathbf{x}_N),
$$
\n(2.4)

where $\chi_i(\mathbf{x}_j)$ are single-electron wavefunctions, is insufficient as it would violate that requirement. From Linear Algebra we know that a determinant is totally antisymmetric and thus arrive at the single-determinant Hartree-Fock ansatz for the wavefunction in form of a Slater determinant

$$
\psi_{\text{HF}}(\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N) = \frac{1}{\sqrt{N!}} \begin{vmatrix} \chi_1(\mathbf{x}_1) & \chi_2(\mathbf{x}_1) & \dots & \chi_N(\mathbf{x}_1) \\ \chi_1(\mathbf{x}_2) & \chi_2(\mathbf{x}_2) & \dots & \chi_N(\mathbf{x}_2) \\ \vdots & \vdots & \ddots & \vdots \\ \chi_1(\mathbf{x}_N) & \chi_2(\mathbf{x}_N) & \dots & \chi_N(\mathbf{x}_N) \end{vmatrix} . \tag{2.5}
$$

There are of course multiple possible determinants such that a complete solution should encompass all possible ones, which is the point of the Full Configuration Interaction approach, but which we are not going to pursue further.

To obtain the energy from the Schrödinger equation we take a look at the expectation value of the Hamiltonian

$$
\langle \psi | \mathcal{H} | \psi \rangle = \langle \psi | E | \psi \rangle \Rightarrow E[\psi] = \frac{\langle \psi | \mathcal{H} | \psi \rangle}{\langle \psi | \psi \rangle}, \tag{2.6}
$$

with the usual definition of the Dirac notation of the expectation value

$$
\langle \psi | \mathscr{A} | \psi \rangle = \int \psi^*(\mathbf{x}) \mathscr{A}(\mathbf{x}) \psi(\mathbf{x}) d\mathbf{x}.
$$
 (2.7)

The variational principle dictates the existence of a uniquely defined energy value E_0 – the ground state energy – along with its ground state wave function ψ_0 for which for any other trial wave function ψ the inequality $E[\psi] \ge E[\psi_0] = E_0$ holds. Based on this we define the Hartree-Fock energy as the variational minimum

$$
E_{\text{HF}} := \min_{\chi_i} \left\langle \psi_{\text{HF}} \, | \, \mathcal{H} \, | \, \psi_{\text{HF}} \right\rangle \tag{2.8}
$$

Additionally, we mandate that the χ_i in this minimization procedure form an orthonormal set (which will allow us to apply the Slater-Condon rules for the one- and two-body integrals), e.g.

$$
\int \chi_i^*(\mathbf{x}) \chi_j(\mathbf{x}) d\mathbf{x} = \delta_{ij}.
$$
 (2.9)

Inserting the electronic Hamiltonian of [Equation](#page-16-2) [2.2](#page-16-2) in [Equation](#page-17-0) [2.8](#page-17-0) then yields

$$
E_{\text{HF}} = \langle \psi_{\text{HF}} | \mathcal{H} | \psi_{\text{HF}} \rangle
$$

\n
$$
= \sum_{i}^{N} \underbrace{\int \chi_{i}^{*}(\mathbf{x}) \left[-\frac{1}{2} \nabla^{2} + \nu(\mathbf{x}) \right] \chi_{i}(\mathbf{x}) d\mathbf{x}}_{=:H_{i}}
$$

\n
$$
+ \frac{1}{2} \sum_{i,j,i \neq j}^{N} \underbrace{\iint \chi_{i}(\mathbf{x}_{1}) \chi_{i}^{*}(\mathbf{x}_{1}) \frac{1}{\|\mathbf{r}_{2} - \mathbf{r}_{1}\|} \chi_{j}^{*}(\mathbf{x}_{2}) \chi_{j}(\mathbf{x}_{2}) d\mathbf{x}_{1} d\mathbf{x}_{2}}_{=:J_{ij}}
$$

\n
$$
- \frac{1}{2} \sum_{i,j,i \neq j}^{N} \underbrace{\iint \chi_{i}^{*}(\mathbf{x}_{1}) \chi_{j}(\mathbf{x}_{1}) \frac{1}{\|\mathbf{r}_{2} - \mathbf{r}_{1}\|} \chi_{i}(\mathbf{x}_{2}) \chi_{j}^{*}(\mathbf{x}_{2}) d\mathbf{x}_{1} d\mathbf{x}_{2}}_{=:K_{ij}}
$$

\n
$$
- \underbrace{\iint \chi_{i}^{*}(\mathbf{x}_{1}) \chi_{j}(\mathbf{x}_{1}) \frac{1}{\|\mathbf{r}_{2} - \mathbf{r}_{1}\|} \chi_{i}(\mathbf{x}_{2}) \chi_{j}^{*}(\mathbf{x}_{2}) d\mathbf{x}_{1} d\mathbf{x}_{2}}_{=:K_{ij}}
$$

\n(2.10)

where $v(x)$ as the external potential captures the electron-nuclei interaction.

By restricting ourselves to the closed-shell approximation where each orbital is double occupied (hence we always have an even number of electrons) and a product ansatz in which we express the spin orbitals as a product of spatial orbitals and spin functions $\chi_i(\mathbf{x}) = \chi_i(\mathbf{x}) \alpha_i(\omega_i)$, [Equation](#page-18-0) [2.10](#page-18-0) can be simplified to

$$
E_{\rm HF} = 2 \sum_{i=1}^{N/2} H_i(\mathbf{r}) + \sum_{i,j}^{N/2} (2J_{ij}(\mathbf{r}) - K_{ij}(\mathbf{r})), \qquad (2.11)
$$

where the Hartree- and Exchange-integrals J, K but also the one-particle kinetic energy term H depend only on the spatial coordinates. Based on those integrals J and K we can now define new operators j and k with the following actions on a function $f(\mathbf{r})$

$$
j(\mathbf{r}_1)f(\mathbf{r}_1) = 2\sum_{j}^{N/2} \int f(\mathbf{r}_1) \frac{1}{\|\mathbf{r}_2 - \mathbf{r}_1\|} \chi_j(\mathbf{r}_2) \chi_j^*(\mathbf{r}_2) d\mathbf{r}_2
$$

$$
k(\mathbf{r}_1)f(\mathbf{r}_1) = \sum_{j}^{N/2} \int \chi_j^*(\mathbf{r}_1) \frac{1}{\|\mathbf{r}_2 - \mathbf{r}_1\|} \chi_j(\mathbf{r}_2)f(\mathbf{r}_1) d\mathbf{r}_2
$$
 (2.12)

which in turn lets us define the Fock operator

$$
F(\mathbf{r}) = -\frac{1}{2}\nabla^2 + v(\mathbf{r}) + j(\mathbf{r}) - k(\mathbf{r}),
$$
 (2.13)

and leads us to the Hartree-Fock eigenvalue equations

$$
F(\mathbf{r})\chi_i(\mathbf{r}) = \sum_j \epsilon_{ij}\chi_j(\mathbf{r}).
$$
\n(2.14)

Since j and k depend on a sum over an integral over spatial orbitals, the Hartree-Fock theory is inherently orbital-dependant, yet $j - k$ can be interpreted in the same way as v , as an average potential controlling the behaviour of each orbital. This orbital dependency, despite the meanfield characteristics of the operators, can thus computationally only be resolved by an iterative procedure, starting from an initial guess for the orbitals (for example for isolated atoms) and repeated until consistency is reached, recalculating $j - k$ again from the newly obtained orbitals χ_i . This approach is known as a self-consistent field (SCF) method.

To be able to solve the Hartree-Fock [Equation](#page-18-1) [2.14](#page-18-1) practically, we have to choose a basis in which we are going to express our orbitals, allowing us to solve the SCF problem by optimizing the coefficients. With $\{\phi_{\mu}(\mathbf{r})\}$ as our basis we write

$$
\chi_i(\mathbf{r}) = \sum_{\mu} C_{\mu i} \phi_{\mu}(\mathbf{r}) \tag{2.15}
$$

and call the C_{ui} the [Molecular Orbital \(MO\)](#page-12-18) coefficients. The variational minimisation therefore becomes a linear variational problem, solveable by diagonalisation of the corresponding operator matrix.

As for the previously defined Hartree-Fock equations: Given that the Fock operator is a Hermitian operator, we can always find a unitary transformation U, which diagonalizes ϵ_{ij} , such that the Hartree-Fock equations can be written in the canonical form (e.g. without a sum) of

$$
F(\mathbf{r})\chi_i(\mathbf{r}) = \epsilon_i \chi_i(\mathbf{r}).
$$
\n(2.16)

Inserting the basis expansion then leads from

$$
F(\mathbf{r})\sum_{\mu}C_{\mu i}\phi_{\mu}(\mathbf{r})=\epsilon_{i}\sum_{\mu}C_{\mu i}\phi_{\mu}(\mathbf{r}).
$$
\n(2.17)

by integrating after multiplying with ϕ^\ast_ν to

$$
C_{\mu i} \underbrace{\int \phi_{\nu}^{*}(\mathbf{r}) F(\mathbf{r}) \phi_{\mu}(\mathbf{r}) d\mathbf{r}}_{=:F_{\nu\mu}} = \epsilon_{i} \sum_{\mu} C_{\mu i} \underbrace{\int \phi_{\nu}^{*}(\mathbf{r}) \phi_{\mu}(\mathbf{r}) d\mathbf{r}}_{=:S_{\nu\mu}}
$$
\n
$$
\Leftrightarrow \sum_{\mu} F_{\nu\mu} C_{\mu i} = \epsilon_{i} \sum_{\mu} S_{\nu\mu} C_{\mu i}.
$$
\n(2.18)

The final equations are nothing else but a matrix equation written out, in proper matrix notation they read as follows and are called the *Roothan equations*

$$
FC = \epsilon SC,\tag{2.19}
$$

where ϵ is a diagonal matrix with the ϵ_i on its diagonal. When using a finite-sized basis set, this is therefore a solvable matrix eigenvalue problem. F and S are consequently called the Fock and Overlap matrices.

As we will see later, we will need the isolated [Hartree-Fock Exchange](#page-12-1) [\(HFX\)](#page-12-1) energy term K_{ii} from [Equation](#page-18-0) [2.10](#page-18-0) in this basis set representation (for the closed-shell case). The other components we will also need are the electron density $\rho(\mathbf{r})$ and the corresponding density matrix P. They let us write the [HFX](#page-12-1) energy in a more concise way.

As we know from general quantum mechanics, the square modulus of the wave function can be interpreted as a probability density (in our case) to find an electron at position **r**. Again for the closed-shell case and expressed in our basis $\{\phi_i\}$ this means

$$
\rho(\mathbf{r}) = 2 \sum_{i}^{N/2} |\chi_i(\mathbf{r})|^2
$$

= $2 \sum_{i}^{N/2} \chi_i^*(\mathbf{r}) \chi_i(\mathbf{r})$
= $\sum_{\mu\nu} 2 \sum_{i}^{N/2} C_{\mu i} C_{\nu i} \phi_{\mu}(\mathbf{r}) \phi_{\nu}^*(\mathbf{r})$
= $\sum_{\mu\nu} P_{\mu\nu} \qquad \phi_{\mu}(\mathbf{r}) \phi_{\nu}^*(\mathbf{r}).$ (2.20)

The exchange term elements of the Fock matrix then becomes

$$
F_{\mu\sigma}^{\mathbf{x}} = -\frac{1}{2} \sum_{\nu\lambda} P_{\nu\lambda} \iint \phi_{\mu}^{*}(\mathbf{r}_{1}) \phi_{\nu}(\mathbf{r}_{1}) \frac{1}{|\mathbf{r}_{2} - \mathbf{r}_{1}|} \phi_{\lambda}^{*}(\mathbf{r}_{2}) \phi_{\sigma}(\mathbf{r}_{2}) d\mathbf{r}_{1} d\mathbf{r}_{2}
$$

=
$$
-\frac{1}{2} \sum_{\nu\lambda} P_{\nu\lambda}(\mu\nu \mid \lambda\sigma),
$$
 (2.21)

where we have used the standard expression of two-electron integrals (in Mulliken notation with round brackets to emphasise that the integral is over spatial rather than spin orbitals, e.g. the spin has already been integrated out)

$$
(\mu v \mid \lambda \sigma) = \iint \phi_{\mu}^*(\mathbf{r}_1) \phi_{\nu}(\mathbf{r}_1) \frac{1}{|\mathbf{r}_2 - \mathbf{r}_1|} \phi_{\lambda}^*(\mathbf{r}_2) \phi_{\sigma}(\mathbf{r}_2) d\mathbf{r}_1 d\mathbf{r}_2.
$$
 (2.22)

And thus follows the Hartree-Fock energy as a contraction of density matrix elements and four-center integrals

$$
E_{\rm x}^{\rm HF} = -\frac{1}{2} \sum_{\mu\nu\lambda\sigma} P_{\mu\sigma} P_{\nu\lambda}(\mu\nu \mid \lambda\sigma). \tag{2.23}
$$

The restriction to take only a single determinant is an artificial one, as already mentioned, to keep computational cost at bay. Together with the ansatz of spin function separation for the spin-orbital, this leads to an error compared to a truly exact exchange energy, which is the Hartree-Fock correlation energy [\[6](#page-122-0)]

$$
E_C^{\text{HF}} = E_{\text{exact}} - E_{\text{HF}}.\tag{2.24}
$$

This correlation energy arises because of the missing excitations given by additional determinants due the interaction of single electrons with the mean field of electrons, while the same-spin exchange interaction In the context of [Density Functional](#page-12-3) (Pauli principle) is still included. This correlation energy can be corrected by either expanding the wavefunction in linear combinations of Slater determinants, or a number of other post-Hartree-Fock methods, which will then increase the computational complexity again.

2.2. Density Functional Theory

Density Functional Theory is based on using the electronic density as a primary quantity rather than directly the orbitals which generate this density. Respectively, while in Hartree-Fock theory the Hamiltonian is solely defined by the potential ν and the number of electrons N , in DFT it is the density which determines the external potential and hence the Hamiltonian, according to the first Hohenberg-Kohn theorem[[13](#page-122-4)].

The density in this case is defined as an integral over the $3N$ -dimensional wave function $\psi(\mathbf{r})$ as

$$
\rho(\mathbf{r}_1) = N \int \cdots \int |\psi(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N)|^2 d\mathbf{r}_2 \cdots d\mathbf{r}_N, \tag{2.25}
$$

with the integral over this density yielding the total number of electrons in the system

$$
\int \rho(\mathbf{r}) = N. \tag{2.26}
$$

This allows us to write the energy expressed as a functional of this density in a similarly separated way as the Hartree-Fock energy in [Equation](#page-18-0) [2.10](#page-18-0), namely

$$
E[\rho] = \underbrace{T[\rho] + V_{ee}[\rho]}_{\text{HK}} + V_{\text{ne}} \\
= F_{\text{HK}}[\rho] + \int \rho(\mathbf{r}) \nu(\mathbf{r}) d\mathbf{r},
$$
\n(2.27)

with the kinetic term T , and the electron-electron and nuclei-electron interaction terms V_{ee} and V_{ne} . The terms independent of the nuclei are collected in the common Hohenberg-Kohn functional F_{HK} , while the electronelectron interaction can be expressed as a sum of the classical Hartree repulsion term J and a non-classical part (which turns out to be part of the exchange-correlation energy term):

$$
V_{ee} = J[\rho] + \text{non-classical term.} \tag{2.28}
$$

While this formulation is convenient, it all hinges on the availability of the HK functional, which unfortunately can only be determined for very

[Theory \(DFT\),](#page-12-3) [Hartree-Fock Exchange](#page-12-1) sometimes also referred to as *exact exchange* because of the absence of any [self-interaction error \(SIE\)](#page-12-19) [[12](#page-122-3)].

simple systems[[14](#page-122-5)]. Luckily, the second Hohenberg-Kohn theorem introduces an analogue to the variational approach of the wave function theory in [Equation](#page-17-0) [2.8.](#page-17-0) Namely that there is a ground state energy E_0 to the true ground state density ρ_0 and that for each trial density $\tilde{\rho}$ the inequality

$$
E_0 \le E[\tilde{\rho}] \tag{2.29}
$$

holds. Together with a reformulation of the kinetic energy term T which still contains interacting and non-interacting parts, let us derive a solu-tion. Kohn-Sham [\[15\]](#page-122-6) introduced this by rewriting T as a sum of the kinetic energies of non-interacting electrons T_S (the non-interacting reference system) and a still unknown term V , together with the reintroduction of orbitals as defined before, allowing us to write

$$
(T_s + V)\psi_s = E_s \psi_s
$$

and

$$
T_s[\rho] = \sum_{i}^{N} \left\langle \psi_i \left| -\frac{1}{2} \nabla^2 \right| \psi_i \right\rangle,
$$
 (2.30)

with the density now again defined as in [Equation](#page-20-1) [2.20.](#page-20-1)

This allows us to rewrite [Equation](#page-21-2) [2.27](#page-21-2) and [Equation](#page-21-3) [2.28](#page-21-3) as

$$
E[\rho] = T[\rho] + J[\rho] + T_s[\rho] - T_s[\rho] + \text{non-classical term}
$$

= $T_s[\rho] + J[\rho] + E_{\text{xc}}[\rho],$ (2.31)

where the non-classical term and the missing correlation in the noninteracting kinetic energy are captured in the new E_{xc} energy. Together with the re-introduction of orbitals, the minimization procedure has to be adjusted in the sense that the orthonormality constraint from [Equa](#page-17-1)[tion](#page-17-1) [2.9](#page-17-1) takes the place of the integration yielding the total number of electrons N . It must also be noted that this extension does not invalidate the variational principle introduced by the second Hohenberg-Kohn theorem. Hence the density-dependent energy term we want to minimize reads by putting [Equation](#page-22-0) [2.30](#page-22-0) and as [Equation](#page-22-1) [2.31](#page-22-1) together:

$$
E[\rho] = \sum_{i}^{N} \left\langle \psi_{i} \left| -\frac{1}{2} \nabla^{2} \left| \psi_{i} \right\rangle + J[\rho] + E_{\text{xc}}[\rho] + \int v(\mathbf{r}) \rho(\mathbf{r}) d\mathbf{r} . \right. \tag{2.32}
$$

This allows us now to define the Kohn-Sham operator which now contains functional derivatives of the density

$$
K(\mathbf{r}) = -\frac{1}{2}\nabla^2 + \nu(\mathbf{r}) + \frac{\delta J[\rho]}{\delta \rho(\mathbf{r})} + \frac{\delta E_{\text{xc}}[\rho]}{\delta \rho(\mathbf{r})}
$$

= $\nu(\mathbf{r}) + \int \frac{\rho(\mathbf{r'})}{|\mathbf{r} - \mathbf{r'}|} d\mathbf{r'} + \nu_{\text{xc}}(\mathbf{r}),$ (2.33)

with the exchange-correlation potential v_{xc} . Again, as *K* is hermitian, we can find a unitary transformation which diagonalizes our energy eigenvalues such that we can without loss of generality write the Kohn-Sham equations in their canonical form

$$
K(\mathbf{r})\psi_i(\mathbf{r}) = \epsilon_i \psi_i(\mathbf{r}),\tag{2.34}
$$

which can again be turned into a general matrix eigenvalue problem by introducing a (finite) basis, to be solved numerically.

2.2.1. Exchange-Correlation Functionals of DFT

As we have been investigating the performance of basis sets (and pseudopotentials) with different exchange-correlation functionals, we will quickly discuss them here. While the Kohn-Sham equations are easier to solve, due to their density dependency, they now depend on the quality of the exchange-correlation potential v_{xc} . This leads to the exchangecorrelation energy via $E_{\text{xc}}[\rho] = \int \rho(\mathbf{r})v_{\text{xc}}(\rho(\mathbf{r}))$. Even though this has been intensively studied in the past and new functionals are still being proposed, there is no formally systematic way of improving those functionals. Yet, there is a scheme proposed by Perdew[[16](#page-122-7)] called "Jacob's Ladder", allowing for categorisation of them. The start at the lowest rung make functionals which depend solely on the density ρ . As they depend only on the functional at that given point in space or in other words on a constant electron density, they are called *Local (Spin) Density Approximation* (LDA). One step higher, the XC potentials depend additionally on the gradient of the density $\nabla \rho(\mathbf{r})$, giving them the name [Generalized Gra](#page-12-13)[dient Approximation \(GGA\)](#page-12-13) and making them semi-local in the process. Going a step further, the *meta-GGA* are adding either a second derivative or orbital kinetic energy density τ , rendering them more accurate but making property calculation more sensitive to numerics. The next rungs towards chemical accuracy are then the *Hybrid Functionals*, which add exact exchange (as given above) to either GGA or meta-GGA functionals, rendering those functionals fully non-local. The final rung (for completeness) then includes the *Double-Hybrids*, which in turn include *Random Phase Approximation* (RPA) contributions or possibly others.

In the following, we are going to look at the explicit forms of the functionals used in this work: PBE, TPSS, PBEsol and PBE0. While all the functionals discussed here are based on the separation into an exchange and a correlation part $E_x + E_c$, this is not a general requirement.

PBE

The *Perdew, Burke, Ernzerhof* functional is arguably one of the most widely used functionals, especially in materials science [\[17\]](#page-122-8). As a GGA functional it depends on both the density and its gradient

$$
E_{\rm xc}^{\rm GGA}[\rho] = \int \rho(\mathbf{r}) \nu_{\rm xc}(\rho(\mathbf{r}), \nabla \rho(\mathbf{r})). \tag{2.35}
$$

The exchange part relies on the *Local Density Approximation* and augments it by an enhancement factor $F_{\rm x}$, while introducing a reduced density gradient s

$$
E_{\rm X} = \int \rho v_{\rm X}^{\rm LDA}(\rho) F_{\rm X} \left(s(\mathbf{r}) \right) d\mathbf{r}
$$
 (2.36)

$$
F(s) = 1 + \alpha - \frac{\alpha}{1 + \beta(s^2)}
$$
 (2.37)

$$
\nu_{\rm x}^{\rm LDA}(\mathbf{r}) = -\frac{3}{4} \left(\frac{3}{\pi}\right)^{1/3} \rho(\mathbf{r})^{4/3} \tag{2.38}
$$

$$
s(\mathbf{r}) = \frac{|\nabla \rho(\mathbf{r})|}{\rho^{4/3}(\mathbf{r})},
$$
\n(2.39)

where the exchange energy density $v_{\rm x}^{\rm LDA}({\bf r})$ has been obtained from the generalisation of the homogeneous electron gas to an inhomogeneous system under the assumption of a locally constant electron density[[18](#page-123-0)].

The correlation part also derives directly from the LDA functional by

$$
v_{\rm c}^{\rm PBE} = v_{\rm c}^{\rm LDA} + H(t),\tag{2.40}
$$

where *t* is a dimensionless density gradient (e.g. of the form $|\nabla \rho|/\rho$, similar to *s* in [Equation](#page-24-0) [2.39\)](#page-24-0).

Even though highly parameterised (α , β but also the parameters contained in H), it must be stressed that those parameters are not derived from fitting the functional but rather from required asymptotic behaviour of the functional in different settings and additional constraints the functional should satisfy. The exact form and discussion can be found in Perdew, Burke, and Ernzerhof[[19](#page-123-1)].

TPSS

The meta-GGA *Tao-Perdew-Staroverov-Scuseria* (TPSS) functional adds a dependency on τ , the Kohn-Sham orbital kinetic energy

$$
E_{\text{xc}}^{\text{GGA}}[\rho] = \int \rho(\mathbf{r}) \nu_{\text{xc}}(\rho(\mathbf{r}), \nabla \rho(\mathbf{r}), \tau(\mathbf{r})) \tag{2.41}
$$

$$
\tau(\mathbf{r}) = \frac{1}{2} \sum_{i}^{\text{occ}} |\nabla \phi_i(\mathbf{r})|^2.
$$
 (2.42)

The exchange part again depends on the previously shown $\rm v_x^{LDA}$ with the enhancement factor now depending on τ , but similar to [Equation](#page-24-1) [2.36](#page-24-1) on auxiliary parameters:

$$
F_{\rm x}(p, z) = 1 + \kappa - \frac{\kappa}{1 + x(p, z)/\kappa} \tag{2.43}
$$

$$
p = s^2 \tag{2.44}
$$

$$
z = \frac{\tau^W}{\tau}, \text{ with } \tau = \tau_{\uparrow} + \tau_{\downarrow}, \text{ and } \tau^W = \frac{1}{8} \frac{|\nabla \rho|^2}{\rho}
$$
 (2.45)

Theform of F_x is again chosen to obey the Lieb-Oxford bound [[20](#page-123-2)] with a fixed κ .

The correlation part derives in a similar manner from the PBE correlation energy shown above, adding a τ dependency in the process.

For this and the full form of $x(p, z)$ we are referring again to the original source of Tao et al. [\[21\]](#page-123-3). What makes this functional interesting to be used as a prototype for meta-[GGAs](#page-12-13) in the following work, is its property of correcting for the one-electron [SIE](#page-12-19), by ensuring the correlation energy vanishes exactly in the valence region.

PBEsol

Even though the parametrization of PBE relies on general physical requirements towards the functional, there is still a significant degree of freedom when it comes to which and how well those constraints are respected. While PBE respects and reproduces atomization energies well in the process, it is far less accurate when it comes to weakly-varying densities in densely packed solids, something the LDA gets right. To remedy this issue, two parameters in the PBE functional were adjusted (part of the *beta* and H functions mentioned above), by fitting to the behaviour of the previously mentioned TPSS functional for surface densities in a homogeneous electron gas setup. As the GGA form itself is limited, this worsens for example atomization energies (but not worse than LDA) and makes it less suitable for molecular calculations, but improves upon bulk properties like lattice constants and surface energies[[22](#page-123-4)].

PBE0

The PBE0 functional is a hybrid functional, directly mixing PBE and the exact exchange energy from Hartree-Fock in a straightforward way, while maintaining the complete correlation energy from PBE:

$$
E_{\text{xc}}^{\text{PBE0}} = \frac{1}{4} E_{\text{x}}^{\text{HF}} + \frac{3}{4} E_{\text{x}}^{\text{PBE}} + E_{\text{c}}^{\text{PBE}} \tag{2.46}
$$

The motivation for this comes from the re-introduction of orbitals in Kohn-Sham DFT, which allows us to define an exact Kohn-Sham exchange energy and one of the major differences between Hartree-Fock and DFT when it comes to Self-Interaction Correction (SIC): While in Hartree-Fock self-interaction is cancelled because the respective contribution is present in both Hartree and Exchange terms, no equivalent mechanism is available in DFT due to the density "intermediary" which gets integrated over to obtain the energies. With the mixing one is able to

(partially) recover some of the properties most influenced by this, namely atomisation energies, bond lengths and vibration frequencies[[23](#page-123-5)].

Even though this way of mixing [DFT](#page-12-3) and [Hartree-Fock \(HF\)](#page-12-2) exchange energy may look arbitrary, with mixing coefficients in hybrid functionals either determined empirically or by required asymptotic behaviour, their use is rigorously justified from [DFT](#page-12-3) itself via the *adiabatic connection* of the Exchange-Correlation energy[[24](#page-123-6)]

$$
E_{\text{XC}} = \int_0^1 U_{\text{XC}}^\lambda d\lambda. \tag{2.47}
$$

Which connects a non-interacting Kohn-Sham system with its fully-interacting real counterpart. In the case of PBE0, the $\frac{1}{4}E_{\rm X}^{\rm HF}$ can be exactly recovered by an analysis of the behaviour of electron pair spin states in [DFT](#page-12-3) [\[25\]](#page-123-7).

An important part worth mentioning is that physical meaning is only obtained for the whole of the Exchange-Correlation energy, hence a segmentation into E_X and E_C and then replacing either does not work, as realized by Becke [\[26\]](#page-123-8), which subsequently led to the creation of the B88 functional[[27](#page-123-9), [28\]](#page-123-10).

2.3. Basis Sets and Pseudopotentials

As mentioned in the previous section, to actually be able to solve the Schrödinger equation numerically, we have to introduce a basis in which we express the [MOs.](#page-12-18) For the largest part of this work, we relied on the CP2K software package, which utilises atom-centred Gaussian-type orbitals (GTO).

While a natural choice for a basis would be Slater functions of the type $e^{-\alpha r}$ as they form the analytical solution to the single particle Schrödinger equation, we rely in several parts – like in the Fock matrix – on [Electron](#page-12-16) [Repulsion Integrals \(ERIs\)](#page-12-16), which do not have an analytical solution for such functions. For that purpose Gaussian functions $e^{-\alpha r^2}$ are much more efficient to calculate as the product of two Gaussian functions around different centres A and B can be rewritten as a single Gaussian function around a common centre C . The disadvantage of functions of the form $e^{-\alpha r^2}$ is that they do not reproduce the cusp forming at the nucleus (e.g. $\frac{\partial \phi(r)}{\partial r} \neq 0$ at $r = 0$) and that they decay too quickly in the long-range (due to the r^2 in the exponent).

For both types of functions, α determines the *diffuseness* of the basis, a larger value leading to a narrower and a lower coefficient to a broader distribution.

Using single (or primitive) Gaussian functions in place of a Slater-type orbital would require a lot of basis functions to recover the same characteristics, which is why contracted Cartesian Gaussian basis functions (centred around a nucleus A) are being used for a single Slater function with the contraction coefficients c_i either fitted to Slater orbitals or to data. Such a Gaussian function is then written as

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$$
\psi_{v}(\mathbf{r} - \mathbf{A}) = \sum_{i=1}^{L} c_{i}(x - A_{x})^{l}(y - A_{y})^{m}(z - A_{z})^{n}e^{-\alpha_{i}(\mathbf{r} - \mathbf{A})^{2}}, \qquad (2.48)
$$

with L determining the *length of the contraction*, and $l+m+n$ corresponds to the Cartesian angular momenta. With that, the [MOs](#page-12-18) of [Equation](#page-19-1) [2.15](#page-19-1) and the Electron Repulsion Integrals of [Equation](#page-20-2) [2.22](#page-20-2) become

$$
\phi_i(\mathbf{r} - \mathbf{A}) = \sum_{v} C_{vi} \sum_{i=1}^{L} c_i (x - A_x)^l (y - A_y)^m (z - A_z)^n e^{-\alpha_i (\mathbf{r} - \mathbf{A})^2}
$$
(2.49)

and

$$
(\mu v \mid \lambda \sigma)_g = \sum_{a=1}^{L_A} \sum_{b=1}^{L_B} \sum_{c=1}^{L_C} \prod_{d=1}^{L_D} \iint \frac{1}{|\mathbf{r}_2 - \mathbf{r}_1|} \n\cdot c_a (x - A_x)^{l_A} (y - A_y)^{m_A} (z - A_z)^{n_A} \n\cdot c_b (x - B_x)^{l_B} (y - B_y)^{m_B} (z - B_z)^{n_B} \n\cdot c_c (x - C_x)^{l_C} (y - C_y)^{m_C} (z - C_z)^{n_C} \n\cdot c_d (x - D_x)^{l_D} (y - D_y)^{m_D} (z - D_z)^{n_D} \n\cdot e^{-\alpha_a(\mathbf{r}_1 - \mathbf{A})^2} e^{-\alpha_b(\mathbf{r}_1 - \mathbf{B})^2} e^{-\alpha_c(\mathbf{r}_2 - \mathbf{C})^2} e^{-\alpha_d(\mathbf{r}_2 - \mathbf{D})^2} \nd\mathbf{r}_1 d\mathbf{r}_2,
$$
\n(2.50)

each a function of length of the contraction L , the angular momenta l , m , and atomic centres **A**, **B**, **C** and **D**. From the above it is immediately clear then that the number of [ERIs](#page-12-16) to calculate depends heavily on the size of the basis set, favouring small and heavily contracted basis sets (low number of contractions).

Expanding atomic orbitals in terms of atom-centred Gaussians comes naturally and is standard for quantum chemistry codes as it permits direct insight into chemical properties like bonds. Expressing the electron density required in KS[-DFT](#page-12-3) in [plane wave \(PW\)](#page-12-8) instead, which are independent of the atomic positions, instead has several benefits as well. In particular can the Hartree and [Exchange-Correlation \(XC\)](#page-13-0) energies be calculated more easily and the complexity of computing the Kohn-Sham matrix follows $\mathcal{O}(N \log(N))$ (the underlying discrete [Fast-Fourier Trans](#page-12-20)[formation \(FFT\)](#page-12-20)) if combined with the Gaussian expansion approach in a dual [Gaussian and Plane Waves Method \(GPW\)](#page-12-9) approach[[29\]](#page-123-11). The weakness of [PWs](#page-12-8) lies in their approximation of the density near the atomic centres: to represent the density accurately enough, a large number of [PWs](#page-12-8) must be employed (i.e. a high cutoff must be chosen), which comes at a large cost in terms of memory and computation as the same representation must be maintained for regions where the accuracy is not needed. This can be remedied by using [pseudopotentials \(PPs\)](#page-12-10) which collect the potential generated by the nucleus together with the non-valence electrons into one effective core potential, often based on a frozen-core assumption. The role of the [PP](#page-12-10) is then to ensure that valence electrons are

kept out of the core and within the valence space, and must thus contain a repulsive short-range and an attractive long-range part. [\[30\]](#page-123-12)

For both [PW](#page-12-8) and [Gaussian-type Orbital \(GTO\)](#page-12-0) approaches do [PPs](#page-12-10) reduce the number of required basis functions within a calculation since the (localised) core behaviour does not have to be captured anymore. For [GTOs](#page-12-0) this comes also into play during basis set construction by permitting more compact basis functions. It should be noted that [PP](#page-12-10) rely on a valence and core electron partition which must be obtained prior to the generation of [PP](#page-12-10) by some other method. This is accurate enough for many calculations but physically not fully correct. For species where this becomes a problem (for example heavier alkali) this can be remedied by treating more electrons as valence electrons (then called *semi-core* electrons), resulting in fewer core electrons covered by the [PP](#page-12-10).

For heavier atoms also relativistic effects can be directly taken into account via the [PP,](#page-12-10) simplifying the calculations.

While there are many different forms of [PP](#page-12-10) as illustrated by Dolg and Cao [[31\]](#page-123-13), we are only going to mention the ones relevant for this work, the norm-conserving[[32](#page-123-14)] Separable Dual-Space Pseudopotentials of Goedecker, Teter, and Hutter [\[33\]](#page-123-15) (GTH), respectively Hartwigsen, Goedecker, and Hutter[[34](#page-123-16)] (HGH).

This means that they take the general form

$$
V(\mathbf{r}, \mathbf{r}') = V_{\text{loc}}(r)\delta(|\mathbf{r} - \mathbf{r}'|) + \sum_{l} V_{l}(\mathbf{r}, \mathbf{r}') + \Delta V_{l}^{\text{SO}}(\mathbf{r}, \mathbf{r}') \mathbf{L} \cdot \mathbf{S}, \quad (2.51)
$$

with the local part given by

$$
V_{\text{loc}}(r) = \frac{-Z_{\text{ion}}}{r} \operatorname{erf}\left(\frac{r}{\sqrt{2}\eta_{\text{oc}}}\right) + \exp\left[-\frac{1}{2}\left(\frac{r}{\eta_{\text{oc}}}\right)^2\right] \cdot \left[C_1 + C_2\left(\frac{r}{\eta_{\text{oc}}}\right)^2 + C_3\left(\frac{r}{\eta_{\text{oc}}}\right)^4 + C_4\left(\frac{r}{\eta_{\text{oc}}}\right)^6\right],
$$
\n(2.52)

where erf is the error function, Z_{ion} the ionic charge of the core (i.e. without the charge of the valence elctrons).

The non-local part V_1 is given as

$$
V_{\rm l}(\mathbf{r}, \mathbf{r}') = \sum_{i=1}^{3} \sum_{j=1}^{3} \sum_{m=-l}^{+l} Y_{l,m}(\hat{\mathbf{r}}) p_i^l(r) h_{ij}^l p_j^l(r') Y_{l,m}^*(\hat{\mathbf{r}}'), \qquad (2.53)
$$

with the projectors p_i^l being products of a polynomial and a Gaussian ļ function in both real and reciprocal space (*dual-space*) and $Y_{l,m}$ the spherical harmonics.

A different solution than the use of [PP](#page-12-10) to the issue of modelling the true wave functions around the core is the use of separate grids. In a [PW](#page-12-8) code this can be resolved by replacing the plane-wave functions by a rangeseparated basis, which uses a sum of products of radial functions again with spherical harmonics inside a certain *muffin-tin* radius, and planewaves outside (the *interstitial region*). The radii are then chosen as big as possible without overlap. This gives rise to the [Full-Potential Linearized](#page-12-15)

[Augmented Plane Wave method \(FP-LAPW\)](#page-12-15)[[35](#page-123-17)], as implemented for example by SIRIUS, Exciting and WIEN2K.

In a [GPW](#page-12-9) code such as CP2K, one can use a conceptually similar approach of treating regions around atoms differently, keeping in mind that only the density is expanded into [PW](#page-12-8), the [Gaussian and Augmented](#page-12-12) [Planewave \(GAPW\)](#page-12-12) method[[36](#page-124-0)[–38\]](#page-124-1). In [GAPW,](#page-12-12) the sharp variations of the density close to the nuclei is captured on (radial) atomic grids, while the smoothly varying density in the interstitial regions can be described by a low amount of [PW.](#page-12-8) The requirement for this is the ability of separating the Hartree and [XC](#page-13-0) functionals into independent global and local contributions as proven possible in the [Projector Augmented-](#page-12-21)[Wave method \(PAW\)](#page-12-21) approach by Blöchl [\[39\]](#page-124-2). For the local atom centred representation one chooses again a projector basis based on Gaussians. Despite that, by ensuring non-overlapping regions (and assuming contributions by other centres are negligible), the cost of calculating the local densities is system-size independent. Finally, even though there is a partitioning of space for consistency of the theory, no explicit boundaries where functions have to match, as in the [FP-LAPW](#page-12-15) approach, appear. And, the [GAPW](#page-12-12) method is not limited to [All-Electron \(AE\)](#page-12-11) calculations but can also employed together with [PP](#page-12-10) for improved accuracy.

From the above, it becomes clear that any non-[AE](#page-12-11) basis set depends on a corresponding [PP](#page-12-10) in terms of number of valence electrons. And since the GTH[-PPs](#page-12-10) depend on the functional used when obtaining their parameters, so do the matching basis sets. Because basis sets are not transferable between different computational methods (e.g. [DFT](#page-12-3) and correlated wave function methods) [\[40,](#page-124-3) [41](#page-124-4)], in this work we will investigate their transferability within the same rung of [DFT.](#page-12-3)

Focusing on the basis functions primarily used in this work, we are quickly looking at how the MOLOPT basis sets are constructed. They are generally (respectively fully) contracted[\[42](#page-124-5)] [GTO](#page-12-0) basis sets with the general form of

$$
\varphi_j = \sum_i c_{i,j} \chi_i
$$

$$
\chi_i(\alpha, n, m, l; r, \theta, \phi) = N Y_{l,m}(\theta, \phi) r^{2n - 2 - l} e^{-\alpha r^2},
$$
\n(2.54)

meaning that the same exponents, respectively primitive Gaussians, are shared across all contracted Gaussian functions forming the basis set, with non-zero contraction coefficients. This is in contrast to minimal and segmented basis sets, where contractions are carefully built based on the anticipated representation of [MOs](#page-12-18), and diffuse Gaussians (small exponents) are therefore often retained as single basis functions. Consequently a double- or triple- ζ MOLOPT basis set again uses the same exponents for the second and third contracted functions, but with different contraction coefficients. Originally drafted as basis sets to be used with [PP,](#page-12-10) the MOLOPT basis sets contain cover only *valence* electrons and must be used with matching [PP.](#page-12-10) Starting at double- ζ they also contain additional polarisation functions in the same way as the **** variants of the popular Pople 6-31G basis sets[[43\]](#page-124-6) (e.g. the polarisation functions are not doubled/tripled), but again based on the full contraction instead, and denoted with a P suffix. The general series of contractions in the MOLOPT basis sets is therefore: SZV (1s1p/1s), DZVP

(2s2p1d /2s1p), TZVP (3s3p1d/3s1p), TZV2P (3s3p2d/s2p), and TZV2PX (3s3p2d1f/3s2p1d) , whereas the newly optimised set evaluated in this thesis only covers DZVP, TZVP and TZV2P.

The rational behind those decisions is based on the observations that for [DFT](#page-12-3) the computationally intensive task is the update of the density matrix, which depends on the number of basis functions [\[44,](#page-124-7) [45\]](#page-124-8), rather than the primitives. More relevant are small [basis set superposition errors](#page-12-22) [\(BSSEs\)](#page-12-22) and a small condition number¹ of the overlap matrix to achieve 1: ratio of largest energy to the smallest stable optimisation. The latter is important since the usual techniques of treating this problem is by removing eigenvectors belonging to small eigenvalues, which may lead to discontinuities in the energy in either geometry optimisation or [molecular dynamics \(MD\)](#page-12-23) use cases as the system evolves. The former can be alleviated by the addition of diffuse functions, which also a requirement for the proper description of weak interactions such as hydrogen bonding. It has been shown, that these highly contracted MOLOPT basis sets satisfy all those criteria [\[46–](#page-124-9)[49](#page-124-10)].

With the same primitives reused across basis functions, a final design decision was then that larger basis sets extend their respective smaller ones. E.g. by neglecting the third basis function of a TZVP basis for each angular momentum, one ends up at the DZVP basis of the same species. This makes it much easier to argue that larger basis sets extend the quality of their respective smaller ones.

In contrast to the original MOLOPT procedure, the revised set follows the *even-tempered* approach[[50](#page-124-11), [51\]](#page-124-12) for selecting the exponents of the primitive Gaussians. What this means is that rather than using N independent exponents, they are instead related via

$$
\alpha_k = \alpha_1 \varepsilon^{k-1}.\tag{2.55}
$$

This greatly simplifies the non-linear optimisation procedure, but there is also another aspect. The overlap of Gaussian primitives for the same angular momentum only depends on the ratio of their exponents. If the exponents are defined as in [Equation](#page-30-1) [2.55](#page-30-1) this means that the ratio between two adjacent primitives is exactly ε . Not only that, but it can be shown that "such a constant overlap will lead to even coverage of the Hilbert space" [\[52\]](#page-124-13).

The new [AE](#page-12-11) variants of the MOLOPT basis sets follow the *def2-SVP*, *- TZVPP*, *-QZVPP* contraction scheme [\[53,](#page-125-0) [54](#page-125-1)] instead.

The smaller number of basis functions is useful to reduce the size of the density matrix important for [DFT](#page-12-3) calculations. But the large number of primitives becomes problematic for hybrid calculations in which the [HFX](#page-12-1) [ERI](#page-12-16) must be calculated. This is due to the dependency on the primitive Cartesian Gaussian functions as shown in [Equation](#page-27-1) [2.50](#page-27-1), whose number is at least equal or even larger than the spherical ones [\[55\]](#page-125-2). Another problem for [HFX](#page-12-1) are the diffuse functions as they limit the application of Schwarz-screening discussed in [Section 2.4.1](#page-33-0) and lead to significantly larger number of quartets contributing.

eigenvalue, directly affects the sparsity and hence the performance of the overlap and matrices derived from it

2.4. Periodic Hartree-Fock Exchange

One of the results of condensed matter theory is the realisation that in a periodic system (e.g. a crystal) the solutions to the Schrödinger equation – the wave functions – must satisfy the Bloch theorem, stating that they can always be written as Bloch functions

$$
\psi_{\mathbf{k}}(\mathbf{r}) = e^{i\mathbf{k}\cdot\mathbf{r}}u(\mathbf{r}),\tag{2.56}
$$

with $u(\mathbf{r}) = u(\mathbf{r}+\mathbf{R})$ being of lattice periodicity and **R** being a periodic cell displacement vector. As a further consequence, the uniqueness of $\psi_{\mathbf{k}}$ is only guaranteed up to a displacement of a reciprocal lattice vector **G**

$$
\psi_{\mathbf{k}+\mathbf{G}}(\mathbf{r}) = \psi_{\mathbf{k}}(\mathbf{r}).\tag{2.57}
$$

allowing us to restrict **k** to lie within the first [Brillouin Zone \(BZ\).](#page-12-24) If we are to introduce primitive vectors a_1 , a_2 , a_3 such that

$$
R = \sum_{i=1}^{3} n_i a_i,
$$
 (2.58)

with n_i being integer numbers, spawns our Bravais lattice, we can also define a set of reciprocal lattice vectors by

$$
\mathbf{b}_1 = 2\pi \frac{\mathbf{a}_2 \times \mathbf{a}_3}{\mathbf{a}_1 \cdot (\mathbf{a}_2 \times \mathbf{a}_3)}, \quad \mathbf{b}_2 = 2\pi \frac{\mathbf{a}_3 \times \mathbf{a}_1}{\mathbf{a}_1 \cdot (\mathbf{a}_2 \times \mathbf{a}_3)}, \quad \mathbf{b}_3 = 2\pi \frac{\mathbf{a}_1 \times \mathbf{a}_2}{\mathbf{a}_1 \cdot (\mathbf{a}_2 \times \mathbf{a}_3)}
$$
(2.59)

in which to express **k** as

$$
\mathbf{k} = \sum_{i=1}^{3} x_i \mathbf{b}_i, \tag{2.60}
$$

with x_i being real valued numbers, and the relationship $a_i \cdot b_j = 2\pi \delta_{ij}$ between the two basis.

Applying the [Born-von Kármán \(BvK\)](#page-12-25) boundary conditions by defining our crystal to consist of a finite number $N = N_1 N_2 N_3$ of primitive cells such that $\psi_{\mathbf{k}}(\mathbf{r} + N_i \mathbf{a}_i) = \psi_{\mathbf{k}}(\mathbf{r})$ then leads to

$$
e^{i\mathbf{k}\cdot(\mathbf{r}+N_i\mathbf{a}_i)} = e^{i\mathbf{k}\cdot\mathbf{r}} \Rightarrow e^{i\mathbf{k}\cdot N_i\mathbf{a}_i} = 1 \,\forall i \in \{1, 2, 3\},\tag{2.61}
$$

and thus

$$
\mathbf{k} = \sum_{i=1}^{3} \frac{m_i}{N_i} \mathbf{b}_i,
$$
\n(2.62)

with m_i being integer numbers again. The reciprocal space can therefore be sampled at a finite number of k -points given by the N_i .

For our [linear combination of atomic orbitals \(LCAO\)](#page-12-26) basis, this means that the [MOs](#page-12-18) are now dependent on **k**

$$
\psi_i(\mathbf{r}; \mathbf{k}) = \sum_{\mu} C_{\mu i}^{\mathbf{k}} \phi_{\mu}(\mathbf{r}; \mathbf{k}) \tag{2.63}
$$

and are now in fact [Crystalline Orbitals \(COs\)](#page-12-27).

Plugging those back into the [HF](#page-12-2) [Equation](#page-19-2) [2.18](#page-19-2) then directly leads to

$$
\sum_{\mu} F_{\nu\mu}^{\mathbf{k}} C_{\mu i}^{\mathbf{k}} = \epsilon_i^{\mathbf{k}} \sum_{\mu} S_{\nu\mu}^{\mathbf{k}} C_{\mu i}^{\mathbf{k}}, \tag{2.64}
$$

with the important distinction that the integration for the overlap matrix $S_{v\mu}$ and the Fock matrix $F_{v\mu}$ is now over the space defined by the [BvK](#page-12-25) boundary condition.

While this is very convenient to evaluate in [PW](#page-12-8) codes, for a [GPW](#page-12-9) code such as CP2K we need a real space formulation. The key to this is to start from the atom centred functions φ_{μ} in a reference unit cell and expand them into a Bloch sum [\[56,](#page-125-3) [57](#page-125-4)]

$$
\phi_{\mu}(\mathbf{r}; \mathbf{k}) = \frac{1}{\sqrt{N}} \sum_{\mathbf{R}} e^{i\mathbf{k} \cdot \mathbf{R}} \phi_{\mu}(\mathbf{r} - \mathbf{R}), \qquad (2.65)
$$

which is essentially a discrete Fourier transform when taking [Equation](#page-31-2) [2.62](#page-31-2) into account. This satisfies the Bloch theorem in [Equation](#page-31-3) [2.56,](#page-31-3) considering that the summation is in principle over infinite *.*

Extending this to the overlap matrix then let's us define real space (neighbour cell dependent) variants as

$$
S_{V\mu}^{k} = \sum_{\mathbf{R}, \mathbf{R}'} \frac{1}{N} \int e^{i\mathbf{k}(\mathbf{R}'-\mathbf{R})} \phi_{V}^{\star}(\mathbf{r}-\mathbf{R}) \phi_{\mu}(\mathbf{r}-\mathbf{R}') d\mathbf{r}
$$

\n
$$
= \sum_{\mathbf{Q}=\mathbf{R}'-\mathbf{R}} \frac{1}{N} \int e^{i\mathbf{k}\mathbf{Q}} \phi_{V}^{\star}(\mathbf{r}) \phi_{\mu}(\mathbf{r}-\mathbf{Q}) d\mathbf{r}
$$

\n
$$
= \frac{1}{N} \sum_{\mathbf{Q}} e^{i\mathbf{k}\mathbf{Q}} \int \phi_{V}^{\star}(\mathbf{r}) \phi_{\mu}(\mathbf{r}-\mathbf{Q}) d\mathbf{r}
$$

\n
$$
= \frac{1}{N} \sum_{\mathbf{Q}} e^{i\mathbf{k}\mathbf{Q}} S_{V\mu}^{\mathbf{Q}},
$$
\n(2.66)

and likewise for the density matrix, but with the integration taking place over the Brillouin zone.

As a four-centre quantity, the same transformation becomes slightly more involved when looking at the exchange matrix from [Equation](#page-20-3) [2.21](#page-20-3), which now reads as follows and where the expansion leads to additional summations over $\mathbf{R}_1, \mathbf{R}_2, \mathbf{R}_3, \mathbf{R}_4$ in the same way as the summation over \mathbf{R}, \mathbf{R}' before:

$$
F_{\mu\sigma}^{\mathbf{k}} = -\frac{1}{2} \sum_{\nu\lambda\mathbf{k}'} P_{\nu\lambda}^{\mathbf{k}'} \iint \phi_{\mu}^{*}(\mathbf{r}_{1}; \mathbf{k}) \phi_{\nu}(\mathbf{r}_{1}; \mathbf{k}') \frac{1}{\|\mathbf{r}_{2} - \mathbf{r}_{1}\|} \phi_{\lambda}^{*}(\mathbf{r}_{2}; \mathbf{k}') \phi_{\sigma}(\mathbf{r}_{2}; \mathbf{k}) d\mathbf{r}_{1} d\mathbf{r}_{2}
$$

\n
$$
= -\frac{1}{2N^{2}} \sum_{\nu\lambda\mathbf{k}'} P_{\nu\lambda}^{\mathbf{k}'} \sum_{\mathbf{R}_{1}, \mathbf{R}_{2}, \mathbf{R}_{3}, \mathbf{R}_{4}} e^{-i\mathbf{k}(\mathbf{R}_{1} - \mathbf{R}_{4})} e^{-i\mathbf{k}(\mathbf{R}_{2} - \mathbf{R}_{3})}
$$

\n
$$
\iint \phi_{\mu}^{*}(\mathbf{r}_{1} - \mathbf{R}_{1}) \phi_{\nu}(\mathbf{r}_{1} - \mathbf{R}_{2}) \frac{1}{\|\mathbf{r}_{2} - \mathbf{r}_{1}\|} \phi_{\lambda}^{*}(\mathbf{r}_{2} - \mathbf{R}_{3}) \phi_{\sigma}(\mathbf{r}_{2} - \mathbf{R}_{4}) d\mathbf{r}_{1} d\mathbf{r}_{2}. \tag{2.67}
$$

By translation symmetry of the crystal we can shift the entirety again by **R**¹ and introduce new displacement vectors **Q**, **S**, **T** instead, together with the definition of the real space density matrix $P_{\nu\mu}^{\mathbf{Q}} = \frac{1}{\lambda}$ $\frac{1}{N} \sum_{\mathbf{k}} e^{i\mathbf{k}\mathbf{Q}} P_{\nu\mu}^{\mathbf{k}},$ which then leads to the general expression for the exchange part of the periodic Fock matrix of

$$
K_{\rm x}^{\rm T} = -\frac{1}{2} \sum_{\rm Q} \sum_{\nu \lambda} P_{\nu \lambda}^{\rm Q} \sum_{\rm S} (\mu^0 \nu^{\rm S} \mid \lambda^{\rm T} \sigma^{\rm S + \rm Q}). \tag{2.68}
$$

Contracting with the density matrix $P_{\mu\nu}$ then leads to the periodic Hartree-Fock exchange energy

$$
E_{\rm x} = -\frac{1}{2} \sum_{Q,T} \sum_{\nu \lambda} P_{\mu \sigma}^T P_{\nu \lambda}^Q \sum_S (\mu^0 \nu^S \mid \lambda^T \sigma^{S+Q}). \tag{2.69}
$$

When only taking the Γ point into consideration, the density matrix in real space becomes the same for each periodic image, letting us simplify the sum to

$$
E_{\rm x} = -\frac{1}{2} \sum_{\lambda \mu \nu \sigma} P_{\mu \sigma} P_{\nu \lambda} \sum_{S,Q,T} (\mu^0 \nu^S \mid \lambda^T \sigma^{S+Q}), \tag{2.70}
$$

which is what prior to this work has been implemented in CP2K by Guidonet al. [[58](#page-125-5)]. Since the 4c-ERIs $(\mu^0 \nu^S | \lambda^T \sigma^{S+Q})$ do not depend on the [MOs](#page-12-18) which are being optimised in the [self-consistent field \(SCF\)](#page-12-28) loop, but only on the atom centre, they only have to be updated when the geometry changes, e.g. in a [MD](#page-12-23) or geometry optimisation run. Together with a precision truncation scheme, usage of symmetries and screening at different levels of the calculation, this allowed implementation of an in-memory and an on-disk cache between [SCF](#page-12-28) cycles, speeding up the calculation significantly.

Unfortunately, this caching implementation turns unfeasible for the general **k** point case as the number of coefficients to store grows quadratically with the number of neighbour cells to consider, given that only the sum over S can be executed before contraction with the density matrix.

2.4.1. Screening

Reducing the number of [ERIs](#page-12-16) to calculate is of utmost importance to keep the calculations for larger systems tractable. In particular if [HFX](#page-12-1) is to be combined with [DFT](#page-12-3), which can scale quasi-linearly, an $\mathcal{O}(N^4)$ scaling

with the system size as derived in [Equation](#page-27-1) [2.50](#page-27-1) is undesirable. The ability to determine a-priori which integrals are significant is therefore key to reducing the scaling. Since the Fock matrix F^X is a contraction of the density matrix $P_{\lambda\nu}$ with [ERIs](#page-12-16) $F_{\nu\lambda} = \sum_{\mu\sigma} (\mu\nu|\lambda\sigma)$, the selection of which integrals to calculate based on their contribution – the *screening* – can be based on either quantity.

For the integral screening on the [ERI](#page-12-16), the main idea is the (Cauchy-)Schwarzinequality

$$
|(\mu v \mid \lambda \sigma)| \le |(\mu v \mid \mu v)|^{1/2} \cdot |(\lambda \sigma \mid \lambda \sigma)|^{1/2}, \tag{2.71}
$$

which holds for for any inner product. While the requirements for an inner product like conjugate symmetry and linearity are fulfilled by the integral definition, the positive definiteness has been shown by Roothaan [[59\]](#page-125-6) for the Coulomb metric, while [\[60](#page-125-7)] have shown this to be rigorous upper bound.

Together with the maximum of the respective density matrix element \bar{P} = $\max\{|P_{\mu\lambda}|, |P_{\nu\lambda}|, |P_{\mu\sigma}|, |P_{\nu\sigma}|\}$ we can then define an estimate, which when smaller than a given threshold (named EPS_SCHWARZ in CP2K) leads to a neglect of the integral in [Equation](#page-34-2) [2.71:](#page-34-2)

$$
EST = |(\mu v \, | \, \mu v)|^{1/2} \cdot |(\lambda \sigma \, | \, \lambda \sigma)|^{1/2}.\tag{2.72}
$$

This means by evaluating a subset of integrals, and continued application of the inner product, one can obtain a hierarchy of screenings for:

- 1. pairs of basis functions belonging to the same atom (in fact their atomic kinds) by evaluating their largest estimate,
- 2. sets of of Gaussian basis functions (a grouping based on equal angular momentum) where again their maximum contribution is estimated,
- 3. and finally uncontracted [primitive Gaussian functions \(PGFs\)](#page-12-29).

The buildup of large screening matrices can further be avoided by instead calculating fitting parameters for a second-order polynomial for the product of the co-densities at different distances

$$
(\mu v \, | \, \mu v)(r_{\mu\nu}) = c_2 \cdot r_{\mu\nu}^2 + c_0. \tag{2.73}
$$

2.5. The Auxiliary Density Matrix Method

In Kohn-Sham Density Functional Theory (DFT) the total energy of the system

$$
E[\rho] = T_s[\rho] + J[\rho] + E_{\rm xc}[\rho] + \int v(\mathbf{r})\rho(\mathbf{r})d\mathbf{r}
$$
 (2.74)

is defined as a functional dependency of the density

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$$
\rho(\mathbf{r}) = \sum_{i=1}^{N_e} |\psi_i(\mathbf{r})|^2, \qquad (2.75)
$$

with N_e being the number of electrons in the system, and $\psi_i(\mathbf{r})$ the (realvalued) single particle wave functions. The terms in the total energy denote (in that order) the kinetic, Hartree and exchange-correlation energies followed by the part from the external potential.

For a Hybrid DFT calculation, a fraction α of the exchange energy E_r of the exchange-correlation potential E_{xc} is replaced by the Hartree-Fock exact exchange

$$
E_{\text{xc}}^{\text{hybrid}}[\rho] = E_{\text{xc}}^{\text{DFT}}[\rho] + \alpha \left(E_{\text{x}}^{\text{HFX}}[\{\psi_i\}] - E_{\text{x}}^{\text{DFT}}[\rho] \right)
$$

=
$$
E_{\text{c}}^{\text{DFT}}[\rho] + \alpha E_{\text{x}}^{\text{HFX}}[\{\psi_i\}] + (1 - \alpha) E_{\text{x}}^{\text{DFT}}[\rho].
$$
 (2.76)

When using a [LCAO](#page-12-26) as a basis set, the single-particle wave functions can be written as

$$
\psi_i(\mathbf{r}) = \sum_{\mu} C_{\mu i} \phi_{\mu}(\mathbf{r}) \tag{2.77}
$$

with $C^{\mu i}$ the [MO](#page-12-18) coefficients. From this, the Hartree-Fock exchange energy can be expressed as a functional of the density matrix

$$
P^{\mu\nu} = \sum_{i} C_{\mu i} C_{\nu i} \tag{2.78}
$$

and two-electron four-centre electron repulsion integrals (4c-ERIs)

$$
E_{x}^{\text{HFX}}[P] = -\frac{1}{2} \sum_{\lambda \sigma \mu \nu} P^{\mu \sigma} P^{\nu \lambda} (\mu \nu | \lambda \sigma), \tag{2.79}
$$

With the matrix-matrix multiplication scaling as $\mathcal{O}(N^3)$ of the number of basis functions, the calculation of the HFX energy scales per [Equation](#page-35-1) [2.79](#page-35-1) as $O(N^4)$. We will shortly see that, while in periodic calculations at the Γ-point sums of ERIs can be cached, effectively trading computation time with storage, the same trick can not be applied in the more general K-point formulation. Reducing the basis set size or choosing a basis with a larger minimal exponent to achieve a more rapidly decaying, respectively sparser density matrix is, therefore, desirable to accelerate the evaluation of the HFX energy. The [Auxiliary Density Matrix Method](#page-12-14) [\(ADMM\)](#page-12-14) [[61\]](#page-125-8) solves this by introducing such an auxiliary density matrix $\hat{P} \approx P$. Together with the assumption that the difference in the exchange energies calculated for the primary and the auxiliary density matrix (respectively the corresponding density) between the DFT and the Hartree-Fock exchange is small enough, we can rewrite the HFX energy for the primary density matrix as
$$
E_X^{\text{HFX}}[P] = E_X^{\text{HFX}}[\hat{P}] + \left(E_X^{\text{HFX}}[P] - E_X^{\text{HFX}}[\hat{P}]\right) \approx E_X^{\text{HFX}}[\hat{P}] + \left(E_X^{\text{DFT}}[\rho] - E_X^{\text{DFT}}[\hat{\rho}]\right).
$$
\n(2.80)

While there are multiple ways to construct such an auxiliary density matrix \hat{P} , we are restricting ourselves to the ones constructed by introducing an auxiliary basis set $\hat{\phi_\mu}(\mathbf{r})$ to express the wave function

$$
\hat{\psi}_i(\mathbf{r}) = \sum_{\mu} \hat{C}_{\mu i} \hat{\phi}_{\mu}(\mathbf{r}), \qquad (2.81)
$$

which directly leads us to an auxiliary density matrix

$$
\hat{P}^{\mu\nu} = \sum_{i} \hat{C}_{\mu i} \hat{C}_{\nu i}.
$$
\n(2.82)

The [MO](#page-12-0) coefficients $\hat{C}^{\mu i}$ can be determined by minimising the square difference for the occupied wave functions expressed in the auxiliary and primary basis set:

$$
\min_{\hat{C}} \sum_{j} \int \left(\psi_j(\mathbf{r}) - \hat{\psi}_j(\mathbf{r}) \right)^2 dr.
$$
 (2.83)

With the overlap matrices for the auxiliary basis and the one between the auxiliary and primary basis

$$
\hat{S}_{nn'} := \int \hat{\phi}_n(\mathbf{r}) \hat{\phi}_{n'}(\mathbf{r}) dr \quad \text{and} \quad Q_{nm} := \int \hat{\phi}_n(\mathbf{r}) \phi_m(\mathbf{r}) dr \tag{2.84}
$$

we can write the solution for the auxiliary [MO](#page-12-0) coefficients subject to the minimising [Equation](#page-36-0) [2.83](#page-36-0) as

$$
\hat{C} = \underbrace{\hat{S}^{-1}QC}_{=:A}
$$
\n(2.85)

Additional constraints – like the required orthonormality – can be integrated in [Equation](#page-36-0) [2.83](#page-36-0) using Lagrange multipliers:

$$
\min_{\tilde{C}} \left[\sum_{j} \int \left(\psi_j(\mathbf{r}) - \hat{\psi}_j(\mathbf{r}) \right)^2 d\mathbf{r} + \sum_{k,l} \Lambda_{k,l} \left(\int \hat{\psi}_k(\mathbf{r}) \hat{\psi}_l(\mathbf{r}) d\mathbf{r} \right) - \delta_{kl} \right].
$$
 (2.86)

Which yields the solution

$$
\tilde{C} = \hat{C}\Lambda^{-1/2} = \hat{C}(\hat{C}^T \hat{S} \hat{C})^{-1/2}.
$$
 (2.87)

The density matrices required for the HFX energy are therefore analogue to [Equation](#page-35-0) [2.78](#page-35-0) given by

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$$
\hat{P} = \hat{C}\hat{C}^T = APA^T
$$
\n
$$
\tilde{P} = \tilde{C}\tilde{C}^T = \hat{C}\Lambda^{-1}\hat{C}^T
$$
\n(2.88)

The total energy of the system can be written as a sum of the energy depending on the primary design matrix $E[P]$ and one depending on the auxiliary matrix $\tilde{E}[\tilde{P}]$:

$$
E_{\text{total}} = E[P] + \tilde{E}[\tilde{P}]. \tag{2.89}
$$

For the final Kohn-Sham matrix, this then means that it too can be expressed by a simple sum of the original and projected auxiliary Kohn-Sham matrices

$$
K_{\text{total}} = K[P] + A^T \tilde{K} A. \tag{2.90}
$$

The [ADMM](#page-12-1) implementation in which the auxiliary density matrix is obtained by solving the optimisation in [Equation](#page-36-0) [2.83](#page-36-0) is referred to as *ADMM2* or *non-purified wavefunction fitting*, the one based on [Equation](#page-36-1) [2.86](#page-36-1) yielding orthonormal orbitals *ADMM1*, or *purified* wavefunction fitting).

A third variant *ADMM3* can be derived for systems where the density matrix is blocked due to the physical setup, i.e. where the system can be divided into subsystems and most of the significant exchange between those subsystems is captured by the *GGA* functional. In this case one can express the auxiliary density matrix as the Hadamard product $(A \circ B)_{ii} =$ $(A)_{ii}(B)_{ii}$ of the original density matrix and a blocking matrix

$$
\stackrel{\circ}{P} := P \circ B,\tag{2.91}
$$

with $B_{ii} \in \{1, 0\}$, and thus setting coefficients corresponding to intersubsystem interaction to 0.

The term *purification* refers to the fact that a regular or *pure* density matrix is symmetric, idem-potent and conserves the number of particles:

$$
P = PT,
$$

\n
$$
PSPS = PS,
$$

\n
$$
tr(PS) = N_e,
$$
\n(2.92)

which is naturally only the case for *ADMM1*. For *ADMM2* however one can recover the *ADMM1 pure* density matrix with the purification algorithm by McWeeny[[62](#page-125-0)], here given in its original form

$$
\begin{aligned}\n\tilde{P}_{n+1} &= 3\tilde{P}_n S \tilde{P}_n - 2\tilde{P}_n S \tilde{P}_n S \tilde{P}_n, \\
\tilde{P} &:= \lim_{n \to \infty} \tilde{P}_n,\n\end{aligned} \tag{2.93}
$$

with $\bar{P}_0 = \hat{P}$ as initial guess. It also exists in a Cauchy integral form instead, which permits to formulate it directly as a function of the nonpurified density matrix [\[61,](#page-125-1) [63](#page-125-2)].

Since the density matrix \tilde{P} of *ADMM1* can not be calculated directly from the original P, the *ADMMO* and its variations *ADMMS* and *ADMMP* have been developed[[64\]](#page-125-3). The main idea being to directly enforce the charge conservation by modifying the Lagrangian from [Equation](#page-36-1) [2.86](#page-36-1) to forgoe the orthogonality in lieu of an overall charge constraint N_e . This results in an [ADMM](#page-12-1) where the resulting auxiliary density matrix satisfies all but the idem-potency and where the density matrix is directly related to the one from $ADMM2$ via a scaling coefficient ξ

$$
P_Q = \xi \hat{P}
$$

\n
$$
\xi = \frac{\text{tr}(PS)}{\text{tr}(\hat{P}\hat{S})}.
$$
\n(2.94)

The unmodified *ADMMQ* has the issue of exhibiting a different effective scaling for the exact and [DFT](#page-12-2) exchange energy in [Equation](#page-36-2) [2.80,](#page-36-2) resulting in a larger deviation of the total energy compared to *ADMM2*, depending on the functional. The remedy in *ADMMS* is to directly counter this difference by rescaling DFT energy contribution but otherwise maintaining the scaled projected density from *ADMMQ*. *ADMMP* on the other hand assumes the functional being used to be [Local Density Approximation](#page-12-3) [\(LDA\)](#page-12-3) (or [LDA](#page-12-3) being a good enough first-order approximation of the employed functional), permitting to factor out ξ^2 from both exact and DFT exchange energy. As Merlot et al.[[64](#page-125-3)] already mentioned, applying the *McWeeny* transformation on top of *ADMMQ* (and by extension *ADMMS*, *ADMMP*) is indeed possible, but brings back the non-trivial dependence of the auxiliary density matrix on the full one.

It should also be noted that in any case the auxiliary orbitals obtained are not directly connected to the primary ones in a physical sense, i.e. the resulting energy eigenvalues may be different. This is particularly the case for the *purified* variant which should subsequently not be used for calculation of band gaps where correct orbital energies are relevant.

The concrete choice of the functional has been intentionally left out of the initial definition in [Equation](#page-36-2) [2.80,](#page-36-2) other than the requirement having to be of the [GGA](#page-12-4) type to capture the necessary interactions. A natural choice – and the default in CP2K – is be the *PBE* Exchange functional, adapted to the interaction potential used for the [ERI](#page-12-5) in the respective [HFX](#page-12-6) calculation itself. Other popular choices are either the full *PBE*, the *OPTX* [[65,](#page-125-4) [66](#page-125-5)] or the *B88* [[28](#page-123-0)] Exchange functionals.

2.6. k-point-enabled Hartree-Fock Exchange for ADMM

Finally we are going to extend the [ADMM](#page-12-1) approximation to a **k**-point dependent density matrix. As the density matrix $P_{\mu\nu}$ depends on the [MO](#page-12-0) coefficients $C_{\mu i}$ the extension of \hat{P} to the periodic case at the same **k**-points as the density matrix for the full basis becomes

$$
\hat{P}^{\mathbf{k}}_{\mu\nu} = \sum_{i} \hat{C}^{\mathbf{k}}_{\mu i} \hat{C}^{\mathbf{k}}_{\nu i}.
$$
 (2.95)

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Where $\hat{C}_{\mu i}^{\mathbf{k}}$ is given by

$$
\hat{C}_{\mathbf{k}} = \underbrace{\hat{S}_{\mathbf{k}}^{-1} Q_{\mathbf{k}}}_{=:A_{\mathbf{k}}} C_{\mathbf{k}} \tag{2.96}
$$

with \hat{S}_k and Q_k being the reciprocal space pure auxiliary basis and mixed basis overlaps from in [Equation](#page-36-3) [2.84](#page-36-3) written in a similar way as the overlap matrix S of the full basis from [Equation](#page-32-0) [2.66,](#page-32-0)

$$
\hat{S}_{nn'}^{\mathbf{k}} = \int \hat{\phi}_n(\mathbf{r}; \mathbf{k}) \hat{\phi}_{n'}(\mathbf{r}; \mathbf{k}) dr,
$$
\n
$$
Q_{nm}^{\mathbf{k}} = \int \hat{\phi}_n(\mathbf{r}; \mathbf{k}) \phi_m(\mathbf{r}; \mathbf{k}) dr,
$$
\n(2.97)

and then expanding $\phi_k(\mathbf{r}; \mathbf{k})$ into a Bloch sum with consistent cell displacements.

Given the linearity of this transformation for each of required quantities, this means that the full [ADMM](#page-12-1) fitting procedure for *ADMM2* can be done straight forward in real space (e.g. for each of the neighbours **R**), after Fourier transformed real-space density matrices have been obtained. By extension this also applies to the *ADMMQ* variations *ADMMS* and *ADMMP* mentioned in the preceeding section.

ADMM3 on the other hand may not be properly defined, since it relies on the notion of being able to define subsystems based on some physical property. While this makes sense for the primary unit cell, it becomes difficult to reason the same holds true for a density matrix $P_{\nu\mu}^{\bf R}$ which depends on an additional cell displacement vector. Whether or not the original blocking matrix should be reused for displacements beyond the Γ-point, is therefore unclear. Furthermore *ADMM3* relies on the sparsity of the density matrix, something which comes not as easily for the solid state case where **k**-points are being used in particular.

While the orthonormality-constrained *ADMM1* would be properly defined, it is much more complex and would require a minimisation procedure to determine the Lagrangian coefficients in each [SCF](#page-12-7) step and for each **k**-point. Hence it stands to reason whether an implementation is computationally reasonable. In particular since with *ADMMS* a similar or better performing variant of [ADMM](#page-12-1) is available, which is computationally less expensive[[64\]](#page-125-3).

It must be noted that care must be taken when it comes to building the list of neighbour cells to consider in the calculation: Due to the different reach of the primary and the auxiliary basis sets, the larger of both lists must be applied consistently for both sets.

Finally, we would like to point out that while density fitting approaches for periodic **k**-point-sampled [HFX](#page-12-6) with atom-centred [GTO](#page-12-8) have been implemented for example in Patterson[[67\]](#page-125-6), [ADMM](#page-12-1) differs from this approach by employing the auxiliary basis not only for the expansion of the [ERI,](#page-12-5) but also for the calculation of the [DFT](#page-12-2) correction term in [Equation](#page-36-2) [2.80](#page-36-2).

Implementation 3.

3.1. The revised MOLOPT protocol for Basis Set and Pseudopotential generation

Unless otherwise noted, we have used newly generated GTH [PP](#page-12-9) for all non-all-electron calculations, and a new family of [GTO](#page-12-8) basis sets for all CP2K calculations. As they have not been formally published before, we are giving some overview of the generation procedure and their general properties, here where not already covered by [Section 2.3](#page-26-0).

The MOLOPT [PP](#page-12-9) are norm-conserving separable dual-space Pseudopotentials as shown in [Equation](#page-28-0) [2.51](#page-28-0) and [Equation](#page-28-1) [2.53,](#page-28-1) but with neglected spin-orbit part, i.e.

$$
V_{\rm I}(\mathbf{r}, \mathbf{r}') = \sum_{i=1}^{3} \sum_{j=1}^{3} \sum_{m=-l}^{+l} Y_{l,m}(\mathbf{r}) p_i^l(r) h_{ij}^l p_j^l(r') Y_{l,m}^*(\mathbf{r}'). \tag{3.1}
$$

This means they contain all scalar parts of the relativistic [PP](#page-12-9), but not more.

Their generation followed the same procedure as the previously published GTH potentials by Krack [\[68\]](#page-125-7), which involves fitting of the local and non-local coefficients $\eta_{\rm oc}$, C_i and $h_i j^l$ (see [Equation](#page-28-2) [2.52](#page-28-2)) against ĺ atomic scalar-relativistic [AE](#page-12-10) calculations. The pseudopotentials were generated up to Radon and are included in the file POTENTIAL_UZH of the CP2K software package. As mentioned before, the dual-space [PP](#page-12-9) have a dependency on the [DFT](#page-12-2) functional being used during optimisation. Therefore three sets of [PP](#page-12-9) were generated, for the functionals PBE, SCAN and PBE0 as representatives for GGA, Meta-GGA and Hybrid functionals. Following the discussion about the the split into valence and core electrons, for several elements one more semi-core [PP](#page-12-9) have been generated. This includes all the alkali, as well as all elements starting from Scandium onward. The reference wave functions were generated using the CP2K integrated ATOM code within KS-[DFT](#page-12-2), and a third-order Douglas-Kroll Hamiltonian[[69](#page-125-8), [70](#page-126-0)]. For the optimisation, Powell's method [\[71\]](#page-126-1) was employed with a target accuracy of 0.003 eV for valence, semi-core and virtual state eigenvalues.

The procedure for generating the accompanying basis set family has been slightly altered compared to the previously published MOLOPT basis sets [\[46\]](#page-124-0) as explained in [Section 2.3.](#page-26-0) While the basis set family covers all chemical elements up to Rn as well, not all semi-core configurations have been included. The new valence basis set family (DZVP, TZVP, TZV2P) is therefore released as a revision and extension of the existing MOLOPT basis set family. As with the [PP](#page-12-9), the basis sets have been optimised with the three functionals PBE, SCAN and PBE0 as representatives for GGA, Meta-GGA and Hybrid functionals, as can be seen from their aliases. They are included in the CP2K package in the file BASIS_- MOLOPT_UZH.

Figure 3.1.: Number of molecules from the SMDB covering an individual element.

The contraction schemes for the all-electron variants (SZV, TZVPP, QZVPP) follow the *Ahlrichs def2* [\[53\]](#page-125-9) basis sets and are available for use with [GGA](#page-12-4) functionals (obtained with PBE) and with the [GAPW](#page-12-11) method. Their optimisation scheme followed the same protocol outlined below.

First, as a reference set of molecules, the database published by Weigend and Ahlrichs [\[53\]](#page-125-9) – in the following referred to as the [Small Molecules](#page-13-0) [Database \(SMDB\)](#page-13-0) – was used. This database covers most of the periodic table [Figure](#page-41-0) [3.1,](#page-41-0) except for the Lanthanides, and ensures optimising the basis set for use within a molecular environment rather than just an isolated atomistic one. For elements not (sufficiently) covered by the [SMDB,](#page-13-0) in particular the noble gases, the set of structures was augmented by single atomic systems.

The reference calculations were done with sufficiently large and fully uncontracted basis sets obtained from atomistic calculations with the ATOM code contained in CP2K.

Secondly, for the optimisation procedure, the new (to be optimised) basis was treated as an auxiliary basis set for the uncontracted one in the same way as an ADMM auxiliary basis for the primary basis set. The optimisation procedure then involved simultaneously maximising the overlap and minimising the condition number, as well as the difference in the generated electronic densities.

While the optimisation relied on the [SMDB](#page-13-0) for the selection of molecular systems to obtain reference calculations, it must be stressed that this part of the optimisation procedure did not aim for reproduction of any particular quantity other than the generated density itself.

3.2. The FLexible Automated Testing MANager

Orchestrating thousands of calculations while maintaining reproducibility and load balancing across different systems is a complex problem, as the vast number of available workflow managers illustrates [\[72\]](#page-126-2), of which many target data science or bioinformatics in particular. Adapating such a workflow manager is possible, but as the integration with

AiiDA later in this chapter shows, requires much adaption to generate input for or parse output from electronic structure codes while making structures and parameter sets, like basis sets or pseudopotentials, traceable. In the realm of materials science, available codes are Python ASE – which gained workflow capabilities rather recently –, AiiDA and pymatgen, with an additional number of more specialised solutions. Some larger computational materials science consortia concerned with highthroughput calculations and computational studies have setup online data sharing platforms, like Materials Cloud¹, Materials Project² MAD^3 and AFLOW⁴. While some of them existed when this project started, many of them were still heavily in flux, had or still have a different focus, and were, as such, not directly usable for our purpose or required extra infrastructure for the deployment.

In particular, we needed the following functionality covered:

- ▶ Explicit management of parameters like pseudopotentials and basis sets, including different versions of a basis set or pseudopotential in the same family as they are being tested and had to be occasionally reoptimised.
- ▶ Integration of unmanaged computes nodes (e.g. without a queueing manager like SLURM or PBS) is crucial to incorporate local resources in high-throughput calculations.
- \triangleright Load balancing over multiple single nodes to employ multiple local disconnected compute nodes.
- ▶ Integration of computing centres with queueing systems to accelerate calculations for structures with a high number of basis functions.
- \triangleright Asset tracking (in- and output) across all calculations for reproducibility across compute nodes and code versions.
- ▶ Templating of input configurations for CP2K.

Some of the required features, like the asset tracking (*Data Provenance*), would have been already covered by domain-specific workflow managers like AiiDA [\[73\]](#page-126-3) when the project started. Others, like the load balancing across multiple disconnected nodes, are still not natively supported in their latest version[[2](#page-122-0)] but would be achievable with additional plugins, some of which we have implemented as part of this work.

This has led us to develop the lean custom workflow management system "FLexible Automated Testing MANager" (FLATMAN), specifically tailored to testing computational chemistry parameters like basis sets and pseudopotentials. Given that many computational chemistry or materials science tools are written in Python, including the prominent Python ASE[[74](#page-126-4)], the AiiDA workflow tool, and the pymatgen library[[75](#page-126-5)], we followed the same direction and chose Python as the primary language. By an ongoing collaboration with the AiiDA community we ensured that components developed for FLATMAN could be reused in AiiDA or as standalone tools independently of FLATMAN to foster a growing software ecosystem around the CP2K software package. An excellent example of a similar endeavour for the ABINIT code is the AbiPy 5 package, 5: [https://github.com/abinit/](https://github.com/abinit/abipy) which has been instrumental for the setup of many high-throughput anal-
 a_{bipy} yses, such as a large-scale validation study for *GW* [[76](#page-126-6)].

1: [https://www.materialscloud.](https://www.materialscloud.org/) [org/](https://www.materialscloud.org/)

- 2: <https://materialsproject.org>
- 3: <https://nomad-lab.eu/>

4: <https://aflow.org/>

Figure 3.2.: Lifecycle of (calculation) tasks within FLATMAN. Deferring a task can prevent it from being run momentarily, but it is also used for importing already-run calculations for further processing. The transition from *new* to *pending* is used for nodes to allocate tasks to be run. The *running* state is synchronized with that of a workload manager (if used).

3.2.1. Architecture

The basic architecture of FLATMAN is based on the client-server model, with a communication protocol based on [Representational state transfer](#page-12-12) [\(REST\)](#page-12-12) [\[77](#page-126-7)] over encrypted HTTP with the [JavaScript Object Notation](#page-12-13) [\(JSON\)](#page-12-13) file format as the data interchange format. As a direct consequence must the web-, respectively, the application-server running the FLATMAN Application Server be accessible by all clients. This is illustrated in [Figure](#page-44-0) [3.3.](#page-44-0)

For task distribution over single compute nodes (as available in many lab setups), the easiest principle we found was a single task queue of jobs with each node running a worker (in FLATMAN called *runners*) picking tasks from that queue in a First In First Out (FIFO) order. Sites with workload managers like SLURM can be easily integrated by running a separate runner targeting that queuing manager and using a specific account for submission. And although not implemented, this same principle could be used to push jobs to sites from which the FLATMAN Application Server is not accessible, lifting the restriction of the FLATMAN Application Server having to be publicly available. To avoid a runner fetching jobs it can not run (e.g. due to missing code setup), jobs can be restricted to certain hosts and users, with the runners having to submit their hostname and the credentials of the FLATMAN user when requesting a new job from the task queue.

As typical in a [REST](#page-12-12)ful architecture, the clients – including the FLATMAN runners – are mostly stateless with the task state tracked on the server as illustrated in [Figure](#page-43-0) [3.2.](#page-43-0) By tracking the activity of runners by hostname and monitoring the task queue, interrupted runners (for example, due to node failures) can be easily determined and their work rescheduled. While this does not allow more complex automated error recovery as can be achieved with a more general solution like the work chains in AiiDA, this design has proven quite resilient to intermittent node failure while achieving a good task distribution over heterogeneous compute nodes and sites.

The stateless architecture of the clients also requires that most of the output data processing occurs on the server side. Since this data processing, which involves output parsing as well as fitting procedures, can be timeconsuming in terms of HTTP requests, this work is controlled by using 6: <https://celeryproject.org> a separate task queue managed by Celery⁶ as illustrated in [Figure](#page-45-0) [3.4](#page-45-0) and can be scaled as needed by adding more workers. The drawback of such a solution is that FLATMAN Workers (subprocesses started by Celery) must contain explicit support for each test type. In contrast to an architecture like AiiDA, where a code plugin contains the code to parse its code's output and parsing is done when fetching the output from the remote side (and that data node becoming immutable), FLATMAN allows regenerating results from the original as needed. The architecture makes use of the possibility to specify dependencies and event listeners in the Celery task queue such that a forced refresh of the parsed data automatically leads to the regeneration of dependent values, such as a Birch-Murnaghan equation of state fitting procedure to obtain an equilibrium volume and bulk modulus. This allowed us to add additional code output parsers (like the one to parse condition numbers from the CP2K output) later in the project or improve our existing parsers without

having to rerun calculations or having to resort to more complex caching mechanisms.

To verify the format of the [JSON](#page-12-13) data in the communication and parse additional data (query parameters, extra HTTP headers) in the requests, a serialization/deserialization schema using the *webargs* and *marshmal* low^7 packages were used, with the venerable Flask⁸ web development kit τ : [https://marshmallow.](https://marshmallow.readthedocs.io/) to implement a WSGI-compatible application served by uWSGI⁹. Strict use of database transactions have been implemented to ensure data integrity. When a runner allocates a task (e.g. a task is set to *pending*), files need to get generated and corresponding database records stored. Only when all succeed is the whole transaction committed. This transactional functionality is provided by the underlying PostgreSQL SQL Database Management System (DBMS) and made readily accessible within Python by the Object Relational Mapper (ORM) of SQLAlchemy¹⁰. While inter- 10: <https://www.sqlalchemy.org/> mittent failures mean that files are temporarily stored in the data directory which lack a reference in the database These can easily be cleaned out by a periodic task pruning orphaned files. On the other hand it can never occur that a database entry is created with missing files, which we consider much more important. This improves robustness significantly, while allowing us to keep the database and data tree compact.

The web frontend (FLATMAN Web Application) is written as a Single Page Application (SPA) in TypeScript with the Angular¹¹ web frame- 11: <https://angular.io/> work. It uses the same [REST](#page-12-12) [Application Programming Interface \(API\)](#page-12-14) as the FLATMAN runners and the command line client (CLI) to get the data from the application server. Such an architecture avoids a divergence in functionality between the different interfaces and forces proper asynchronous task management on the server side to avoid blocking requests. However it requires synchronisation of the front- and backend-code to be able to give the user early feedback on input validation. With the web-interface implemented mainly for browsing, this could be kept minimal.

Figure 3.3.: FLATMAN software components and their dependencies. Items set in italic are off-the-shelf components. The FLATMAN web application can be served by the same server, which in turn uses the Javascript XMLHttpRequest method to make a request to the *FLATMAN REST [API](#page-12-14)* served by the *FLATMAN Application*. While some code is shared between the *Worker* and the *Application Server*, the communication between them is strictly asynchronous via *Celery*, which in turn uses *Redis* as its backend.

[readthedocs.io/](https://marshmallow.readthedocs.io/) 8: [https://flask.palletsprojects.](https://flask.palletsprojects.com/) [com/](https://flask.palletsprojects.com/) 9: [https://uwsgi-docs.](https://uwsgi-docs.readthedocs.io) [readthedocs.io](https://uwsgi-docs.readthedocs.io)

Figure 3.4.: Sequence diagram of the FLATMAN calculation output upload on the user's behalf by either the command line interface (CLI) or the *fdaemon* service to generate a test result (Δ-test, GW100). The calls to *Celery/Redis* from the application are done asynchronously and are linked: Only if the function execution of generate_calculation_results in the context of the *FLATMAN Worker* succeeds, will *Celery* schedule the execution of generate_test_result. Only the initial call and the link are specified in the *FLATMAN Application* context. Also, the execution of the functions generate_calculation_results, generate_test_result and generate_test_result_<X> do not have to be run by the same worker but can be executed by any of the workers in the worker pool. By locking the database for an update, the execution of the actual test result generation (consisting of a fitting procedure and database record generation) is serialized.

3.3. Comparison of automation approaches

In this work, we have implemented three different methods of calculation automatisation: With the bespoke workflow management solution FLATMAN, the more general but materials science specific AiiDA and a manual approach using CP2K preprocessor directives. The Δ-test values for the previously published MOLOPT basis sets $[1, 46]$ $[1, 46]$ $[1, 46]$ as well as preliminary results for the [SMDB](#page-13-0) have been obtained with FLATMAN. At the same time, AiiDA has been used for running the Δ-test with the revised MOLOPT basis sets, and the CP2K preprocessor directives approach was used for the molecular database calculations.

With hundreds of available workflow projects, as we uncovered in a recent survey[[72\]](#page-126-2), the development of any new general-purpose workflow management system must be met with scrutiny. As already observed by da Silva et al.[[78](#page-126-8)], workflow management tools are often spun out of scripting frameworks already in use in a workgroup, rather than developed from scratch. Gradually adding additional features which may cover features otherwise found in full-fledged workflow management tools is from that perspective then only part of the progress to satisfy immediate needs. In particular, since often thought-after features such as running commands or copying data are easily implemented in any scripting language, if only a very limited number of methods must be supported (e.g. only running calculations directly via mpirun). In contrast, many general purpose workflow managers for [High-performance](#page-12-15) [computing \(HPC\)](#page-12-15) have a rather steep learning curve due to the higher abstraction, or non-negligible setup cost, and are often coupled with nomenclature likely foreign to a domain scientist [\[79\]](#page-126-9). General-purpose workflow managers often lack support for tools and applications used in a scientific domain, increasing the initial cost of adoption. After that initial hurdle though, they quickly start to outpace bespoke frameworks

since they often provide rich ecosystems of plugins (such as the AiiDA registry ¹²) and support for various transport mechanisms and workload 12: [https://aiidateam.github.io/](https://aiidateam.github.io/aiida-registry/) managers (SLURM, PBS, etc.). But if bespoke frameworks are developed [aiida-registry/](https://aiidateam.github.io/aiida-registry/) in a way such that their components are reusable components, as in the design of FLATMAN, which now shares code with the AiiDA CP2K plugin and other tools, transitioning between the two paradigms as-needed becomes easier.

While this work shares many characteristics with the high-throughput efforts mentioned above, its immediate goals are different. While different model systems are calculated, we are mainly interested in the evaluation of the codes (CP2K, SIRIUS) and their respectively calculation parameters (basis sets, pseudopotentials, functional). More explicitly stated, we are not varying the structures under investigation for the same parameter set, but we are varying the parameters for the same structures. This directly implies that the database (the molecular or solid-state description) remains largely unchanged over the course of the project. Instead, it must be expected that manual adjustments to parameters are required more frequently in the initial stage of such a project. This covers both parameters applied to all calculations in a test, like the calculation of initial magnetisation parameters or reference cells, as well as systemspecific corrections. In a suitable workflow system, the possibility of quickly iterating between modifications of the templating engine (taking the abstract input parameters, a specification of the physical system, and a description of the target machine on which to run the workload) is therefore crucial. The templating engine itself must be flexible enough to allow the specification of custom rules to make per-system parameters possible in the first place. An a-posteriori connection between the abstract input, the generated input for the code, and the output of both the electronic structure code and the fitting procedure must be establishable for publication. Another important feature is the efficient usage of available resources, which can vary over the course of such a project from local compute nodes to running on clusters and mixed environments. Finally, it must be assumed that codes have many failing modes, requiring proper output parsing to detect them properly. Any workflow manager relying on caches to determine whether to rerun calculations must be able to determine whether a calculation has finished correctly.

CP2K preprocessor directives Relying purely on the CP2K preprocessor and a small number of scripts (shell scripts, GNU Makefiles) can avoid any friction introduced by intermediate layers like templating layers. It allows for quick iteration between running codes and adjusting runtime parameters. It is suitable for calculations running on mostly one machine and where calculations can be assumed to be robust enough to succeed. The drawback of this approach is that one must manually track reruns in case of changed parameters (including basis sets) and overall progress itself. Distribution of the work on multiple compute nodes must be done manually unless a workflow manager specialised only in task distribution is introduced at this point. This incurs the least upfront cost while shifting most of the required time to manual a-posteriori evaluation of the output.

Bespoke workflow manager FLATMAN This approach had the advantage of combining much of the simplicity of the simple scripting approach above with a high degree of automation, enabled by the design of FLATMAN. It allows for both manual single runs making it possible to inspect automatically generated code input and trial runs, and fully automated load-balanced task distribution across single node instances and workload manager (SLURM) driven supercomputing centres. The task queue model permits automated parameter fitting as soon as enough data is generated and live status overview to detect sudden systematic errors early. It still has limited retry capabilities in case of intermittent failures, yet the task pull architecture limits the effect of such failures. Automated reruns due to changed parameters must still be done manually and thus require careful tracking of changes. The drawback of this approach was clearly the time required for development of basic facilities and extensions, even if a large part of it could be salvaged by the component based architecture.

AiiDA with CP2K and custom workflow plugins The AiiDA workflow manager provides facilities for automated task submission to various types of computing resources. It features strong provenance tracking allowing for graph-assisted tracking of input parameters to output data and automated export and publishing capabilities to the Materials Cloud project. While this resolves various tedious tasks around running calculations, additional plugins are needed to handle other aspects. An extended version of the aiida-cp2k plugin and a separate data plugin were developed to manage GTO basis sets and pseudopotentials. Relying solely on the built-in file data plugin was not possible as this would track basis sets and pseudopotentials only via implicit code parameters and file content, requiring either manual tracking of calculations to rerun in the case of updated basis sets or having to avoid rerunning unaffected calculations due to the changed file contents. This is due to how the caching of calculations within AiiDA works: based on changes in the input AiiDA determines whether a calculation step needs to be rerun (and which generates new output nodes) or whether the existing output nodes can be reused. If all calculations were to use the same data file, an update or extension to this file would trigger AiiDA to rerun all calculations using this data file if the workflow were to be called again. Another restriction imposed by the architecture of AiiDA is using specific resources for a single workflow rather than distributing tasks onto available resources at runtime. E.g. a code node is always directly tied to a computing resource. Hence the computing resource being used is determined for all sub-workflows and steps at the beginning of a workflow, together with the code. Loadbalancing over different computing resources, therefore, must be done externally to the workflow. The immutability of the code or compute nodes requires a manual restart of whole workflows, in case of changes to the compute or code configuration. This invalidates any already run single-point energy calculation and requires them to be rerun in such an event. Therefore, the implemented workflow in the forked aiida-cp2k plugin still requires explicit specification of the chemical element to run the Δ-test workflow for, with the iteration over elements having to be scripted separately. While this separate scripting was also used as an opportunity for load-balancing on the level of model systems, it partially defies the point of workflow automation. A workflow management sys-

tem should be efficiently usable beyond final benchmark runs. A final point in which the caching failed was the parsing of code output. The experimental nature of our protocol again influenced this and is unlikely to occur in a setting where the focus is on the simulated systems instead. In our case, we encountered many cases where the code (CP2K and SIRIUS) could not converge but also did not return proper error codes due to intermittent failures (e.g. compute node errors, scientific libraries). Such cases AiiDA (together with the present version of the aiida-cp2k plugin) considered successful runs, requiring time-consuming post-processing and analysis, followed by manually invalidating (e.g. deleting) affected calculations.

This comparison hopefully also illustrates how quickly the complexity of running seemingly simple tasks can increase. If strong data provenance is required or complex workflows must be orchestrated, a fully-fledged workflow manager like AiiDA has a clear advantage. Its current limitations considering task distribution make it difficult to be used in mixed computing environments and projects where the object under investigation is the code rather than the simulated system. Automation via code-provided tools (like the CP2K preprocessor definitions to include shared definitions) has the advantage of being easily accessible to any domain specialist, which is the intended audience in a project like ours. Combining this with a workflow manager to automate the process of task distribution (including up- and download to computing centres) will likely solve most issues. And in our case, the modular development of the FLATMAN components has proven invaluable.

3.4. CP2K Input Tools Python Package

While running CP2K calculations with the two workflow managers FLATMAN introduced in [Section 3.2](#page-41-1) and AiiDA[[73\]](#page-126-3), a common challenge emerged: validating, converting and importing CP2K input configuration. When running high-throughput calculations, a scientist will eventually use the workflow tools and language – in the example of AiiDA, the Python language and its dictionary syntax or YAML in the protocols, for FLATMAN, a [JSON](#page-12-13) representation – to write the CP2K input as part of their larger workflow. But more often than not, scientists will already have some CP2K configuration they would like to run via a workflow manager like AiiDA or FLATMAN or use as a template for a new project with a workflow management tool. Furthermore, CP2K writes its restart files in the same input format, making it possible to parse output data from it, given a CP2K input format parser. And last, tools which integrate CP2K as part of their workflow (e.g. as a force calculator) must be able to parse a CP2K input file to obtain required data like the cell information and then generate modified CP2K input files. An example of this class of applications is Phonopy [\[80\]](#page-126-10), where the user specifies an input file of their code, and Phonopy will generate derived inputs for single site displacements to obtain the forces. For codes where the geometries are easily parseable because they are either in a specific place of the input configuration with a limited syntax variability (Quantum-Espresso) or even kept in a separate file (PODCAR) this is an easy enough task, but CP2K offers a much richer syntax when it comes to its input configuration which is

readily exploited by its users and thus requires greater care when parsing. A pure-Python package that can parse the CP2K input configuration and different data files like the basis set and pseudopotential formats is, therefore, crucial for the continued support of CP2K in the expanding quantum chemistry and material science software ecosystem.

The overall design of the input parsing framework is shown in [Figure](#page-51-0) [3.5.](#page-51-0) A layered approach has been taken, using Python iterators extensively to separate the different parsing tasks and to avoid extra copies of data structures. CP2K also features a preprocessor which allows for including other files, conditional blocks and variable assignments. The CP2KInputTokenizer class responsible for parsing a single configuration key is a state machine, making the whole architecture a one-pass parser which uses a stack to track any preprocessor variables and state, building a kind of syntax tree of the input configuration. Implementations of the CP2KInputParser will then use this tree to provide different representations of the CP2K input configuration. We are constantly maintaining the source context to give the user proper feedback on syntax errors, as seen in the screenshot in [Figure](#page-51-1) [3.6](#page-51-1), including the specific line and column. Together with a base language server protocol (LSP), this made it possible to easily implement a CP2K language server, permitting syntax checking of CP2K input directly in any editor supporting the LSP.

To validate a CP2K input configuration against a specific version of CP2K, the parsing framework uses the CP2K input configuration XML, which is a description of the available options and the input structure that CP2K can generate with the --xml, initially intended for the CP2K manual generation. In contrast to most other quantum chemistry code configurations, the CP2K configuration consists of not only sections with keywords but also nested sections (a tree-like structure). This generally maps very well to maps (*dictionaries* in Python) and lists available in most programming languages, together with their primitive datatypes. Complications for a simple one-to-one mapping without further descriptive elements (e.g. explicit *section* or *keyword* tags) arise in the case of having in the same section the identical word for both a section and a keyword (which within CP2K is resolved by the & marker to indicate the start of a section). Further inconsistencies are introduced by repeatable (parametrised) sections like the usual &KIND section, which calls either for a list of maps or a map of maps since the parameters must still be unique. The latter requires a special being introduced to capture the section parameter. This leads to the following rules for a (canonical) representation of the CP2K input configuration in Javascript Object Notation 13: The following rules and the refer- (JSON) in terms of Python objects as illustrated in [Figure](#page-52-0) 3.7^{13} 3.7^{13} :

enced code examples have also been published as part of the *cp2k-input-tools* package.

- \rightarrow repeatable sections are mapped to dictionaries
- \triangleright keywords or subsections are key/value entries in sections
- ▶ all repeatable elements (sections and keywords) are mapped to lists of their respective mapped datatype
- \triangleright section parameters are mapped to a special key named \preceq
- ▶ default section keywords are mapped to a special key name *
- ▶ sections in JSON must be prefixed to avoid the double definition of a key in case of the same name for a section and a keyword (like the POTENTIAL in KIND), to avoid quotation marks, instead of CP2K's & we are using the + character

 \triangleright keyword values are mapped based on their datatypes: a list of values is always mapped to a list of their respective datatypes

Based on the above restrictions, the format specification can be relaxed under the conditions followed below, leading to a simplified format as illustrated with JSON and YAML¹⁴ (YAML Ain't Markup LanguageTM) in 14: <https://yaml.org/> [Figure](#page-53-0) [3.8](#page-53-0). A derivation of this simplified object notation (with small differences in how multi-valued values for keywords are specified) is used in the AiiDA CP2K Plugin. It can also be emitted by the *cp2k-input-tools* library and command line interfaces.

- \triangleright a section only has to be prefixed with a + if a keyword with the same name is present at the same time in the same section. Given the XML input specification, we can resolve any ambiguities while parsing
- \triangleright if a repeated keyword or section contains only one entry, the list can be omitted. In case of ambiguity, priority is given to multiple values per keyword rather than keyword repetition
- ▶ sections with default parameters can be formulated as dictionaries as long as the default parameter values are unique and do not match section keywords or subsection names

Using a [JSON](#page-12-13) or YAML-derived format rather than the original CP2K input format in orchestration tools like FLATMAN or AiiDA has other advantages than a direct mapping to language constructs. They can be syntactically validated before the logical validation, they can be stored directly in JSON database columns as implemented in PostgreSQL or SQLite (as opposed to opaque text objects on disk or in a textual column), and last, there are already tools available to manipulate structured data like [JSON](#page-12-13) (e.g. *jq*) which facilitates the integration of CP2K itself in workflow orchestration tools.

The functionality described is implemented as a library, together with the command line tools (converters, language server, linters, prettifiers) on Github ¹⁵ under the MIT license. Release versions are automatically 15: [https://github.com/cp2k/](https://github.com/cp2k/cp2k-input-tools) deployed on Pypi 16 , after successful testing with code coverage above $^{cp2k-$ input-tools 90%. This library is used in Phonopy [\[80\]](#page-126-10) to read and generate CP2K input and has been integrated into the *aiida-gaussian-datatypes* plugin to parse CP2K basis set and pseudopotential files.

16: [https://pypi.org/project/](https://pypi.org/project/cp2k-input-tools/) [cp2k-input-tools/](https://pypi.org/project/cp2k-input-tools/)

Figure 3.5.: Class diagram of the main CP2K input tools classes. Different core parts of the parser have been split into separate classes to use *separation of concerns*, using *Generators* to avoid full storage of parsed segments. The parsed options are stored in a tree-like structure with the Section and Keyword dataclasses. The Context class stores original source file, line and character numbers across the complete input, allowing exact determination and feedback of parsing errors, including tracking of references of preprocessor variables and respective sections of the input schema definition.

1 **\$** cp2klint mysystem.inp

-
- 2 Syntax error: unterminated string detected, in mysystem.inp: 3 line 14: BASIS_SET_FILE_NAME "BASIS_MOLOPT_UCL
- . There \sim

Figure 3.6.: Example of a cp2klint output returning exact line number and column indicator.

1 &GLOBAL 2 PRINT LEVEL MEDIUM 3 **PROJECT** test RUN_TYPE ENERGY 5 &END GLOBAL 6 &FORCE_EVAL METHOD Quickstep 8 &DFT 9 BASIS_SET_FILE_NAME ./BASIS_SETS
10 POTENTIAL_FILE_NAME ./POTENTIALS 10 POTENTIAL_FILE_NAME ./POTENTIALS
11 &XC 11 &XC 12 &XC_FUNCTIONAL PBE 13 **&END XC_FUNCTIONAL** 14 &END XC 15 &END DFT 16 &SUBSYS
17 &CELI 17 & CELL
18 A 18 A [angstrom] 4.07 0.0 0.0
19 B [angstrom] 2.03 3.52 0.0 19 B [angstrom] 2.03 3.52 0.0 20 C [angstrom] 2.03 1.17 3.32 21 **PERIODIC XYZ**
22 **&END CELL** 22 &END CELL
23 &KIND Ge 23 &KIND Ge
24 ELEMEI ELEMENT Ge 25 POTENTIAL ALL-q32 26 BASIS_SET ORB pob-TZVP 27 &END KIND
28 &TOPOLOGY 28 &TOPOLOGY
29 COORD_ 29 **COORD_FILE** ./struct.xyz
30 **COORD_FILE_FORMAT** XYZ 30 COORD_FILE_FORMAT XYZ 31 &END TOPOLOGY 32 &END SUBSYS 33 &END FORCE_EVAL

```
\{ 1
 "+global": { 2
   "print_level": "medium", 3
"project_name": "test", 4
   "run_type": "energy" 5
 }, 6
"+force_eval": [ 7
   { 8
"method": "quickstep", 9
     "+DFT": {<br>
"basis_set_file_name": [ 10
      "basis_set_file_name": [ 11
        "./BASIS_SETS" 12
], 13
"potential_file_name":
↪ "./POTENTIALS"
                                  14
     \}, 15
     "+XC": { 16
"+xc_functional": { 17
"_": "PBE" 18
      \} 19
     \}, 20
     +subsys": {<br>"cell": { 22<br>22
      "cell": {<br>
"A": [4.07, 0, 0], 22<br>
23"A": [4.07, 0, 0], 23<br>
"B": [2.03, 3.52, 0], 24
        "B": [ 2.03, 3.52, 0 ], 24
"C": [ 2.03, 1.17, 3.32], 25
"periodic": "XYZ" 26
      \}, \frac{27}{1}, \frac{27}{2}<br>\frac{27}{2}<br>\frac{28}{2}<br>\frac{28}{2}"+kind": [<br>
"<br>
"_": "Ge",<br>
"element": "Ge",<br>
"potential": "ALL-q32", 33<br>
"basis_set": [<br>
[ "ORB", "pob-TZVP" ] 34
          \frac{1}{35}\} 36
        \frac{1}{2}, \frac{37}{2}"+topology": { 38
        "coord_file_name":
   ↪ "./struct.xyz",
                                  39
        "coord_file_format": "XYZ" 40
      } 41
     } 42
   \} 43
 \frac{1}{44}} 45
```
Figure 3.7.: Comparison of a CP2K input and its canonical JSON representation.

```
1\; {
 2 "global": {
  3 "print_level": "medium",
4 "project_name": "test",
            5 "run_type": "energy"
  6 },
7 "force_eval": {
 8 "method": "quickstep",
 9 "DFT": {
10 "basis_set_file_name":
↪ "./BASIS_SETS",
11 "potential_file_name":
           ↪ "./POTENTIALS"
12 },
13 "xc": {
14 "xc_functional": {
15 "_": "PBE"
16 }<br>
17 },<br>
"subsys": {<br>
20 "A": [ 4.07, 0.0, 0.0 ],<br>
21 "B": [ 2.03, 3.52, 0.0],<br>
22 "C": [ 2.03, 1.17, 3.32],<br>
"periodic": "XYZ"<br>
24 },<br>
"kind": {
26 "_": "Ge",
27 "element": "Ge",
28 "potential": "ALL-q32",
29 "basis_set": [ "ORB", "pob-TZVP"
     \leftrightarrow ]
\begin{array}{ccc} 30 & & & \frac{1}{2} \\ 31 & & & \frac{1}{2} \end{array}31 "topology": {
32 "coord_file_name":
               7struct.xyz",
33 "coord_file_format": "XYZ"
           }<sup>3</sup>
\begin{array}{cc} 35 \\ 36 \end{array} \qquad \qquad \Big\}3637 }
```


Figure 3.8.: Example of the same CP2K input as in [Figure](#page-52-0) [3.7](#page-52-0), but with simplification rules applied. The YAML format (used for the example on the right) as a superset of JSON can contain the same information, but due to its rules for structured indentation and quoting, it becomes even more condensed as the CP2K original in [Figure](#page-52-0) [3.7](#page-52-0) but retains the same legibility.

3.5. CP2K and Gaussian Output Tools Python Packages

In high-throughput calculations, being able to parse the output of codes efficiently, correctly and in a fault-tolerant way is vital as it directly affects further calculations and hence compute resources. While some codes like BigDFT[[81](#page-126-11)] have implemented a human and machine-readable output by adopting YAML as their primary format, this becomes quickly unfeasible with a highly complex code as CP2K and impossible for a closed source code like Gaussian[[82](#page-126-12)].

With the implementation of the *cp2k-output-tools*¹⁷ package, we provide 17: [https://github.com/cp2k/](https://github.com/cp2k/cp2k-output-tools) a Python library and command line tools which implement parsing the $\epsilon_{\text{p2k-output-tools}}$ most common blocks of CP2K output in an efficient way using regular expressions (regex). The package is organised as a set of parser functions acting on a string and which can be reused individually by any Python project as needed. The parsed data is stored in Python dataclasses as they provide a clear advantage over simple dictionaries in the form of semantic completion within text editors and, by integrating typing annotations, allow for additional correctness checks. Based on the integration of the Pint¹⁸ library, the data fields carry physical units to incorporate unit doc-

18: <https://pint.readthedocs.io> umentation in the code, making unit conversion easier and avoiding unit conversion errors in the process. In addition to the parsing blocks, the library also contains a more structured parser which returns a tree structure containing the various data objects. An example of such a tree structure in textual representation is shown in [Figure](#page-54-0) [3.9](#page-54-0). This tree structure corresponds to the nested method calls of CP2K, for example, employed in a geometry optimisation where each geometry optimisation step consists of an [SCF](#page-12-7) loop, which may be split into an inner and outer loop. Monitoring quantities and outputs across levels allows for quick analysis in high-throughput calculations, even in the presence of errors.

Additional tools – for example, Projected Density of States (PDOS) interpolation or bandstructure conversions – have also been implemented. Still, among those tools, the technique behind the *trajectory restart cleaner* is worth highlighting. When running [MD](#page-12-16) simulations, CP2K continuously writes trajectory files in XYZ format, which can be used to evaluate observables statistically. Upon restarts of the calculation, the restoration point may be several frames before the last entry in the trajectory, leading to multiple duplicated frames and statistically noticeable noise. As

CP2K: started at: 2021-02-23 22:57:53.427000 ended at: 2021-02-23 22:58:11.587000 CellInfoType.top cell volume: 39.167875 angstrom ** 3 CellInfoType.default cell volume: 39.167875 angstrom ** 3 CellInfoType.reference cell volume: 39.167875 angstrom ** 3 SCF: converged: True Total FORCE_EVAL energy: -7.944253454478329 hartree 10 Mulliken Population Analysis:
11 (present) 11 (present)
12 [warning]: Pr [warning]: Print MO Cubes not implemented for k-point calculations!! [warning]: Localization and MO related output not implemented for k-point calculations! Inner SCF: converged: True number of steps: 8

Figure 3.9.: Shortened example of a parsed CP2K output, showing proper Inner and Outer SCF loop detection with correct warning assignment.

CP2K includes a step number in the XYZ comment line, filtering the duplicated frames is possible. The challenge is the trajectories' size, which can easily grow to a couple of gigabytes. Handling huge text files efficiently is still an ongoing research topic [\[83\]](#page-126-13). However, the challenges we face here are limited computer memory and avoiding costly conversion operations and string handling by Python due to its extra conversion steps, often a performance bottleneck. To avoid the costly Python string operations, we are again resorting to regular expressions to find frames in the output, implemented behind Python iterator objects. The regex library is implemented in C and acts directly on text buffers, with string conversion to Python delayed until needed. To avoid loading the entire content of the trajectory into memory as a Python string and work around limited memory, we are directly using the operating systems (OS) memory mapping capabilities (*mmap*) in which the file gets mapped to an OS-managed buffer. As the regex engine sequentially accesses bytes in the array, the operating system automatically loads only required parts of the file in page units into memory, evicting previous pages. Buffering the loaded frames before writing until a restart point is detected (or a maximum number of frames has been buffered in memory) prevents high-frequency seeking, which for network filesystems like NFS works around the issue of higher latency for quick file system access. Combining those two techniques allowed us to clean gigabyte-sized trajectories several times faster than a previously implemented naive parsing approach based on line-based file iteration.

The *cp2k-output-tools* library and its accompanying command line utilities are published under the MIT license on Github, including a Continuous Integration setup with high coverage and released as an installable Python package on Pypi. It has been integrated into the *aiida-cp2k* plugin to parse additional data from CP2K output files in AiiDA workflows.

Since we also needed to parse Gaussian output as part of this thesis (see [Chapter 4\)](#page-60-0), a package following the same design principles as the *cp2k*19: [https://github.com/dev-zero/](https://github.com/dev-zero/gaussian-output-tools) *output-tools* was implemented, the *gaussian-output-tools*¹⁹.

[gaussian-output-tools](https://github.com/dev-zero/gaussian-output-tools)

3.6. Software Engineering in Computational Science

Software engineering techniques have not only played a role in the development of the FLATMAN workflow manager and its component-based architecture, which allowed the reuse of components across different projects. With long-running open-source projects like CP2K with many contributors, organisation and code quality become increasingly important to enable continued development. To that end the author contributed significantly to three aspects: the migration of the CP2K from the Subversion to the Git version control system, making the embedded Distributed Block Compressed Sparse Row (DBCSR) Matrix library a standalone project, and the introduction of the CMake build system first for said DBCSR library and then CP2K itself.

On Version Control Systems While collaboration and development do not necessarily rely on a Version Control System (VCS) to manage the project's source code or parameter data, using a VCS has significant advantages. Tracking changes to the source code alongside meaningful comments not only serves as a documentation of labour but also as an implicit form of documentation since most VCS provide an annotated source code view in which source code lines are shown next to the comment entered for that code change (e.g. for Git: git blame). This, in turn, allows tracing bugs back across releases and identifying copyright holders for individual files. The former is important for the reproducibility of results. At the same time, the latter becomes important in the case of relicensing, sometimes required to ensure collaboration with industry, which relies on more permissive licensing than potentially chosen at the beginning of a project (e.g. BSD-style license instead of GPL). The continuous recording of authorship also permits easy tracking down people for collaborative work within a specific area. Something which becomes increasingly difficult for a large project like CP2K.

For new projects, the choice of VCS is often not done consciously but decided based on what the original authors are familiar with, which VCS is most popular or for which free online resources for sharing are available. For CP2K, the collaborative platform chosen at the time was Sourceforge, which initially offered the hosting of CVS and later Subversion code repositories. Both VCS have a clear client-server model in which the server hosts the master version, and each commit done by a contributor is uploaded to the server (on the master version or a branch). Any conflicts arising due to the master version having advanced while the changes in a commit still rely on a previous state of the source code have to be resolved at the time of commit by the user. While this client-server paradigm makes for a linear development model with a low entry barrier, it has shortcomings when it comes to collaboration and ensuring coding standards. The dedicated master service requires everyone who wants to commit on either the master or a separate branch to have an account with the service, often leading to patches being sent by email to the maintainers who then commit the changes with their credentials. Besides the time required by the maintainers to adapt and incorporate such patches, it also meant the occasional loss of authorship since credentials for committing and author of the commit are coincident in such systems. A second challenge arises from the fact that branching in either CVS or Subversion – while possible – is rather cumbersome and again requires the person who wishes to create such a branch certain access rights to the repository. It furthermore makes running tests such as code style compliance checks before a commit unfeasible, often requiring a-posteriori work.

Distributed Version Control Systems (DVCS) like Git, together with publicly hosted services like Github or Gitlab, solve the issues mentioned above. The distributed aspect of a DVCS means that every participant will automatically get a fully separate copy of a project's complete versioned source code. On this copy, a contributor can then create branches and submit commits. The implication of such a model is that conflicts arising when merging changes from one repository to another (in whatever fashion) need to be resolved at the time of the merge rather than at the time of commit, potentially requiring multiple conflict resolutions, one for each commit. This further implies that the immutability of commits from non-distributed VCS is relaxed so that commits can be rearranged and altered. Each commit then also carries both an author and a committer, solving the problem of losing authorship. Services like Github not only host repositories, but they also provide workflows to send and incorporate commits from other copies (called *forks*) in what the services call *Pull* or *Merge* Requests. Furthermore, they provide tasks to be run on such requests, allowing for a priori checks to be run, solving the other mentioned challenge of non-distributed VCS. Altogether this allows for a much more dynamic development in which different parties can work largely independently while making their changes publicly available once they see fit. Being able to commit independently results in commits being more atomic rather than lumping multiple unrelated changes together into one, helping with code review and therefore code quality.

The migration of CP2K from Subversion to Git involved not only a simple import (for which tools are available) but to preserve copyright holders and history. Care had to be taken to mirror each commit. This required several passes in which usernames were mapped, directory reorganizations had to be correctly tracked, and tags and branches to be recreated. With the service migration, existing workflows (both automated and manual) had to be adjusted, and users were guided towards using the new system. It must also be noted that even though Git is centred around the concept of *merging* in which changes can be pulled into a copy with many conflicts being resolved automatically, this has the negative effect of rendering the commit history of a project quickly unreadable as it becomes unclear where a specific commit originated from. To avoid this cluttering of the history, it was decided for the main repository only to permit a linear history, requiring authors to *rebase* their work onto the latest master before sending a *Pull Request*. Incidentally, this also prevents the issue common in DVCS in which tests on *Pull Requests* succeed, but once merged into the *main* branch, they start to fail despite not having generated any conflicts during the said merge. In the *rebase* development workflow, the *Pull Request* becomes the new state of the *main* branch once merged and thus prevents this corner case as well as shifts the integration work to the submitter of the *Pull Request*. Unfortunately, this *rebasing* workflow was, and occasionally still is, the source of some confusion within the developer community as it often requires more manual adjustment of commits than the more prominent *merge* strategy.

On Build Systems The scientific software ecosystem has seen drastic changes within the last twenty years. While most HPC software like CP2K was previously buildable with just BLAS/LAPACK, MPI and ScaLA-PACK, modularization and consolidation have led to large dependency trees. While this has allowed the field to advance more quickly by allowing to easily share common code like implementations of integration routines, correlation-exchange functionals and others, building software has become much more difficult. This can easily be illustrated by a dependency tree in [Figure](#page-59-0) [3.10](#page-59-0), generated with the Spack package manager for the CP2K package, which the author maintains. Such a dependency tree depends not only on the available packages on a system (compiler, scientific libraries) but also on the project's configuration. Advancing language standards while providing the developers with more advanced

constructs and simplifying development also have the potential of breaking unexpectedly with untested compilers.

A build system is therefore not only used to invoke the compiler and linker to build an executable reproducibly but also to configure the software (e.g. enable or disable code passages) based on features requested by the user via flags, check the consistency of the requested features, and to check whether the environment (compiler, provided libraries) satisfy the requirements. CP2K has been using a custom build system based on GNU Make and Python, focusing primarily on the building. The user then writes a configuration file specifying the preprocessor directives and compiler and linker flags. The separation of the DBCSR library into a separate project opened up the possibility of introducing the CMake build system for DBCSR, which is a slightly smaller codebase than CP2K itself, before adapting it for CP2K itself.

The CMake-based build system for DBCSR has the following additional features compared to the custom CP2K build system. It checks at configuration time for a series of required Fortran language constructs. This helps the user to identify potentially incompatible compilers before starting the compilation with an understandable error message. Required libraries are automatically discovered based on multiple mechanisms (pkgconfig, CMake, common library paths), accommodating most setups, including the Cray Programming Environment. Preprocessing the source code with the Fortran preprocessor Fypp has been integrated. The use of accelerator software development kits (CUDA, HIP/ROCm, OpenCL) has been integrated, and their use can be controlled via a single build configuration, which triggers respective discovery mechanisms. Likewise, for different small matrix multiplication libraries. The discovered BLAS library is checked for OpenMP compatibility, avoiding hard-to-debug numerical errors due to concurrency issues when using non-thread-safe libraries. The build system automatically builds complete [API](#page-12-14) documentation with the FORD documentation tool, which gets automatically deployed via a CI/CD system on GitHub. This makes it possible that most users can get a working configuration of DBCSR with a single command, avoiding common mistakes and potentially devastating inconsistencies in the library configuration.

Based on the above principles of the CMake build system adoption for the DBCSR library, a CMake-based build system for the whole CP2K project has been recently added.

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Figure 3.10.: Dependency tree for CP2K 2022.1 as generated with the Spack package manager for the *spec* cp2k +cosma +cuda +elpa +libint +libvori +libxc +mpi +openmp +pexsi +plumed +sirius +spglib cuda_arch=70 smm=libxsmm. The edges of the graph are colour coded depending on the type of dependency (build, link, run, test). Such a graph depends on available compilers and scientific libraries, in this case on OpenBLAS, Netlib ScaLAPACK, and OpenMPI with the GNU Compilers.

MOLOPT **Basis Sets and Pseudopotentials Benchmarks 4.**

4.1. Motivation

While localised basis sets like the Gaussian basis sets have been successfully used for decades in quantum chemistry and materials science, they do have some limitations. Unlike with plane-waves, it is not possible to increase the precision at will by simply increasing a cutoff, but larger basis sets must be explicitly generated. This is done by optimising contraction coefficients and exponents in the Gaussian basis sets such that calculations adequately reproduce specific properties (often the energy), obtained for example from databases of molecular energies or other quantities. Since optimising a larger number of exponents is still difficult, multiple approaches exist to directly construct them via recursion formulas[[51,](#page-124-1) [52](#page-124-2), [84](#page-126-14), [85\]](#page-126-15). By now, a vast number of of basis sets have been published [\[86,](#page-126-16) [87](#page-127-0)]; the *Basis Set Exchange* [[88\]](#page-127-1) lists almost 700 families of basis sets. Although many of them are attuned to specific systems or methods, and often cover only a subset of the elements on the periodic table. Yet, new basis sets are still developed[[89](#page-127-2), [90](#page-127-3)].

Additionally, they are closely tied to the underlying method of handling the core electrons and the charge distribution near the nucleus, segmenting them into either *all-electron* or *pseudopotential* (resp. *valence*) basis sets. Finally, the specific method (Density Functional Theory or Hartree-Fock and post-HF) to approximate the wave function is inherently reflected in the generated coefficients. This becomes clearer when looking at *correlation-consistent* basis set families attuned to post-Hartree-Fock calculations, but also for DFT basis sets this may add a dependency on the functional being used. Failure to use the correct basis sets for the respective methods[[40](#page-124-3)] may then in fact lead to unreasonably large errors [\[41\]](#page-124-4). Finally, optimising basis sets with respect to energy alone does not guarantee convergence for other properties as they may not be cor-related[[91](#page-127-4)], thus careful validation is required. A basis set *family* describes a collection

In this work we will benchmark a revised edition of the *MOLOPT* family of basis sets and pseudopotentials [\[46\]](#page-124-0), particularly quantifying their improvements for increasing numbers of exponents and added polarisation terms, covering three rungs of Jacob's ladder (see [Chapter 2](#page-16-0)). This revised MOLOPT set now also features an [AE](#page-12-10) basis set, generated in the tradition of the *Karlsruhe def2* basis sets[[53\]](#page-125-9). A special focus will also be given towards assessing how well such a benchmark can be automated.

These MOLOPT basis sets and pseudopotentials are extensively used in, and shipped with the CP2K software package [\[1](#page-122-1)].

[4.1](#page-60-1) [Motivation](#page-60-1) [47](#page-60-1) [4.2](#page-61-0) [Methodology](#page-61-0) [48](#page-61-0) [4.3](#page-63-0) [Solid state benchmark](#page-63-0) [results](#page-63-0) [50](#page-63-0) [4.3.1](#page-64-0) [FP-LAPW](#page-64-0) [51](#page-64-0) [4.3.2](#page-64-1) [GTH Pseudopotentials](#page-64-1) . . . [51](#page-64-1) [4.3.3](#page-65-0) [MOLOPT Basis Sets](#page-65-0) [52](#page-65-0) [4.3.4](#page-66-0) [All-Electron MOLOPT](#page-66-0) [Basis Sets](#page-66-0) [53](#page-66-0) [4.3.5](#page-68-0) [All-Electron POB Basis Set](#page-68-0) [55](#page-68-0) [4.3.6](#page-69-0) [PBEsol](#page-69-0) [56](#page-69-0) **[4.4](#page-70-0) [Molecular benchmark](#page-70-0) [results](#page-70-0) [57](#page-70-0)** [4.4.1](#page-70-1) [Geometry](#page-70-1) [57](#page-70-1) [4.4.2](#page-72-0) [Dipole moments and](#page-72-0) [polarizability](#page-72-0) [59](#page-72-0) [4.4.3](#page-73-0) [Vibrational Spectra](#page-73-0) [60](#page-73-0) [4.4.4](#page-73-1) [ADMM](#page-73-1) [60](#page-73-1) [4.4.5](#page-74-0) [GAPW/All-Electron com](#page-74-0)[parison](#page-74-0) [61](#page-74-0) **[4.5](#page-79-0) [Conclusion](#page-79-0) [66](#page-79-0)**

of basis sets for a number of chemical elements. Often with multiple sets per element, where the different sets contain an increasing number of exponents ζ for the same momenta and/or cover increasingly higher momenta. A *family* basis set on the other hand describes a generally contracted basis set in which the exponents are shared between the contractions.

4.2. Methodology

To assess the quality of the MOLOPT basis sets and pseudopotentials we are looking at both a quantum chemical and a solid-state setting. There exist many different data bases of molecules along with referenced numbers for various use cases, quantities, functionals, or methods (of which [\[92–](#page-127-5)[98](#page-127-6)] cover a mere fraction), sometimes collected into even larger sets [\[99\]](#page-127-7). For this work we used as database for the quantum chemical case the already mentioned [SMDB](#page-13-0) by Weigend and Ahlrichs [\[53\]](#page-125-9), which consists of more than 300 small molecules. The reason is that it has a good coverage of most of the periodic table (excluding the Lanthanides, see also [Figure](#page-41-0) [3.1](#page-41-0) for coverage of elements by structures) and has been used in a similar function before.

This set of small molecules was also instrumental in the generation of this basis set family, but given the optimisation procedure outlined in [Section](#page-40-0) [3.1,](#page-40-0) there is no direct correlation between the calculated properties of those molecules and the basis set itself and it can therefore still serve as a reference database for performance comparison.

For the molecular database, we compare multiple properties for the GGA functional PBE, the meta-GGA TPSS and the hybrid PBE0 functionals of DFT which are described in [Chapter 2,](#page-16-0) each with the three different sizes of the basis set *DZVP*, *TZVP* and *TZV2P* and their respective pseudopotentials. The properties range from simple geometric comparisons of how well bond lengths and angles are reproduced to electronic properties like dipole moments, polarisability, as well as vibrational frequencies. For PBE this is done in a three-way comparison between G16 reference calculations, all-electron and pseudopotential calculations with CP2K, while the comparison for TPSS and PBE0 is between the G16 reference and the CP2K pseudopotential-based approach as shown in table [Table](#page-61-1) [4.1](#page-61-1).

The external reference values for these molecules have been obtained from calculations with the G16 software package [\[82\]](#page-126-12) and the all-electron *Def2-QZVP* basis set of Ahlrichs[[53\]](#page-125-9) with *tight* SCF conditions and an *ultrafine* integration grid.

To run the calculations with CP2K a cutoff and relative cutoff of 720 Ry and 60 Ry were used, with a decreased default epsilon of 1×10^{-14} for improved precision in integration grids. The convergence criteria for the energy was set to 1×10^{-7} .

To assess the quality of the basis set and pseudopotentials for the solidstateuse case, we relied on the Δ -test database of elemental solids [[100](#page-127-8)] and the Δ -gauge[[101](#page-127-9)] given by

$$
\Delta_i(a,b) := \sqrt{\frac{\int_{0.94V_{0,i}}^{1.06V_{0,i}} \left(E_{b,i}(V) - E_{a,i}(V) \right)^2 dV}{0.12V_{0,i}}},\tag{4.1}
$$

and where i denotes a chemical element and a and b for two results obtained with different codes, methods or parameter sets.

The function $E(V)$ is the internal energy function derived from the Birch-Murnaghan equation of states[[102](#page-128-0)]

Table 4.1.: Overview of available calculation sets for the Small Molecules Database

	G ₁₆ CP ₂ K	CP2K
	GPW	GAPW
PBE.		
TPSS		
PBE ₀		
ADMM		

$$
P(V) = \frac{3}{2}B_0 \left[\left(\frac{V_0}{V} \right)^{7/3} - \left(\frac{V_0}{V} \right)^{5/3} \right] \left\{ 1 + \frac{3}{4} (B_1 - 4) \left[\left(\frac{V_0}{V} \right)^{2/3} - 1 \right] \right\}
$$
 (4.2)

by integration over P , as

$$
E(V) = E_0 + \frac{9}{16} V_0 B_0 \left\{ \left[\left(\frac{V_0}{V} \right)^{2/3} - 1 \right]^3 B_1 + \left[\left(\frac{V_0}{V} \right)^{2/3} - 1 \right]^2 \left[6 - 4 \left(\frac{V_0}{V} \right)^{2/3} \right] \right\},
$$
\n(4.3)

with $B_1 = \frac{\partial B}{\partial P}\Big|_{P=0}$ the derivative of the bulk modulus B_0 . B_0 , B_1 and V_0 are determined from a fit on the energy of a bulk system for different volumes and the energy E_0 aligned such that the curves have their minimum at the same energy. The difference expressed in the Δ-gauge, therefore, comes from a shift in V_0 and skewness and opening of the slopes.

While this metric has been proven useful as a way to broadly assess differences in method implementations, it can not be used as a fitness function for optimisation, nor are values between different elements meaningfully comparable. The latter is a result of the naturally varying energies per atom around V_0 (and thus the integral value) for the different elements and the missing normalisation in [Equation](#page-61-2) [4.1](#page-61-2). Hence a direct comparison of the equilibrium volumes or bulk moduli may still be required to recover the full picture or to verify the quality of a pseudopotential or basis set for the required quantity to be reproduced.

For the calculations with CP2K (both [GPW](#page-12-17) and [GAPW](#page-12-11)), we have been using a high cutoff of 1000 Ry and relative cutoff of 200 Ry (for GAPW CP2K automatically reduces this, the stated numbers are the specified values in the input). To avoid spurious numerical artefacts in the integration, we are using a fixed reference cell for all the volume points based on 120 % of the anticipated V_0 cell. For [GAPW](#page-12-11) we used 100 and 250 grid points for the Lebedev and radial grids and decreased the default epsilon to 1×10 $^{-14}$. The energy convergence threshold was set to 1×10^{-8} except for a small number of elements which would otherwise not have succeeded. The **k**-point-mesh densities for the different elements are based on the initial suggestions of the Δ-test protocol used for the Wien2k reference calculations.

To obtain pure pseudopotential calculations without Gaussian basis sets we used the CP2K-integrated SIRIUS plane-wave code which was able to make use of the GTH pseudopotentials. The aforementioned reference grid was not employed for these calculations. The G_k and plane-wave cutoffs were set based on plane-wave Δ-test calculations with Quantum Espresso[[103](#page-128-1)] leading up to the SSSP library of pseudopotentials [\[104\]](#page-128-2), the same holds for the cold smearing and the **k**-point-mesh density.

To test the full potential linearized augmented plane wave (FP-LAPW+lo) implemention in SIRIUS as a means to obtain a full set of reference calculations from within one code (CP2K + SIRIUS), we used settings based

[be/sites/default/files/](https://molmod.ugent.be/sites/default/files/deltadftcodes/supplmat/SupplMat-Exciting.pdf) [deltadftcodes/supplmat/](https://molmod.ugent.be/sites/default/files/deltadftcodes/supplmat/SupplMat-Exciting.pdf) [SupplMat-Exciting.pdf](https://molmod.ugent.be/sites/default/files/deltadftcodes/supplmat/SupplMat-Exciting.pdf)

Table 4.2.: Overview of available CP2K (+SIRIUS) calculation sets for the solidstate benchmark in this work.

Table 4.3.: Mean Δ-values across the periodic table (rows 1-4 for GAPW) against the official Wien2k and SIRIUS LAPW and PW references from this work. Where multiple pseudopotentials with different numbers of valence electrons are available, the better one (usually the smaller core) has been used.

on the Exciting code as published in [\[105\]](#page-128-3), since SIRIUS' FP-LAPW facilities were carefully verified against the Exciting code. At this point it must be noted that the effectively used values for the calculation differ 1: [https://molmod.ugent.](https://molmod.ugent.be/sites/default/files/deltadftcodes/supplmat/SupplMat-Exciting.pdf) $from$ the summarised report at 1 , the effectively employed values were taken for this work and *IORA* [[106\]](#page-128-4) was used as the relativistic scheme. The Muffin-tin basis functions were generated with SIRIUS' atom command line utility with --auto_enu --order=2 --type=lo1, lo2, lo3, LO1, LO2 to allow an automatic search of the linearisation energy and include the maximum order of available local orbitals. While the Exciting basis used for the Δ-test reference calculations could be used after a format conversion, practical usage failed due to unsupported higher-order energy derivatives within SIRIUS at the point of the experiment.

> For the PBE [GPW](#page-12-17) calculations, we used the CP2K built-in implementation of the Exchange-Correlation functional, while the rest of the calculations (for CP2K with [GAPW](#page-12-11), SIRIUS) use the implementation provided by the *libxc* library [\[107\]](#page-128-5).

> For the extraction of the data from CP2K and G16 output files the cp2koutput-tools and gaussian-output-tools from [Section 3.5](#page-54-1) have been used, and the procedure to automate the Δ -test calculations is described in [Chapter 3](#page-40-1).

4.3. Solid state benchmark results

To assess the quality of the newly generated MOLOPT basis sets and pseudopotentials and to some extent, the CP2K and SIRIUS codes themselvesfor the solid-state case we are relying on the Δ -test-metric [[101](#page-127-9)] and the Δ-test-database[[100](#page-127-8)] since it provides a well-researched and curated database of values to compare against. [Table](#page-63-1) [4.2](#page-63-1) shows the different test sets generated for this evaluation, based on variations of the functional, method and basis set. In the following we are conducting a more thoroughdiscussion of the results. The raw data is available at $[108]$ $[108]$ $[108]$ and tables with the fitted Birch-Murnaghan coefficients can be found in [Chapter B.](#page-98-0) To complete the picture we also compare our all-electron basis sets with the second revised *pob* basis set family[[109](#page-128-7)–[112](#page-128-8)] which has been optimised for the use in, and verified against, crystalline systems.

Figure 4.1.: Δ-values for FP-LAPW obtained with SIRIUS compared against the published Wien2k reference.

Figure 4.2.: Δ-values for the GTH pseudopotentials obtained with the planewave code of SIRIUS integrated within CP2K compared against the published Wien2k reference. O, Cr-Ni are unavailable due to a bug in the interface between CP2K and SIRIUS while Sc, Ti are outliers under investigation.

4.3.1. FP-LAPW

The breakdown of the Δ-values for the [FP-LAPW](#page-12-18) method provided by SIRIUS within CP2K with the automatically generated muffin tin basis can be seen in [Figure](#page-64-2) [4.1.](#page-64-2) For most of the periodic table, an excellent match can be observed, especially for the first four rows which are well within the range of best-in-class codes with usually < 1 meV /atom. For the heavier elements in the sixth row of the transition metals, an unusual discrepancy can be observed, which could be attributed to either the generated muffin tin basis (and missing higher-order energy derivatives) or differences in how the relativistic effects are calculated. Another oddity is the failures in convergence for the lower part of the noble gases due to numerical issues, which, together with aluminium, phosphorus, chlorine and bromine, should be investigated further.

4.3.2. GTH Pseudopotentials

The verification of the GTH pseudopotentials is done via the plane-wave capabilities within CP2K provided by the SIRIUS integration and shown in [Figure](#page-64-3) [4.2](#page-64-3), with mean and median values of 3.04 meV /atom and 1.08 meV /atom respectively. When comparing this to the best-in-class GTH pseudopotentials at ² which are around in average 1 meV/atom, with non-linear 2: [https://molmod.ugent.be/](https://molmod.ugent.be/deltacodesdft) corecorrection (NLCC) [[113\]](#page-128-9), we fail to reproduce this value when including all converged and fitted systems. Removing the most obvious outliers (V, Cu, Zn, Nb-Pd, Ta-Ir, Au) from the comparison as similarly done in the published values, we can reproduce an average of 1 meV /atom

Table 4.4.: For most systems a pseudopotential with a larger number of valence electrons (*q* number) improves the agreement with the high-precision calculations as indicated for the selected elements with the Wien2k reference. Likely due to the more accurate modelling of delocalized electrons in the crystals. The opposite can be observed for a minor number of elements, likely due to effects previously captured in their pseudopotentials.

without applying NLCC. Limiting our analysis to the main group alone even yields an average of 0.93 meV /atom. As [Table](#page-65-1) [4.4](#page-65-1) shows, the pseudopotential selection can make a significant difference for the Δ-test value and possibly condensed systems in general.

4.3.3. MOLOPT Basis Sets

The results for the different sizes of the newly generated MOLOPT basis sets are shown in [Figure](#page-67-0) [4.4](#page-67-0), against the Wien2k and SIRIUS plane-wave references from Lejaeghere et al.[[100](#page-127-8)] and [Section 4.3.2](#page-64-1) respectively.

[Table](#page-66-1) [4.5](#page-66-1) shows a deviation of less than 10 % for the largest TZV2P basis sets compared to the plane-wave results. It is furthermore clear that the errors originating from the GTO basis sets are in the same order of magnitude as from the pseudoization approach. This is further confirmed by the detailed analysis in [Figure](#page-67-0) [4.4](#page-67-0), often showing a minor error as in the H-C, Si-Ti, Kr-Sn ranges. For some element ranges, an "overcorrection" can be observed, as in F case or the Cu-Ge series or in the stark case of Vanadium. This is not entirely surprising as the Δ-test does not allow a normalisation on the single atom energy and a small shift of V_0 can have a disproportionate effect.

Nonetheless, this analysis indicates elements for which further optimisation may be required to achieve more accurate results in the solid-state case. We can easily identify two categories: the first is elements with a significant difference but which improve measurably when increasing the basis set size. In the first three rows, Nitrogen and Oxygen fall into this category. The second is elements with a significant deviation from the mean but which do not improve with a larger basis, like the series As-Br.

Fluorine and Iridium require a short discussion as they allow additional insight. The first is an example of the *overcorrection* in the GPW approach compared to the plane-wave approach as illustrated in [Figure](#page-66-2) [4.3.](#page-66-2) In the plane-wave approach, the volume is underestimated while the GPW approach overestimates by almost the same percentage. This leads to error accumulation when comparing the GPW values against the PW values directly as verified in [Figure](#page-67-0) [4.4.](#page-67-0) It also serves as an example in which the bulk modulus and its derivative deviate significantly from the reference, yet this is not reflected in the Δ-value([Table](#page-66-3) [4.6](#page-66-3)). The GPW results for Iridium on the other hand have been omitted from the comparison in [Figure](#page-67-0) [4.4](#page-67-0) due to its large error on the Δ-value as reported in [Table](#page-66-3) [4.6](#page-66-3). The likely cause of this poor behaviour on the basis sets is the underrepresentation of Iridium in the Small Molecules Database [\(Figure](#page-41-0) [3.1\)](#page-41-0). Comparing the Δ-value for Iridium with the TZV2P basis set and Flourine in the plane-wave basis unearths a more critical deficiency in the Δ -test itself: despite a similar error in the equilibrium volume V_0 between Flourine and Iridium and smaller errors in B_0 and B_1 for Iridium is the Δ-value for Iridium an order of magnitude larger. The root cause is an absent energy normalisation which can not be implemented due to the missing general reference energy within electron structure theory. This leads to larger deviations in the Δ-value than would be expected due to the change in one of the parameters, and questions the meaning of an unweighted global average of Δ-values across the periodic table. Finally, for the practitioner, this again highlights the importance of direct quantity comparison rather than relying solely on Δ-values.

4.3.4. All-Electron MOLOPT Basis Sets

Besides the pseudopotential-based MOLOPT basis sets explored in the previous section, we also report the behaviour of the newly generated MOLOPT all-electron basis sets SZV, TZVPP and QZVPP. As the naming indicates, these basis sets use the same contraction patterns as the *def2* basis sets by Weigend and Ahlrichs [\[53\]](#page-125-9) and Weigend[[54\]](#page-125-10). For CP2K, the [GAPW](#page-12-11) method [\[36\]](#page-124-5) must be employed to model electron density around the atom centre with high enough accuracy without requiring an impractical amount of plane waves. At this point we are only interested

Table 4.5.: Mean Δ-values for the MOLOPT basis sets and pseudopotentials across all elements, respectively only the main group. The values for systems with non-vanishing magnetic moments are missing for the planewave values and reference due to initialisation issues in the code.

Figure 4.3.: Energy-Volume curve for Fluorine and Iridium, for Wien2k, SIRIUS and CP2K with the MOLOPT basis set for the *q7*, *q17* pseudopotential variants respectively.

Table 4.6.: Percent error for V_0 , B_0 and B_1 , and Δ-values with respect to Wien2k for Fluorine and Iridium for SIRIUS planewave and CP2K GPW for the *q7*, *q17* pseudopotential variants respectively.

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Figure 4.4.: PBE Δ-values for the MOLOPT basis sets against the Wien2k and CP2K + SIRIUS plane-wave references.

Table 4.7.: Average Δ-values for the first four rows of the periodic table for the allelectron MOLOPT basis set families SVP, TZVPP & QZVPP in meV /atom and the respective values of the GPW MOLOPT families DZVP, TZVP and TZV2P for the same subset of elements (see also [Fig](#page-69-1)[ure](#page-69-1) [4.5a\)](#page-69-1), both against the Wien2k reference.

in the all-electron basis sets, hence we limit ourselves to the first four rows of the periodic table since for rows five and six a pseudoization approach is used. Some transition metal values are further excluded due to challenges in reaching convergence.

As with the [GPW](#page-12-17) approach before, we can first note the consistent improvement of the Δ-values with larger basis sets, with a minor number of exceptions like nitrogen and sodium as shown in [Figure](#page-69-1) [4.5a.](#page-69-1) In particular, the averages for the QZVPP family are below 1 meV /atom as indicated in [Table](#page-68-1) [4.7](#page-68-1), placing this family and method amongst the bestperforming codes of the Δ-test benchmark. Comparing averages for the same subset of elements furthermore shows a significant improvement over the (GPW) families DZVP, TZVP & TZV2P. One can further observe the significantly larger error for the SVP family, drastically corrected at the TZVPP level.

4.3.5. All-Electron POB Basis Set

To obtain an additional external point of reference for the improvements of our MOLOPT family, we selected the revised POB basis set families DZVP and TZVP, and TZVPP[[111](#page-128-10), [112](#page-128-8)]. Besides the fact that these basis sets have been optimised for use in solid-state calculations, they also follow the same contraction scheme as the *def2* families and thus our own MOLOPT basis sets, but they use less diffuse primitives in general. We again restrict the comparison to the first four periods as the fifth and sixth periods employ effective core potentials (ECP), for which CP2K has only basic support, and which has been shown to require further improvements. [Figure](#page-69-1) [4.5b](#page-69-1) contains the overview of the converged calculations. The optimization procedure behind the generation of the POB basis set relied on a variational optimization approach for a database of compounds with single point energies obtained with the CRYSTAL09 code with the hybrid functional PW1PW. The verification was done against the CRYSTAL09-provided basis set by comparing lattice constants and other properties for both the PW1PW functional and Hartree-Fock calculations.

We observe an error which is on average an order of magnitude larger than obtained with any of the MOLOPT basis set families. Additionally, we do not observe the same systematic improvement for larger basis sets seen from the MOLOPT family. For the TZVPP variant, this may not be necessarily expected since it has not yet been revised, but also a comparison between the revised DZVP and TZVP does not exhibit this behaviour. A reason for this difference could be the optimization for hybrid calculations rather than plain DFT functionals.

(a) Δ-test values for the MOLOPT SVP, TZVPP, QZVPP all-electron basis sets against the Wien2k reference.

(b) Δ-test values for the POB DZVP-rev2, TZVP-rev2 and TZVPP all-electron basis sets against the Wien2k reference.

Figure 4.5.: GAPW-based all-electron Δ-test calculation results for MOLOPT and POB basis sets for the first 4 rows of the periodic table.

4.3.6. PBEsol

The support for [FP-LAPW](#page-12-18) calculations directly available within CP2K via the SIRIUS integration opens up a route to a complete chain of verification for arbitrary supported functionals within the same code [\(Figure](#page-69-2) [4.6\)](#page-69-2).

As a first example, we have chosen PBEsol due to its similarity to the well-validated PBE functional. As the overview in [Table](#page-63-2) [4.3](#page-63-2) illustrates, the difference in the mean Δ-value between plane-wave and LAPW values is less than 0.05 meV /atom. Unfortunately, this hides the fact that numerical instabilities in the SIRIUS LAPW code have thinned out the number of converged calculations across the periodic table from 56 to 35 elements. The results are therefore now limited to rows 1-3, 5 and the first two groups of the periodic table as shown in [Figure](#page-70-2) [4.7.](#page-70-2) Casual testing has shown that some of those instabilities vanish with smaller cutoffs than employed with our high accuracy settings.

The exact source of these instabilities could not be determined as for all calculations involving SIRIUS the LIBXC library has been used for the implementation of the exchange-correlation functional. With PBEsol being a reparametrisation of PBE and similar numerical issues having occurred for a smaller number of elements with the PBE functional, this may hint to a more fundamental issue with the numerics in the SIRIUS LAPW implementation in combination with the employed high precision settings

Figure 4.6.: The route to a fully automated GTH pseudopotential and GTO basis set verification within a single code.

Figure 4.7.: PBEsol Δ-values for planewave with MOLOPT pseudopotentials with SIRIUS LAPW as a reference.

or the automatically generated muffin tin basis. Further investigation of these issues, which have to be resolved to succeed at a fully automated benchmark with SIRIUS within CP2K, will be part of future work.

4.4. Molecular benchmark results

While for the solid-state benchmark only the alignment of the energyvolume curve was evaluated as a proxy for the overall performance of code and parameters, does the molecular benchmark permit a much more nuanced analysis.

4.4.1. Geometry

For the comparison of purely geometric properties, we are looking at relative errors for the bond lengths, and at absolute errors for the angles. Due to convergence issues when obtaining the reference values with G16 or comparison values with CP2K, not all molecules from the database are taken into account in the statistics. The frequency analysis in the following [Section 4.4.3](#page-73-0) has furthermore been used to filter molecules where the calculation inadvertently converged to a transient state rather than a minimum. Appendix [Chapter A](#page-94-0) and the data set[[114](#page-128-11)] contain the details of the setup and the raw data of the included molecules.

Analysis of the relative errors of bonds to their respective all-electron reference for each of the functionals PBE, TPSS and PBE0 in [Figure](#page-71-0) [4.8](#page-71-0) shows a consistent improvement for larger basis sets, reflected in lower median values and narrower interquartile ranges. The median values are consistently below 6 ‰ which corresponds to a difference of 0.01Å on the average bond length of 1.73Å in the database.

To verify this behaviour across different chemically important bonds, the same analysis has been repeated in [Figure](#page-75-0) [4.13](#page-75-0) for hydrogen and carbon bonds, the first 2 rows of the oxygen, nitrogen and fluorine groups, and metal complexes. The results from the inter-group comparison do not show a significant deviation for any particular element. We nonetheless observe larger errors for the oxygen and fluorine groups for the smaller basis sets *DZVP* and *TZVP*, which are only recovered when introducing an additional polarisation term in the *TZV2P* set. Carbon bonds are in general reproduced at a relative error of an order of magnitude lower

(b) Distribution of relative errors across all bonds. The outliers have been hidden to focus on the behaviour around the median, whiskers are drawn at 1.5x of the interquartile range $Q3 - Q1$.

(a) Mean relative errors across all bonds.

(c) Histograms are normalised to account for different availability of calculations across basis sets.

Figure 4.8.: Both (b) and (c) show the same trend, larger basis sets leading to a narrower spread as they reproduce the all-electron bond lengths much more accurately.

Figure 4.9.: For NiF₃ the largest angle may not always be located between the same Fluorine atoms, applying also to other highly symmetric molecules in the database like AuCl₃, AlH₃, etc.

than the average, although the number of such bonds within the database is rather low.

To automatically identify non-linear and dihedral angles we relied on the facilities of the G16 software package. As shown in [Figure](#page-72-1) [4.10](#page-72-1) the previously observed and anticipated trend for larger basis sets leading to narrower spread continues, in particular for the all-electron basis sets. The one notable exception here would be the TPSS functional, where larger basis sets tended to reproduce dihedral angles slightly worse. Comparing angles in a fully automated fashion and without additional chemical information has its difficulties: for highly constraint or even linear systems, many if not all angles are essentially fixed due to symmetries. Comparing such angles is then rather akin to a sanity check but its expressive power is reduced. Furthermore, for almost symmetrical systems, numerical noise can lead to obtuse angles occurring between different sites of the same kind, even with the same functionals but different basis sets, as the example of NiF_3 in [Figure](#page-71-1) [4.9](#page-71-1) illustrates. This could be solved on a case-by-case basis by simple permutation of equivalent sites if this information would be available in the database. We, therefore, limited ourselves to looking at the distribution of the maximum relative angle error and keeping trivial angles in the statistics.

(a) Distribution of the maximum relative error of angles per structure.

(b) Distribution of the maximum relative error of dihedral angles per structure.

Figure 4.10.: Relative errors of angles (non-linear and dihedral) for the small molecules database across functionals and basis sets.

4.4.2. Dipole moments and polarizability

For a number of selected molecules with non-vanishing dipole (and availability across all functionals), we compare the magnitude of the dipole moments with the resulting statistics of the relative errors plotted in [Fig](#page-72-0)[ure](#page-72-0) [4.11a.](#page-72-0) Comparing just the order of the relative errors to the purely geometric quantities from [Section 4.4.1](#page-70-0) we see a much larger variance in the results, which is not completely resolved by employing the [GAPW](#page-12-0) method in the same manner as for the vibrational modes discussed in [Section 4.4.3.](#page-73-0) The general trend for larger basis sets to improve the error continues nonetheless here, leading to median relative errors well below 2 %.

The comparison of the average molecular polarizability reveals the effect of basis set quality and size in the most striking manner, as illustrated in [Figure](#page-72-0) [4.11b](#page-72-0). The error continuously and significantly improves going from smallest to largest basis set within the same functional and method (pseudopotential vs. all-electron). On the other hand, the sensitivity of this quantity due to second-order derivatives and high-order geometric dependency leads to the largest relative errors of the studied properties.

(a) Distribution of the relative error of dipole moments (for 87 converged structures with non-vanishing dipole moment).

(b) Distribution of the relative error of the trace, TPSS missing due to unavailability of this property in CP2K for meta-GGA.

Figure 4.11.: Relative errors of dipole moments & average molecular polarizability.

4.4.3. Vibrational Spectra

When calculating and comparing vibrational spectra in a high-throughput fashion, the difficulty lies in correctly identifying and pruning low frequencies and matching the remaining ones. Pruning is required because different codes may not identify the same degenerate frequencies, and collapse them into one. Matching is needed since the list of frequencies produced by the codes are unlikely to agree in order or exact value. One reason for such mismatches to occur is the numerical differentiation, which may amplify differences in geometric properties or lead to nonnegligible low frequencies, indicating either an underlying problem with the structure itself or requiring even finer integration grids. Others are when a simulation inadvertently converged to a transient state instead of the true minimum, identifiable by significant negative frequencies. In either way, we have used a pre-screening on the vibrational spectra to exclude such structures completely from the analysis, assuming any good agreement in geometry (or other properties) would have been incidental and further manual investigation would be required to assess whether or not a structure is still meaningfully converged. Doing this in an automated fashion would require more elaborate machinery and likely more than just geometrical information in the database (e.g. validated chemical information). To compare the frequencies we are thus looking at the minimal relative error per frequency (when compared to the list of frequencies obtained from the reference), with the final comparison shown in [Figure](#page-76-0) [4.14](#page-76-0) based on the mean of the relative errors of the matched frequencies.

What can be observed in [Figure](#page-76-0) [4.14](#page-76-0) is the much larger average relative error as compared to the bond length comparisons, and while the median gradually improves for TPSS and PBE0, the same can not be observed for PBE with [GPW](#page-12-1) (e.g. pseudopotentials), or for the spread for all functionals with GPW. With the all-electron basis sets SVP, TZVPP and QZVPP, which employ the [GAPW](#page-12-0) method, we can recover the usual behaviour of significantly improved spread and median when going to larger basis sets. While the aforementioned difficulties for obtaining frequencies could be at play here, it is also possible that the improved precision by using [GAPW](#page-12-0) – which gives a finer radial grid around the atom to model the core charge distribution – resolves some of the numerical issues often plaguing frequency calculations.

4.4.4. ADMM

When applying Hartree-Fock exchange as part of a hybrid-functional calculation like PBE0, the computation becomes more expensive than a pure DFT calculation. Indeed, a $\mathcal{O}(N^4)$ dependency on the system size as previously outlined in [Section 2.5](#page-34-0) is introduced. This makes methods like the Auxiliary Density Matrix Method (ADMM) worthwhile to consider as it allows us to replace the basis used to calculate the Hartree-Fock exchange energy with a smaller one, provided it is able to reproduce the required observables accurately enough. Even though the systems in the [SMDB](#page-13-0) will not profit from a significant speedup, they will allow us to assess the quality of [ADMM](#page-12-2) and the newly generated [ADMM](#page-12-2) basis. This

Figure 4.12.: Comparison of relative errors for PBE0+ADMM calculations against PBE0, with CP2K.

new basis was generated with a matching size for each of the Hybrid subsets of the *DZVP*, *TZVP* and *TZV2P* of MOLOPT basis sets. Interesting in this case is therefore not only the error against the G16 reference value but also the error compared to the CP2K PBE0 calculation.

[Figure](#page-77-0) [4.15](#page-77-0) contains the comparison of a subset of 200 molecules for which ADMM calculation data was available for both PBE0 and PBE0 with ADMM, against the G16 reference values. While minor deviations and shifts in spread and median can be be observed for the smaller DZVP basis set, this effect vanishes for the larger TZVP and TZV2P basis sets completely. This is confirmed by a direct comparison of the [ADMM](#page-12-2) data against the CP2K PBE0 calculations in which the average errors for purely geometric values like bond lengths and angles drop below 2 ‰ and the more sensitive electronic properties below 1 %, as shown in [Fig](#page-74-0)[ure](#page-74-0) [4.12.](#page-74-0)

The indicated sizes describe the main basis set. For the auxiliary basis set we used the *admm-dzp* together with *DZVP*, and *admm-tzp* for both *TZVP* and *TZV2P*.

4.4.5. GAPW/All-Electron comparison

While the first sections have been focused on comparing CP2K and its basis sets and pseudopotentials against reference values obtained from G16 with an all-electron *def2* basis set, we are now focusing on an intra-CP2K comparison by comparing the pseudopotential MOLOPT basis sets for PBE against [AE](#page-12-3) *QZVPP* reference values. Since the previous evaluations have shown a very narrow error between *QZVPP* and the G16 values we believe that *QZVPP* can itself serve as a reference and will allow us to verify the consistency of the data within CP2K itself. Indeed, the sideby-side comparison in [Figure](#page-78-0) [4.16](#page-78-0) shows only small statistical deviations between the *MOLOPT* basis sets DZVP, TZVP, TZV2P and G16 on the left and CP2K with the QZVPP as a reference on the right.

Figure 4.13.: Distribution of relative errors across all bonds (with outliers hidden) for different groups of bonds, comparing different basis set sizes. For *C-C* bonds the range has been adjusted as their error is at an order of magnitude lower, but given the low number of such bonds, the results are skewed, especially for the all-electron basis sets. A similar situation occurs at the distribution for the SVP basis and bonds involving Fluorine or Chlorine where the spread is higher than for all other basis sets and functionals. For easier comparison and legibility reasons, we refrained from rescaling the axis again to accompany this specific boxplot where the upper whisker is at $E_R = 0.033$.

(a) Mean relative errors across a mean of minimal relative errors of frequencies.

(b) Distribution of minimal relative errors. The outliers have been hidden to focus on the behaviour around the median, whiskers are drawn at 1.5*x* of the interquartile range $Q3 - Q1$.

(c) Histograms are normalised to account for different availability of calculations across basis sets.

Figure 4.14.: Distribution of averages of minimal relative errors of vibrational modes.

Figure 4.15.: Comparison of relative (for angles: absolute) errors between PBE0/PBE0+ADMM and G16.

Figure 4.16.: Comparison of relative (for angles: absolute) errors between the MOLOPT basis sets DZVP, TZVP, TZV2P and the G16 and CP2K QZVPP reference values. Axis is truncated to focus on the distribution around the median.

4.5. Conclusion

We have shown that the revised *MOLOPT* basis sets are well-defined for a broad number of quantities and for both solid-state and molecular systems. As expexted, the results improve as one adds more functions or angular momenta. This behaviour has been shown to hold across the three functionals PBE, TPSS and PBE0, as well as with an ADMM calculation for PBE0. For the meta-GGA TPSS, it even shows that a pseudopotential and basis set optimised for a different functional of the same rung (SCAN) performs at a high enough precision to warrant its usage despite being optimised for a different functional.

For the solid-state case, we observed that semi-core pseudopotentials tend to lead to better results, likely due to the delocalization of electrons. The all-electron MOLOPT basis sets perform exceptionally well, also in cross-comparison with other basis sets based on similar principles of generation. This may indicate that the pseudopotentials can be a substantial source of deviation in such a high-accurracy calculation.

To be able to automate this analysis further, several improvements to either the database itself or the analysis tools must be made. For the database one likely has to follow the tradition of quantum chemistry data bases (like the GMTKN) and include validated reference data. This is in particular relevant for integer data, such as the number of vibrational frequencies and their degeneracies. But also identifying only (chemical) relevant frequencies would help to discover transition states. Other required data are symmetries, which can then be used to automatically validate the configuration and to match results between codes by e.g. automatic rotation of the molecules to minimize the RMSE of the position differences. Relying only on heuristic approaches, such as the ones we have implemented, is ultimately error-prone.

ADMM with k-point support in periodic Hartree-Fock Exchange 5.

In the previous [Chapter 4](#page-60-0) we have been using PBE0 as an example for a hybrid DFT functional, testing the portability of basis sets and pseudopotentials otherwise optimized for the GGA functional PBE on a set of molecular structures. It is in this context of Hybrid functionals that [HFX](#page-12-4) – despite its early introduction in Computational Chemistry[\[115](#page-128-0), [116\]](#page-128-1) – is still a very relevant target for optimization as it becomes the rate-limiting factor in the calculation of larger systems.

One aspect which has not been discussed previously in [Section 2.4](#page-31-0) is the challenge arising in the calculation of the [HFX](#page-12-4) energy in the reciprocal space, i.e. the sum of the diagonal terms of the [ERI](#page-12-5)

$$
E_{\mathbf{X}} = -\frac{1}{N^2} \sum_{\mu \nu \mathbf{k} \mathbf{k}'} P_{\mu \nu}^{\mathbf{k}} P_{\nu \mu}^{\mathbf{k}'} \iint \phi_{\mu}^* (\mathbf{r}_1; \mathbf{k}) \phi_{\nu}(\mathbf{r}_1; \mathbf{k}') \frac{1}{\|\mathbf{r}_2 - \mathbf{r}_1\|} \phi_{\nu}^* (\mathbf{r}_2; \mathbf{k}') \phi_{\mu}(\mathbf{r}_2; \mathbf{k}) d\mathbf{r}_1 d\mathbf{r}_2,
$$
\n(5.1)

which when expanded with Bloch functions for the ϕ_{μ} as in [Equation](#page-31-1) [2.56](#page-31-1) becomes a divergent series due to non-vanishing co-densities for $\mathbf{k} = \mathbf{k}'$, e.g.

$$
\int e^{(\mathbf{k'}-\mathbf{k})\cdot\mathbf{r}_1} \mathbf{u}(\mathbf{r}_1). \tag{5.2}
$$

There are different ways to resolve this divergence, one of them is based on adding an auxiliary function to the Exchange energy which cancels the divergent term and separately subtract it[[117\]](#page-128-2). The disadvantage of this auxiliary function is that it must match the crystal class for which E_X is to be calculated. Instead, we follow the Γ-point periodic [HFX](#page-12-4) implementation of CP2K, which directly replaces the Coulomb metric in the integration with a truncated Coulomb operator, based on the work bySpencer and Alavi [[118](#page-128-3)]. That is, the 1/ $\|\mathbf{r}_2 - \mathbf{r}_1\|$ in [Equation](#page-80-0) [5.1](#page-80-0) gets replaced by

$$
g_{\rm TC}(\mathbf{r}) = \begin{cases} \frac{1}{|\mathbf{r}|} & \text{if } |\mathbf{r}| \le R_c, \\ 0 & \text{otherwise} \end{cases} \tag{5.3}
$$

A well established value for this truncation radius is found to be at half the cell distance $L/2$. For the [DFT](#page-12-6) correction in [ADMM](#page-12-2) (the DFT Exchange functional, see [Equation](#page-36-0) [2.80\)](#page-36-0) it is then only natural to apply the same truncation as for the Exchange energy. This is also the default within CP2K.

As we have shown in [Chapter 2,](#page-16-0) actually calculating the [HFX](#page-12-4) energy in a Gaussian-Type basis set based code for a periodic system with **k**-point sampling is not entirely trivial and computationally expensive. Yet, there are some codes which have supported this for some time [\[119\]](#page-128-4) or have gained experimental support as of late[[120](#page-129-0)]. Our contribution, which

we are going to discuss here is not only the addition of [HFX](#page-12-4) implementation which supports **k**-point sampling to CP2K, but also its novel combination with [ADMM](#page-12-2). The latter allows us to use a significantly smaller basis without a noticeable reduction in accuracy, which is crucial to reduce the number of four-centre integrals to calculate.

We consider the implementations above, as well as our own, canonical implementations. In the sense that besides employing usual identities like $P_{\mu\nu}^T = P_{\nu\mu}^{-T}$ (and corresponding for the Exchange matrix) as well as applying required truncation schemes to avoid the divergence and limit the problem to a finite number of neighbour cells, no other optimisations are being used to tackle the actual computational complexity.

This is in contrast to [Resolution of Identity \(RI\)](#page-12-7) approaches with suitable auxiliary basis sets to reduce the [ERIs](#page-12-5) from 4- to 3 or 2-centre integrals in [HF](#page-12-8) $[121, 122]$ $[121, 122]$ $[121, 122]$ or Post[-HF](#page-12-8) methods $[123-125]$ $[123-125]$ $[123-125]$ $[123-125]$ $[123-125]$, as well as the more refined approaches developed in the group of Head-Gordon[[126,](#page-129-5) [127](#page-129-6)]. In their [occupied orbital RI-K \(occ-RI-K\)](#page-12-9) approach, several components are combined to obtain a very efficient (in both compute and memory usage) algorithm. The focus herein lies on the efficient construction of the exchange matrix K since fast methods for the J matrix which covers the classical Coulomb interaction have already been established prior[[128](#page-129-7)– [130](#page-129-8)]. The [RI](#page-12-7) approach reduces the the [ERI](#page-12-5) to a 2-centre quantity by introducing an auxiliary basis in which to expand the co-densities

$$
\phi_{\mu}^{*}(\mathbf{r}_{1})\phi_{\lambda}(\mathbf{r}_{1}) = \sum_{Q} C_{Q}^{\mu\lambda} \chi_{Q}(\mathbf{r}_{1}), \qquad (5.4)
$$

leading to a simpler expression for K

$$
K_{\mu\nu} = \sum_{\lambda\sigma} \sum_{PQ} C_P^{\mu\lambda} C_Q^{\nu\sigma}(P|Q) P_{\lambda\sigma r}.
$$
 (5.5)

The improvement then comes by exploiting the fact that for both the energy (which requires only the diagonal elements of the exchange matrix in the first place) and gradient only the occupied [MO](#page-12-10) must be taken into account. When employing the [Direct Inversion of the Iterative Sub](#page-12-11)[space \(DIIS\)](#page-12-11) method, this finds direct application as in that case only the product of the Fock and density matrix are required to construct the [DIIS](#page-12-11) error vector, and thus only elements corresponding to occupied [MO](#page-12-10) contribute. The combination of this *compression* of the *K* matrix together with [RI](#page-12-7) approach then loads to a reported speed-up from 3-5x compared to other [RI](#page-12-7) approaches [\[131\]](#page-129-9) in a molecular setting. This can then be extended to the solid state use case[[126,](#page-129-5) [132](#page-129-10)] by following the same construction of the periodic [HFX](#page-12-4) in a [GTO](#page-12-12) framework. Going further, the group then progresses by combining this with the Tensor Hypercontraction framework[[133](#page-129-11)–[135](#page-129-12)] (respectively, [interpolative separable density](#page-12-13) [fitting \(ISDF\)](#page-12-13)) into a *THC-oo-K* algorithm. The main idea being the expansion of products of atomic orbitals into a sum of interpolation vectors, weighted by the orbitals

$$
\phi_{\mu}(\mathbf{r})^* \phi_{\nu}(\mathbf{r}) \approx \sum_{P}^{N_{\text{ISDF}}} \phi_{\mu}(\mathbf{r}_P)^* \phi_{\nu}(\mathbf{r}_P) \xi_P^{[nn]}(\mathbf{r}), \qquad (5.6)
$$

which then leads to a simplified (approximated) exchange matrix which only needs the basis functions at a set of interpolation points N_{ISDF} and integration between the the interpolation vectors $\xi_P(r)$

$$
M_{PQ} = \iint d\mathbf{r}_1 d\mathbf{r}_2 \frac{\xi_P(\mathbf{r}_1) \xi_Q(\mathbf{r}_2)}{r_{12}}.
$$
 (5.7)

This is then extended towards a periodic **k**-point [ISDF](#page-12-13) and adapted to fit only occupied orbitals.

5.1. Verification of HFXk

As base for the verification path as depicted in [Figure](#page-82-0) [5.1](#page-82-0) we are using the well-studied [Hexagonal boron nitride \(h-BN\)](#page-12-15) and [Lithiumhydrid \(LiH\)](#page-12-16) systems as examples for 2D and 3D systems. We are furthermore using the fact that when taking the supercell or superlattice of a primitive unit cell and calculating the system at the Γ-point, this corresponds to a sampling of the reciprocal space. Due to the Fourier transformation between real and reciprocal space, identifying special points relevant for studying bulk or surface materials is not as easily done in the supercell approach as when employing solely **k**-point sampling [\[136\]](#page-129-13). Likewise, band structures obtained from supercell calculations are folded upon themselves, requiring extra treatment [\[137,](#page-130-0) [138\]](#page-130-1). To sample the **k**-point space we are using a regular Monkhorst-Pack [\[139\]](#page-130-2) grid. The issue of the band-folding or explicitly identifying relevant symmetry points in reciprocal space is not relevant for achieving converged total energies given fine enough mesh grids, number of supercells respectively. The detailed results of this can be seen in [Figure](#page-83-0) [5.2](#page-83-0) and [Figure](#page-84-0) [5.3](#page-84-0), respectively. We can conclude that an MKP grid of $9x9(x9)$, respectivly a supercell of $5x5(x5)$ is enough to achieve convergence for both systems as well as an agreement between the total energies of 1.106×10−5 E^h for [LiH](#page-12-16) and 1.254×10−4 E^h for [h-BN,](#page-12-15) using the revised all-electron POB DZVP basis set[[112\]](#page-128-5) employing the [GAPW](#page-12-0) method, and a moderate EPS_SCF of 1×10^{-6} . The truncation radius was kept constant across the different supercells. As the timing plots in [Figure](#page-84-1) [5.4](#page-84-1) illustrate do the different calculations exhibit different scaling behaviour for constant resources. As long as the primitive integrals fit into the cache, only the first SCF cycle of the periodic [HFX](#page-12-4) takes a significant amount of time. But once the cache is exhausted, the scaling of the [HFX](#page-12-14)**k** implementation becomes significantly more favourable in terms of sampling of the reciprocal space.

5.1.1. Schwarz-Screening

While we are not relying on additional screening methods, including screening on the density matrix, for now in this reference implementation, we are still using the Schwarz-inequality to reduce the number of 4-center [ERI](#page-12-5) to calculate[[60](#page-125-0), [140](#page-130-3)[–143\]](#page-130-4).

As [Figure](#page-84-2) [5.5](#page-84-2) illustrates, the default value of CP2K for EPS_SCHWARZ of 1×10^{-10} which has been used throughout the calculations is still justified. Making it larger leads to unphysical energies, while lowering it increases

Figure 5.1.: With the addition of the [Hartree-Fock Exchange with](#page-12-14) **k**-point [\(HFX](#page-12-14)**k**) implementation together with the [ADMM](#page-12-2) integration we are validating the different code parts as illustrated. While the the practical use of([ADMM-](#page-12-2))[HFX](#page-12-14)**k** may be limited for larger systems, it serves as a stepping stone for other methods within CP2K.

					$x^{\mu\nu}$	2222		37373	x^+
Mesh	E_{tot} [a.u.]	Supercell	E_{tot} [a.u.]	-7.70					
3x3x3	-7.718231	1x1x1	-7.94597	-7.75					
6x6x6	-7.717316	2x2x2	-7.697665						
9x9x9	-7.717312	3x3x3	-7.718219	energy [a.u.] -7.80					
12x12x12	-7.717312	4x4x4	-7.717115	Total -7.85					
15x15x15	-7.717312	5x5x5	-7.717323						
18x18x18	-7.717312			-7.90					
21x21x21	-7.717312								K-Point Superc $\overline{}$
24x24x24	-7.717312			-7.95					
27x27x27	-7.717312			3-23-23	67676	orby runn	15-15-15	1871878 21-21-21	21-27-27 24-24-24
30x30x30	-7.717312							k point mesh	

Figure 5.2.: Convergence of the total energy for ever finer **k**-point meshes, larger supercell configurations respectively, of [LiH](#page-12-16). The *mesh* column refers to the MKP grid, while the *supercell* refers to the supercell configuration. The respective energies (per cell) are given next to it. There is no direct correspondence between supercell configuration and **k**-point mesh.

the time to solution significantly without any significant improvement on the total energy.

 λ

 Ω

 \sim

number of supercells

30x30x30

bint sampling ercell

ststs

5.1.2. ADMMk

For the verification of the [ADMM](#page-12-2) implementation with **k**-point support with [HFX](#page-12-4) we are limiting ourselves to the [h-BN](#page-12-15) system. As shown in [Figure](#page-85-0) [5.6,](#page-85-0) the energy converges continuously with the increased size of the [ADMM](#page-12-2) basis up to an agreement of −0.035 E^h with *admm-tz2p*. We also show the speedup and total timing in [Figure](#page-85-0) [5.6](#page-85-0) and conclude that the time savings by using smaller [ADMM](#page-12-2) basis sets are significant given the small improvement in total energy. Detailed analysis during calculations has shown that the simple parallelisation scheme occasionally leads to sub-optimal core utilisation, which becomes more important for larger basis sets. While the timing for the reference calculation at the full *TZVP* basis could therefore be improved, the speedups seen between the the different [ADMM](#page-12-2) basis sets will remain.

number of supercells

					x^{\uparrow}		$v^{\mathcal{D}^{\star}}$		3-23-1			$x+x^2$		5551
Mesh	E_{tot} [a.u.]	Superlatt.	E_{tot} [a.u.]	-78.550								- K-Point sampling X Supercell		
3x3	-78.73841	1x1	-78.54089	-78.575										
6x6	-78.74149	2x2	-78.69401	-78.600										
9x9	-78.74149	3x3	-78.73841	$\begin{array}{r} \n\frac{1}{11} - 78.600 \\ \frac{1}{100} - 78.625 \\ \frac{1}{100} - 78.650 \\ \frac{1}{100} - 78.675\n\end{array}$										
12x12	-78.74149	4x4	-78.74085											
15x15	-78.74149	5x5	-78.74136											
18x18	-78.74149			-78.700										
21x21	-78.74149			-78.725										
24x24	-78.74149			-78.750										
27x27	-78.74149				Grot e^{35}	$e^{i\theta}$	21-22-	155-57-	187871	2121+1	24-24-1		21-27% 2020%	
30x30	-78.74149								k point mesh					

Figure 5.3.: Convergence of the total energy for ever finer **k**-point meshes, larger supercell configurations respectively, of [h-BN.](#page-12-15) The *mesh* column refers to the MKP grid, while the *superlattice* refers to the superlattice configuration. The respective energies (per cell) are given next to it. There is no direct correspondence between superlattice configuration and **k**-point mesh.

Figure 5.4.: Average SCF timings for each system, with an integral cache of 128GB.

Figure 5.5.: Combined effect of the Schwarz-screening parameter on total energy and average SCF duration.

Figure 5.6.: Convergence of the total energy of [h-BN](#page-12-15) with [HFX,](#page-12-4) **k**-point mesh of 18x18, a cut-off of 2Å and for different sizes of the respective [ADMM](#page-12-2) *MOLOPT* basis set compared to the reference with a *MOLOPT TZVP* basis. Speedup is given in respect to the non-[ADMM](#page-12-2) reference calculation.

5.2. Basis Set Convergence

As mentioned in [Section 2.5](#page-34-0) is the scaling of the number of primitive integrals to calculate with regard to the size of the basis set unfavourable. A demonstration of this can be seen in [Figure](#page-86-0) [5.7,](#page-86-0) indicating that with increasing size of the MOLOPT basis, the total energy is indeed converging. At the same time is the [time to solution \(TTS\)](#page-13-1) increasing, following the $N⁴$ dependence. While [TTS](#page-13-1) might not be the right quantity as it is dependent on algorithmic and implementation factors, as [Chapter C](#page-120-0) illustrates, it is the measure the user is usually interested in. The respective total number of calculated ERIs is given in [Table](#page-86-1) [5.1](#page-86-1) for completeness. While caching the cartesian primitive integrals at TZVP level may still be feasible at single precision where it amounts to \approx 10 TB, this becomes quickly unfeasible if higher precision and larger basis sets are needed or more complex systems are to be investigated.

Figure 5.7.: Behaviour of the total energy for [h-BN](#page-12-15) using [HFX](#page-12-4) with the MOLOPT-HYB-GTH basis set family and its corresponding pseudopotential. On a dual AMD EPYC 7742 64-Core Processor, running with 256 OpenMP threads and an MKP grid of $18x18x1$. Slow convergence of the total energy is indicated. The scaling of the average SCF duration follows the expected N^4 scaling, although with some minor deviation.

For a comparison of different sizes of MOLOPT-ADMM basis sets, we are again using the Δ -test metric [\[101\]](#page-127-0). As an example for a hybrid functional, we selected *HSE06*, an improved parametrisation of the original Heyd-Scuseria-Ernzerhof (HSE) screened hybrid functional[[144\]](#page-130-5). It is a range separated functional of the form

$$
E_{\text{xc}}^{\text{HSE}} = aE_{\text{x}}^{\text{HF,SR}}(\omega) + (1 - a)E_{\text{x}}^{\text{PBE,SR}}(\omega) + E_{\text{x}}^{\text{PBE,LR}}(\omega) + E_{\text{c}}^{\text{PBE}}.
$$
\n(5.8)

where *SR* and *LR* refer to the short- and long-range components of the the *PBE* exchange functional, based on the partition of the Coulomb potential by

Table 5.1.: Total number of calculated cartesian primitive [ERIs,](#page-12-5) resp. spherical [ERIs](#page-12-5) for different sizes of the MOLOPT basis for [h-BN.](#page-12-15)

$$
\frac{1}{r} = \underbrace{\frac{1 - \text{erf}(\omega r)}{r}}_{SR} + \underbrace{\frac{\text{erf}(\omega r)}{r}}_{LR}.
$$
\n(5.9)

The system is again [h-BN,](#page-12-15) and as the main orbital basis set we are using the MOLOPT TZVP, to account for the observation that hybrid functionals require basis sets at least at the triple- ζ (or larger) quality level [\[145,](#page-130-6) [146](#page-130-7)].

The results for this experiment can be seen in [Figure](#page-88-0) [5.8](#page-88-0). We have used the MOLOPT TZVP as the main basis for all calculations, with varying ADMM basis set sizes. The truncation radius was adjusted to the scaling of the volume.

The total energy converges towards the non[-ADMM](#page-12-2) case with a delta of 0.0208 E^h with *admm-dz* down to 0.0089 E^h at *adm-tzp*. The equilibrium volume converges in a similar manner with a final Δ-value of 5.2 eV for the complete system.

For all the series not denoted with corr we used the *PBE* Exchange functional adapted to the truncated coulomb operator and its radius, while the corr series employs a full *PBE* Exchange operator in the [ADMM](#page-12-2) correction term

$$
E_x^{\text{HFX}}[P] = E_x^{\text{HFX}}[\hat{P}] + \left(E_x^{\text{HFX}}[P] - E_x^{\text{HFX}}[\hat{P}]\right) \approx E_x^{\text{HFX}}[\hat{P}] + \left(E_x^{\text{DFT}}[\rho] - E_x^{\text{DFT}}[\hat{\rho}]\right).
$$
\n(5.10)

Using the full *PBE* exchange operator improves the energy towards the non-ADMM reference, and better than the *admm-dzp*. It also increased the average [SCF](#page-12-17) time significantly, but still remained below that of *admmdzp*.

Figure 5.8.: Energy-volume curves fitted to the Birch-Murnaghan equation of states with scalings of 0.98, 0.99, … , 1.04 of the volume corresponding to the lattice parameter $a = 2.503$ Å. The Δ -values are given for the complete system rather than normalised for a single atom as in [Section 4.3](#page-63-0). The table shows the Δ-value between each of the ADMM basis sets (with the MOLOPT TZVP as primary basis), resp. between the ADMM basis sets and the non-ADMM reference with the TZVP basis set.

5.3. Conclusion

We have shown an implementation of the [Hartree-Fock Exchange](#page-12-4) with **k**-point support for the [Auxiliary Density Matrix Method](#page-12-2), with verification using the [LiH](#page-12-16) and [h-BN](#page-12-15) systems. The comparison has shown a well-defined behaviour in terms of convergence with reasonable cutoffs for the [Truncated Coulomb](#page-13-2) operator with a mix of direct density mixing and [DIIS](#page-12-11) in the [SCF](#page-12-17) iterations. Significant instabilities with the [Trun](#page-13-2)[cated Coulomb \(TC\)](#page-13-2) operator as mentioned in Irmler, Burow, and Pauly [[147](#page-130-8)] have not been observed. The [ADMM](#page-12-2) implementation shows clear advantage in terms of number of [ERI](#page-12-5) to calculate and therefore timing, compared to the reference [HFX](#page-12-4) **k**-point implementation. An advantage in timing of the **k**-point-enabled implementation could also be observed in terms of convergence for sampling of the reciprocal space when compared to the Γ-point supercell approach. Although it must be stressed that this advantage occurs in the limited setup of a primitive cell and does not necessarily apply to cases where a supercell or a mixed approach is needed, such as adsorption and surface effect studies. Possible improvements to this reference implementation could be made in the following areas:

▶ Quantization and compression: the usual avenue of accelerating [HFX](#page-12-4) calculations is the separation of the primitive integrals and the contraction with the density matrix, allowing to cache the result of the [ERI](#page-12-5) calculation between [SCF](#page-12-17) iterations. While it was still possible to implement this technique for the periodic implementation by Guidon, Hutter, and VandeVondele [\[148\]](#page-130-9), the N^2 dependency in terms of neighbor cells makes this more challenging for the **k**-point implementation. Nonetheless, if a reduction of precision (Quantization) can be applied, together with improved screening methods (possibly on the basis of density matrix for extended systems), newer memory sharing paradigms like disaggregated and [Fabric-attached memory](#page-12-18) could be applied to successfully continue the implementation of caches.

- ▶ Using the occupation: approaches like the *Adaptively Compressed Exchange operator* by Lin [\[149\]](#page-130-10) but also the *RI-occ-K* approach successfully exploit locality and reduce the computational complexity by limiting the calculation to occupied orbitals.
- \triangleright [Resolution of Identity](#page-12-7) approaches: the [RI](#page-12-7) approaches already present within CP2K could be extended towards **k**-point-enabled [HFX](#page-12-4) (with or without [ADMM\)](#page-12-2). As recent work shows [\[126,](#page-129-5) [127](#page-129-6), [131](#page-129-9)] is the reduction of the [ERI](#page-12-5) to a 3- or 2-center quantity a lucrative approach. While the choice of an additional basis may add an additional set of parameters which must be studied and controlled for well-defined behaviour, this basis must not necessarily follow the same construction scheme (safe for some properties) as a *full* basis sets but can be generated on-the-fly. We note here that the implementation of such an [RI](#page-12-7) scheme is likely to be done in separate algorithm as it changes the algebraic form of the overall schema and provides different possibilities in terms of parallelisation. As shown in the aforementioned references a direct analysis and optimisation of the required quantities for specific iteration schemes proof fruitful as well.

There are also more recent proposals on accelerating [HFX](#page-12-4) calculations, such as combining a range-separated operator with the advantages of the dual-nature of the [GPW](#page-12-1) approach itself[[150](#page-130-11)].

Overall this shows that despite the decades passed since the first implementations [HFX](#page-12-4) in computer codes, the field is still very active and the final optimisation has not yet been reached. We think that this reference implementation serves as another stepping stone towards more efficient [HFX](#page-12-4) implementations, in particular within CP2K.

Summary and Outlook 6.

6.1. Summary

This work was divided into three parts, all evolving around the use of [Gaussian-type Orbital \(GTO\)](#page-12-12) as the basis to solving the time-independent Schrödinger equation within electronic structure theory using the software package CP2K.

In the first part we have illustrated the generation of the revised MOLOPT pseudopotential and basis set family, the latter now being available as an all-electron basis set. From there we have analysed the performance of both pseudopotential and basis sets in a molecular setting, comparing the accuracy of both code and parameters against well-known references. In doing so, we were able to confirm once more the well-behaved nature of the MOLOPT basis set towards the complete basis set limit. This behaviour has been shown to hold consistently across the three functionals PBE, TPSS and PBE0, as well as with ADMM. With the meta-GGA TPSS we could also show the transferability of the basis set to other functionals in the same rung.

Since software packages like CP2K excel at the intersection of quantum chemistry and solid state physics, evaluating the performance of both the software package and its underlying simulation parameters in a condensed matter setting is crucial. To that end, we employed the Δ-test and not only compared against literature values, but also established a full workflow to obtain reference values from within CP2K, with help of the SIRIUS library for implementation of the [Full-Potential Linearized](#page-12-19) [Augmented Plane Wave method \(FP-LAPW\)](#page-12-19) and [plane wave \(PW\)](#page-12-20) methods. This we have demonstrated for the PBEsol functional. We could again observe well-defined behaviour for most elemental crystals with some minor exceptions for elements with more difficult electronic structure (magnetisation) or some heavier elements. In particular with the newly generated all-electron basis set together with [Gaussian and Aug](#page-12-0)[mented Planewave \(GAPW\)](#page-12-0), we were able to obtain results in very good agreement with other state-of-the-art codes.

These sort of benchmarks require a considerable amount of calculations, as well as proper tracking of the parameters such as the pseudopotentials and basis sets under test, as these may be revised during the testing. Hence, a significant effort was made towards automation and therefore counted as a separate part in this thesis. Molecular calculations were far easier to converge and computationally not as demanding, hence they could be run directly on local machines and thus required far less automation. Nonetheless, in the spirit of improving the software ecosystem around CP2K, we developed and released extendable open-source parsing libraries for both CP2K and G16. Automating the more complex solidstate benchmarks took more effort. While at the beginning of the project, the AiiDA framework was still in early development and lacked tracking functionalities for different versions of [GTO](#page-12-12) basis sets, a bespoke workflow manager was written. To make the transition to AIIDA easier, its architecture was again based on separately released open-source libraries

to handle CP2K input and output. This workflow manager was used for the initial batch of Δ-test results, while the latter were obtained using an AiiDA workflow with additional plugins. We compared the different approaches of running benchmarks, from simple ad-hoc scripting over custom to adaption of a larger existing workflow manager. In that comparison it has become clear that established workflow managers hold a clear advantage when it comes to standardised tasks in a more complex workflow, such as data transport, scheduling, error recovery. On the contrary, the process of adoption can grow more complex as a consequence of the levels of abstraction and the idiosyncratic design of any given workflow management tool. We have also seen that the availability of well-designed code interface libraries, such as the *cp2k-input-tools* and *cp2k-output-tools* developed as part of this thesis, make it significantly easier to transition between the different approaches and to retain a high grade of automation for directly code related tasks (such as parsing or input generation). Despite appropriate tooling, endeavours such as large scale benchmarking still retain some of their complexity. Both the setup of a workflow management system, but also the full automation still require considerable amount of work and respective know-how. Based on our work, it should be possible to create a simple and fully automated validation suite based on small molecular benchmarks, such as the [Small Molecules Database \(SMDB\)](#page-13-0) with additional information. More intricate benchmarks necessitating greater orchestration or compute resources still elude simple usability and execution. Several of the improvements as well as the libraries and tools developed as either effort are now directly available to the community, either as plugins for AiiDA or within the software itself[[2,](#page-122-0) [3](#page-122-1)].

To be able to extend the aforementioned solid state benchmarks towards Hybrid functionals such as PBE0, a periodic **k**-point [Hartree-Fock Ex](#page-12-4)[change \(HFX\)](#page-12-4) implementation is necessary. As has been shown is the scaling of a naïve implementation in the order of N^4 of the system size. Even though this can be improved by appropriate screening of the integrals, many problems still remain out of reach. As a remedy, the existing [Auxiliary Density Matrix Method \(ADMM\)](#page-12-2) implementation within CP2K was extended to support periodic calculations with **k**-points as well, and validated with systems commonly found in literature. This concluded the third and final part of this thesis.

6.2. Outlook

6.2.1. Benchmarking

The need for validating results in terms of accuracy and agreement amongst different electronic structure codes will remain high. For [GTO](#page-12-12) based codes, this does not only include the implementation and any [pseudopo](#page-12-21)[tential \(PP\)](#page-12-21) involved, but also the basis set employed in such calculations. While we have shown that the MOLOPT basis sets are qualitatively high performing basis sets for many different use cases able to reproduce various quantities accurately enough, further work may be needed to extend this in different directions. A next step towards automation of such benchmarks has already been taken with the *aiida-common-workflows*

package [\[151\]](#page-130-12) which has been used for a new verification study encompassing the whole periodic table from Z=1 to 96 and characterising 10 prototypical cubic compounds for each element (4 unaries and 6 oxides), spanning a wide range of coordination numbers and oxidation states. This resulted in a vast collection of equations of state, verified between all-electron and [PP](#page-12-21)-based approaches[[3\]](#page-122-1). In doing so, this also expands the landscape towards system beyond simple solids. Another direction would be to try for different functionals. While this is often explored in the context of new basis sets or computational methods, it is rarely explored across different codes and approaches [\(PW,](#page-12-20) [GTO](#page-12-12)). Finally, in particular towards the basis set limits, many codes exhibit unclear instabilities when it comes to convergence of the [self-consistent field \(SCF\).](#page-12-17) Monitoring of specific observables during a calculation run could proof very useful to avoid losing compute time in such cases, in particular for high-throughput calculations. The difficulty lies in identifying which quantities to monitor and detecting anomalies reliably.

6.2.2. ADMM-HFXk Implementation

The primary intention of the implementation given in this work was that of a reference code, in the sense of correctness. As such it is thought to serve as a stepping stone to improved-scaling methods such as the mentioned [Resolution of Identity \(RI\)](#page-12-7) approaches. Since these improvements will always have to start at the level of the **k**-point enabled [HFX](#page-12-4) implementation itself, the combination with [ADMM](#page-12-2) will most likely automatically benefit from the improvements as well. As outlined in the *occ-RI-K* approach, optimising for [SCF](#page-12-17) methods which require only a subset of the full [HFX](#page-12-4) matrix has some potential as well, in particular with larger or more diffuse basis sets such as the MOLOPT.

The reference implementation itself could also be improved. One such area of improvement could be the screening, for which we relied mostly only on the classical Schwarz-screening. Extending the integral estimates to Multipole-methods[[141](#page-130-13), [143](#page-130-4), [152](#page-130-14)[–154\]](#page-131-0) as in the work of Irmler [\[155\]](#page-131-1) has the potential of reducing the number of [Electron Repul](#page-12-5)[sion Integral \(ERI\)](#page-12-5) to calculate further by providing stricter bounds. Algorithmic improvements could be considered as well. Another avenue could be new computer architecture techniques of pooling memory between nodes using fabric-attached memory, which greatly enhances the amount of memory available to each node. Such an architecture would have the potential to simplify the otherwise explicit distribution of matrices and permit to cache the full list of [ERI](#page-12-5) (whether obtained in an RI-approximation or with the reference four-centre approach) in a transparent fashion. Furthermore, with the data cached on memory-like storage, accessing it in a variable ordering without performance penalty as for example required by post-Hartree-Fock methods such as MP2 would be directly supported.

6.2.3. Tooling

Finally, the development of external integration libraries such as the *cp2kinput-tools* and *cp2k-output-tools* for CP2K has already proven useful. By

collecting common tasks, they can greatly accelerate the development of simple custom workflows, which despite the existence of larger and all-encompassing frameworks such as AiiDA still have their place, as we have seen in this thesis. While a proper understanding of the underlying physics and methods of electronic structure theory will always be necessary to setup and run calculations and interpret their results, the commoditisation of [High-performance computing \(HPC\)](#page-12-22) makes software such as CP2K more accessible in general. By providing corresponding tooling around it, such as a Language Server Protocol implementation, which provides live feedback in a text editor when crafting the input for a calculation, adaption could be accelerated even further.

Small Molecules Database Calculation Details A.

The full data set for our benchmark with the [SMDB](#page-13-0) can be found in Hutter and Müller [\[114\]](#page-128-6) and the original geometries in the appendix to Weigend and Ahlrichs[[53](#page-125-1)].

The protocol is run in four steps

- 1. Gaussian reference calculation, with OPT and FREQ keywords to optimise the geometry and obtain the vibrational frequencies.
- 2. Geometry optimisation with CP2K.
- 3. Properties calculation with the wave function and positions from the previous step as initial guess, using the LINEAR_RESPONSE run type.
- 4. Vibrational Analysis with the VIBRATIONAL_ANALYSIS run type, again with initial guess for wave function and positions obtained from the previous steps.

In Listings [1](#page-95-0) and [3](#page-96-0) we are reproducing exemplary G16 and CP2K input configurations (for the latter only for the geometry optimisation).

The file included as kinddef contains CP2K basis set and [PP](#page-12-21) definitions for all elements, for the basis set size and type under test. The xcdef contains the definition of the functional to be used for a specific test run, here we reproduce the one used for the [ADMM](#page-12-2) as it the most complex and complete one in Listing [2](#page-96-1). The [ADMM](#page-12-2) input illustrates the use of *ADMM2* with the full *PBE* exchange functional.

Listing 1: CP2K input for the geometry optimisation of the Ag₂ structure from the [SMDB](#page-13-0)

&END FORCE_EVAL

Listing 2: A CP2K input segment for the [ADMM](#page-12-2) calculations for the [SMDB](#page-13-0) benchmark.

%mem=8GB 2 %NProcShare=8 3 #N RPBEPBE/Def2QZVPP scf=tight Int(Grid=ultrafine) OPT FREQ

 5 Mol job 1 7 0 1

Listing 3: G16 input for the Ag_2 structure from the [SMDB](#page-13-0)

Solid State Calculation Details B.

We have been using single point energy calculations at seven volume scales. Non-convergent single point energies were ignored if a fit could be obtained with the remaining points. The fitted coefficients can be found in [Table](#page-110-0) [B.2](#page-110-0) and [Table](#page-99-0) [B.1](#page-99-0), unphysical values were filtered out in a later stage.

In Listing [4](#page-118-0) we have reproduced an exemplary input for the Δ-test with CP2K for Ag with the DZVP MOLOPT basis set and a corresponding GTH [PP,](#page-12-21) run with [Gaussian and Plane Waves Method \(GPW\).](#page-12-1) Inputs for other basis sets have been prepared in the same manner and with similar tolerances, with specific parameters as given in the main text. The raw data set can be found in Müller [\[108\]](#page-128-7).

Table B.1.: Fitted Birch-Murnaghan coefficients for all PBEsol calculations.

				E ₀	V ₀	B ₀	B1
element	method	pseudo	basisset	[eV]	$[\text{Å}^3/\text{atom}]$	[GPa]	
		GTH-PBE-q22		-5202.3770	32.2811	39.6458	4.1789
	GPW	GTH-PBE-q4	DZVP-MOLOPT-PBE-GTH-q4	-96.2003	32.8723	39.9307	4.8842
			TZVP-MOLOPT-PBE-GTH-q4	-96.2508	32.4604	41.4390	5.0003
			TZV2P-MOLOPT-PBE-GTH-q4	-96.2528	32.4203	41.4017	4.9883
Bi	LAPW			-587253.2612	36.7274	16.0218	3.0000
	GAPW	GTH-PBE-q23	SVP-MOLOPT-PBE-GTH-q23	-5780.7539	36.6911	44.0538	4.7980
			TZVPP-MOLOPT-PBE-GTH-q23	-5783.6829	0.0115	42.8991	7.2225
			QZVPP-MOLOPT-PBE-GTH-q23	-5782.6815	29.7441	84.4283	4.3809
	PW	GTH-PBE-q5		-149.3625	37.0574	43.2011	4.5897
		GTH-PBE-q15		-1920.6651	36.9289	42.7744	4.6820
		GTH-PBE-q23		-5790.5350	36.7780	42.5205	4.6857
	GPW	GTH-PBE-q5	DZVP-MOLOPT-PBE-GTH-q5	-149.2726	37.4683	42.1366	4.5977
			TZVP-MOLOPT-PBE-GTH-q5	-149.2973	37.2946	42.4017	4.6188
			TZV2P-MOLOPT-PBE-GTH-q5	-149.3068	37.2634	42.4404	4.6372
Po	LAPW						
	GAPW	GTH-PBE-q24	SVP-MOLOPT-PBE-GTH-q24	-6448.9450	37.2959	44.0253	4.9844
			TZVPP-MOLOPT-PBE-GTH-q24	-6455.3571	34.2403	57.4580	4.7942
			QZVPP-MOLOPT-PBE-GTH-q24	-6455.7853	30.5736	103.2762	3.4301
	PW	GTH-PBE-q6		-219.2938	37.5453	45.8776	4.9142
		GTH-PBE-q16		-2248.5516	37.3075	45.2492	4.9807
		GTH-PBE-q24		-6460.9174	36.9941	45.3715	4.2765
	GPW	GTH-PBE-q6	DZVP-MOLOPT-PBE-GTH-q6	-219.1878	37.9580	44.4075	5.0600
			TZVP-MOLOPT-PBE-GTH-q6	-219.2102	37.8878	44.3168	5.0018
			TZV2P-MOLOPT-PBE-GTH-q6	-219.2145	37.8955	44.2307	4.9417
Rn	LAPW						
	GAPW	GTH-PBE-q26	SVP-MOLOPT-PBE-GTH-q26	-11681.7605	54.3012	502.0782	-992.0318
			TZVPP-MOLOPT-PBE-GTH-q26	-7977.6944	62.7742	2.3488	7.2259
			QZVPP-MOLOPT-PBE-GTH-q26				
	PW	GTH-PBE-q8		-407.1189	93.2580	0.5387	7.2186
		GTH-PBE-q18		-2975.9580	90.2585	0.2744	-18.1617
		GTH-PBE-q26		-7996.3985	95.1867	3.0496	-32.4445
	GPW	GTH-PBE-q8	DZVP-MOLOPT-PBE-GTH-q8	-407.0654	95.5170	0.3983	6.1548
			TZVP-MOLOPT-PBE-GTH-q8	-407.0758	88.9960	0.6043	6.3695
			TZV2P-MOLOPT-PBE-GTH-q8	-407.0788	88.8468	0.5827	6.4658

Table B.2.: Fitted Birch-Murnaghan coefficients for all PBE calculations.

TZV2P-MOLOPT-PBE-GTH-q5

Br LAPW

Se LAPW -66084.9035 28.4390 40.1278 -2.3959

PW GTH-PBE-q6 -256.0970 28.8477 51.9211 4.4596

PW GTH-PBE-q7 -364.2143 37.6754 25.5437 4.8774

GPW GTH-PBE-q7 DZVP-MOLOPT-PBE-GTH-q7 -363.9828 38.2935 24.9086 4.9758
TZVP-MOLOPT-PBE-GTH-q7 -363.9917 38.2817 24.7928 4.9579

GTH-PBE-q16 -3270.1771 23.5581 22.5093 0.5703 $\begin{array}{lclll} \textrm{GTH-PBE-q24} & & & -9521.7618 & & 24.0679 & & 29.8087 & & 2.3439 \\ \textrm{GTH-PBE-q6} & & \textrm{DZVP-MOLOPT-PBE-GTH-q6} & & & -255.8821 & & 29.3119 & & 51.5117 & & 4.4156 \\ \end{array}$ GPW GTH-PBE-q6 DZVP-MOLOPT-PBE-GTH-q6 -255.8821 29.3119 51.5117 4.4156

GTH-PBE-q17 -3848.4697 -3848.4697 -54.5234 -16.1783 -0.1202 GTH-PBE-q25 -10644.9084 36.5154 64.2625 11.9812

TZVP-MOLOPT-PBE-GTH-q6 -255.8910 29.2946 51.2162 4.4206 TZV2P-MOLOPT-PBE-GTH-q6 -255.8993 29.2683 51.1665 4.4270

TZVP-MOLOPT-PBE-GTH-q7 -363.9917 38.2817 24.7928 4.9579

Continued on next page

$$
^{102}
$$

Listing 4: CP2K input for the deltatest calculation of Ag with PBE for the DZVP MOLOPT basis set and GTH [PP](#page-12-0) for the 1.00 scaling.

1 &GLOBAL 2 PROJECT aiida 3 RUN_TYPE ENERGY 4 &END GLOBAL 5 &FORCE_EVAL 6 &DFT 7 BASIS_SET_FILE_NAME BASIS_SETS 8 &KPOINTS 9 C.R. SERIO .FALSE. 10 PARALLEL_GROUP_SIZE -1
11 SCHEME MONKHORST-PACK 11 SCHEME MONKHORST-PACK 24 24 24
12 SYMMETRY .FALSE. 12 SYMMETRY .FALSE.
13 &END KPOINTS &END KPOINTS 14 &MGRID 15 CUTOFF 1000.0 16 REL_CUTOFF 100.0
17 &END MGRID &END MGRID 18 POTENTIAL_FILE_NAME POTENTIAL 19 &PRINT 20 **8OVERLAP** CONDITION ON 21 $1-NORM$. TRUE. 22 **DIAGONALIZATION .TRUE.**
23 **&END OVERLAP_CONDITION** 23 &END OVERLAP_CONDITION
24 &END PRINT 24 & END PRINT
25 & QS 25 &QS 26 EXTRAPOLATION USE_GUESS
27 METHOD GPW METHOD GPW 28 &END QS 29 &SCF
30 A 30 ADDED_MOS 30
31 EPS_SCF 1e-08 31 EPS_SCF 1e-08 32 MAX_SCF 200 33 &MIXING 34 ALPHA 0.4
35 METHOD BR 35 METHOD BROYDEN_MIXING
36 & & & RID MIXING 36 &END MIXING
37 &SMEAR 37 &SMEAR 38 ELECTRONIC TEMPERATURE 300.0 39 METHOD FERMI_DIRAC 40 &END SMEAR
41 &END SCF 41 &END SCF
42 &XC 42 &XC
43 & 43 &XC_FUNCTIONAL PBE 44 &END XC_FUNCTIONAL 45 &END XC 46 &END DFT
47 METHOD Q 47 METHOD Quickstep
48 &SUBSYS 48 &SUBSYS
49 &CEL 49 &CELL 50 A 4.16424 0.0 0.0 51 B 2.54986159e-16 4.16424 0.0 52 C 2.54986159e-16 2.54986159e-16 4.16424 53 &CELL_REF
54 A 4.42 4 A 4.425165320132997 0.0 0.0

B 2.7096322688430977e-16 4. 55 B 2.7096322688430977e-16 4.425165320132997 0.0 56 C 2.7096322688430977e-16 2.7096322688430977e-16 4.425165320132997 57 PERIODIC XYZ 58 &END CELL_REF 59 PERIODIC XYZ
60 &END CELL 60 &END CELL
61 &KIND Ag &KIND Ag 62 BASIS_SET ORB DZVP-MOLOPT-PBE-GTH-q11 63 ELEMENT Ag 64 POTENTIAL GTH GTH-PBE-q11 65 &END KIND 66 &TOPOLOGY
67 COORD_ 67 **COORD_FILE_FORMAT XYZ**
68 **COORD FILE NAME aiida** 68 COORD_FILE_NAME aiida.coords.xyz &END TOPOLOGY 70 &END SUBSYS 71 &END FORCE EVAL

HFXk implementation details

In the development of the *k point enabled Hartree-Fock Exchange* reference implementation, scaling with regard to threads quickly became a challenge. The existing Γ-point code relied on a complex cost-model calculation together with a load-balancing algorithm to distribute tasks across both MPI and OpenMP parallelisation with both levels essentially being treated on an equal footing. For **k**-point support a different loop structure had to be employed in which the summation over the indices Q and T had to be pulled out of the primitive integrals calculation and only the summation over S remained:

$$
K_{\mathbf{x}}^{\mathbf{T}} = -\frac{1}{2} \sum_{\mathbf{Q}} \sum_{\nu \lambda} P_{\nu \lambda}^{\mathbf{Q}} \sum_{\mathbf{S}} (\mu^0 \nu^{\mathbf{S}} \mid \lambda^{\mathbf{T}} \sigma^{\mathbf{S} + \mathbf{Q}}). \tag{C.1}
$$

It is this change which makes caching an unresolved challenge with currently available single-node memory as a cache would now have to scale with $N_{\rm img}^2 \cdot N_{\rm sgf}^2$, e.g. requiring $N_{\rm img}^2$ more memory than the periodic Γ point implementation. This is equates to ∼14 TB of memory at double precision for a two-atomic hBN system with ∼1100 neighbour cells considered and a *MOLOPT-TZVP* basis.

Using an adequate (possibly lossy) compression scheme could help here, but care must be taken with regard to error propagation since this truncation would now be applied to individual values rather than a sum as before. From the infrastructure point of view, Fabric-attached memory together with a framework like OpenFAM[\[156\]](#page-131-0) could be a solution as it would allow for memory pooling across nodes.

For the current implementation we therefore recalculate all primitive integrals on each iteration. Since we nowadays can assume that OpenMP runtimes, compilers together with modern computer architectures are capable of caching read-only data and that OpenMP threads are lightweight, we went with a simpler parallelisation scheme without active load-balacing but with much smaller tasks. Parallelising over the 10 loops (2 neighbour image, 4 atom, 4 basis set indices) with the DO PARALLEL COLLAPSE construct is not possible since it requires iteration boundaries to be known at the entry of the parallel section and no branching between the loops. This constraint is not straightforward satisfiable since the number of sets depends on the atom kind and we maintain several earlier screening checks on the individual iteration levels. Collapsing over only T , i and k to avoid locking to serialise access to the Exchange matrix has lead to limited core utilisation since some tasks take can take much longer than others.

Instead we are using task-based OpenMP parallelisation at the level of the contraction of the primitive integrals with the Fock matrix which leads to excellent core utilisation and associated speedup up to 384 threads (verified on AMD Genoa). To prevent corruption of the Fock matrix we employ a locking scheme. While benchmarking different locking schemes (omp critical, omp_set_lock(), omp atomic) we discovered that some OpenMP implementations do not scale well with larger

Figure C.1.: Timing behaviour of a model example using repeated squares with small tasks, intentionally underemploying cores to explore tasking and scheduling overhead.

(a) The GNU OpenMP implementation shows a larger overhead for a singlevalue atomic scheme for small number of threads, and a large linear scaling cost associated with threading.

(b) The Cray/LLVM OpenMP implementation shows the same overhead for the atomic scheme and the desired sublinear scaling.

number of threads as shown in [Figure](#page-120-0) [C.1](#page-120-0) and for smaller systems this can become an issue.

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