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Abstract

Abstract goes here [e.g. 5, page 300].

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Chapter 1

Introduction

In recent years the field of artificial intelligence has made great strides, particularly in applications such as computer vision, natural language processing, speech recognition and user behaviour analytics. The exponential growth of available and high quality data has brought about a large demand for accurate, efficient and semi-automated algorithms, capable of building complicated mathematical models and making predictions without human supervision. Artificial neural networks in particular, partially inspired by simple models of human cognition, have found success in a large variety of task, largely owing to their ability to scale efficiently as the size of the dataset increases.

Data analysis and machine learning have become important parts of many subfields of physics, such as observational astronomy, condensed matter, biophysics and subatomic particle physics. Electronic structure calculations are well suited for the adoption of machine learning methods, as large datasets can be produced on demand and relatively free of noise which obscures patterns.

1.0.1 Electronic structure calculations

Electronic structure calculations - or numerical solutions to the manybody Schrödinger equation - are methods of modelling physical systems based on the principles of quantum mechanics. They involve very few parameters, and the results are found to be very accurate compared to laboratory measurements. However, exponential scaling greatly limits their applications, and we are typically limited to very small and simple systems. Approximations can be made which reduces the scaling to polynomial, but this limits the accuracy

of the method. The most successful and widely applied methods are the Density Functional Theory (DFT) method and the Hartree-Fock (HF) family of methods. The Hartree-Fock method scales nominally as $\mathcal{O}(N^4)$, where N is the number of particles in the system (i.e. electrons), owing to the number of two-electron integrals which must be computed. However, as the system grows in size many of these spatial integrals become vanishingly small and can be neglected, at the cost of introducing a small and adjustable error. A major weakness of Hartree-Fock methods is the neglect of electron correlation energies, which can lead to large deviations from experiment. The Density Functional Theory method scales in a similar manner, but often with a larger proportionality term. Density Functional Theory can treat both exchange and correlation interactions, but this must be done approximately, and developing accurate and numerically stable approximations remains an active area of research. **Rewrite section.**

Molecular Dynamics (MD) freezes out the degrees of freedom of the electrons, and treats the atoms as point particles centered on the nucleus using a mean-field approach. The dynamics of the particles are treated as Newtonian, meaning the position and velocity can be integrated using a symplectic integrator such as Verlet integration. This treatment allows for systems much larger than ab-initio methods, but at the cost of neglecting both nuclear and electronic phenomena. However, the development of molecular dynamics potentials involves a large amount of parameters for any realistic system, and determining their functional form is more of an art than an exact science.

An application of machine learning which has shown some promise is the development of molecular dynamics potentials or Potential Energy Surfaces (PES). Using for example Artificial Neural Networks (ANNs) the parameters (i.e. weights and biases) are fully determined from the training data. Under mild assumptions imposed on the activation functions in the hidden layers, ANNs have been proven to be able to approximate any continuous functions on compact subsets of \mathbb{R}^N . This offers the potential of developing potential energy surfaces directly from ab-initio data or from well-developed and tested empirical potentials. **Minor rewrite.**

1.0.2 Atom-centered descriptors

For electronic structure calculations the potential energy, forces and other derived properties are determined by the cartesian coordinates. However, it

is not sufficient to feed neural networks cartesian coordinates labeled with the energy. From physical theory we know that any molecular dynamics potential must be invariant w.r.t. translation, rotation, and permutation of like atoms. **Slight re-phrasing.** In order to apply machine learning methods we require a mapping from the cartesian coordinates to a 1D feature vector which conserves all of these properties.

The idea is to approximate the potential energy with a regression model:

$$\{\mathbf{R}\} \xrightarrow{\text{regression}} E = E(\{\mathbf{R}\}), \quad (1.1)$$

where $\{\mathbf{R}\}$ represents the cartesian coordinates of our system. We will refer to a mapping which satisfies the constraints of translation, rotation and permutation invariance as a *descriptor*. **Slight re-phrasing.** The descriptor is a multidimensional function \mathbf{G} that serves as input to the regression method:

$$\{\mathbf{R}\} \rightarrow \mathbf{G}(\{\mathbf{R}\}) \xrightarrow{\text{regression}} E = E(\mathbf{G}(\{\mathbf{R}\})) \quad (1.2)$$

Once we have a descriptor and a regression model the dynamics can be readily obtained by taking derivatives:

$$\begin{aligned} \mathbf{F}_i &= -\nabla_i E \\ &= -\nabla_i E(\mathbf{G}(\{\mathbf{R}\})) \\ &= -\sum_j \frac{\partial E}{\partial G_j} \frac{\partial G_j}{\partial \mathbf{R}_i}, \end{aligned} \quad (1.3)$$

where we have applied the chain rule to break the gradient into derivatives with respect to the network inputs (obtained through backpropagation) and derivatives of the network inputs with respect to the coordinates of atom i . The potential energy is typically also broken into atomic contributions:

$$E = \sum_{i=1}^N E_{\text{atom}}(\mathbf{R}_i, \{\mathbf{R}\}), \quad (1.4)$$

where each atomic contribution is determined by the atom’s local environment. This allows us to treat systems with a varying amount of particles without retraining the machine learning method each time.

1.0.3 Goals

The goal of this thesis was to investigate machine learning as a tool for bridging the gap between ab-initio electronic structure calculations and molecular dynamics. Previous theses at the University of Oslo Computational Physics group have investigated the Behler-Parrinello method of atom-centered symmetry functions, in particular the theses of [23, Stende, John A.] and [26, Treider, Håkon Vikør]. In these theses they have evaluated the numerical speed and accuracy of potentials trained on data produced from the Lennard-Jones and Stillinger-Weber potentials. We sought to continue this work, and demonstrate and validate machine-learned potentials developed using the Behler-Parrinello method, but also apply the method to data obtained using ab-initio molecular dynamics and compare these potentials to empirical potentials. This was initially attempted using a combination of Tensorflow and LAMMPS. However, this was later abandoned, as connecting software packages written in different programming languages proved to be tedious and error-prone, and the Atomic Simulation Environment (ASE) package provided a Python interface to electronic structure calculations. Initially we sought to implement and test the Deep Potential Molecular Dynamics method by [27, Zhang et al.], but it proved difficult to obtain acceptable results for the energy and force Root Mean Squared Errors (RMSEs), and calculating the forces efficiently proved too difficult to implement. This was therefore abandoned in favor of the more tried and tested Behler-Parrinello method.

We finally settled on a combination of using the ASE package for producing molecular dynamics trajectories and the Atomistic Machine-learning Package (AMP) for training them. The AMP package provides an interface for generating Behler-Parrinello "fingerprints" of atomic environments and training them using neural networks (and potentially other machine-learning) models. This allowed us to focus on the accuracy, speed and scaling when training neural networks on empirical potentials and ab-initio data in molecular dynamics, and how well equilibrium properties can be replicated using trained neural networks.

1.0.4 Contributions

Ideally we might have liked to make our own implementation, and I would have especially liked to build a neural network interface through the recently released Tensorflow 2.0 (beta). Unfortunately there was no time for this, and

we settled for working through the AMP interface and making modifications as necessary. Developing code from scratch could have given insights into the structure and process of calculating fingerprints and feeding them through neural networks to produce energies and forces. However, the nature of AMP is modular and the code is well documented and readable, so settling on making modifications to the package can allow one to focus more on the process of generating and sampling data, training and deploying the trained neural networks on novel systems and evaluating the results. Suggestions for future work on the topic is included in our final conclusion. In this thesis we have:

- Produced and sampled from atomistic data obtained from ab-initio molecular dynamics and empirical potential energy surfaces
- Trained neural networks on atomistic data sampled from molecular dynamics and evaluated the accuracy of the energies and forces
- Evaluated the ability of trained neural networks to reproduce equilibrium properties of molecular dynamics trajectories
- Analysis and processing scripts, and minor modifications to the AMP code

1.0.5 Structure

This thesis is divided into four parts. First we build from first principles to connect classical molecular dynamics with the laws of quantum mechanics, and introduce machine learning through the concept of atom-centered descriptors. Thereafter we discuss the implementation details of using ASE, AMP and Tensorflow. Third we train neural networks potentials on empirical potentials and on data from ab-initio molecular dynamics. Fourth we conclude the thesis and discuss future applications and work.

Part I

Theory

Chapter 2

Quantum Mechanics

In order to proceed to electronic structure calculations we require a solid foundation in the principles of quantum mechanics. This chapter will give a brief overview of the basic tenets of quantum mechanics and describe briefly how these rules lead to the Schrödinger equation, which is the equation governing all non-relativistic quantum mechanics. We will assume an undergraduate understanding of calculus and linear algebra, and some knowledge of mechanics is also helpful. The discussion in this chapter follows closely the discussion in [Sakurai 20, pages 10-76], and the reader is referred there for more details.

2.0.1 Kets and bras

In quantum mechanics, the state of a quantum system is represented by a *state vector* in a complex vector space. Such a vector is called a *ket*, denoted by $|\alpha\rangle$, following the notation of Paul Dirac. The state ket is postulated to contain all information about the state of the quantum system, such as energy, angular momentum, mass and so on. Two kets can be added to produce a new ket:

$$|\alpha\rangle + |\beta\rangle = |\gamma\rangle . \quad (2.1)$$

They can also be multiplied by a complex number:

$$c|\alpha\rangle = |\alpha\rangle c = |\delta\rangle . \quad (2.2)$$

If c is zero the resulting ket is called a *null ket*. If c is non-zero it is postulated that the resulting ket contains the same information as the initial ket. **Is this**

true if $|c| \neq 1$?

Observables such as momentum and spin are represented by operators acting on the vector space in question. Operators act on a ket from the left to produce a new ket:

$$A|\alpha\rangle = |\delta\rangle. \quad (2.3)$$

Of particular importance is when the action of an operator on a ket is the same as multiplication:

$$A|\alpha\rangle = c|\alpha\rangle = |\delta\rangle. \quad (2.4)$$

These kets are known as *eigenkets* and the corresponding complex numbers are known as *eigenvalues*. The physical state represented by an eigenket is known as an *eigenstate*. The eigenvalues of an operator A represent the only possible values of a measurement of the observable. For observables such as position and momentum, the operators will have a continuous spectrum of eigenvalues, whereas operators such as energy and spin have a discrete or *quantized* spectrum, whereby the term *quantum* mechanics is derived. The eigenkets of a physical observable form a complete orthogonal set, meaning any ket can be written as an expansion of eigenkets $|a'\rangle$:

$$|\alpha\rangle = \sum_{a'} c_{a'} |a'\rangle, \quad (2.5)$$

where $c_{a'}$ is a complex coefficient. In principle there are infinitely many linearly independent eigenkets, depending on the dimensionality of the vector space.

A *bra space* is a vector space "dual" to the ket space. We postulate that for every ket $|\alpha\rangle$ there exists a bra $\langle\alpha|$. The bra space is spanned by eigenbras $\langle a'|$ corresponding to the eigenkets $|a'\rangle$. The ket and bra spaces have a dual correspondence:

$$\begin{aligned} |\alpha\rangle &\leftrightarrow \langle\alpha| \\ |a'\rangle, |a''\rangle, \dots &\leftrightarrow \langle a'|, \langle a''|, \dots \\ |\alpha\rangle + |\beta\rangle &\leftrightarrow \langle\alpha| + \langle\beta|. \end{aligned} \quad (2.6)$$

The bra dual to $c|\alpha\rangle$ is postulated to be $c^* \langle\alpha|$, and more generally:

$$c_\alpha |\alpha\rangle + c_\beta |\beta\rangle \leftrightarrow c_\alpha^* \langle\alpha| + c_\beta^* \langle\beta|. \quad (2.7)$$

The *inner product* of a bra and a ket is a complex number written as a bra on the left and a ket on the right. It has the fundamental property:

$$\langle\alpha|\beta\rangle = \langle\beta|\alpha\rangle^*, \quad (2.8)$$

meaning they are complex conjugates. For this to satisfy the requirements of an inner product we must have

$$\langle\alpha|\alpha\rangle \geq 0, \quad (2.9)$$

with equality if and only if $|\alpha\rangle$ is a null ket. We define the *norm* of a ket as

$$\sqrt{\langle\alpha|\alpha\rangle}, \quad (2.10)$$

which can be used to form normalized kets

$$|\tilde{\alpha}\rangle = \frac{1}{\sqrt{\langle\alpha|\alpha\rangle}} |\alpha\rangle, \quad (2.11)$$

with the property

$$\langle\tilde{\alpha}|\tilde{\alpha}\rangle = 1. \quad (2.12)$$

Two kets are said to be *orthogonal* if

$$\langle\alpha|\beta\rangle = 0. \quad (2.13)$$

2.0.2 Operators

As we mentioned briefly above, operators act on kets from the left to produce a new ket. Two operators A and B are equal $A = B$ if

$$A|\alpha\rangle = B|\alpha\rangle, \quad (2.14)$$

for an arbitrary ket in the relevant ket space. An operator A is said to be the *null operator* if

$$A|\alpha\rangle = 0. \quad (2.15)$$

Operators can be added, and addition operations are commutative and associative.

$$X + Y = Y + X, \quad (2.16)$$

$$(X + Y) + Z = X + (Y + Z). \quad (2.17)$$

Operators act on bras from the right to produce a new bra

$$\langle\alpha| A = \langle\beta|. \quad (2.18)$$

The ket $A|\alpha\rangle$ and the bra $\langle\alpha|A$ are in general not dual to each other. We define the *hermitian adjoint* A^\dagger through the dual correspondence:

$$A|\alpha\rangle \leftrightarrow \langle\alpha|A^\dagger. \quad (2.19)$$

An operator is said to be *hermitian* if

$$A = A^\dagger. \quad (2.20)$$

Hermitian operators have real eigenvalues, and since the result of any measurement must be a real number any operator that represents a physical observable must be Hermitian.

Operators can be multiplied. Multiplication is associative, but non-commutative:

$$XY \neq YX, \quad (2.21)$$

$$X(YZ) = (XY)Z. \quad (2.22)$$

The left product of a ket and a bra is known as the *outer product*:

$$|\alpha\rangle\langle\beta|. \quad (2.23)$$

The outer product should be treated as an operator, while the inner product $\langle\alpha|\beta\rangle$ is a complex number. If an operator is to the left of a ket $|\alpha\rangle A$ or to the right of a bra $A\langle\beta|$ these are illegal products, in other words not defined within the ruleset of quantum mechanics. The associative properties of operators are postulated to hold true as long as we are dealing with legal multiplications among kets, bras and operators. As an example, the outer product acting on a ket:

$$(|\alpha\rangle\langle\beta|)|\gamma\rangle, \quad (2.24)$$

can be equivalently regarded as scalar multiplication

$$|\alpha\rangle(\langle\alpha|\gamma\rangle) = |\alpha\rangle c = c|\alpha\rangle, \quad (2.25)$$

where $c = \langle\alpha|\gamma\rangle$ is just a complex number.

2.0.3 Time evolution

In quantum mechanics, time is treated not as an observable, but as a parameter. Relativistic quantum mechanics treats space and time on the same footing, but only by demoting position to a parameter.

Suppose we have a physical system $|\alpha\rangle$ at a time t_0 . Denote the ket at a later time $t > t_0$ by

$$|\alpha, t; t_0\rangle. \quad (2.26)$$

Time evolution is assumed to be continuous and symmetric, meaning that if we evolve the system backwards in time we should arrive at the initial state:

$$\lim_{t \rightarrow t_0} |\alpha, t; t_0\rangle = |\alpha\rangle. \quad (2.27)$$

The kets separated by a time $\Delta t = t - t_0$ are related by the *time-evolution operator* \mathcal{U} :

$$|\alpha, t; t_0\rangle = \mathcal{U}(t, t_0) |\alpha, t_0\rangle. \quad (2.28)$$

If the state ket is normalized to unity at a time t_0 , it must remain normalized at a later time:

$$\langle\alpha, t_0|\alpha, t_0\rangle = \langle\alpha, t; t_0|\alpha, t; t_0\rangle = 1. \quad (2.29)$$

This is guaranteed if the time evolution operator \mathcal{U} is a *unitary* operator:

$$\mathcal{U}^\dagger \mathcal{U} = 1. \quad (2.30)$$

We also require that the time evolution operator exhibits a composition property:

$$\mathcal{U}(t_2, t_0) = \mathcal{U}(t_2, t_1) \mathcal{U}(t_1, t_0), \quad (t_2 > t_1 > t_0), \quad (2.31)$$

meaning that the time evolution between two points t_0 and t_2 remains the same if we first evolve the system to an intermediate time t_1 .

If we consider an infinitesimal time-evolution operator

$$|\alpha, t_0 + dt; t_0\rangle = \mathcal{U}(t_0 + dt, t_0) |\alpha, t_0\rangle, \quad (2.32)$$

it must reduce to the identity operator as the infinitesimal time interval dt goes to zero:

$$\lim_{dt \rightarrow 0} \mathcal{U}(t_0 + dt, t_0) = 1, \quad (2.33)$$

and we expect the difference between the operators to be of first order in dt . These requirements are all satisfied by the operator

$$\mathcal{U}(t_0 + dt, t_0) = 1 - i\Omega dt, \quad (2.34)$$

where Ω is a Hermitian operator:

$$\Omega^\dagger = \Omega. \quad (2.35)$$

The operator Ω has the dimension inverse time. Frequency or inverse time is related to energy through the Planck-Einstein relation:

$$E = \hbar\omega. \quad (2.36)$$

In classical mechanics the Hamiltonian is the generator of time evolution, so we postulate that Ω is related to the Hamiltonian operator H :

$$\Omega = \frac{H}{\hbar}. \quad (2.37)$$

The Hamiltonian operator represents the energy of our system, which is a physical observable and must therefore be Hermitian.

2.0.4 The Schrödinger equation

The Schrödinger equation is the fundamental equation governing non-relativistic quantum mechanics. It can be assumed as a postulate, but is usually derived from more fundamental principles. By exploiting the composition property of the time-evolution operator we find that:

$$\mathcal{U}(t + dt, t_0) = \mathcal{U}(t + dt, t)\mathcal{U}(t, t_0) = (1 - \frac{iHdt}{\hbar})\mathcal{U}(t, t_0), \quad (2.38)$$

where the time difference $t - t_0$ is not required to be infinitesimal. Subtracting from both sides of this equation:

$$\mathcal{U}(t + dt, t_0) - \mathcal{U}(t, t_0) = -\frac{iHdt}{\hbar}\mathcal{U}(t, t_0). \quad (2.39)$$

Rearranging this equation and taking the limit $dt \rightarrow 0$ leads to the equation:

$$i\hbar \frac{\partial}{\partial t} \mathcal{U}(t, t_0) = H\mathcal{U}(t, t_0). \quad (2.40)$$

This is known as the Schrödinger equation for the time-evolution operator. We multiply both sides by a ket $|\alpha, t_0\rangle$:

$$i\hbar \frac{\partial}{\partial t} \mathcal{U}(t, t_0) |\alpha, t_0\rangle = H \mathcal{U}(t, t_0) |\alpha, t_0\rangle. \quad (2.41)$$

This ket does not depend on t , leading us to the famous equation:

$$i\hbar \frac{\partial}{\partial t} |\alpha, t; t_0\rangle = H |\alpha, t; t_0\rangle. \quad (2.42)$$

This is known as the time-dependent Schrödinger equation, and gives the description for how a quantum system evolves with time. It is possible to show that in the classical limit $\hbar \rightarrow 0$, the expectation value of the operator H takes on the role of the energy in classical mechanics. The Schrödinger equation takes on the role of Newton's laws in quantum mechanics. However, it is not the only way to study quantum systems, as it has been shown to be an equivalent interpretation to the matrix mechanics of Werner Heisenberg and the path-integral formulation developed by Richard Feynman.

Chapter 3

Manybody Quantum Mechanics

The Schrödinger equation only offers exact solutions for very small and simple systems, such as the hydrogen atom or a system of non-interacting harmonic oscillators. If we want to study most systems of interest we must turn instead to numerical methods and solutions. The most prominent methods in the field of manybody quantum mechanics are the Hartree-Fock (HF) and the Density Functional Theory families of solvers. This chapter will give a brief overview of both methods, focused more on understanding and intuition than rigor. Eventually we will take these methods to be black boxes of electronic structure calculations, given some cartesian coordinates and outputting energies and forces. This section will give a brief overview of the discussion of the electronic Hamiltonian in [Szabo 24, pages 39-89], which also covers Hartree-Fock theory which will be expanded upon in the next section.

We want to find solutions to the non-relativistic time-independent Schrödinger equation:

$$\hat{H} |\Psi\rangle = E |\Psi\rangle, \quad (3.1)$$

with the Hamiltonian \hat{H} describing a system of nuclei and electrons with cartesian coordinates \mathbf{R}_a , $a = 1, 2, \dots, A$ and \mathbf{r}_i , $i = 1, 2, \dots, N$ respectively. The distance between nuclei a and electron i is given as the euclidean distance $R_{ai} = |\mathbf{R}_a - \mathbf{r}_i|$ and correspondingly for the nuclei-nuclei and electron-electron distances. The full Hamiltonian for a set of N electrons and A nuclei in atomic

units is:

$$\begin{aligned} \hat{H} = & - \sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{a=1}^A \frac{1}{M_a} \nabla_a^2 - \sum_{i=1}^N \sum_{a=1}^A \frac{Z_a}{R_{ia}} \\ & + \sum_{i=1}^N \sum_{j=i+1}^N \frac{1}{r_{ij}} + \sum_{a=1}^A \sum_{b=a+1}^A \frac{Z_a Z_b}{R_{ab}}. \end{aligned} \quad (3.2)$$

The first two terms describe the kinetic energy operators of the electrons and nuclei, with M_a the ratio of the mass of nuclei a to the electron mass. The third term describes the coulomb attraction between electrons and nuclei, while the fourth and fifth terms describe the repulsion between electrons and nuclei respectively.

Since the nuclei are approximately 2000 times heavier than the electrons, the electrons can to a good approximation be described as moving in the field of fixed nuclei. In practice we neglect the kinetic energy terms of the nuclei, while considering an averaged effect from the nuclei-nuclei repulsion. The nuclei-nuclei repulsion energy averaged over adds a constant to the energy eigenvalues, but has no effect on the energy eigenfunctions. The remaining terms are known as the electronic Hamiltonian:

$$\hat{H}_e = - \sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{i=1}^N \sum_{a=1}^A \frac{Z_a}{R_{ia}} + \sum_{i=1}^N \sum_{j=i+1}^N \frac{1}{r_{ij}}. \quad (3.3)$$

The electronic wavefunction $\Psi_e = \Psi_e(\{r_i\}; \{R_a\})$ is a function of the electronic coordinates with a parametric dependence on the fixed nucleic coordinates. The electronic energy is obtained in the usual way $E_e = \langle \Psi_e | \hat{H}_e | \Psi_e \rangle$. The total energy of our system must now include the constant nuclear repulsion:

$$E_{tot} = E_e + \sum_{a=1}^A \sum_{b=a+1}^A \frac{Z_a Z_b}{R_{ab}}. \quad (3.4)$$

If one has solved the Schrödinger equation for the electronic Hamiltonian, one can subsequently solve for the nucleic motion using the same trick, i.e. substituting the electronic coordinates for their average values, averaged over

the electronic wave function. We are then left with a nuclear Hamiltonian \hat{H}_n :

$$\begin{aligned}\hat{H}_n &= -\sum_{a=1}^A \frac{1}{2M_a} \nabla_a^2 + \left\langle -\sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{i=1}^N \sum_{a=1}^A \frac{Z_a}{R_{ia}} + \sum_{i=1}^N \sum_{j=i+1}^N \frac{1}{r_{ij}} \right\rangle \\ &\quad + \sum_{a=1}^A \sum_{b=a+1}^A \frac{Z_a Z_b}{R_{ab}} \\ &= -\sum_{a=1}^A \frac{1}{2M_a} \nabla_a^2 + E_{tot}.\end{aligned}\tag{3.5}$$

Under this approximation the nuclei move on a potential energy surface obtained by solving the electronic Hamiltonian. We will however remain focused on the electronic structure problem. For the electronic Hamiltonian we would like to make one more approximation. The electronic Hamiltonian further simplifies if instead of considering the relative positions of the nuclei, we fix the coordinate system in the center of mass of the nucleus. This gives us the final expression we want for the electronic Hamiltonian:

$$\hat{H} = -\sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{i=1}^N \frac{Z}{r_i} + \sum_{i=1}^N \sum_{j=i+1}^N \frac{1}{r_{ij}}\tag{3.6}$$

3.0.1 Hartree-Fock

The Hartree-Fock method is a method for finding solutions to the electronic Hamiltonian assuming the electron-electron repulsion can be approximated with a set of single-particle functions or *orbitals*, moving in a mean field generated by the presence of other electrons. The theory in this section is based upon the [22, Sherrill] lecture notes from the Georgia Institute of Technology and the lecture notes on Computational Physics II [8, Hjorth-Jensen] from the University of Oslo. Assuming that the electrons do not interact the Hamiltonian is separable and the wavefunction is simply a product of orbitals ψ which are solutions to a onebody Hamiltonian. This gives us an ansatz for the manybody wavefunction Ψ known as the *Hartree product*:

$$\Psi(\mathbf{r}_1, \dots, \mathbf{r}_N) = \psi(\mathbf{r}_1) \cdot \dots \cdot \psi(\mathbf{r}_N).\tag{3.7}$$

Since we are dealing with fermions this ansatz fails to satisfy the antisymmetry principle, i.e. the wavefunction is not antisymmetric with respect to the interchange of any two particles. Fermions in addition to three spatial degrees of freedom also have a spin degree of freedom σ which means the fermion can be described by the space-spin coordinate $\mathbf{x} = (\mathbf{r}, \sigma)$ with $\mathbf{x} \in \mathbb{R}^3 \otimes \sigma$. The problem of antisymmetry in a system of N fermions is satisfied by the introduction of *Slater determinants*

$$\Psi(\mathbf{x}_1, \dots, \mathbf{x}_N) = \frac{1}{\sqrt{N!}} \begin{vmatrix} \chi_1(\mathbf{x}_1) & \chi_2(\mathbf{x}_1) & \dots & \chi_N(\mathbf{x}_1) \\ \chi_1(\mathbf{x}_2) & \chi_2(\mathbf{x}_2) & \dots & \chi_N(\mathbf{x}_2) \\ \vdots & \vdots & \ddots & \vdots \\ \chi_1(\mathbf{x}_N) & \chi_2(\mathbf{x}_N) & \dots & \chi_N(\mathbf{x}_N) \end{vmatrix}, \quad (3.8)$$

with $\chi(\mathbf{x})$ spin orbitals and a normalization factor $(N!)^{-1/2}$. The introduction of this ansatz is equivalent to assuming that all electrons move independently of each other in a mean field generated by the electron-electron repulsion. Define the one-electron operator of the electronic Hamiltonian as:

$$\hat{h}_1(\mathbf{x}_i) = -\frac{1}{2}\nabla_i^2 - \frac{Z}{r_i}, \quad (3.9)$$

with a twobody interaction term

$$\hat{v}(\mathbf{x}_i, \mathbf{x}_j) = \frac{1}{r_{ij}}, \quad (3.10)$$

which allows us to write the electronic Hamiltonian more compactly as:

$$\hat{H} = \sum_i \hat{h}_1(\mathbf{x}_i) + \sum_{i < j} \hat{v}(\mathbf{x}_i, \mathbf{x}_j). \quad (3.11)$$

The expectation value of the energy is given as the usual inner product:

$$\langle \Psi | \hat{H} | \Psi \rangle. \quad (3.12)$$

The *variational theorem* states that the expectation value of any normalized wavefunction with respect to the energy represents an upper bound to the ground state energy. This suggests a procedure wherein we vary the parameters of a set of approximate wave functions Ψ_T until an energy minimum

is reached. The Hartree-Fock energy can be written in terms of integrals over the onebody and interaction terms:

$$E_{HF} = \sum_i \langle i | \hat{h} | i \rangle + \sum_{i < j} \langle ij | \hat{v} | ij \rangle_{AS}, \quad (3.13)$$

where we have introduced an antisymmetrized matrix element:

$$\langle ij | \hat{v} | ij \rangle_{AS} = \langle ij | \hat{v} | ij \rangle - \langle ij | \hat{v} | ji \rangle, \quad (3.14)$$

and the shorthand integrals:

$$\langle i | \hat{h}_1 | i \rangle = \int d\mathbf{r} \chi_i^*(\mathbf{r}) \hat{h}_1 \chi_i(\mathbf{r}), \quad (3.15)$$

and

$$\langle ij | \hat{v} | ij \rangle = \int d\mathbf{r}_i d\mathbf{r}_j \chi_i^*(\mathbf{r}_i) \chi_j^*(\mathbf{r}_j) \hat{v} \chi_i(\mathbf{r}_i) \chi_j(\mathbf{r}_j). \quad (3.16)$$

In order to derive the Hartree-Fock equations we perform a linear expansion of the spin orbitals χ in terms of a fixed orthogonal basis ϕ :

$$\chi_i = \sum_{\nu} C_{i\nu} \phi_{\nu}, \quad (3.17)$$

in principle an infinite sum, but in practice truncated. This basis is usually obtained as the eigenfunctions of parts of the electronic Hamiltonian, e.g. solutions to the Schrödinger equation with a harmonic oscillator or Coulomb potential. If the coefficients belong to an orthogonal or unitary matrix, the resulting basis will preserve orthogonality. This expansion allows us to rewrite the Hartree-Fock energy as:

$$E_{HF} = \sum_i \sum_{\alpha\beta} C_{i\alpha}^* C_{i\beta} \langle \alpha | \hat{h}_1 | \beta \rangle + \sum_{i < j} \sum_{\alpha\beta\delta\eta} C_{i\alpha}^* C_{j\beta}^* C_{i\delta} C_{j\eta} \langle \alpha\beta | \hat{v} | \delta\eta \rangle. \quad (3.18)$$

Using the method of Lagrangian multipliers we can define a functional to be minimized:

$$\begin{aligned} F[\Psi] &= E_{HF}[\Psi] - \sum_i \epsilon_i \langle i | j \rangle \\ &= E_{HF}[\Psi] - \sum_i \epsilon_i \sum_{\alpha} C_{i\alpha}^* C_{i\alpha}, \end{aligned} \quad (3.19)$$

with Lagrange multipliers ϵ_i , where we have exploited the orthogonality of the basis functions to introduce the coefficients. The Lagrange multipliers are identified with the energy eigenvalues of the single-particle orbitals. Minimizing with respect to $C_{i\alpha}^*$ yields the eigenvalue equation:

$$\sum_{\beta} \hat{h}_{\alpha\beta}^{HF} C_{i\beta} = \epsilon_i C_{i\alpha}, \quad (3.20)$$

where we have introduced the Fock matrix elements:

$$\hat{h}_{\alpha\beta}^{HF} = \langle \alpha | \hat{h}_1 | \beta \rangle + \sum_j^N \sum_{\delta\eta} C_{j\delta}^* C_{j\eta} \langle \alpha \delta | \hat{v} | \beta \eta \rangle_{AS}. \quad (3.21)$$

The single-particle integrals are usually tabulated in advance, and depend upon the choice of basis functions. Often the single-particle integrals $\langle \alpha | \hat{h}_1 | \beta \rangle$ have analytical expressions, while the antisymmetric matrix elements must be evaluated using numerical integration. The eigenvalue problem can be written more compactly as:

$$FC = C\epsilon, \quad (3.22)$$

where F is the Fock matrix defined above, C is the matrix of coefficients and ϵ is now a vector of single-particle energies. The Hartree-Fock equations are solved in an iterative way, starting with an initial guess for the coefficients C . Solving the eigenvalue problem yields new eigenvectors and eigenvalues. The process continues until the change in eigenvalues is within some tolerance ν :

$$\frac{\sum_p |\epsilon_i^n - \epsilon_i^{n-1}|}{m} \leq \nu, \quad (3.23)$$

where p runs over all the single-particle energies and m is the number of single-particle states.

3.0.2 Density-functional theory

Density-functional theory (DFT) is a method for investigating the electronic structure of a manybody system by finding approximations to the ground state density $n(\mathbf{r})$. It holds many similarities to the Hartree-Fock method, since the usual method of obtaining the ground-state density involves constructing

a single-determinant wave function from a set of orthonormal single-particle states, and expanding these single-particle states in terms of a known basis. However, DFT methods offer the benefit of dealing with a function of only three spatial coordinates, while Hartree-Fock methods require you to keep track of the spatial and spin coordinates of every single-particle state.

This section is a brief summary of the material covered in the [Toulouse 25, pages 1-12] lecture notes from the Université Pierre et Marie Curie, which the reader is encouraged to check out for more detail. Our starting point is again the electronic Hamiltonian:

$$\hat{H} = - \sum_{i=1}^N \frac{1}{2} \nabla_i^2 - \sum_{i=1}^N \frac{Z}{r_i} + \sum_{i=1}^N \sum_{j=i+1}^N \frac{1}{r_{ij}}. \quad (3.24)$$

Any electronic wavefunction Ψ which solves this equation is in principle a function of $4N$ coordinates $\mathbf{x}_i = (\mathbf{r}_i, \sigma_i)$, $i = 1, \dots, N$ where N is the number of electrons. Once we have obtained a solution to the Schrödinger equation we can obtain the one-electron density $n(\mathbf{r})$ as:

$$n(\mathbf{r}) = N \int |\Psi(\mathbf{r}, \sigma, \mathbf{x}_2, \dots, \mathbf{x}_N)|^2 d\sigma d\mathbf{x}_2 \dots d\mathbf{x}_N. \quad (3.25)$$

Since the wavefunction is a unique functional of the Hamiltonian \hat{H} , the one-electron density is uniquely determined by the Hamiltonian. Hohenberg and Kohn showed in 1964 [9] in their first theorem that this mapping can be inverted, i.e. that the one-electron density uniquely determines the Hamiltonian of our system (up to an arbitrary constant). Taken altogether, this means that all properties of our system, including the Hamiltonian and the manybody wavefunction are fixed by a one-electron density carrying a dependency on only 3 spatial coordinates. The electronic Hamiltonian can be rewritten as:

$$\hat{H} = \hat{F} + \hat{V}_{ne}, \quad (3.26)$$

where \hat{F} is an operator consisting of the kinetic energy and electron-electron operators and \hat{V}_{ne} is the electron-nuclei interaction. For their second theorem, Hohenberg and Kohn defined the universal density-functional:

$$F[n] = \langle \Psi[n] | \hat{F} | \Psi[n] \rangle, \quad (3.27)$$

and the total electronic energy functional:

$$E[n] = F[n] + \int \hat{V}_{ne} n(\mathbf{r}) d\mathbf{r}. \quad (3.28)$$

Hohenberg and Kohn showed that the energy functional with respect to one-electron densities $n(\mathbf{r})$ is an upper bound to the ground state energy:

$$E_0 \leq F[n] + \int \hat{V}_{ne} n(\mathbf{r}) d\mathbf{r}, \quad (3.29)$$

with equality if and only if the one-electron density is the one-electron density corresponding to the Hamiltonian \hat{H} . This suggests a variational procedure, wherein we vary the total electronic energy functional until we reach an energy minimum:

$$E_{min} = \min_n E[n], \quad (3.30)$$

which serves as our best estimate for the ground state one-electron density $n(\mathbf{r})$. Levy and Lieb [14, 18, 17] proposed to redefine the universal density-functional in terms of normalized antisymmetric wavefunctions Ψ which yield a fixed density n :

$$F[n] = \min_{\Psi \rightarrow n} \langle \Psi | \hat{F} | \Psi \rangle = \langle \Psi[n] | \hat{F} | \Psi[n] \rangle, \quad (3.31)$$

wherein the minima search is performed over wavefunctions which yield the fixed density n . A search is then performed over densities n until we reach an energy minimum. This method is known as the *constrained search formulation*. Kohn and Sham proposed to decompose $F[n]$ as:

$$F[n] = T_s[n] + E_{Hxc}[n], \quad (3.32)$$

where $T_s[n]$ is a non-interacting kinetic-energy functional which can be defined through the constrained-search formulation:

$$T_s[n] = \min_{\Phi \rightarrow n} \langle \Phi | \hat{T} | \Phi \rangle = \langle \Phi[n] | \hat{T} | \Phi[n] \rangle, \quad (3.33)$$

wherein the minima search is now performed over normalized single-determinant wavefunctions Φ which yield the fixed density n . The functional

$E_{\text{Hxc}}[n]$ is known as the Hartree-exchange-correlation functional. The variational procedure is now performed over single-determinant wavefunctions which yield a fixed density n and then minimized over densities:

$$\begin{aligned}
E_0 &= \min_n \left\{ F[n] + \int \hat{V}_{ne} n(\mathbf{r}) d\mathbf{r} \right\} \\
&= \min_n \left\{ \min_{\Phi \rightarrow n} \langle \Phi | \hat{T} | \Phi \rangle + E_{\text{Hxc}}[n] + \int \hat{V}_{ne} n(\mathbf{r}) d\mathbf{r} \right\} \\
&= \min_n \min_{\Phi \rightarrow n} \left\{ \langle \Phi | \hat{T} + \hat{V}_{ne} | \Phi \rangle + E_{\text{Hxc}}[n_\Phi] \right\} \\
&= \min_\Phi \left\{ \langle \Phi | \hat{T} + \hat{V}_{ne} | \Phi \rangle + E_{\text{Hxc}}[n_\Phi] \right\}.
\end{aligned} \tag{3.34}$$

These equations now involve only a single-determinant wave function, which is a large simplification over a variational method involving multi-determinant wave functions. Now a major part of the kinetic energy contribution can be treated through the single-determinant wave function, while only the Hartree-exchange-correlation needs to be approximated as a functional of the density. As with the Hartree-Fock method, the single determinant wavefunctions are constructed from an orthonormal basis of spin orbitals $\chi_i(\mathbf{x})$, $i = 1, \dots, M$ with spin-spatial coordinates $\mathbf{x}_i = (\mathbf{r}_i, \sigma_i)$. The total electronic energy can be expressed in terms of spatial orbitals $\phi_i(\mathbf{r})$ after integrating out the spin variables:

$$E[\{\phi_i\}] = \sum_i \int \phi_i^*(\mathbf{r}) \left(-\frac{1}{2} \nabla^2 + \hat{V}_{ne} \right) \phi_i(\mathbf{r}) d\mathbf{r} + E_{\text{Hxc}}[n], \tag{3.35}$$

with the density expressed as:

$$n(\mathbf{r}) = \sum_i |\phi_i(\mathbf{r})|^2. \tag{3.36}$$

The energy minimum is obtained using the method of Lagrangian multipliers, with the constraint that the spatial orbitals be normalized we introduce the following Lagrangian:

$$\mathcal{L}[\{\phi_i\}] = E[\{\phi_i\}] - \sum_i \epsilon_i \left(\int \phi_i^*(\mathbf{r}) \phi_i(\mathbf{r}) d\mathbf{r} - 1 \right), \tag{3.37}$$

with ϵ_i the associated Lagrangian multiplier. The energy minimum is where the Lagrangian is stationary with respect to the spatial orbitals:

$$\frac{\partial \mathcal{L}}{\partial \phi_i^*(\mathbf{r})} = 0, \quad (3.38)$$

which gives us the functional derivative:

$$\left(-\frac{1}{2}\nabla^2 + \hat{V}_{ne}\right)\phi_i(\mathbf{r}) + \frac{\partial E_{\text{Hxc}}[n]}{\partial \phi_i^*(\mathbf{r})} = \epsilon_i \phi_i(\mathbf{r}). \quad (3.39)$$

The second term can be expressed through the chain rule as:

$$\frac{\partial E_{\text{Hxc}}[n]}{\partial \phi_i^*(\mathbf{r})} = \int \frac{\partial E_{\text{Hxc}}}{\partial n(\mathbf{r}')} \frac{\partial n(\mathbf{r}')}{\partial \phi_i^*(\mathbf{r})} d\mathbf{r}'. \quad (3.40)$$

The second factor can be expressed as:

$$\frac{\partial n(\mathbf{r}')}{\partial \phi_i^*(\mathbf{r})} = \phi_i(\mathbf{r}) \delta(\mathbf{r} - \mathbf{r}'). \quad (3.41)$$

Defining the Hartree-exchange-correlation potential as the functional derivative:

$$\hat{V}_{\text{Hxc}} = \frac{\partial E_{\text{Hxc}}}{\partial \phi_i^*(\mathbf{r})}, \quad (3.42)$$

we arrive at the Kohn-Sham eigenvalue equations:

$$\left(-\frac{1}{2}\nabla^2 + \hat{V}_{ne} + \hat{V}_{\text{Hxc}}\right)\phi_i(\mathbf{r}) = \epsilon_i \phi_i(\mathbf{r}). \quad (3.43)$$

The eigenfunctions satisfying these equations are known as the Kohn-Sham orbitals, and are eigenfunctions of the Kohn-Sham one-electron Hamiltonian:

$$\hat{h}_{KS} = -\frac{1}{2}\nabla^2 + \hat{V}_{KS}, \quad (3.44)$$

with the Kohn-Sham potential defined as:

$$\hat{V}_{KS} = \hat{V}_{ne} + \hat{V}_{\text{Hxc}}. \quad (3.45)$$

The Kohn-Sham one-electron Hamiltonian defines a system of N non-interacting electrons in an effective external potential \hat{V}_{KS} ensuring that the one-electron density is the same as that of the ground-state one-electron

density of a system of interacting electrons. The Hartree-exchange-correlation potential is further decomposed as:

$$\hat{V}_{\text{Hxc}} = \hat{V}_{\text{H}} + \hat{V}_{\text{XC}}, \quad (3.46)$$

where \hat{V}_{H} is the Hartree potential and \hat{V}_{XC} is the exchange-correlation potential. The Hartree potential can be expressed through the density:

$$\hat{V}_{\text{H}} = \int \frac{n(\mathbf{r})}{|\mathbf{r} - \mathbf{r}'|} d\mathbf{r}'. \quad (3.47)$$

The exchange-correlation potential is decomposed into the exchange potential and the correlation potential:

$$\hat{V}_{\text{XC}} = \hat{V}_{\text{X}} + \hat{V}_{\text{C}}. \quad (3.48)$$

For practical calculation the spatial orbitals are expanded as a linear combination of a known basis, such as hydrogen-like functions or Gaussian-type orbitals:

$$\phi_i(\mathbf{r}) = \sum_{\nu} C_{\nu i} \chi_i(\mathbf{r}). \quad (3.49)$$

We insert these into the Kohn-Sham equations, multiply by $\chi_i^*(\mathbf{r})$ and integrate over \mathbf{r} to arrive at the eigenvalue equations:

$$\sum_{\nu} F_{\mu\nu} C_{\nu i} = \epsilon_i \sum_{\nu} S_{\mu\nu} C_{\nu i}, \quad (3.50)$$

where $F_{\mu\nu} = \int \chi_{\mu}^*(\mathbf{r}) \hat{h}_{KS} \chi_{\nu}(\mathbf{r}) d\mathbf{r}$ are the elements of the Kohn-Sham Fock matrix and $S_{\mu\nu} = \int \chi_{\mu}^*(\mathbf{r}) \chi_{\nu}(\mathbf{r}) d\mathbf{r}$ are the elements of the overlap matrix of basis elements. The Fock matrix is decomposed into its constituent parts:

$$F_{\mu\nu} = H_{\mu\nu} J_{\mu\nu} + V_{XC,\mu\nu}, \quad (3.51)$$

where $H_{\mu\nu}$ are the one-electron integrals:

$$H_{\mu\nu} = \int \chi_{\mu}^*(\mathbf{r}) \left(-\frac{1}{2} \nabla^2 + \hat{V}_{ne}(\mathbf{r}) \right) \chi_{\nu}(\mathbf{r}) d\mathbf{r}, \quad (3.52)$$

$J_{\mu\nu}$ is the Hartree-potential contribution:

$$J_{\mu\nu} = \sum_{\lambda} \sum_{\gamma} P_{\lambda\gamma} (\chi_{\mu} \chi_{\nu} | \chi_{\lambda} \chi_{\gamma}), \quad (3.53)$$

where we have defined the density matrix $P_{\lambda\gamma}$ as:

$$P_{\gamma\lambda} = \sum_i C_{\gamma i} C_{\lambda i}^*, \quad (3.54)$$

and the two-electron integrals are defined as:

$$(\chi_\mu \chi_\nu | \chi_\lambda \chi_\gamma) = \int \int \frac{\chi_\mu^*(\mathbf{r}_1) \chi_\nu(\mathbf{r}_1) \chi_\lambda^*(\mathbf{r}_2) \chi_\gamma(\mathbf{r}_2)}{|\mathbf{r}_1 - \mathbf{r}_2|} d\mathbf{r}_1 d\mathbf{r}_2. \quad (3.55)$$

and finally the exchange-correlation potential contribution:

$$\hat{V}_{\text{XC},\mu\nu} = \int \chi_\mu^*(\mathbf{r}) \hat{V}_{\text{XC}}(\mathbf{r}) \chi_\nu(\mathbf{r}) d\mathbf{r}. \quad (3.56)$$

The Kohn-Sham equations can be written more compactly as the matrix equation:

$$FC = SC\epsilon, \quad (3.57)$$

where ϵ is a vector containing the energy eigenvalues of the basis elements. The equations are then solved iteratively through diagonalization to obtain the matrix of coefficients C . Once we have obtained the coefficients the density $n(\mathbf{r})$ is calculated as:

$$n(\mathbf{r}) = \sum_\gamma \sum_\lambda P_{\gamma\lambda} \chi_\gamma(\mathbf{r}) \chi_\lambda^*(\mathbf{r}), \quad (3.58)$$

where the summation is over the number of basis functions M . The total electronic energy can now be expressed as:

$$E = \sum_\mu \sum_\nu P_{\nu\mu} H_{\mu\nu} + \frac{1}{2} \sum_\mu \sum_\nu P_{\nu\mu} J_{\mu\nu} + E_{\text{XC}}. \quad (3.59)$$

Typically the energy contribution from the exchange-correlation E_{XC} has a complicated non-linear dependence on the density and must therefore be evaluated through numerical integration.

Chapter 4

Molecular Dynamics

The ab-initio methods discussed in the previous chapter are appropriate for systems with a relatively small amount of electrons, but suffer from cubic scaling as the number of electrons grows. If we would like to study systems of molecules, nanoscale structures or calculate transport coefficients we have to make further approximations limiting the degrees of freedom of our system. Instead of solving Schrödinger's equation to obtain the wave function, classical approximations are made to treat the atoms as point particles, with their interactions governed by a classical potential. This eliminates both the nucleonic and electronic degrees of freedom and allows for much larger systems to be simulated, though at the cost of quantum effects exhibited by the electrons. In addition, the construction of molecular dynamics potentials involves guessing at a functional form, and typically a large amount of parameters to be determined from experiments and simulations. In this chapter we will show how quantum mechanics and classical mechanics can be bridged semi-rigorously, and also give an introduction to central concepts of molecular dynamics, such as initialization, integration and construction and evaluation of potentials.

4.0.1 From quantum mechanics to molecular dynamics

We will follow the route described in the lecture notes [Marx, Dominik and Hutter, Jörg 15, pages 1-10] given at the Winterschool 2000 at the John von Neuman Institute for Computing, Jölich. Our starting point is the full

Hamiltonian for a set of N electrons and A nuclei:

$$\begin{aligned} \hat{H} = & - \sum_{i=1}^N \frac{\hbar^2}{2m_e} \nabla_i^2 - \sum_{a=1}^A \frac{\hbar^2}{2M_a} \nabla_a^2 - \sum_{i=1}^N \sum_{a=1}^A \frac{e^2 Z_a}{R_{ia}} \\ & + \sum_{i=1}^N \sum_{j=i+1}^N \frac{e^2}{r_{ij}} + \sum_{a=1}^A \sum_{b=a+1}^A \frac{e^2 Z_a Z_b}{R_{ab}}. \end{aligned} \quad (4.1)$$

We want to find solutions to the time-dependent non-relativistic Schrodinger equation:

$$i\hbar \frac{\partial}{\partial t} \Psi = \hat{H} \Psi. \quad (4.2)$$

The wave function is separated in terms of the electronic and nuclear coordinates with the ansatz:

$$\Psi(\{\mathbf{r}\}_i, \{\mathbf{R}\}_a, t) \approx \Phi(\{\mathbf{r}\}_i) \chi(\{\mathbf{R}\}_a) \exp \left[\frac{i}{\hbar} \int_{t_0}^t dt' E_e(t') \right], \quad (4.3)$$

with the electronic and nuclear wave functions normalized to unity at every instance of time. A phase factor is introduced to make the equations look nice:

$$E_e = \int d\mathbf{r} d\mathbf{R} \Phi^* \chi^* \hat{H} \Phi \chi, \quad (4.4)$$

where the integration occurs over all spatial coordinates $\{\mathbf{r}\}_i, \{\mathbf{R}\}_a$. This is a single determinant ansatz which must lead to a mean-field description of the dynamics. Inserting this ansatz into the Schrodinger equation reveals the following set of equations:

$$i\hbar \frac{\partial \Phi}{\partial t} = - \sum_i \frac{\hbar^2}{2m_e} \nabla_i^2 \Phi + \left\{ \int d\mathbf{R} \chi^* V_{ne} \chi \right\} \Phi, \quad (4.5)$$

$$i\hbar \frac{\partial \chi}{\partial t} = - \sum_a \frac{\hbar^2}{2M_a} \nabla_a^2 \chi + \left\{ \int d\mathbf{r} \Phi^* \hat{H} \Phi \right\} \chi. \quad (4.6)$$

These coupled equations form the framework for the time-dependent self-consistent field (TDSCF) method. The electrons and nucleons move on a

potential energy surface obtained from averages over the opposite class of degrees of freedom (the nuclear and electronic wave functions respectively). In the framework of classical molecular dynamics we approximate the nuclei as classical point particles. This can be done by rewriting the nuclear wave function as

$$\chi = A \exp[iS/\hbar], \quad (4.7)$$

with an amplitude factor A and a phase S which are both considered to be real. The TDSCF equations are rewritten in terms of these variables

$$\frac{\partial S}{\partial t} + \sum_a \frac{1}{2M_a} (\nabla_a S)^2 + \int d\mathbf{r} \Phi^* \hat{H} \Phi = \hbar^2 \sum_a \frac{1}{2M_a} \frac{\nabla_a^2 A}{A}, \quad (4.8)$$

$$\frac{\partial A}{\partial t} + \sum_a \frac{1}{M_a} (\nabla_a A)(\nabla_a S) + \sum_a \frac{1}{2M_a} A(\nabla_a^2 S) = 0. \quad (4.9)$$

This set of equations is known as the "quantum fluid dynamical representation". The term for S contains a term for \hbar which vanishes in the classical limit $\hbar \rightarrow 0$:

$$\frac{\partial S}{\partial t} + \sum_a \frac{1}{2M_a} (\nabla_a S)^2 + \int d\mathbf{r} \Phi^* \hat{H} \Phi = 0. \quad (4.10)$$

This formulation of the nuclear dynamics is isomorphic to the Hamilton-Jacobi formulation:

$$\frac{\partial S}{\partial t} + \hat{H} = 0, \quad (4.11)$$

with the classical Hamilton function

$$\hat{H} = T(\{P_a\}) + V(\{R_a\}), \quad (4.12)$$

with coordinates $\{R_a\}$ and conjugate momenta $\{P_a\}$. If we identify the conjugate momenta with the phase S as:

$$\mathbf{P}_a = \nabla_a S, \quad (4.13)$$

we obtain the following Newtonian equations of motion:

$$\begin{aligned}\frac{d\mathbf{P}_a}{dt} &= -\nabla_a V = -\nabla_a \int d\mathbf{r} \Phi^* \hat{H} \Phi \quad \text{or} \\ M_a \frac{d^2 \mathbf{R}_I}{dt^2} &= -\nabla_a \int d\mathbf{r} \Phi^* \hat{H} \Phi \\ &= -\nabla_a V_e^E(\{\mathbf{R}_a(t)\}).\end{aligned}\tag{4.14}$$

Under this formulation of nuclear dynamics the nuclei move according to the laws of classical mechanics in an effective potential V_e^E generated by the electrons. After averaging out the electronic degrees of freedom this potential is now only a function of the nuclear coordinates. the electronic degrees of freedom. For consistency the nuclear wave function appearing in the TDSCF equation for the electronic degrees of freedom has to be replaced by the positions of the nuclei. This is accomplished by replacing the nuclear density $|\chi|^2$ in the limit $\hbar \rightarrow 0$ by a product of delta functions $\prod_a \delta(\mathbf{R}_a - \mathbf{R}_a(t))$ centered at the instantaneous positions $\{\mathbf{R}_a(t)\}$ of the classical nuclei. This leads to a time-dependent wave equation for the electrons:

$$i\hbar \frac{\partial \Phi}{\partial t} = -\sum_i \frac{\hbar}{2m_e} \nabla_i^2 \Phi + \hat{V}_{ne} \Phi, \tag{4.15}$$

which evolve quantum mechanically as the nuclei propagate classically. This mixed approach is commonly referred to as *Ehrenfest molecular dynamics*. Under this formulation of nuclear dynamics the nuclei evolve classically while the electrons evolve according to the laws of quantum mechanics. Although the underlying equations describe a mean-field theory, the Ehrenfest approach includes transitions between electronic states. In order to arrive at a purely classical description of the dynamics of both the nuclei and the electrons we need to make further simplifications. Firstly we restrict the electronic wave function Φ to the ground state wave function Φ_0 at every instant of time. This means the nuclei move on a single potential energy surface:

$$V_e^E = \int d\mathbf{r} \Phi_0^* \hat{H} \Phi_0 = E_0(\{\mathbf{R}_I\}), \tag{4.16}$$

that is obtained by solving the Schrodinger equation for the ground state electron wave function:

$$\hat{H} \Phi_0 = E_0 \Phi_0. \tag{4.17}$$

Since we are now dealing with a single potential energy surface, the problem of computing the energy surface can be decoupled from computing the expectation values from the electronic wave function. First one produces an appropriate set of nuclear configurations by solving the time-independent Schrodinger equation. Second, these configurations are fitted to an analytical functional form to produce a global potential energy surface. Finally the Newtonian equations of motions are solved on this energy surface, producing a set of classical trajectories. To deal with the large number of degrees of freedom as the number of nuclei in the system increases, the global potential energy surface is approximated as an expansion of manybody contributions:

$$V_e^E \approx V_e^{\text{approx}} = \sum_a v_1(R_a) + \sum_{a<b} v_2(R_a, R_b) + \sum_{a<b<c} v_3(R_a, R_b, R_c), \quad (4.18)$$

and is typically truncated at 2, 3 or 4-body interactions depending on the complexity of the atoms and molecules in the system. This renders the problem of computing dynamics purely classical:

$$M_a \frac{d^2 R_I}{dt^2} = -\nabla_a V_e^{\text{approx}}. \quad (4.19)$$

This reduction in the number of degrees of freedom is a huge simplification which allows us to study much larger and more complex systems than ab-initio methods. However, many approximations have to be made to get to this formulation of atomic/molecular mechanics, and neglecting the electronic degrees of freedom effectively precludes chemical transformations from appearing in the simulations. In addition, the analytical functional forms of the potentials usually include many parameters to be determined, and they often have to be tailored to the quantities one is trying to compute.

4.0.2 Molecular dynamics simulations

The theory in this and the following sections is based partly on [Frenkel, Daan and Smit, Berend 6, pages 63-107], which explains the physics behind many popular methods for computer calculation and simulation. Classical molecular dynamics is a method for computing equilibrium and transport properties of manybody systems obeying classical laws of motion. While a large number of simplifications have to be made in order to describe quantum mechanical systems classically, the approximation works surprisingly well

except for atoms which are quite light (He, H²) or for atoms with a vibrational energy which is substantially larger than the thermal energy of the system ($h\nu > k_B T$).

In order to calculate properties of the system they have to be expressed in terms of the positions and velocities of the constituent nuclei. For instance the temperature can be related to the average kinetic energy of the system:

$$\langle \frac{1}{2}mv^2 \rangle = \frac{N_f}{2}k_B T, \quad (4.20)$$

where N_f is the number of degrees of freedom in our system. At every instant of time the total kinetic energy of our system defines an instantaneous temperature, which has to be averaged over a large number of timesteps in order to produce the equilibrium property. In practice, one is satisfied when the fluctuations in the instantaneous temperature appear reasonably small.

To run a molecular dynamics simulation one requires a set of initial conditions, i.e. a set of initial positions and velocities for every atom in the system. Typically the atoms are placed by replicating a unit cell a number of times in every dimension. A unit cell consists of a set of lattice vectors which define the placement of every atom in the unit cell. For instance the face-centered cubic cell (FCC) contains 4 atoms:

$$\begin{aligned} \mathbf{r}_1 &= (0, 0, 0) \\ \mathbf{r}_2 &= \left(\frac{b}{2}, \frac{b}{2}, 0\right) \\ \mathbf{r}_3 &= \left(0, \frac{b}{2}, \frac{b}{2}\right) \\ \mathbf{r}_4 &= \left(\frac{b}{2}, 0, \frac{b}{2}\right), \end{aligned} \quad (4.21)$$

where b is known as the lattice constant and defines the size of the unit cells.

The velocities are typically initialized with a random uniform distribution or the Maxwell-Boltzmann distribution. The Maxwell-Boltzmann distribution is the one most often used, since the equilibrium distribution tends towards this distribution. The exact form however will differ from the one we started with.

Given these initial conditions, the system will not be in an equilibrium state at $t = 0$. To evolve the system to an equilibrium state one most commonly evolves the system for a number of timesteps until fluctuations in

dynamic properties such as the total potential energy or the temperature settle down. Once we are in equilibrium we can start calculating thermodynamic averages.

As we mentioned before, the global energy surface as a function of nuclear coordinates $\{\mathbf{r}\}$ is approximated as an expansion of manybody contributions:

$$V_e^E(\{\mathbf{r}\}) = \sum_i v_1(r_i) + \sum_{i<j} v_2(r_i, r_j) + \sum_{i<j<k} v_3(r_i, r_j, r_k), \quad (4.22)$$

wherein each n -body term is an analytical function of n coordinates. As an atom moves on the energy surface it feels a force which is the gradient of the potential energy surface. This means atom i feels an acceleration:

$$\mathbf{F}_i = m_i \frac{d^2 \mathbf{r}_i}{dt^2} = -\nabla_i V_e^E(\{\mathbf{r}\}). \quad (4.23)$$

For a system of N atoms with only pairwise interactions this means the forces must be calculated $N(N-1)/2$ times for every timestep which means we have a time complexity of order $\mathcal{O}(N^2)$. The force calculation is by far the most important part of any molecular dynamics simulation, and the most time consuming. A number of techniques are employed in order to reduce the time usage, perhaps the most common is the use of neighbor lists. Using neighbor lists, each atom carries a list of neighbors within a cut-off radius r_{cut} and interactions beyond this cut-off are neglected. This reduces the time-complexity to merely $\mathcal{O}(N)$, with a proportionality constant dependent upon the average number of neighbors in the system within a cutoff r_{cut} . For a large system this can be a huge reduction in complexity, but the choice of cut-off can obviously massively impact the dynamics of the system.

In order to simulate the dynamics of a system governed by a conservative force $\mathbf{F} = -\nabla V_e^E$ we need to integrate the Newtonian equations of motion. The equations of motion are typically not solvable analytically, which means we require an effective numerical method for integration. Some important considerations for molecular dynamics are conservation of energy and accuracy for large time steps. The most common method used is the Velocity-Verlet algorithm. At any given time step t , the position $\mathbf{r}(t + \Delta t)$ and velocity

$\mathbf{v}(t + \Delta t)$ at the next time step $t + \Delta t$ is calculated as:

$$\begin{aligned}\mathbf{r}(t + \Delta t) &= \mathbf{r}(t) + \mathbf{v}(t)\Delta t + \frac{1}{2}\mathbf{a}(t)\Delta t^2, \\ \mathbf{a}(t + \Delta t) &= -\frac{1}{m}\nabla V_e^E(\mathbf{r}(t + \Delta t)), \\ \mathbf{v}(t + \Delta t) &= \mathbf{v}(t) + \frac{1}{2}(\mathbf{a}(t) + \mathbf{a}(t + \Delta t))\Delta t.\end{aligned}\tag{4.24}$$

The error in the Velocity-Verlet method is of order $\mathcal{O}(\Delta t^2)$, which means that it is not particularly accurate for large time steps over a long time. However, the long term energy drift of the method is small, which is very desirable. It is also not very memory-intensive, which matters for simulating very large systems.

Molecular dynamics is usually performed within a cubic box of fixed volume $V = L_x \cdot L_y \cdot L_z$, where L_i is the length of the box in direction i . Molecular dynamics is typically limited by the number of particles we are able to simulate, of the order $10^6 - 10^8$, which means the size of the box is often decided by the desired density $\rho = N/V$. Since the number of particles is always much smaller than the number of particles in realistic systems, approximations are required. Periodic boundary conditions can be applied to the box in order to approximate an infinite system. Typically particle coordinates are restricted to the simulation box, which can be expressed in pseudocode as:

Algorithm 1 Continuity

```

if  $x < -L_x/2$  then
     $x += L_x$ 
end if
if  $x > L_x/2$  then
     $x -= L_x$ 
end if

```

Distance and distance vectors between particles should also obey the minimum image convention:

Algorithm 2 Minimum image

```
dx = xj - xi
if dx < -Lx/2 then
    dx += Lx
end if
if dx > Lx/2 then
    dx -= Lx
end if
```

These conditions should be applied in every dimension. This approach runs the risk of introducing nonphysical artifacts of the simulation, such as a macromolecule interacting with its own image, and for coulombic interactions the system must be charge neutral to avoid summing to an infinite charge. The optimal system size with periodic boundary conditions will therefore depend on the intended simulation length, the desired accuracy and the dynamics which are being studied.

Thus far we have discussed molecular dynamics for a system of N particles within a fixed volume V and constant energy E , i.e. in the microcanonical ensemble NVE . Other ensembles are also impossible, such as the canonical ensemble NVT and the isothermal-isobaric ensemble NPT .

Simulations in the canonical ensemble can be achieved by modifying the verlet integration algorithm. The simplest thermostat possible follows from the equipartition theorem:

$$T \propto \langle mv^2 \rangle, \quad (4.25)$$

meaning some amount of kinetic energy i.e. velocity can be added or subtracted to every atom in order to maintain a constant temperature at every timestep. Multiplying every velocity by a factor $\lambda = \sqrt{T_0/T(t)}$ where $T(t)$ is the instantaneous temperature and T_0 is the desired temperature will achieve desired effect. This approach significantly alters the trajectories of the system however, which means this thermostat should only be applied for adjusting the temperature of the system and not for taking ensemble averages in equilibrium.

The most common thermostat used is the Nosé-Hoover thermostat, which is one of the most accurate and efficient algorithms for achieving realistic constant-temperature conditions (see the lecture notes [21, Shell, M. Scott]).

Nosé introduced an extended Hamiltonian with two additional degrees of freedom:

- s - the position of an imaginary coupled heat reservoir
- p_s - the conjugate momentum of the heat reservoir

In addition it introduces an effective mass Q such that $p_s = Q \frac{ds}{dt}$.

Hoover modified Nosé's approach by introducing the Hamiltonian:

$$H = \frac{1}{2} \sum m_i |\mathbf{p}_i|^2 + U(\mathbf{r}) + \frac{\xi Q}{2} + 3Nk_B T \ln s, \quad (4.26)$$

where ξ is a friction coefficient and $\mathbf{p}_i = m_i \mathbf{v}_i \times s$ are the particle momenta. This leads to a new set of Newtonian equations of motions with an additional force that is proportional to the velocity:

$$\begin{aligned} \frac{d\mathbf{r}_i}{dt} &= \mathbf{v}_i \\ \frac{d\mathbf{v}_i}{dt} &= -\frac{1}{m_i} \frac{\partial U(\mathbf{r})}{\partial \mathbf{r}_i} - \xi \mathbf{v}_i \\ \frac{d\xi}{dt} &= \left(\sum m_i |\mathbf{v}_i|^2 - 3Nk_B T \right) / Q \\ \frac{d \ln s}{dt} &= \xi. \end{aligned} \quad (4.27)$$

These can then be solved with a numerical integration scheme such as the velocity-Verlet algorithm.

4.0.3 Molecular dynamics potentials

The dynamics of an ensemble of particles is governed by their interactions. In molecular dynamics we stipulate that the interactions are decided only by the relative positions of the particles, i.e. only conservative forces act on the atoms. This means that the force on atom i is fully described by a potential energy U :

$$\mathbf{F}_i = -\nabla_i U(\{\mathbf{r}\}), \quad (4.28)$$

which in principle depends on the position of atom i and all other atoms in the system. Finding an appropriate potential for the system of atoms

which you intend to study can be arduous work, and usually involves fitting an analytical functional form with a large set of parameters to a potential energy surface from ab initio quantum mechanical calculations.

Potentials can be classified as either bonded or non-bonded. Bonded potentials compute the interactions for a predefined set of atoms and molecules in the simulations, while non-bonded potentials compute the interactions between *all* pairs, triplets etc. of atoms (usually within a certain radius). Larger, more complex systems typically contain a mix of bonded and non-bonded potentials, for example a system of rigid water molecules interacting with a surface of carbon atoms.

One of the simplest potentials meant to simulate a realistic system is the Lennard-Jones potential:

$$U(r_{ij}) = 4\epsilon \left(\left(\frac{\sigma}{r_{ij}} \right)^{12} - \left(\frac{\sigma}{r_{ij}} \right)^6 \right), \quad (4.29)$$

with $r_{ij} = |\mathbf{r}_j - \mathbf{r}_i|$. For the Lennard-Jones potential there are only two parameters to be decided, a characteristic energy ϵ and a characteristic length σ . This potential is meant to emulate the relatively weak interactions between noble gas atoms such as Argon. It can be separated into two terms:

- $-\left(\frac{\sigma}{r}\right)^6$ - owing to the long-term attraction from van der Waals interactions
- $+\left(\frac{\sigma}{r}\right)^{12}$ - owing to the short-term repulsion from the Pauli principle

While the van der Waals term is justified by theory, the repulsion term is justified by numerical efficiency - as it contains the square of the van der Waals term - and because it models the Pauli repulsion accurately.

While the Lennard-Jones potential is very simple, requiring only two parameters to be determined, it has shown to be effective at modelling noble gas atoms and is commonly used as a building block for more complicated interactions.

Another simple and common potential is the Stillinger-Weber potential, which is meant to model the interactions between silicon atoms (see the lecture notes [1, Abrams, Cameron]). Silicon forms tetrahedral bonded structures as well as pairwise interactions which means the potential includes a twobody

and a threebody interaction:

$$U = \sum_{i < j} v_2(r_{ij}) + \sum_{i < j < k} v_3(\mathbf{r}_i, \mathbf{r}_j, \mathbf{r}_k). \quad (4.30)$$

The twobody interaction models the pairwise interaction:

$$v_2(r) = \begin{cases} \epsilon A (B r^{-p} - r^{-q}) \exp[(r - a)^{-1}], & r < a \\ 0 & r \geq a \end{cases} \quad (4.31)$$

This twobody term resembles the Lennard-Jones potential, but with an exponential cutoff. The threebody term models the tetrahedral angles, and is a sum over three triplets:

$$v_3(\mathbf{r}_i, \mathbf{r}_j, \mathbf{r}_k) = h_{jik} + h_{ijk} + h_{ikj}, \quad (4.32)$$

with the angular interaction $h_{jik} = h(r_{ij}, r_{ik}, \theta_{jik})$ and

$$h_{jik} = \begin{cases} \epsilon \lambda \exp \left[\frac{\gamma}{r_{ij} - a} + \frac{\gamma}{r_{ik} - a} \right] (\cos \theta_{jik} - \cos \theta_{jik}^0)^2 & r_{ij} < a \\ 0 & r_{ij} \geq a \end{cases} \quad (4.33)$$

where θ_{jik}^0 is an "equilibrium" angle. The terms $\epsilon, A, B, p, q, \lambda, \gamma$ are parameters to be decided and a is a cutoff radius. The inclusion of the threebody terms prove to be quite important in silicon maintaining its equilibrium crystal structure. The Stillinger-Weber potential agrees quite well with experiment, and its relatively simple form makes it well suited for the testing and evaluation of new potentials.

A more complicated set of potentials is the Effective Medium Theory (EMT) family of potentials, developed to describe the late transition metals in the FCC crystal structure. The potential was first described by [11, Jacobsen, K.W.; Nørskov, J.K. and Puska, M.J.], but the most common set of parameters was published in the later article by [10, Jacobsen, K.W.; Stoltze, P. and Nørskov, J.K.]. These potentials are based on the effective medium theory concept of an electron density with a volume-dependent contribution to the total energy. Effective Medium Theory computes the energy of an atom in an arbitrary environment by computing it first in a reference system and then

estimating the energy difference between the real system and the reference system. The total energy is written as:

$$E = \sum_i E_{c,i} + \left(E - \sum_i E_{c,i} \right), \quad (4.34)$$

where $E_{c,i}$ is the energy of atom i in the reference system. The correction $E - \sum_i E_{c,i}$ is made small enough so that it can be estimated using approximate methods such as perturbation theory. From Density Functional Theory the total energy can be written as:

$$E = \sum_i E_{c,i}(n_i) + \Delta E_{AS} + \Delta E_{1el}, \quad (4.35)$$

where E_c , ΔE_{AS} and ΔE_{1el} are known as the cohesive function, atomic-sphere correction and one-electron correction respectively. The density argument n_i is known as the embedding density, which connects the surroundings of atom i to the reference system of atom i . The atomic-sphere correction is the difference in electrostatic and exchange-correlation energy for the atoms in the system of interest and the reference system. The one-electron correction is the sum of one-electron energies in the two systems. If the one-electron correction is small and can be neglected a pair-potential approximation leads to the expression:

$$\begin{aligned} E &= \sum_i [E_{c,i}(n_i) + \Delta E_{AS}] \\ &= \sum_i \left\{ E_{c,i}(n_i) + \frac{1}{2} \left[\sum_{j \neq i} V_{ij}(r_{ij}) - \sum_{j \neq i}^{\text{ref}} V_{ij}(r_{ij}) \right] \right\} \end{aligned} \quad (4.36)$$

The one-electron correction is often not small, so this is usually referred to as just the atomic-sphere correction. The embedding density n_i is computed by superimposing density contributions from the neighboring atoms:

$$n_i = \sum_{j \neq i} \Delta n_j(s_i, r_{ij}), \quad (4.37)$$

where the density tail $\Delta n(s, r)$ from a neighboring atom a distance r averaged over a sphere of radius s has an exponential form:

$$\Delta n(s, r) = \Delta n_0 \exp [\eta_1(s - s_0) - \eta_2(r - \beta s_0)]. \quad (4.38)$$

The size of the sphere s is chosen so that the total charge within is zero. The geometric factor $\beta = (16\pi/3)^{1/3}/\sqrt{2}$ is related to the nearest-neighbor distance $d_{nn} = \beta s$. For this set of electron densities there is a one-to-one correspondence between the average electron density and its neutral-sphere radius. This relationship has been shown to be approximately exponential:

$$\bar{n}(s) = n_0 \exp[-\eta(s - s_0)]. \quad (4.39)$$

For an FCC crystal of varying nearest-neighbor distance $r = \beta s$ the neutral-sphere radius can be expressed as:

$$s_i = s_0 - \frac{1}{\beta\eta_2} \log\left(\frac{\sigma_{1,i}}{12}\right), \quad (4.40)$$

where

$$\sigma_{1,i} = \sum_{j \neq i} \exp[-\eta_2(r_{ij} - \beta s_0)]. \quad (4.41)$$

The cohesive function is parameterized as a function of the neutral-sphere radius using the functional form:

$$\begin{aligned} E_c(s) &= E_0 f[\lambda(s - s_0)], \\ f(x) &= (1 + x) \exp(-x) \end{aligned} \quad (4.42)$$

where s_0 is the equilibrium (zero pressure) neutral-sphere radius. Finally the atomic sphere correction is written as:

$$\Delta E_{AS}(i) = \frac{1}{2} \left[\sum_{j \neq i} V(r_{ij}) - 12V(\beta s_i) \right], \quad (4.43)$$

where the factor 12 comes from the 12 nearest neighbors at a distance $r = \beta s_i$ in the FCC reference system. The pair potential is parameterized as:

$$V(r) = -V_0 \exp[-\kappa(r/\beta - s_0)]. \quad (4.44)$$

This has been found to give reasonable descriptions of the six fcc metals Cu, Ag, Au, Ni, Pd, Pt and their alloys. Further description and parameters can be found in the article [10, Jacobsen, K.W.; Stoltze, P. and Nørskov, J.K.].

Chapter 5

Machine learning

Machine learning is the study of algorithms and statistical models employed by computing systems capable of performing tasks without explicit instruction. While traditional algorithms rely on some specified input and a ruleset for determining the output, machine learning is instead concerned with a set of generic algorithms which can find patterns in a broad class of data sets. This section will give a brief overview of machine learning, and more specifically the class of algorithms known as neural networks, and will follow closely the review by [Mehta et al. 16, pages 1-64] which the reader is encouraged to seek out for further information.

Examples of machine learning problems include identifying objects in images, transcribing text from audio and making film recommendations to viewers based on their watch history. Machine learning problems are often subdivided into estimation and prediction problems. In both cases, we choose some observable \mathbf{x} (e.g. the period of a pendulum) related to some parameters $\boldsymbol{\theta}$ (e.g. the length and the gravitational constant) through a model $p(\mathbf{x}|\boldsymbol{\theta})$ that describes the probability of observing \mathbf{x} given $\boldsymbol{\theta}$. Subsequently we perform an experiment to obtain a dataset \mathbf{X} and use these data to fit the model. Fitting the model means finding the parameters $\hat{\boldsymbol{\theta}}$ that provide the best explanation for the data. *Estimation* problems are concerned with the accuracy of $\hat{\boldsymbol{\theta}}$, whereas prediction problems are concerned with the ability of the model $p(\mathbf{x}|\boldsymbol{\theta})$ to make new predictions. Physics has traditionally been more concerned with the estimation of model parameters, while in this thesis we will be focused on the accuracy of the model.

Many problems in machine learning are defined by the same set of ingredients. The first is the dataset $\mathcal{D} = (\mathbf{X}, \mathbf{Y})$, where \mathbf{X} is a matrix containing

observations of the independent variables \mathbf{x} , and \mathbf{Y} is a matrix containing observations of dependent variables. Second is a model $\mathbf{F} : \mathbf{x} \rightarrow \mathbf{y}$ which is a function of the parameters $\boldsymbol{\theta}$. Finally we have a cost function $\mathcal{C}(\mathbf{Y}, \mathbf{F}(\mathbf{X}; \boldsymbol{\theta}))$ that judges the performance of our model at generating predictions.

In the case of linear regression we consider a set of independent observations $\mathbf{X} = [\mathbf{x}_1 \ \mathbf{x}_2 \ \dots \ \mathbf{x}_N]$ related to a set of dependent observations $\mathbf{y} = (y_1, y_2, \dots, y_N)$ through a linear model $f(\mathbf{x}; \boldsymbol{\theta}) = x_1 \cdot w_1 + x_2 \cdot w_2 + \dots + x_P \cdot w_P$, with parameters $\boldsymbol{\theta} = (w_1, w_2, \dots, w_P)$. The cost function is the well known sum of least squares $\mathcal{C}(\mathbf{y}, f(\mathbf{X}; \boldsymbol{\theta})) = \sum_i^N (y_i - f(\mathbf{x}_i; \boldsymbol{\theta}))^2$ and the best fit is chosen as the set of parameters which minimize this cost function: $\hat{\boldsymbol{\theta}} = \underset{\boldsymbol{\theta}}{\operatorname{argmin}} \mathcal{C}(\mathbf{Y}, f(\mathbf{X}; \boldsymbol{\theta}))$.

5.0.1 Basics of statistical learning

Statistical learning theory is a field of statistics dealing with the problem of making predictions from data. We start with an unknown function $y = f(x)$ and our goal is to develop a function $h(x)$ such that $h \sim f$. We fix a hypothesis set \mathcal{H} that the algorithm is willing to consider. The expected error of a particular h over all possible inputs x and outputs y is:

$$E[h] = \int_{X \times Y} \mathcal{C}(h(x), y) \rho(x, y) dx dy, \quad (5.1)$$

where \mathcal{C} is a cost function and $\rho(x, y)$ is the joint probability distribution for x and y . This is known as the *expected error*. Since this is impossible to compute without knowledge of the probability distribution ρ , we instead turn to the *empirical error*. Given n data points the empirical error is given as:

$$E_S[h] = \frac{1}{n} \sum_i^n \mathcal{C}(h(x_i), y_i). \quad (5.2)$$

The *generalization error* is defined as the difference between the expected and empirical errors:

$$G = E[h] - E_S[h]. \quad (5.3)$$

We say an algorithm is able to learn from data or *generalize* if

$$\lim_{n \rightarrow \infty} G = 0. \quad (5.4)$$

We are in general unable to compute the expected error, and therefore unable to compute the generalization error. The most common approach known as *cross-validation* is to estimate the generalization error by subdividing our dataset into a *training* set and a *test* set. The value of the cost function on the training set is called the *in-sample* error and the value of the cost function on the test set the *out-of-sample* error. Assuming the dataset is sufficiently large and representative of f , and the subsampling into train and test datasets is unbiased, the in-sample error can serve as an appropriate proxy for the generalization error.

In figure 5.1 we show the typical evolution of the errors as the number of data points increase. It is assumed that the function being learned is sufficiently complicated that we cannot learn it exactly, and that we have a sizeable number of data points available. The in-sample error will decrease monotonically, as our model is not able to learn the underlying data exactly. In contrast, the out-of-sample error will decrease, as the sampling noise decreases and the training data set becomes more representative of the underlying probability distribution. In the limit, these errors both approach same value, which is known the model *bias*. The bias represents the best our model could do in the infinite data limit. The out-of-sample error produced from the sampling noise is known as *variance*, and will vanish completely given an infinite representative data set.

In figure 5.2 we show the typical evolution of the out-of-sample error as the model *complexity* increases. Model complexity is a measure of the degrees of freedom in the model space, for example the number of coefficients in a polynomial regression. In the figure we can see that bias decreases monotonically as model complexity increases, as the model is able to fit a larger space of functions. However, the variance will also increase as the model becomes more susceptible to sampling noise. In general the lowest out-of-sample error, and therefore generalization error, is achieved at an intermediate model complexity. We also find that as model complexity increases, a larger amount of data points is required to be able to reasonably fit the true function.

5.0.2 Bias-variance decomposition

Consider a dataset $\mathcal{D}(\mathbf{X}, \mathbf{y})$ of n pairs of independent and dependent variables. Assume the true data is generated from a noisy model:

$$y = f(\mathbf{x}) + \epsilon, \tag{5.5}$$

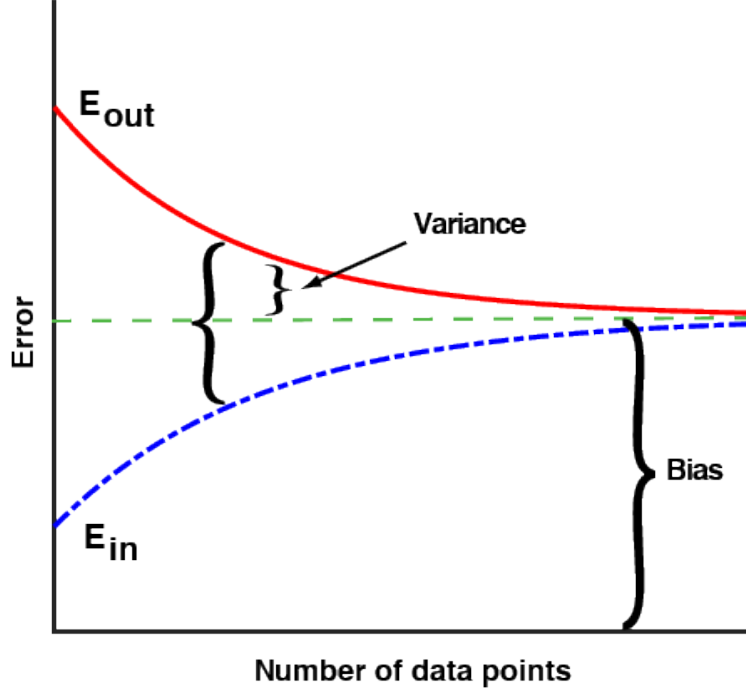


Figure 5.1: Typical in-sample and out-of-sample error as a function of the number of data points. It is assumed that the number of data points is not small, and that the true function cannot be exactly fit.

where ϵ is normally distributed with mean μ and standard deviation σ . Assume that we have an estimator $h(\mathbf{x}; \boldsymbol{\theta})$ trained by minimizing a cost function $\mathcal{C}(\mathbf{y}, h(\mathbf{x}))$ which we take to be the sum of squared errors:

$$\mathcal{C}(\mathbf{y}, h(\mathbf{x})) = \sum_i^n (y_i - h(\mathbf{x}_i; \boldsymbol{\theta}))^2. \quad (5.6)$$

Our best estimate for the model parameters:

$$\boldsymbol{\theta}_{\mathcal{D}} = \arg \min_{\boldsymbol{\theta}} \mathcal{C}(\mathbf{y}, h(\mathbf{x}; \boldsymbol{\theta})), \quad (5.7)$$

is a function of the dataset \mathcal{D} . If we imagine we have a set of datasets $\mathcal{D}_j = (\mathbf{y}_j, \mathbf{X}_j)$, each with n samples, we would like to calculate the expectation value of the cost function over all these datasets $E_{\mathcal{D}, \epsilon}$. We would also like to calculate the expectation value over different instances of the noise ϵ . The

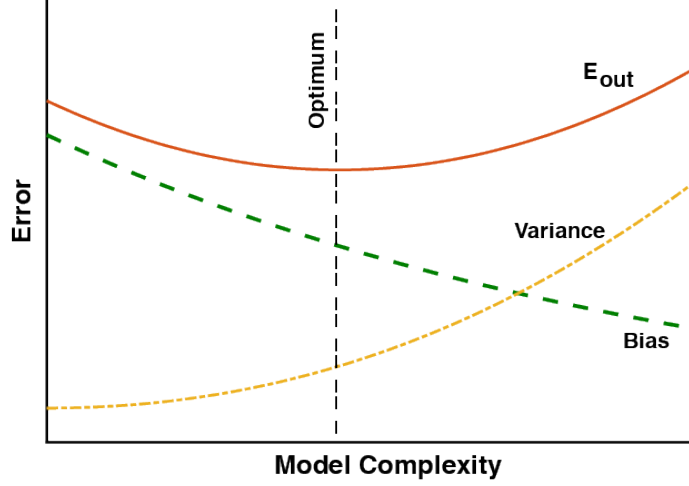


Figure 5.2: Typical out-of-sample error as a function of model complexity for a fixed dataset. Bias decreases monotonically with model complexity, while variance increases as a result of sampling noise.

expected generalization error can be decomposed as:

$$\begin{aligned} E_{\mathcal{D}, \epsilon}[\mathcal{C}(\mathbf{y}, h(\mathbf{X}; \boldsymbol{\theta}_{\mathcal{D}}))] &= E \left[\sum_i (y_i - h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}}))^2 \right] \\ &= \sum_i \sigma_{\epsilon}^2 + E_{\mathcal{D}}[(f(\mathbf{x}_i) - f(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}}))^2]. \end{aligned} \quad (5.8)$$

The second term can be further decomposed as

$$\begin{aligned} E_{\mathcal{D}}[(f(\mathbf{x}_i) - f(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}}))^2] \\ = (f(\mathbf{x}_i) - E_{\mathcal{D}}[h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}})])^2 + E[(h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}}) - E[h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}})])^2] \end{aligned} \quad (5.9)$$

The first term is what we have referred to as the bias:

$$\text{Bias}^2 = \sum_i (f(\mathbf{x}_i) - E_{\mathcal{D}}[h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}})])^2. \quad (5.10)$$

The bias measures the expectation value of the deviation of our model from the true function, i.e. the best we can do in the infinite data limit.

The second term is what we have referred to as the variance:

$$\text{Var} = \sum_i E[(h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}}) - E[h(\mathbf{x}_i; \boldsymbol{\theta}_{\mathcal{D}})])^2] \quad (5.11)$$

The variance measures the deviation of our model due to finite-sampling effects. Combining these effects we can decompose the out-of-sample error into:

$$E_{\text{out}} = \text{Bias}^2 + \text{Var} + \text{Noise}, \quad (5.12)$$

with $\text{Noise} = \sum_i \sigma_{\epsilon}^2$.

In general it can be much more difficult to obtain sufficient good data than to train a very complex model. Therefore it is often useful in practice to use a less complex model with higher bias, because it is less susceptible to finite-sampling effects.

5.0.3 Neural networks

Artificial Neural Networks (ANN) or Deep Neural Networks (DNN) are supervised learning models vaguely inspired by biological neural networks. The building blocks of neural networks are neurons that take a vector input of d features $\mathbf{x} = (x_1, \dots, x_d)$ and produce a scalar output $a(\mathbf{x})$. A neural networks consists of layers of these neurons stacked together with the output of one layer serving as input for another. The first layer is typically known as the *input layer*, the middle layers as *hidden layers* and the final layer the *output layer*. The basic architecture is shown in figure 5.3. In almost all cases the output $a_i(\mathbf{x})$ of neuron i can be decomposed into a linear operation on the inputs passed through a non-linear activation function:

$$a_i(\mathbf{x}) = \sigma_i(z_i), \quad (5.13)$$

where σ_i is a non-linear function and z_i is the dot product between the inputs \mathbf{x} and a set of neuron-specific weights \mathbf{w}_i :

$$z_i = \mathbf{x}^T \mathbf{w}_i + b_i. \quad (5.14)$$

The term b_i is a neuron-specific re-centering of the input. Typical choices of non-linearities/activation functions include the sigmoid and hyperbolic tangent functions, and Rectified Linear Units (ReLU). When the activation function is non-linear, the neural network with a single hidden layer

can be proven to be a *universal function approximator*, given an arbitrarily large number of neurons. We typically also want functions that are monotonic and smooth with a monotonic derivative.

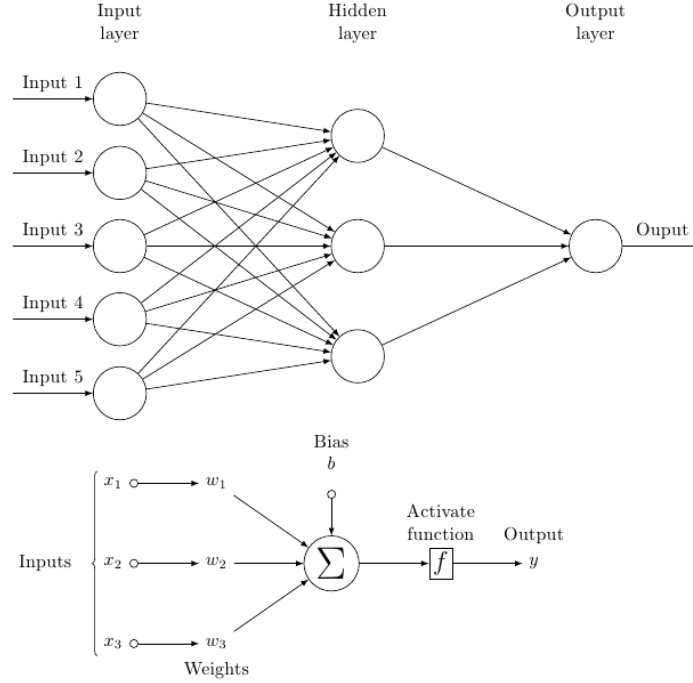


Figure 5.3: Text.

The simplest neural networks are known as *feed-forward* neural networks (FNN). The input layer is the vector \mathbf{x} of inputs, while each neuron in the first hidden layer performs a dot product between its weights \mathbf{w}_i and the inputs and passes it through a non-linearity σ_i . The activation function is typically shared across one or multiple layers $\sigma_i = \sigma$. The vector of neuron outputs \mathbf{a}_i serves as input to the next hidden layer until we reach the final layer. In the final layer the choice of activation function is dependent on the problem we are trying to solve. If we are performing non-linear regression the final activation function is often the identity $\sigma_i(z) = z$, or if we are doing classification the soft-max function is often employed.

Let \mathbf{x} be a vector of $d = 1, \dots, D$ inputs or *features*. Let $a_i^{(h)}$ denote the output of neuron $i = 1, \dots, N_l$ in layer $l = 1, \dots, L$. The output of neuron i in the first hidden layer $a_i^{(1)}$ is thus:

$$\begin{aligned} z_i^{(1)} &= \mathbf{x}^T \mathbf{w}_i^{(1)} + b_i^{(1)}, \\ a_i^{(1)} &= \sigma_i^{(1)}(z_i^{(1)}). \end{aligned} \tag{5.15}$$

The inputs are iterated through each hidden layer until we reach the final layer. Denote the vector of outputs $\mathbf{o} = (o_1, \dots, o_O)$:

$$\begin{aligned} z_i^{(L)} &= (\mathbf{a}_{L-1})^T \mathbf{w}_i^{(L)} + b_i^{(L)}, \\ a_i^{(L)} &= o_i \\ &= \sigma_i^{(L)}(z_i^{(L)}) \\ &= \sigma_i^{(L)} \left((\mathbf{a}_{L-1})^T \mathbf{w}_i^{(L)} + b_i^{(L)} \right) \\ &= \sigma_i^{(L)} \left(\left(\sigma_1^{(L-1)}, \dots, \sigma_{N_{L-1}}^{(L-1)} \right)^T \mathbf{w}_i^{(L)} + b_i^{(L)} \right). \end{aligned} \tag{5.16}$$

This allows us to compose a complicated function $\mathbf{F} : \mathbb{R}^D \rightarrow \mathbb{R}^O$, with D the number of inputs and O the number of outputs. The *universal approximation theorem* tells us that this simple architecture can approximate any of a large set of continuous functions given appropriate choice of weights \mathbf{w}_i^h and mild assumptions on the activation functions. The theorem requires only a single hidden layer, where the strength of the approximation relies on the number of neurons. In practice it has been found that adding more layers produces faster convergence and higher accuracy, which has given rise to the field of *deep learning*.

5.0.4 Backpropagation

Given a set of datapoints (\mathbf{x}_i, y_i) , $i = 1, \dots, n$, the value of the cost function is entirely determined by the weights and biases of each neuron in the network. We define learning narrowly as adjusting the parameters of the network in order to minimize the cost function.

Gradient descent is a simple, but powerful method of finding the minima of

differentiable functions. Given a function $F : \mathbb{R}^d \rightarrow \mathbb{R}$, and an initial value \mathbf{x}_0 we define an iterative procedure:

$$\mathbf{x}_{n+1} = \mathbf{x}_n - \eta \nabla F(\mathbf{x}_n), \quad (5.17)$$

where η is known as the *learning rate*. The procedure terminates when the norm $|\nabla F(\mathbf{x}_n)|$ or $|\mathbf{x}_{n+1} - \mathbf{x}_n|$ is appropriately small.

The learning rate is not necessarily fixed throughout the procedure, and proves crucial to the convergence of the method. If f is convex, and η is reasonably small, convergence is guaranteed. Convergence may be very slow however, and if f is not convex you are only guaranteed to find local minima, and this makes the method very sensitive to initial conditions.

In order to train the model, we need to calculate the derivative of the cost function with respect to a very large number of parameters multiple times. However, numerical calculation of gradients is very time consuming. The *backpropagation* algorithm is a clever use of the chain rule that allows us to calculate gradients efficiently.

Assume that there are L layers in our network with $l = 1, 2, \dots, L$ indexing the layers, including the output layer and all the hidden layers. Let w_{ij}^l denote the weight for the connection from the i -th neuron in layer $l - 1$ to the j -th neuron in layer l . Let b_j^l denote the bias of this j -th neuron.

The activation a_j^l of the j -th neuron in the l -th layer is related to the activities of the neurons in the layer $l - 1$ by:

$$a_j^l = f \left(\sum_i w_{ij}^l a_i^{l-1} + b_j^l \right) = f(z_j^l), \quad (5.18)$$

where f is some activation function.

The cost function \mathcal{C} depends directly on the activations in the output layer, and indirectly on the activations in all the lower layers. Define the error Δ_j^L of the j -th neuron in the L -th (final) layer as the change in cost function with respect to the weighted input z_j^L :

$$\Delta_j^L = \frac{\partial \mathcal{C}}{\partial z_j^L}. \quad (5.19)$$

Define analogously the error Δ_j^l of neuron j in the l -th layer as the change

in cost function with respect to the weighted input z_j^l :

$$\Delta_j^l = \frac{\partial \mathcal{C}}{\partial z_j^l}. \quad (5.20)$$

This can also be interpreted as the change in cost function with respect to the bias b_j^l :

$$\Delta_j^l = \frac{\partial \mathcal{C}}{\partial z_j^l} = \frac{\partial \mathcal{C}}{\partial b_j^l} \frac{\partial b_j^l}{\partial z_j^l} = \frac{\partial \mathcal{C}}{\partial b_j^l}, \quad (5.21)$$

since $\partial b_j^l / \partial z_j^l = 1$.

The error depends on neurons in layer l only through the activation of neurons in layer $l + 1$, so using the chain rule we can write:

$$\begin{aligned} \Delta_j^l &= \frac{\partial \mathcal{C}}{\partial z_j^l} = \sum_i \frac{\partial \mathcal{C}}{\partial z_i^{l+1}} \frac{\partial z_i^{l+1}}{\partial z_j^l} \\ &= \sum_i \Delta_i^{l+1} \frac{\partial z_i^{l+1}}{\partial z_j^l} \\ &= \sum_i \Delta_i^{l+1} w_{ij}^{l+1} f'(z_j^l) \\ &= \left(\sum_i \Delta_i^{l+1} w_{ij}^{l+1} \right) f'(z_j^l). \end{aligned} \quad (5.22)$$

The sum comes from the fact that any error in neuron j in the l -th layer propagates to all the neurons in the layer $l + 1$, so we have to sum up these errors.

This gives us the equations we need to update the weights and biases of our network:

$$\frac{\partial \mathcal{C}}{\partial w_{ij}^l} = \frac{\partial \mathcal{C}}{\partial z_j^l} \frac{\partial z_j^l}{\partial w_{ij}^l} = \Delta_j^l a_i^{l-1}. \quad (5.23)$$

$$\frac{\partial \mathcal{C}}{\partial b_j^l} = \Delta_j^l. \quad (5.24)$$

Now, if we have the error of every neuron j at the output layer, Δ_j^L , equation 5.22 gives us the recipe for calculating the error in the preceding

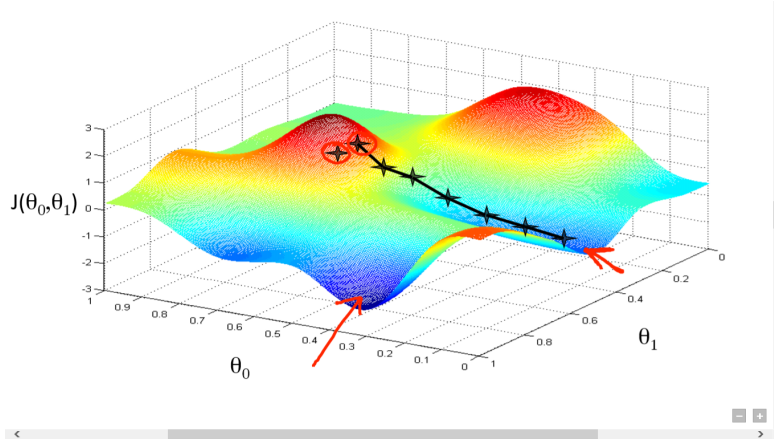


Figure 5.4: Text.

layer until we reach the first hidden layer, and we are done. All we are missing is the error at the output layer:

$$\Delta_j^L = \frac{\partial \mathcal{C}}{\partial z_j^L} = \frac{\partial}{\partial z_j^L} \left(\sum_o \frac{1}{2} (z_o^L - y_o)^2 \right) = z_j^L - y_j. \quad (5.25)$$

Now, since the derivatives for the weights depend on the activations in the preceding layer, this suggests an iterative procedure for training the network. First we feed the input data through the network and obtain activations and an output, then these outputs are backpropagated through the network to update the weights and biases. This is then repeated for some number of steps or until the network achieves acceptable accuracy.

5.0.5 Optimization

In order to begin the minimization procedure and find an optimal set of weights and biases for our network we first need some initial values. Often weights are initialized with small values distributed around zero, drawn from a uniform or normal distribution. The bias can be initialized to zero, but enforcing that all biases have some small value ensures that every neuron has output which can be backpropagated in the first training cycle. In the Pytorch neural network framework - which is the one we will be using - weights are

initialized uniformly as

$$\begin{aligned}\sigma &= 1/N_{in} \\ w &= \mathcal{U}(-\sigma, \sigma)\end{aligned}\tag{5.26}$$

where N_{in} is the number of inputs to the weight/layer of weights and \mathcal{U} is the uniform distribution.

A critical choice for building neural networks is the choice of activation function. As we have mentioned briefly above, we have a small set of requirements in order for the neural network to be a universal function approximator, namely that the function be nonconstant, bounded, continuous and monotonically increasing. We also desire that the function be fast to evaluate, with a derivative that is simple to calculate.

A function that fulfills all of these criteria is the sigmoid function:

$$\begin{aligned}\sigma(x) &= \frac{1}{1 + e^{-x}}, \\ \sigma'(x) &= \sigma(x)(1 - \sigma(x)).\end{aligned}\tag{5.27}$$

The sigmoid function is defined on the entire real number line, and outputs a number between 0 and 1. It also has a continuous derivative which is simple to calculate. The sigmoid function is well suited for binary classifiers, since it easily creates a decision boundary between two categories 0 and 1, and is often the first goto for AI programmers.

Another simple and commonly used activation function is the hyperbolic tangent

$$\begin{aligned}\tanh(x) &= \frac{e^{2x} - 1}{e^{2x} + 1}, \\ \tanh'(x) &= (1 - \tanh(x)^2).\end{aligned}\tag{5.28}$$

The hyperbolic tangent is defined on the real number line and outputs a number between -1 and 1 .

Both the sigmoid and the hyperbolic tangent functions exhibit the problem of vanishing gradients. In deep learning, you typically have several layers of neurons outputting some linear combination of the activation functions. Through the backpropagation algorithm, each neuron receives a weight update

proportional to the partial derivative of the loss with respect to its weights. For the sigmoid and hyperbolic tangent activations these gradients will be in the range $(-1, 1)$, and therefore often exceedingly small. This means that many neurons may receive effectively no weight update in any given training epoch, which severely impedes training.

The Rectified Linear Unit (ReLU) has gained popularity in recent years for its effectiveness in the field of convolutional neural networks. The ReLU function is defined as:

$$\begin{aligned}\text{ReLU}(x) &= \begin{cases} x & x \geq 0 \\ 0 & x < 0 \end{cases} \\ \text{ReLU}'(x) &= \begin{cases} 1 & x \geq 0 \\ 0 & x < 0 \end{cases}\end{aligned}\tag{5.29}$$

Since the ReLU function in principle has no upper bound, it does not suffer the effect of vanishing gradients. Instead, the ReLU function can produce exploding gradients, if one or more activations becomes very large. In practice the gradients are often "clipped", i.e. truncated above a certain upper bound. With the ReLU function one can also encounter "dying" neurons, since the input to any neuron that does not exceed zero is set to zero, which means that the number of neurons receiving an effective weight update

From the point of view of the neural network, the inputs are just dimensionless numbers, which are passed through layers until it spits out some outputs. It is therefore often useful to standardize the inputs. A common method is to shift the inputs by their mean and normalize by their standard deviation:

$$x'_i = \frac{x_i - \bar{x}}{\sigma_x}.\tag{5.30}$$

This is often useful in speeding up the training of neural networks. In theory any shifting and rescaling can be reproduced simply by updating the weights and biases of the network. In practice however, as the weights often start as small numbers, it can take quite a few training cycles before the weights are of appropriate size. Standardizing the inputs also makes it impose to impose a penalty on the weights in order to reduce overfitting.

The most common methods for training neural networks are variations on the simple gradient descent scheme as mentioned above:

$$\mathbf{x}_{n+1} = \mathbf{x}_n - \eta \nabla F(\mathbf{x}_n). \quad (5.31)$$

Since we are interested in training neural networks, \mathbf{x}_n represents the weights and biases of the network after n training cycles, η is our learning rate and $\nabla F(\mathbf{x}_n)$ is the gradient of the loss function.

The learning rate η controls how fast we reach a given minimum. A small learning rate will require more training cycles and a larger learning rate will require fewer. The learning rate also controls the numerical stability of the method, if it is too large the weights may diverge and if it is too small the weight may never converge. Gradient descent also tends to exhibit oscillating behaviour around the minimum. Often a schedule is imposed on the learning rate, such as reducing it by a fixed amount every few epochs or incorporating an exponentially decaying learning rate. [cite: Mehta et al] As discussed in Mehta et. al. using gradient descent to optimize our neural network imposes some limitations:

- *Gradient descent finds local minima* - if the GD algorithm converges, it will converge to a local minimum. This can lead to poor performance in complicated cost function landscapes
- *Gradients are expensive to compute* - the loss function often includes a term for each data point, which means the gradient also does.
- *GD is sensitive to learning rate* - as mentioned above, GD is very sensitive to learning rate
- *GD is sensitive to initial conditions* - gradient descent can take two different initial values and converge at two drastically different values
- *GD does not take curvature into account* - the learning rate for gradient descent is the same in all directions of parameter space, which means the maximum learning rate is set by the behaviour of the steepest direction

A common method for ameliorating some of these concerns is minibatching the inputs. Instead of calculating the gradient on the entire dataset for every epoch, we instead calculate the gradient on a subset of the data called a minibatch. If there are n datapoints and a minibatch size of m the total

number of batches is n/m . If we denote each minibatch b_k , $k = 1, 2, \dots, n/m$ the gradient becomes:

$$\nabla \mathcal{C} = \frac{1}{n} \sum_{i=1}^N \nabla \mathcal{L}_i \rightarrow \frac{1}{m} \sum_{i \in b_k} \nabla \mathcal{L}_i, \quad (5.32)$$

i.e. instead of averaging the loss over the entire dataset we instead average over a minibatch. This significantly speeds up the calculation, since we do not use the entire dataset for every update. In addition, introducing stochasticity in the division of the dataset into minibatches introduces stochasticity to the weights update, which should help gradient descent in overcoming local minima.

It is also common to introduce regularization to the weights and biases of the networks. Regularization in the context of neural networks means adding a term proportional to the L_p norm of the weights and biases. For example using the L2-norm our cost function becomes:

$$\nabla \mathcal{C} = \frac{1}{n} \sum_i \nabla \mathcal{L}_i \rightarrow \frac{1}{n} \sum_i \nabla \mathcal{L}_i + \lambda \|\mathbf{w}\|^2 = \frac{1}{n} \sum_i \nabla \mathcal{L}_i + \lambda \sum_{ij} w_{ij}^2, \quad (5.33)$$

i.e. we sum up all the weights squared. The parameter λ is known as a regularization parameter. This extra term adds a penalty on the size of the weights dependant on the regularization parameter. This has been shown to reduce overfitting, as the weights cannot be adjusted to arbitrary size in order to fit the training dataset.

Gradient descent is often paired with a momentum parameter that serves as a "memory" of the direction we are moving. This can be implemented as a modification to the gradient descent update:

$$\begin{aligned} \mathbf{v}_n &= \gamma \mathbf{v}_{n-1} + \eta \nabla F(\mathbf{x}_n), \\ \mathbf{x}_{n+1} &= \mathbf{x}_n - \mathbf{v}_n, \end{aligned} \quad (5.34)$$

where $0 < \gamma < 1$ is a memory parameter that controls the time scale for the memory. It is termed a momentum parameter because the equations for updating the parameters \mathbf{x} are analogous to the equations of motion for a particle moving in a viscous medium. Momentum helps the gradient descent algorithm gain speed in directions where the curvature is flat while dampening speed in high curvature directions.

First-order gradient descent methods differ from quasi-Newton methods in that they do not keep track of the curvature which is encoded in the so-called Hessian matrix of second order derivatives. Second-order methods accomplish this by calculating or approximating the Hessian and normalizing the learning rate by the curvature.

The RMSprop algorithm keeps a running average of both the first and second moment of the gradient. If we term the gradient as $\mathbf{g} = \nabla F(\mathbf{x})$ and the first and second orders as $\mathbf{m} = \mathbb{E}[\mathbf{g}]$ and $\mathbf{s} = \mathbb{E}[\mathbf{g}^2]$ we can write the update rule as:

$$\begin{aligned}\mathbf{g}_n &= \nabla F(\mathbf{x}_n) \\ \mathbf{s}_n &= \beta \mathbf{s}_{n-1} + (1 - \beta) \mathbf{g}_n^2 \\ \mathbf{x}_{n+1} &= \mathbf{x}_n - \eta \frac{\mathbf{g}_n}{\sqrt{\mathbf{s}_n + \epsilon}}\end{aligned}\tag{5.35}$$

where β is a parameter which controls the time scale of the averaging and ϵ is a small regularization constant to prevent divergences. Operations involving vectors are understood to be element-wise. This results in a dampening of the learning rate in directions where the gradient is consistently large, and allows us to use a larger learning rate for areas of flat curvature.

Perhaps the most commonly used optimizer today is the closely related ADAM optimizer. In addition to keeping a running average of the first and second-order moments ADAM performs an additional bias correction to account for the fact that we are estimating first and second order moments using a running average. The update rule is given as:

$$\begin{aligned}\mathbf{g}_n &= \nabla F(\mathbf{x}_n) \\ \mathbf{m}_n &= \beta_1 \mathbf{m}_{n-1} + (1 - \beta_1) \mathbf{g}_n \\ \mathbf{s}_n &= \beta_2 \mathbf{s}_{n-1} + (1 - \beta_2) \mathbf{g}_n^2 \\ \hat{\mathbf{m}}_n &= \frac{\mathbf{m}_n}{1 - \beta_1^n} \\ \hat{\mathbf{s}}_n &= \frac{\mathbf{s}_n}{1 - \beta_2^n} \\ \mathbf{x}_{n+1} &= \mathbf{x}_n - \eta \frac{\hat{\mathbf{m}}_n}{\sqrt{\hat{\mathbf{s}}_n + \epsilon}},\end{aligned}\tag{5.36}$$

with β_1 and β_2 as memory parameters for the first and second moments respectively. This update rule effectively normalizes the learning rate by the

standard deviation of the gradient, which is a natural measurement scale. This also has the effect of cutting off directions where the gradient varies by a lot.

Chapter 6

Atom-centered descriptors

Electronic structure calculations are among the most computationally intensive scientific calculations, and the rapid development of modern computers have made many previously unthinkable computer simulations a central part of the scientific toolkit. Because of their computationally demanding nature, electronic structure calculations today occupy a large portion of resources on modern scientific supercomputer facilities.

For small-scale systems, we have discussed the Hartree-Fock and Density Functional Theory methods as the primary workhorses of ab-initio electronic structure calculations. However, these methods suffer from very poor scaling as the system size increases, with Hartree-Fock naively scaling as $\mathcal{O}(N^4)$ with N the number of electrons and Density Functional Theory scaling as $\mathcal{O}(N^4)$, but with a larger proportionality scaling.

In many cases the exact details of the electronic structure are less important than the long-time behaviour of the atoms and molecules involved in the simulation, and classical approximations can be made as in molecular dynamics, which comes close to linear scaling. This allows us to simulate systems of up to millions or hundreds of millions of atoms, which can approximate nano- or micro-scale systems if periodic boundary conditions are applied. However, the question remains as to how you develop an accurate classical potential which can accurately reproduce fundamentally quantum systems, with a speed that allows us to enter into realistic timescales (i.e. nano or microseconds).

The most common approach to developing molecular dynamics potentials is to guess a functional form based on your physical intuition and experience with the systems and calculate appropriate parameters from data obtained

from DFT calculations. The number of parameters involved can range from two in the case of Lennard-Jones or hundreds of parameters in the case of complex, many-atom potentials such as the AMBER and CHARMM force fields. The imposition of functional forms to quantum data is an artform, and the potential must often be tailored to not only the chemical species and number of atoms in your system, but also the specific experimental quantity you are trying to extract, such as the energy, radial distribution function or transport coefficients. Notably there are dozens of MD potentials describing different models of water (H₂O), each fine-tuned for a specific system structure or parameter.

Due to recent developments in the field of machine learning, the question has been raised as to how it may be possible to automate the process of developing potentials. In their article introducing the Atomistic Machine-Learning Package (AMP) [12, Khorshidi, Alireza and Peterson, Andrew A.] outline one potential way forward. The idea is to approximate the potential energy with a regression model:

$$\{\mathbf{R}\} \xrightarrow{\text{Regression}} E = E(\{\mathbf{R}\}), \quad (6.1)$$

where $\{\mathbf{R}\}$ is the set of nuclear coordinates of our system. Most machine learning methods operate over a set of one-dimensional so-called *feature vectors*, where every vector element represents a feature of the data set. For example the amount of precipitation in a given area at a given time is a function of features such as humidity, cloud cover, air pressure etc. This is a vector of some length F , while the nuclear coordinates represent a point in $3N$ -dimensional phase space. This difference in representation requires some way of mapping the nuclear coordinates to features which can be employed by a machine learning method.

The naive approach would be to simply feed in the nuclear coordinates as a 1D vector, and then perform a regression on the dataset in order to obtain the potential energy. However, our physical intuition imposes some constraints on the potential energy. In particular, the potential energy of a microscopic system should be translationally, rotationally and permutationally invariant.

Translational invariance implies that the addition of any three-dimensional vector to every coordinate in the system should not in any way alter the potential energy of the system. This should not be the case with a naive mapping, as for a given set of weights (or equivalent) smaller/larger coordi-

nates values would be mapped to smaller/larger activations, and therefore alter the final output. Rotational invariance implies that the potential energy of the system should not change as the system is rotated about an axis. This also should not be the case in the context of a naive mapping, as any change to any of the inputs would be mapped in a non-linear way to produce a different output. Finally, permutation invariance implies that swapping the coordinates of any two atoms of the same chemical species would produce the same potential energy. This should also not be the case, for the same reasons as we just discussed. These constraints together heavily restrict the functional form that any mapping to the potential energy could have, which means a more careful analysis should be considered.

In order for the mapping to be applicable to systems of varying size, a decomposition into atomic energy contributions is performed:

$$E(\{\mathbf{R}\}) = \sum_{i=1}^N E_{\text{atom}}(\{\mathbf{R}\}). \quad (6.2)$$

The individual energy contributions E_{atom} are then approximated by performing a regression analysis. The atomic energy contributions are usually limited to its local environment through the introduction of a cutoff radius R_c :

$$E_{\text{atom}}(\{\mathbf{R}\}) \approx E_{\text{atom}}(\mathbf{R}_i, \{\mathbf{R}\}_j \mid |\mathbf{R}_{ij}| < R_c) \quad (6.3)$$

meaning that interactions are only treated if the interatomic distance is smaller than the cutoff. This is a good approximation for a sensible choice of cutoff radius if no electrostatic interactions are involved. Long-range interactions can also be treated through the introduction of methods such as Ewald summation, but this will not be discussed here.

A mapping that satisfies the above constraints we will refer to as a *descriptor*, and is used as input to the regression method:

$$\{\mathbf{R}\} \rightarrow \mathbf{G}(\{\mathbf{R}\}) \xrightarrow{\text{regression}} E_{\text{atom}} = E_{\text{atom}}(\mathbf{G}(\{\mathbf{R}\})). \quad (6.4)$$

Once we have a descriptor and a regression model the dynamics can be

readily obtained by taking derivatives:

$$\begin{aligned}
\mathbf{F}_i &= -\nabla_i E \\
&= -\nabla_i \sum_i^{\text{local}} E_{\text{atom}}(\mathbf{G}(\{\mathbf{R}\})) \\
&= -\sum_i^{\text{local}} \sum_j \frac{\partial E_{\text{atom}}}{\partial G_j} \frac{\partial G_j}{\partial \mathbf{R}_i},
\end{aligned} \tag{6.5}$$

where we have applied the chain rule to break the gradient into derivatives with respect to the network inputs (obtained through backpropagation) and derivatives of the network inputs with respect to the coordinates of atom i . Once we have obtained the forces the system can be propagated through time classically using for example the Velocity-Verlet equations.

6.0.1 Gaussian descriptors

In their paper on neural-network representations of potential energy surfaces [3, Behler, Jörg and Parrinello, Michele] suggested the decomposition of the mapping \mathbf{G}_i of atom i into two subvectors \mathbf{G}_i^I and \mathbf{G}_i^{II} representing pairwise and three-body interactions respectively. The components of \mathbf{G}_i^I are comprised of sums of gaussian functions of the pairwise distance R_{ij} :

$$f_i^I = \sum_{j \neq i}^{\text{local}} \exp(-\eta(R_{ij} - R_s)^2/R_c^2) f_c(R_{ij}), \tag{6.6}$$

with the sum over the local environment of atom i . The parameters η and R_s represent the width and center of the gaussian functions respectively. The term f_c is a cutoff function which decays smoothly to zero at the cutoff radius. Behler and Parrinello proposed the following cutoff:

$$f_c(R) = \begin{cases} \frac{1}{2} (1 + \cos(\pi R/R_c)) & R < R_c \\ 0 & R > R_c, \end{cases} \tag{6.7}$$

however other functional forms are possible. For the angular part such terms are multiplied, which means the function decays much more rapidly as we approach the cutoff. The only requirements we pose is that the function

be continuous with a continuous first derivative in $r \in [0, \infty)$, approach one as $R \rightarrow 0$ and zero as $R \rightarrow R_c$.

The components of the three-body subvector are defined incorporating the angles θ_{ijk} between every triplet of atoms:

$$f_i^{II} = 2^{1-\zeta} \sum_{j,k \neq i}^{\text{local}} (1 + \lambda \cos \theta_{ijk})^\zeta \exp \left(-\eta (R_{ij}^2 + R_{ik}^2 + R_{jk}^2) / R_c^2 \right) \times f_c(R_{ij}) f_c(R_{ik}) f_c(R_{jk}). \quad (6.8)$$

The components for each subvector is calculated by varying the different parameters $\eta, R_s, \zeta, \lambda$. The choice of neither symmetry functions, cutoff, nor the parameters employed by Behler and Parrinello are unique. The guiding wisdom is that atomic environments with different potential energies should give differing energies, while remaining invariant under translation, rotation and permutation. Finally we note that the descriptors and the neural network models are not interchangeable, as each neural network is trained for a specific set of input vectors, and must be retrained if the way inputs are composed changes.

6.0.2 Zernike and bispectrum descriptors

Two closely related examples of atom-centered descriptors are the Zernike and Bispectrum descriptors. They are described by [12, Khorshidi, Alireza and Peterson, Andrew A.] in their paper on the Atomistic Machine-learning Package (AMP). Bispectrum descriptors are also discussed by [2, Behler, Jörg] in his perspective on machine learning potentials. Zernike descriptors represent a tensor product between spherical harmonics and Zernike polynomials. The local atomic environment of atom i is represented by an atomic density function $\rho_i(\mathbf{r}_i)$:

$$\rho_i(\mathbf{r}_i) = \sum_{j \neq i}^{\text{local}} \eta_j \delta(\mathbf{r}_i - \mathbf{r}_{ij}) f_c(\|\mathbf{r}_{ij}\|), \quad (6.9)$$

with $f_c(r)$ a cutoff function as described in the previous section. The 3-D Zernike basis set Z is formed by a tensor product between the Zernike

polynomials basis set R and the spherical harmonics Y . The Zernike basis set is defined inside and on the surface of the S^2 unit sphere as:

$$Z_{nl}^m(r, \theta, \phi) = R_n^l(r) Y_l^m(\theta, \phi), \quad (6.10)$$

where $n \geq 0$ is an integer, l is restricted to even $n - l \geq 0$ and m is an integer such that $|m| \leq l$. Functions defined inside and on the S^2 sphere can be represented by the 3-D Zernike basis as:

$$f(r, \theta, \phi) = \sum_{n=0}^{\infty} \sum_l \sum_{m=-l}^l c_{nl}^m Z_{nl}^m(r, \theta, \phi), \quad (6.11)$$

with coefficients $c_{nl}^m = \langle Z_{nl}^m, f \rangle$ computed as projections of f onto the Zernike basis. These projections form the basis of the Zernike fingerprint, \mathbf{G}_i . Centering the atomic density preserves translation invariance of the atomic environment, while the projections onto the Zernike basis set preserves rotational invariance. Permutation invariance is maintained by keeping the constant values η_j the same within each chemical species. The Zernike descriptors are able to incorporate quadruple atomic interactions involving for example dihedral angles, while the gaussian descriptors are truncated at threebody interactions. The Zernike coefficients can also often be represented in terms of monomials, making them computationally cheaper than the bispectrum descriptors.

Bispectrum descriptors are computed much in the same way as the Zernike descriptors. The 4-D spherical harmonics form a complete, orthogonal basis set for the S^3 4-D unit sphere, and the components of the Bispectrum fingerprints \mathbf{G}_i can be computed by projecting the atomic density function onto them. For more information the reader is encouraged to check out the [12, AMP paper].

6.0.3 Deep Potential Molecular Dynamics

Deep Potential Molecular Dynamics (DPMD) is a method proposed by [27, Zhang et al.] in response to the successes of methods such as Behler-Parrinello, Gaussian Approximation Potentials (GAP) and Gradient-Domain Machine Learning (GDML). These methods all involve some amount of handcrafting the inputs, and building these inputs for larger, more complex systems is not always straightforward. The Deep Potential method assigns a local

environment and reference frame to each atom. The total potential energy is a sum of atomic contributions as before:

$$E = \sum_i E_{\text{atom}}(\{\mathbf{R}\}), \quad (6.12)$$

with the atomic energy determined by its nearest neighbors within a cutoff radius R_c :

$$E_{\text{atom},i} = E\left(\mathbf{R}_i, \{\mathbf{R}\}_j : |\mathbf{R}_{ij}| < R_c\right). \quad (6.13)$$

The position of each neighbor of atom i is described by the relative position $\mathbf{R}_{ij} = \mathbf{R}_j - \mathbf{R}_i$, which preserves translational symmetry. Rotational symmetry is conserved by constructing a local frame for each atom. Two neighboring atoms a and b are picked by a user-specified rule (default: two closest). The environment of atom i is then described by three unit vectors:

$$\begin{aligned} \mathbf{e}_{i1} &= \mathbf{e}(\mathbf{R}_{ia}), \\ \mathbf{e}_{i2} &= \mathbf{e}(\mathbf{R}_{ib} - (\mathbf{R}_{ib} \cdot \mathbf{e}_{i1})\mathbf{e}_{i1}), \\ \mathbf{e}_{i3} &= \mathbf{e}_{i1} \times \mathbf{e}_{i2}, \end{aligned} \quad (6.14)$$

where $\mathbf{e}(\mathbf{R})$ denotes the normalized vector $\mathbf{e}(\mathbf{R}) = \mathbf{R}/|\mathbf{R}|$. Together these vectors form an orthonormal basis for the reference frame of atom i . The local coordinates \mathbf{R}_{ij} can then be obtained from the global coordinates \mathbf{R}_{ij}^0 through the transformation:

$$\mathbf{R}_{ij} = \mathbf{R}_{ij}^0 \cdot \mathcal{R}, \quad (6.15)$$

where $\mathcal{R} = [\mathbf{e}_{i1} \ \mathbf{e}_{i2} \ \mathbf{e}_{i3}]$ is a rotation matrix with columns given by the local basis vectors. The neural network input vector for every atom-to-atom interaction \mathbf{D}_{ij} can be given with radial-only or full radial-angular information:

$$\mathbf{D}_{ij}^\alpha = \begin{cases} \left(\frac{1}{R_{ij}}, \frac{\mathbf{R}_{ij}}{|\mathbf{R}_{ij}|} \right) & \text{full information,} \\ \left(\frac{1}{R_{ij}} \right) & \text{radial-only information,} \end{cases} \quad (6.16)$$

with $\alpha = 0$ when only radial information is specified and $\alpha = 0, 1, 2, 3$ when full information is provided. Radial information is typically sufficient for

long-range interactions such as van-der-Waals forces, while covalent bonding can be modeled by including only the closest atoms. We therefore specify two separate cutoff shells, one for the radial information R_c and one for treating angular interactions R_a .

In order to preserve permutation symmetry the inputs vectors \mathbf{D}_{ij} are sorted first according to chemical species, and then within each chemical species according to their inverse distance $1/R_{ij}$. The vector of subvectors \mathbf{D}_i is then fed through a neural network to produce the atomic energy contribution. The network input size is fixed according to the maximum number of neighbors in the system which is being studied, with some entries $\mathbf{D}_{ij} = \mathbf{0}$ if there are fewer neighbors within the radial cutoff.

The authors also propose a scheme of force learning, wherein the force Root Mean Square Error (RMSE) is incorporated into the Loss Function:

$$\mathcal{L} = \frac{p_\epsilon}{N} \sum_i (\Delta E_i^2) + \frac{p_f}{3N} \sum_i |\Delta \mathbf{F}_i|^2, \quad (6.17)$$

with p_ϵ and p_f energy and force pre-factors which are adjusted throughout the learning process. The term ΔE_i denotes the error between the network outputs and the correct potential energy, while the term $\Delta \mathbf{F}_i$ denotes the error in the force output. The pre-factors are adjusted based on the learning rate:

$$p(t) = p^{\text{limit}} \left[1 - \frac{r_l(t)}{r_l^0} \right] + p^{\text{start}} \left[\frac{r_l(t)}{r_l^0} \right], \quad (6.18)$$

with $r_l(t)$ and r_l^0 the learning rate at time step t and time step 0 respectively. The learning rate decays exponentially as:

$$r_l(t) = r_l^0 \cdot d_r^{(t/d_s)}, \quad (6.19)$$

with d_r the decay rate and d_s the decay steps. The decay rate should be less than 1. The force error is often a magnitude or two larger than the energy error, and it is believed that incorporating the force into the loss should improve the learning rate for physics-based applications which incorporate forces. The virial information can also be treated in this manner, but we will not discuss this here.

Part II

Implementation

Chapter 7

Atomic Simulation Environment

The Atomic Simulation environment (ASE¹) [13, Larsen et al.] is a software package written in Python for the purpose of setting up, steering and analyzing atomistic simulations. Python is an interpreted, high-level general purpose language, with a powerful, consise syntax which allows one to perform very complex tasks with few lines of code. Python can also easily be extended and interfaced with fast and mature libraries. The modular interface of Python makes ASE easily extensible; in particular the calculator interface for evaluating energies, forces and much more has been implemented for open- and closed-source software packages such as LAMMPS, VASP, Quantum Espresso and many more. The Atomic Simulation Environment is intended to be:

- Easy to use
- Flexible
- Customizable
- Pythonic
- Open to participation

¹ <https://wiki.fysik.dtu.dk/ase/index.html>

The real drawback of Python is that it is an interpreted language, which results in slow execution. It can also be quite memory-intensive, which makes pure Python unsuitable for large scale computations and simulations. It is therefore common to write the computationally demanding tasks in a lower level compiled language, and build a Python interface for calling functions and classes.

7.0.1 Installation

ASE requires an installation of

- Python 2.7, 3.4-3.6
- Numpy 1.9 or newer
- Scipy 0.14 or newer

This can be easily obtained through the Anaconda or Miniconda packages², or follow the instructions on the Python website³. Once you have the prerequisites ASE can be installed using pip:

```
pip install ase
```

7.0.2 Molecular Dynamics

Here we will demonstrate how to setup a simple Argon crystal, set the velocities and integrate the system using the Velocity Verlet equations. First we import some prerequisites and define the system:

```
1 from ase.lattice.cubic import FaceCenteredCubic
2 from ase import units
3 from ase.md.velocitydistribution import MaxwellBoltzmannDistribution
4 from ase.md.verlet import VelocityVerlet
5
6 symbol = "Ar"
7 size = (3, 3, 3)
```

²<https://anaconda.org/>

³<https://www.python.org/>


```

8 atoms = FaceCenteredCubic(symbol=symbol, size=size, pbc=True)
9 MaxwellBoltzmannDistribution(atoms, 300 * units.kB)

```

This defines a face-centered-cubic (FCC) crystal unit cell with 4 atoms, and a system size of $3 \times 3 \times 3$ unit cells for a total of $4 \cdot 3^3 = 108$ atoms with periodic boundary conditions. We thereafter give the atoms velocities according to the Maxwell-Boltzmann distribution such that the system temperature is approximately 300 Kelvin.

Next we give the atoms a Lennard-Jones *calculator* for calculating dynamics and create a Velocity Verlet *integrator* for evolving the atoms according to their forces. Calculators will be discussed in the next section.

```

1 calc = LennardJones(sigma=3.405, epsilon=1.0318e-2)
2 atoms.set_calculator(calc)
3 dyn = VelocityVerlet(atoms, 2 * units.fs)

```

The parameters σ and ϵ define the well known length and energy scales for the Lennard-Jones potential. The Velocity Verlet integrator is initialized with a timestep of 2 femtoseconds, which strikes a balance between accuracy and the timescale of the simulation. Finally we run the system for 1000 steps:

```

1 for i in range(100):
2     dyn.run(10)

```

Every 10 timesteps the system quantities can be printed, written to file or put through some other form of analysis or post-processing.

7.0.3 Calculators

The calculator interface gives ASE an easy to use, flexible and customizable way of computing dynamics, and makes ASE viable for a wide range of electronic structure calculations. For ASE a calculator is a black box that receives positions, atomic numbers and so on and outputs energies, forces, stresses; all that is required to perform atomistic simulations. The basic interface is defined in the ASE source code as:

```

1 import numpy as np
2
3 class Calculator:
4     def get_potential_energy(self, atoms=None,
5                             force_consistent=False):
6         return 0.0
7
8     def get_forces(self, atoms):
9         return np.zeros((len(atoms), 3))
10
11    def get_stress(self, atoms):
12        return np.zeros(6)
13
14    def calculation_required(self, atoms, quantities):
15        return False

```

There is also an interface for DFT calculators, which also requires the implementation of spins, occupation numbers, the fermi level and so on.

In the previous section we used the Lennard-Jones calculator as an example, however this calculator is not suited for general use. Apart from the Lennard-Jones being a toy potential unsuited for real systems, the ASE implementation is also written in pure Python, which makes it very, very slow. Usually the calculator interface is used as a wrapper for much faster compiled code or software packages; for example the Asap calculator is a Python wrapper for the Effective Medium Theory potential, which is implemented in Fortran and is orders of magnitudes faster. A Python molecular dynamics code is justified since the bulk of computation time is spent on computing forces, however for large scale molecular dynamics simulations one would be advised to use fast compiled code such as LAMMPS⁴ or GROMACS⁵. ASE really shines when it comes to small-scale simulations, experimentation and testing out new methods, and this is why it has been chosen as a basis for this thesis. Fortunately, ASE has an extensive code base of calculators for Molecular Dynamics and Density Functional Theory codes such as Asap, CP2K, LAMMPS, GROMACS which are all implemented in lower-level languages.

⁴ <https://lammmps.sandia.gov/>

⁵ <http://www.gromacs.org/>

Chapter 8

Atomistic Machine-learning Package

The Atomistic Machine-learning Package (AMP) [12, Khorshidi, Alizera and Peterson, Andrew A.] is a software package written in Python with the intent of bringing machine learning to electronic structure calculations. The software is intended to interface with ASE and the OpenKIM API for usage in LAMMPS. The interface to AMP is written purely in Python while computationally intensive tasks are outsourced to Fortran modules and the machine learning performed through a Tensorflow backend. The Python interface makes AMP flexible and easily extended, and this makes the package ideal for prototyping and testing both newer and more established machine learning methods.

A suggested workflow is as follows ¹:

- Use AMP for training, testing and validation of novel descriptors and systems
- Use the AMP calculator for smaller scale simulation in the ASE environment
- Export the network compliant with the OpenKIM API for usage in more mature, large-scale electronic structure calculation software such as LAMMPS

¹<https://bitbucket.org/andrewpeterson/amp/issues/79/parallelize-fingerprint-derivatives>

Unfortunately, the software is not currently fully compliant with the latest version of the OpenKIM API, which introduces artifacts in the simulation involving periodic images. However, the authors have recently received a large grant from the U.S. Department of Energy², which should facilitate further development.

8.0.1 Theory

AMP is intended to interface extensively with ASE, and the primary interface to AMP is the AMP calculator. The AMP calculator is an ASE compliant calculator that accepts cartesian coordinates and outputs energies and forces, just as a classical molecular dynamics calculator. The primary difference between the AMP calculator and ASE calculators such as the Lennard-Jones calculator is the train method, which takes a set of *images*, i.e. a set of snapshots of atomic configurations labeled with the potential energy and forces. The calculator is fitted to the images and can subsequently be used to predict atomic energies and forces from never before seen atomic configurations.

AMP provides interfaces for both atom-centered descriptors, as we discussed in chapter 6, and image-centered descriptors, which are formed from the complete set of cartesian coordinates. A set of feature vectors are formed from an image, which are fed through a neural network to produce the potential energy. The neural network is implemented through a Tensorflow interface, which provides a full neural network graph with weights and activations. The inputs can be backpropagated through the network to produce both weight updates and derivatives with respect to the inputs.

8.0.2 Installation

AMP requires an installation of

- Python 2.7, 3.4-3.6, 3.6 is recommended
- Numpy 1.9 or newer
- Scipy 0.14 or newer
- ASE

²<https://www.brown.edu/news/2018-09-20/simulations>

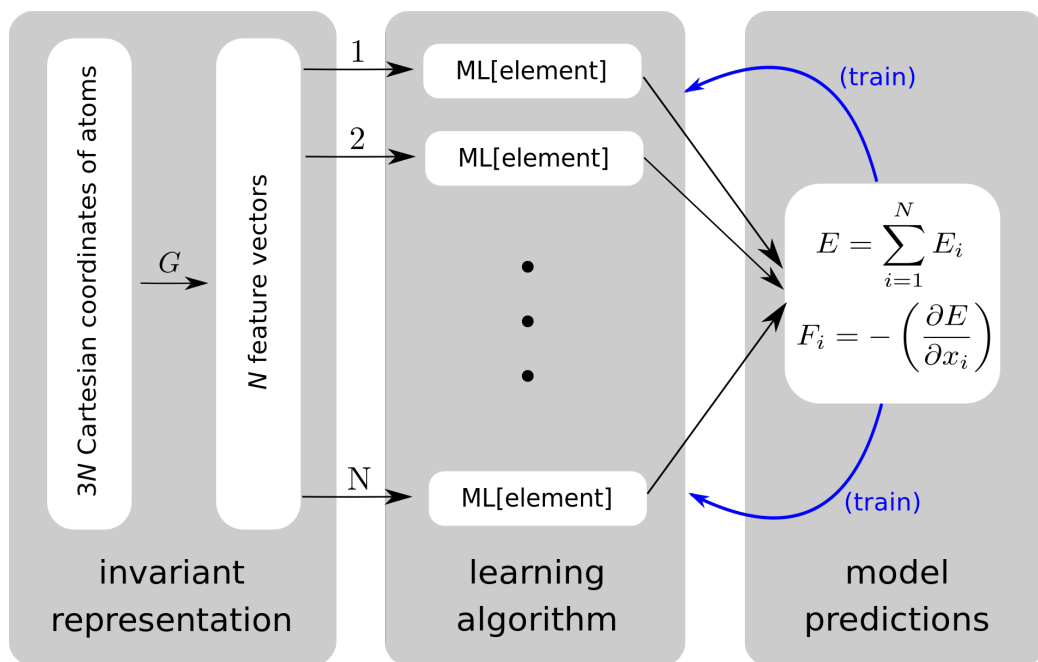


Figure 8.1: Schematics of how AMP works in atom-centered mode. Reprinted from [12, AMP paper].

Python installations can be easily obtained through the Anaconda or Miniconda packages³, or follow the instructions on the Python website⁴. ASE installation is described in the chapter on ASE. Once you have the prerequisites AMP can be installed using pip:

```
pip install amp-atomistics
```

8.0.3 Training example

In the previous chapter we showed how to run a molecular dynamics simulation using ASE. Here we will show how an AMP calculator can be fitted to molecular dynamics data with only minor modifications to the code.

First we import the prerequisites and define the system:

³<https://anaconda.org/>

⁴ <https://www.python.org/>

```

1 import ase.io
2 from ase.lattice.cubic import FaceCenteredCubic
3 from ase import units
4 from ase.md.velocitydistribution import MaxwellBoltzmannDistribution
5 from ase.md.verlet import VelocityVerlet
6
7 from amp import AMP
8 from amp.descriptor.gaussian import Gaussian
9 from amp.model.neuralnetwork import NeuralNetwork
10 from amp.model import LossFunction
11
12 symbol = "Ar"
13 size = (3, 3, 3)
14 atoms = FaceCenteredCubic(symbol=symbol, size=size, pbc=True)
15 MaxwellBoltzmannDistribution(atoms, 300 * units.kB)

```

The class AMP is the primary object of the AMP package, and is implemented through the ASE interface. We will use a neural network machine learning model and Gaussian descriptors, which are an implementation of the Behler-Parrinello method. To implement force training we require access to the LossFunction class. We will also be using the ASE Input/Output (ase.io) module to generate an ASE *Trajectory*, which is an object storing the time-evolution of a simulation and usually interpreted as a time series of atoms.

```

1 traj = ase.io.Trajectory("training.traj", "w")
2 calc = LennardJones(sigma=3.405, epsilon=1.0318e-2)
3 atoms.set_calculator(calc)
4 atoms.get_potential_energy()
5 atoms.get_forces()
6 traj.write(atoms)
7 dyn = VelocityVerlet(atoms, 2 * units.fs)

```

In order to write the potential energy and forces to file they must first be calculated using the ASE Atoms methods, which require a calculator and otherwise raise an error. We can then evolve the system forward in time and save the atomic configuration every 10 time steps:

```

1 for i in range(100):
2     dyn.run(10)
3     atoms.get_potential_energy()
4     atoms.get_forces()
5     traj.write(atoms)

```

After the data has been generated we can train the AMP calculator using the Lennard-Jones calculations as input. We use a neural network model with three hidden layers, each containing 10 neurons. The training will be satisfied once the energy and force root mean squared errors (RMSE) has reached values of 10^{-2} or less:

```

1 calc = Amp(descriptor=Gaussian(),
2             model=NeuralNetwork(hiddenlayers=(10, 10, 10)))
3 calc.model.lossfunction = LossFunction(
4     convergence={"energy_rmse": 1E-2,
5                  "force_rmse": 1E-2})
6 calc.train(images="training.traj")

```

Once the calculator has been trained, the parameters are stored in a file called "amp.amp", and can be loaded using the command:

```

1 calc = Amp.load("amp.amp")

```

From there the calculator can be used as any other ASE calculator, in electronic structure calculations on Atoms objects.

8.0.4 Descriptors and models

Currently AMP provides support for three different descriptors. Gaussian descriptors implement the Behler-Parrinello method of radial and angular symmetry functions. For this descriptor the derivatives are also available, which means it can be used for computing dynamics. Some physical intuition and chemical knowledge is necessary to choose various parameters for the symmetry functions - unless you wish to do it by trial and error - but AMP provides defaults for multiple chemical species. The Zernike and Bispectrum

descriptors are also implemented, but without derivatives, which means the trained calculator cannot be used for example performing molecular dynamics simulations. Currently the neural network model is the only model implemented, and is supported through Tensorflow's interface. However, the modular nature of AMP should enable more additions in time, such as derivatives for the Zernike and Bispectrum descriptors or other regression models which have derivatives available.

Chapter 9

Fitting to the Lennard-Jones potential

In order to demonstrate the construction of a neural network potential, we use Tensorflow to reconstruct the Lennard-Jones potential. The Lennard-Jones potential is the simplest realistic molecular dynamics potential, and since it is a function of only radial distance, symmetry functions are not required. We can thus use neural networks to perform a simple regression on a function accepting one input and producing one output. This serves to illustrate some of the intuitions and problems one runs into when using more complex methods such as atom-centered descriptors and gives a nice introduction into modern Tensorflow. We will be using the Tensorflow 2.0 beta version recently released, since it introduces a wide array of changes which will likely prove influential to the long-term direction of the Tensorflow project.

9.0.1 Tensorflow implementation

The code used to produce this implementation is a modification of the Tensorflow 2.0 for experts guide which is available online¹. We start with some necessary imports from the Numpy and Tensorflow libraries. Tensorflow from 2.0 onwards is now primarily accessed through its Keras interface, which is a general high-level API for constructing and training neural networks. We also use a utility function from the scikit-learn library for splitting the dataset into train and test data, but this is merely for convenience as it is

¹<https://www.tensorflow.org/beta/tutorials/quickstart/advanced>

very simple to implement from scratch. Finally we use the matplotlib and Seaborn libraries for producing the plots.

```
1 import numpy as np
2 import matplotlib.pyplot as plt
3 import tensorflow as tf
4 from tensorflow.keras import Model
5 from tensorflow.keras.layers import Dense
6 from sklearn.model_selection import train_test_split
```

Our neural network is a simple feed-forward artificial neural network which inherits from the tensorflow.keras base model. It contains 2 layers with 50 and 10 neurons respectively using the hyperbolic tangent as the activation function. The neural network produces a single output which represents the potential energy and is computed as a linear function aka a dot product of the activations in the final hidden layer and the weights in the output layer. The gradient of the neural network with respect to the input can be computed using the tensorflow.GradientTape object. The GradientTape monitors the computation from the input to the output and is then able to backpropagate the output in order to obtain the gradient.

```
1 class MyModel(Model):
2     def __init__(self):
3         super(MyModel, self).__init__()
4         self.d1 = Dense(50, activation="tanh")
5         self.d2 = Dense(10, activation="tanh")
6         self.d3 = Dense(1, activation="linear")
7
8     def call(self, x):
9         x = self.d1(x)
10        x = self.d2(x)
11        x = self.d3(x)
12
13        return x
14
15    def derivative(self, x):
16        with tf.GradientTape() as t:
```

```

17         t.watch(x)
18         y = self.call(x)
19
20     return t.gradient(y, x)

```

The data is produced using the Lennard-Jones potential, which is a simple function of radial distance. The inputs need to be in the shape of matrices in order to be fed through the neural network in batches. We split the data into train and test using a test fraction of 0.2, with the remainder used for training.

```

1 def lennard_jones_data():
2     lj = lambda r: 4 * ((1.0 / r) ** (12) - (1.0 / r) ** 6)
3
4     x = np.linspace(0.90, 3.0, 10000).reshape(-1, 1)
5     y = lj(x)
6
7     x_train, x_test, y_train, y_test = train_test_split(
8         x, y, test_size=0.2
9     )
10
11     return (x_train, y_train), (x_test, y_test)

```

The data which is in the form of numpy arrays can easily be converted into tensors which can then be processed by Tensorflow. In order to perform regression we will use the mean squared error for evaluating the loss. We will use the Adam optimizer, which is currently the most popular optimizer for training neural networks, and generally outperforms the other less popular optimizers.

```

1 (x_train, y_train), (x_test, y_test) = lennard_jones_data()
2
3 train_ds = tf.data.Dataset.from_tensor_slices(
4     (x_train, y_train)
5 ).shuffle(1000).batch(32)
6 test_ds = tf.data.Dataset.from_tensor_slices(
7     (x_test, y_test)

```

```

8     ).batch(32)
9
10    model = MyModel()
11    loss_object = tf.keras.losses.MeanSquaredError()
12    optimizer = tf.keras.optimizers.Adam()
13
14    train_loss = tf.keras.metrics.Mean(name="train_loss")
15    test_loss = tf.keras.metrics.Mean(name="test_loss")

```

The train and test steps are wrapped as Tensorflow functions so that they can be efficiently called and applied to tensors. For every train step the loss is computed and then backpropagated so that the optimizer can apply updates to the weights and biases. We subsequently train the neural network for 100 epochs, computing the train and test loss for every epoch.

```

1  @tf.function
2  def train_step(images, labels):
3      with tf.GradientTape() as tape:
4          predictions = model(images)
5          loss = loss_object(labels, predictions)
6          gradients = tape.gradient(loss, model.trainable_variables)
7          optimizer.apply_gradients(zip(gradients, model.trainable_variables))
8
9      train_loss(loss)
10
11  @tf.function
12  def test_step(images, labels):
13      predictions = model(images)
14      t_loss = loss_object(labels, predictions)
15
16      test_loss(t_loss)
17
18  epochs = 100
19
20  for epoch in range(epochs):
21      for images, labels in train_ds:
22          train_step(images, labels)

```

```

23
24     for test_images, test_labels in test_ds:
25         test_step(test_images, test_labels)
26
27     template = "Epoch {}, Loss: {}, Test Loss: {}"
28     print(template.format(
29         epoch + 1, train_loss.result(), test_loss.result()
30     )
31 )

```

9.0.2 Comparison and relative error

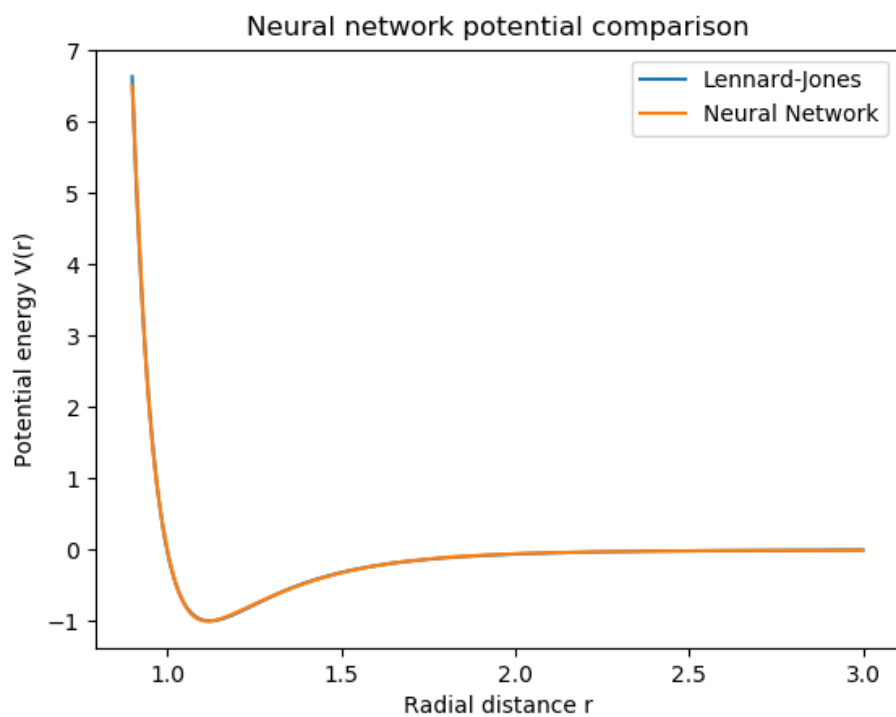


Figure 9.1: Neural network potential compared to Lennard-Jones.

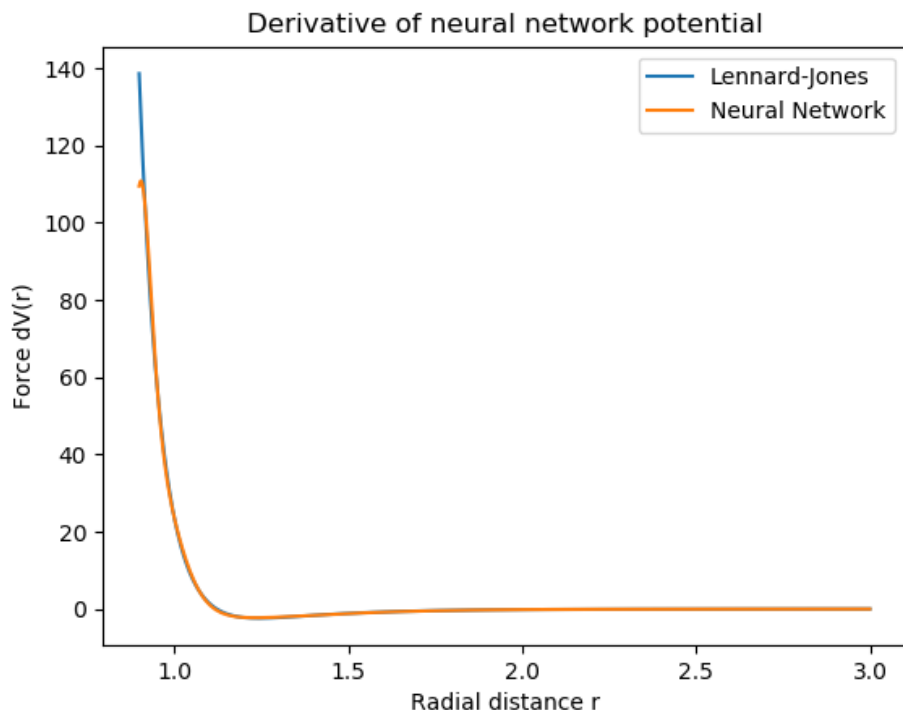


Figure 9.2: Neural network derivative compared to Lennard-Jones.

After training the network we can evaluate its performance on test data. For the potential energy we obtain a root mean squared error of 0.37 (energy units). However, the root mean squared error does not tell the complete story, and the simplest way to evaluate the fit is to plot the potential. In figure 9.1 the neural network potential is plotted with the Lennard-Jones potential. We see that this potential is not difficult to reproduce, as the number of datapoints is relatively small, and we used a small number of epochs, amounting to only a few seconds of training. The potentials agree very well on most of the input space, and we can only spot a small divergence as the potential rises sharply around a radial distance of one.

For the error in the derivative we obtain a force root mean squared error of 61.7 (energy units per length units), which is approximately two orders of magnitude larger. The derivatives are plotted in figure 9.2. The difference in derivatives is more pronounced, as the difference is much larger as the radial

distance decreases from around one, and we can see that the neural network does not have the same asymptotic behaviour. This poses a potential problem for the dynamics, as the forces aka the derivatives keep the atoms from moving too closely and causing massive increases in the potential energy of the system. This implies that we should train the potential on a representative set of points in order to reproduce the correct asymptotic behaviour, especially at the edges of configuration space. It may also be beneficial to include force terms in the loss function, as this is expected to decrease the error in the derivatives.

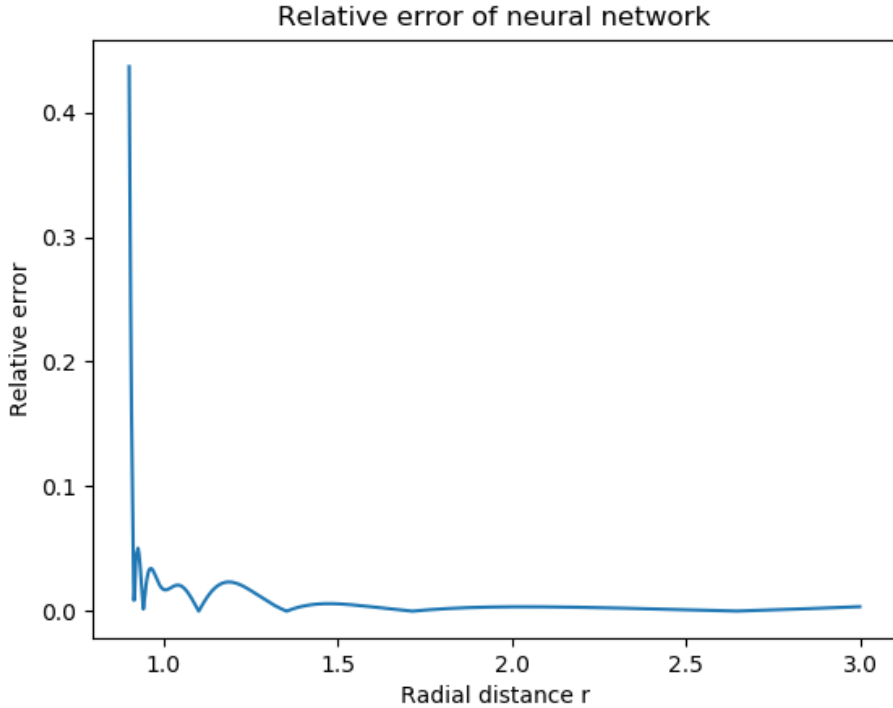


Figure 9.3: Relative error of the neural network potential compared to Lennard-Jones.

In figure 9.3 we have plotted the absolute error of the neural network potential, defined as $|E_p - E_{\text{NN}}|$ where E_{NN} is the potential energy from the neural network. From this we can see that the error in the fit is much larger at one edge of configuration space, as shown in the above plots. The

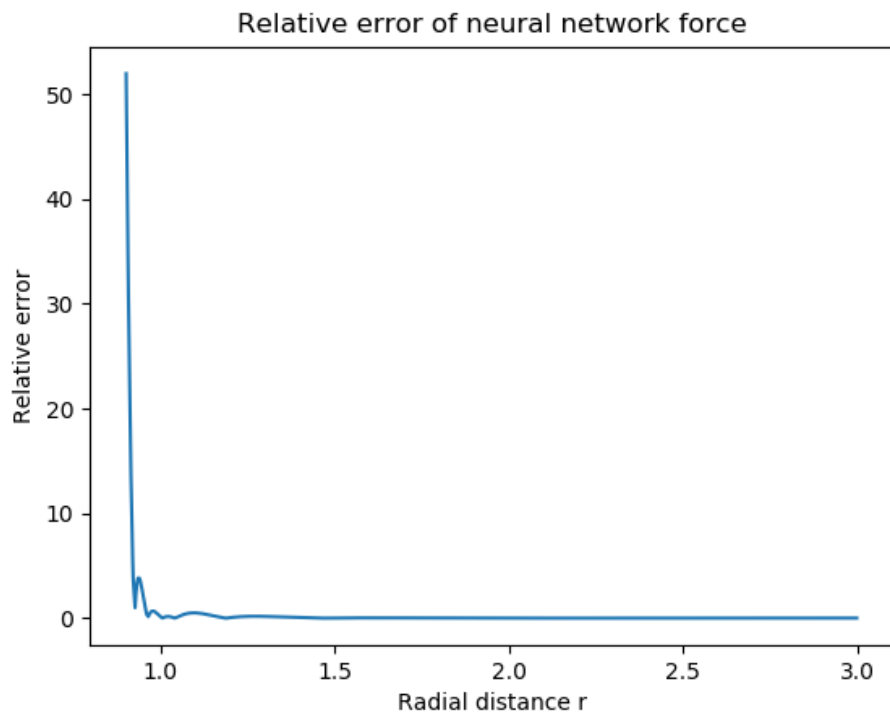


Figure 9.4: Relative error of neural network derivative compared to Lennard-Jones.

neural network is able to reproduce small values at larger distances, but not the asymptotic behaviour as the interatomic distance approaches zero. Additionally, we can observe that the absolute error in the derivative is two orders of magnitude larger than the error in the potential energy fit. However, since this behaviour occurs only at the edge of the input space, dynamics could be preserved by training on a representative set of input data. This may also not be a big problem, as with appropriate timesteps some configurations of interatomic distances should never be observed in molecular dynamics simulations, and would cause problems regardless of the accuracy of the interatomic potential.

Part III

Results

Chapter 10

Parameter search

In order to obtain optimal performance from the neural networks given a set of atomistic configurations we need a careful choice of parameters and neural network architecture. The parameters can be classified as either training parameters - such as learning rate and force loss coefficient - or architectural parameters - such as the number of neurons and hidden layers, or the choice of interaction cutoff radius. The former are important in the training of the neural network, i.e. adjusting weights and biases while the latter influence both the training process and the final deployment of the neural networks on unfamiliar data. In this section we will be employing a grid search over a set of parameters, training multiple neural networks on the same data set and subsequently testing energy and force Root Mean Squared Errors on a smaller test data set. Generally we will only be training the neural networks on the energies, since training with forces is much more CPU- and memory- intensive. However, training with forces would likely affect the final result and improve the force RMSEs, as we will observe in the following section. The parameters are unless otherwise specified the defaults listed in table 10.1. In their paper on Random Search, [4, Bergstra and Bengio] demonstrate that Random Search outperforms Grid Search for dimensions of search space larger than 3 or 4. However, since we have tested a small number of parameters (since training and testing is costly) and we have a general idea of what parameters are appropriate, we have chosen to employ Grid Search. AMP has a built in simulated annealing module, which performs simulated annealing on the weights and biases of the network, in order to find values for which the loss is lowest. The annealing is run for every trained neural network for 2000 steps at the beginning of the training procedure, with

temperatures starting $T_{max} = 20$ and ending $T_{min} = 1$. Simulated annealing is a suitable algorithm for finding minima in a complicated energy landscape, and it reduces somewhat the randomness of initialization so that the results are comparable without having to perform many runs.

Hyperparameters		
Architecture	Symmetry functions	12 radial, 20 angular
	Hidden layers	(10, 10)
	Activation	Hyperbolic tangent
	Cutoff function	Polynomial, $R_c = 6.0, \gamma = 5.0$
Training	Epochs	2000
	Energy coefficient	1.0
	Force coefficient	None
	Optimizer	BFGS

Table 10.1: Training defaults

The AMP package provides a set of defaults for most elements, and these symmetry functions are plotted in figure 10.1. However, we did not feel that these covered the radial and angular space sufficiently so we constructed our own instead which is what we will use for training. AMP only provides centered radial functions, while we use a mix of centered and shifted radial functions since these have demonstrated higher performance, as is discussed in the section on symmetry functions. For the symmetry functions we have chosen a set of 8 uncentered radial, 8 centered radial and 20 angular (G4) symmetry functions. The uncentered radial functions have η s spaced evenly from 1 to 20 and are centered at 0. The centered radial functions are centered evenly from 0.5 to $R_c - 0.5$ with $\eta = 5.0$. The angular functions have η s spaced evenly from 0.01 to 3 with $\zeta = 1$ and $\gamma = \pm 1$. These symmetry functions are displayed in figure 10.2. We also choose to employ the polynomial cutoff introduced in AMP, since this has a wider range of values inside the cutoff boundary.

10.0.1 Force training

When training the neural networks we have the choice of whether to incorporate the forces into our loss function, or only fit the neural network to the

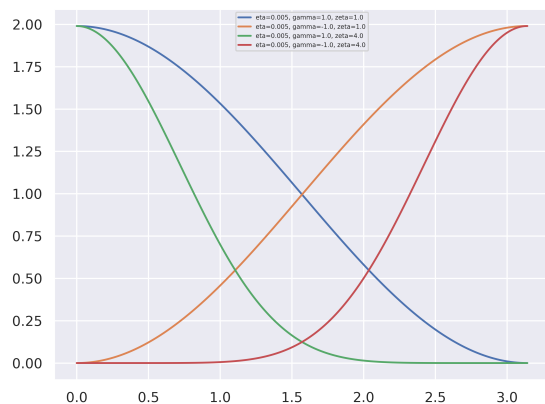
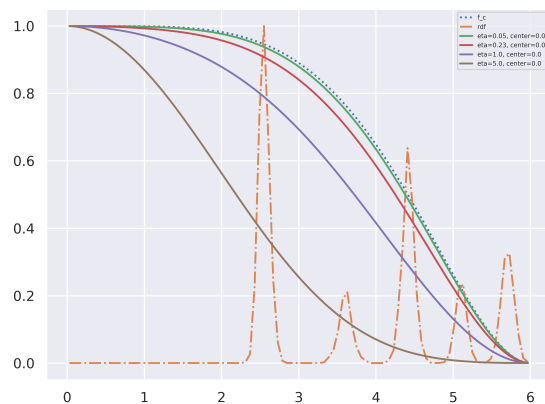


Figure 10.1: My flowers.

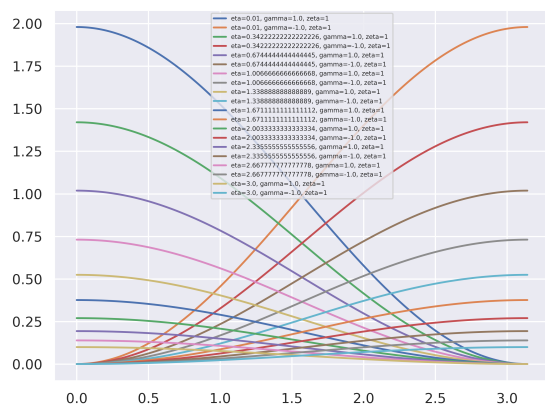
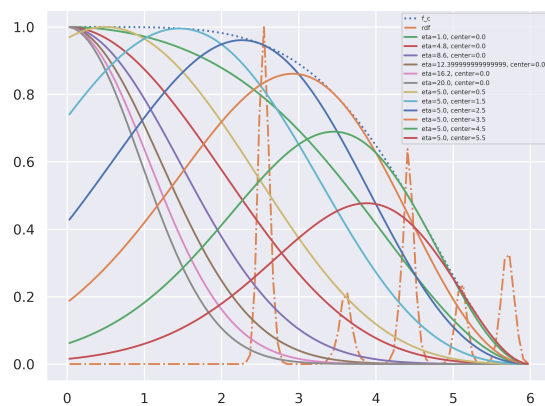


Figure 10.2: My flowers.

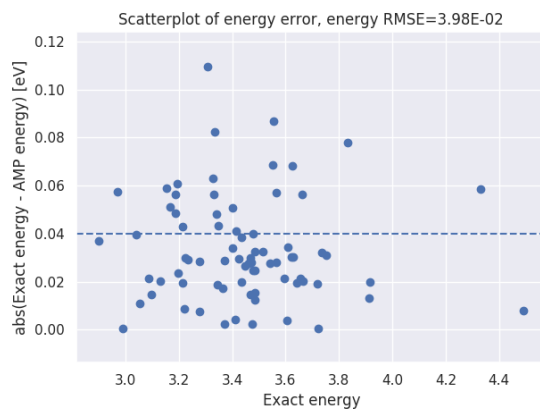
potential energy. By default, unless we have access to a per-atom energy every configuration is labeled with only a single number for a potentially large number of atoms, which limits the improvement in loss metrics for every epoch and the final result. If instead we incorporate the forces into the loss we have potentially $3N + 1$ labels for every epoch, which provides a lot more information for weight updates. In the previous chapter we also showed how adding derivatives to the loss function could significantly improve the accuracy of the derivatives. Since the forces determine the trajectories generated from molecular dynamics we would expect we would expect much better accuracy and numerical stability if we could improve the fit of the derivatives. The real drawback is the calculation of the derivatives in the input layer, aka the fingerprintprimes, of which there are a lot for every coordinate and input symmetry function, and they consume a lot of disk space and memory.

In order to test the performance of neural networks we trained with and without forces on a set of test images. A system of copper atoms is generated in the face-centered cubic (FCC) configuration with 4 atoms in the unit cell and $3 \times 3 \times 3$ unit cells for a total of $4 \cdot 3^3 = 108$ atoms. The atoms are given velocities from the Maxwell-Boltzmann distribution corresponding to a temperature of 500 Kelvin. The potential we will be using is the Effective Medium Theory (EMT), which has a very fast Fortran implementation in the ASE software package¹. The training trajectory is ran for $5 \cdot 10^4$ steps with a timestep of $\Delta t = 1\text{fs}$ and written to file every 100 steps for a total of 500 atomic configurations. The test trajectory is integrated for $1 \cdot 10^4$ steps for a total of 100 atomic configurations.

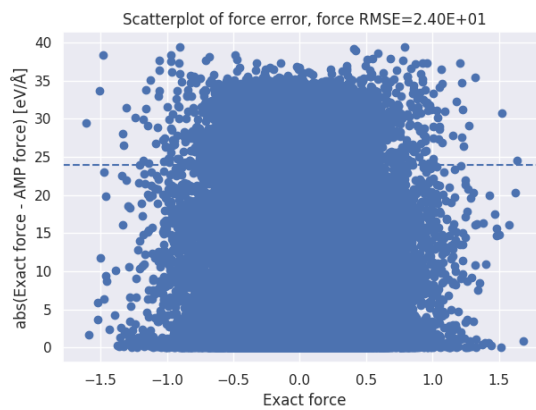
In figure 10.3 we have created a scatterplot of the energies and forces vs the absolute error, and labeled the plots with the energy and force RMSEs. We observe that the potential energies can achieve fairly low error values of approximately 0.02 to 0.10 eV, and the result does not depend very much on the value of the exact potential energy. The force error however is approximately three orders of magnitude larger, which echoes some of the concerns raised in the previous chapter with fitting derivatives. The forces produced by the neural network are still not dependent on the exact value of the force.

In figure 10.4 we have a scatterplot of energies and forces generated from a force-trained neural network. While the error in the potential energy is now an order of magnitude higher, the error in the forces is now two orders of

¹ <https://wiki.fysik.dtu.dk/asap/asap>

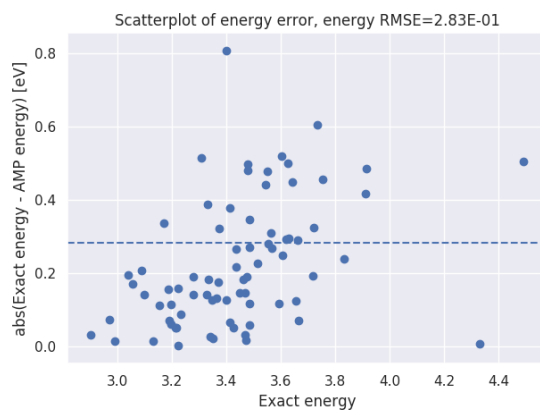


(a) Flower one.

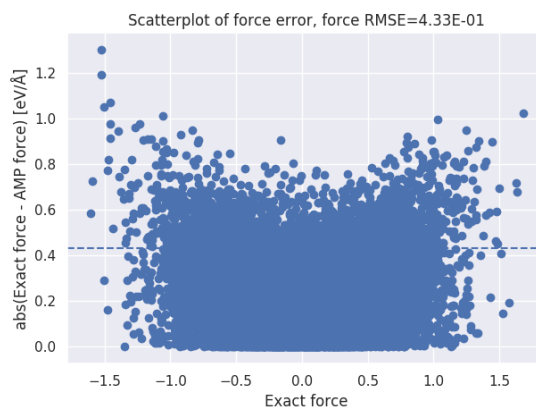


(b) Flower two.

Figure 10.3: My flowers.



(a) Flower one.



(b) Flower two.

Figure 10.4: My flowers.

magnitude smaller. This is arguably a very good tradeoff, since the force error matters much more for long molecular dynamics trajectories, and will make any simulation requiring large amounts of data much more stable. However, force training is as mentioned much costlier in terms of memory and CPU hours. Instead of training with forces on the full set of images, we instead suggest training on a large amount of configurations with only the energies (and arguably a small amount of atoms, since the ratio of fingerprints to labels is higher), and subsequently training with forces on a smaller set of images in order to improve the force fit, at some cost to the energy fit.

10.0.2 Activation, hidden layers

In order to test different network architectures we test different values of the activation functions, and the number of hidden layers and nodes. At this range of values, we do not expect a large variation in the performance, while larger neural networks with a large amount of hidden layers would be expected to overfit the training data and perform poorly on unseen data. In the paper Efficient Backprop by [lecun2012efficient] the authors suggest that the hyperbolic tangent outperforms the sigmoid, since the derivatives are larger, which provides more efficient training. The hyperbolic tangent is somewhat more computationally costly, however this is not a big consideration for our neural networks overall, since they are quite small and can be evaluated relatively fast. To test different architectures a copper system of $4 \cdot 2^3 = 32$ atoms is generated and integrated for $8 \cdot 10^4$ steps with a timestep of $\Delta t = 1.0\text{fs}$ and written to file every 100 steps for a total of 800 training images. By the same procedure we also obtain 100 test images. The velocities are generated according to a Maxwell-Boltzmann distribution with a temperature of 500 Kelvin. The results are shown in table 10.2. The network is trained only on energies, while for the test set we calculate the energy and force Root Mean Squared Errors (RMSEs).

From the results we can see that the results do not differ significantly. The larger networks may perform somewhat better on the energy, but this is also somewhat influenced by the stochasticity of random initialization. For the hyperbolic tangent using a single hidden layer of 10 nodes we also achieve a fairly low value on the force RMSE, though the network has not been trained on forces, but this also matches our intuition that the network should not be very large, with the hyperbolic tangent outperforming the sigmoid. For the remainder of this thesis we have settled on these values for the neural

Activation/Hidden layers	Energy RMSE	Force RMSE
tanh-[10]	3.54E-03	5.84E-02
tanh-[20]	2.01E-03	1.47E-01
tanh-[30]	1.46E-03	9.91E-01
tanh-[40]	1.70E-03	9.35E-01
tanh-[10, 10]	1.84E-03	1.97E-01
tanh-[20, 10]	2.91E-03	9.66E-02
tanh-[30, 10]	3.51E-03	8.29E-02
tanh-[40, 40]	1.80E-03	1.86E-01
sigmoid-[10]	1.85E-03	9.44E-01
sigmoid-[20]	3.73E-03	3.25E-01
sigmoid-[30]	1.79E-03	1.01E+00
sigmoid-[40]	2.09E-03	2.54E-01
sigmoid-[10, 10]	1.93E-03	5.98E-01
sigmoid-[20, 10]	1.83E-03	2.26E-01
sigmoid-[30, 10]	1.52E-03	1.99E+00
sigmoid-[40, 40]	1.94E-03	3.36E-01

Table 10.2: Training defaults

network, though it remains to be seen if a larger network trained for longer could outperform the smaller models.

10.0.3 Cutoff radius

The cutoff radius defines the boundary outside of which no interactions between atoms take place, and the magnitude of the interactions which take place within. We therefore expect it to have a reasonable effect on the final result. Ideally we might like all atoms to interact, as they plausibly do in the real world. However there is a tradeoff between the accuracy and speed when calculating fingerprints and fingerprint derivatives, with substantial CPU and memory cost the larger the cutoff radius, and accuracy can also be impacted if any atom interacts with an atom which in actuality does not have a substantial energy and force contribution. In their original paper on AMP by [12, Khorshidi and Peterson], the authors suggest an alternative cutoff function to the cosine suggested by Behler and Parrinello which covers a wider range of values within the cutoff boundary and can reproduce the cosine at certain values of γ .

$$f_c(r) = \begin{cases} 1 + \gamma(r/R_c)^{\gamma+1} - (\gamma+1)(r/R_c)^\gamma & r \leq R_c \\ 0 & r > R_c \end{cases} \quad (10.1)$$

We choose a value of $\gamma = 5.0$ since it has a substantially wider range than the cosine, and compare the two for different cutoff radii. In figure 10.5 we have plotted the radial distribution function of the copper atoms governed by the EMT potential. We see that the system is strongly peaked at distances of approximately 2 and 4 Ångström, with smaller peaks in between and beyond. It is therefore reasonable to assume that a cutoff between 4 and 8 Ångström would perform well, without sacrificing too much accuracy. As in the previous section we produce a system with 32 atoms, with 800 training configurations and 200 test configurations. The network is only trained on the energy, since this is substantially cheaper, and then the network is evaluated on the energy and force RMSE on the test set. The results are presented in 10.3.

From the energy RMSEs we can see that the middle values of the cutoff produce the lowest values. This is likely due to some kind of overfitting, such that better values are obtained by considering fewer atoms more strongly. The intermediate values also seem to produce somewhat lower values of the force RMSE, of which the lowest is the polynomial with a cutoff of 7

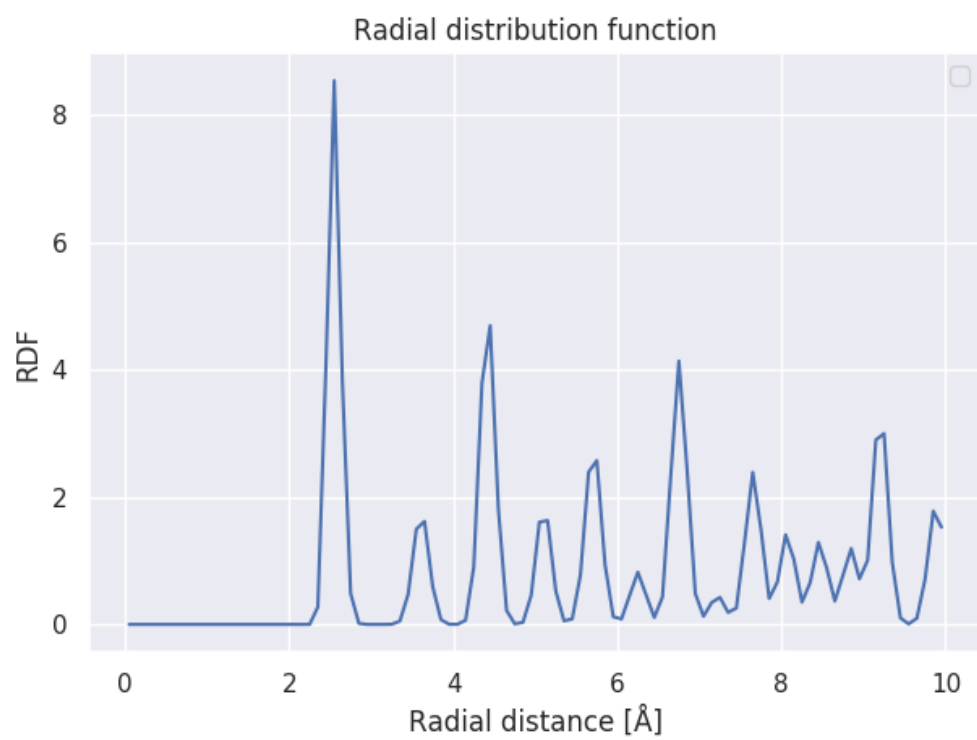


Figure 10.5: Copper RDF

Cutoff	Energy RMSE	Force RMSE
Cosine-2.0	2.22E-01	4.00E-01
Polynomial-2.0	2.22E-01	4.00E-01
Cosine-3.0	4.31E-03	3.42E-01
Polynomial-3.0	4.22E-03	3.54E-01
Cosine-4.0	8.41E-04	1.41E-01
Polynomial-4.0	7.92E-04	1.74E-01
Cosine-5.0	3.74E-04	1.19E-01
Polynomial-5.0	4.94E-04	1.40E-01
Cosine-6.0	2.01E-03	8.19E-02
Polynomial-6.0	2.48E-03	6.93E-02
Cosine-7.0	3.21E-03	1.50E-01
Polynomial-7.0	7.16E-03	4.66E-02
Cosine-8.0	3.14E-03	2.70E-01
Polynomial-8.0	5.95E-03	8.90E-01

Table 10.3: Cutoffs

Ångström. The differences between the cosine and the polynomial do not appear very large, though the polynomial may obtain marginally lower values of the force RMSE. We do not that there is a substantial stochastic element in these tests, and also that longer training periods may have produced more substantial differences, however training is costly in terms of CPU time. For the remainder of this thesis we settled on the polynomial with a cutoff of 6 Ångström, while the cosine may have performed just as well. We also note that since the cutoff radius defines a sphere with a volume $V \propto R_c^3$, the average number of neighbors and therefore calculations increases substantially with the cutoff radius.

10.0.4 Symmetry functions

The symmetry functions determine the local environment of every atom, which is then fed through and backpropagated through a neural network, and should in theory have substantial impact on the final results. The authors of AMP suggest through experience that the most important factors are

the quality of data, the cutoff radius and the symmetry functions ². The symmetry functions should cover both the radial and angular environment of the atoms in the system we are trying to learn from. They should also be distinguishable in order for the neural network to be able to separate different chemical environment. In their article on Weighted Atom-Centered Symmetry Functions [7, Gastegger et al.] suggest that uncentered aka shifted radial symmetry functions perform better than symmetry functions centered at 0, since these offer better coverage of the radial space. They also suggest that this is not the case for angular symmetry functions, since they are products of multiple gaussians which narrows their range of values. They also suggest that for angular symmetry functions the parameter ζ should be limited to values of 1 or 2, and they demonstrate that increasing this parameter narrows the function on a smaller range of angles close to the maxima (i.e. 0 or 90 degrees). We follow some of their suggestions and use a combined set of centered and uncentered radial functions. In the introduction to this chapter we define a method for constructing the set of symmetry functions, with the parameters being the number of radial functions, angular functions, zetas and the type of angular function. To find the optimal set we perform tests of the energy and force RMSE while varying the number of radial and angular symmetry functions, and testing whether the G4 or G5 type of angular functions performs noticeably better than the other type. The results are presented in table 10.4.

From these results we observe that not much is gained with respect to the energy when increasing the number of symmetry functions, as this space tends to be covered reasonably well. However, we may be able to achieve a lower force RMSE with adding more symmetry functions, since the forces generally represent a small perturbation in the position of a single atom, and this may be better represented by having a larger amount of functions sensitive to this change. The G4 functions generally outperform marginally on the force RMSE, and a little poorer on the energy RMSE. As for the number of zetas, we only test two values with $\zeta = 1, 2$, thus doubling the number of angular symmetry functions, and this seems to make the performance somewhat worse, as we might have predicted.

²<https://listserv.brown.edu/cgi-bin/wa?A2=ind1809&L=AMP-USERS&D=0&P=35451>

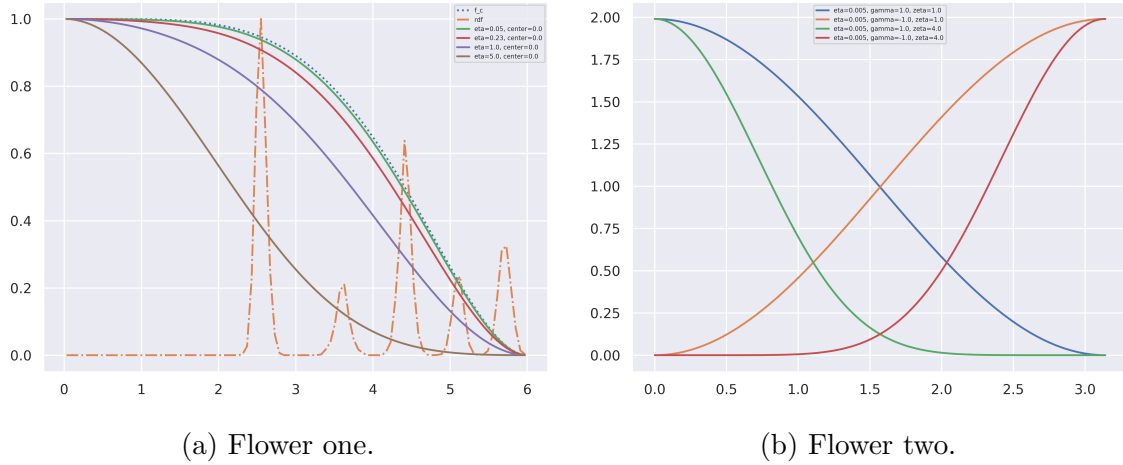


Figure 10.6: My flowers.

Symmetry function	Energy RMSE	Force RMSE
Default	1.99E-02	8.97E+00
Gs-4-8-1-G4	2.26E-03	8.65E-02
Gs-4-8-1-G5	2.44E-03	1.91E-01
Gs-5-9-1-G4	2.07E-03	3.01E-01
Gs-5-9-1-G5	2.59E-03	8.02E-02
Gs-6-10-1-G4	1.88E-03	1.35E-01
Gs-6-10-1-G5	2.45E-03	1.50E-01
Gs-7-11-1-G4	1.78E-03	4.13E-02
Gs-7-11-1-G5	2.34E-03	1.85E-01
Gs-8-12-1-G4	1.76E-03	6.01E-02
Gs-8-12-1-G5	2.51E-03	8.92E-02
Gs-9-13-1-G4	2.07E-03	6.72E-02
Gs-9-13-1-G5	2.36E-03	1.44E-01
Gs-10-14-1-G4	3.80E-03	1.27E-01
Gs-10-14-1-G5	2.48E-03	4.61E-02
Gs-10-14-2-G4	2.99E-03	8.19E-02
Gs-10-14-2-G5	2.31E-03	4.98E-02

Table 10.4: Symmetry functions

10.0.5 Sampling and scaling

In order for the neural network to learn patterns from data the data needs to be of high quality, and atomic configurations should be sufficiently distinguishable while being representative of the underlying distribution. Neural networks typically perform poorly or unexpectedly on unseen data, in addition to being data-hungry requiring fairly large amounts of data in order to train well over many epochs. One approach to learning atomic configurations might be to generate random configurations (not too closely spaced) and calculate energy and forces from these using a suitable calculator. However, this phase space of configurations would be enormous using only a few particles, and we would encounter many highly unlikely configurations. Since we want to train the neural network to perform molecular dynamics, the obvious solution is to sample configurations from molecular dynamics trajectories. However, these configurations are (mostly) in equilibrium, with relatively small forces, and thus the network might struggle if it encounters smaller distances between atoms. In their paper on fitting potential energy surfaces using neural networks, [19, Pukrittayakamee et al.] suggest using a variable time interval dependent on the maximum acceleration:

$$\tau = \begin{cases} \text{trunc}[\alpha/a_{max}]\Delta t & \text{trunc}[\alpha/a_{max}] > 0 \\ \Delta t & \text{trunc}[\alpha/a_{max}] = 0 \end{cases} \quad (10.2)$$

where Δt is a minimum time interval and α is a parameter which must be determined empirically. The rationale behind this is that we will sample more from areas where the forces are large, while skipping areas where the forces are small. In our experiments using this algorithm (slightly modified) we find that appropriate choices of Δt and α can broaden the distribution of force somewhat, however it does not add a substantial amount of larger forces, since these are simply not present in equilibrium. Other sampling algorithms have been suggested, for example iteratively pruning a large data set of images where the energy or force difference is not very large, and then retraining until we are satisfied with the result. One can also check for images where new values of the fingerprints are encountered and add these to the training set, or checking images for large overall values of the feature vector. However these sampling methods have not been tested in this thesis. Other methods such as metadynamics ³ have seen increasing application and there

³ <https://parrinello.ethz.ch/research/metadynamics.html>

Number of images	Energy RMSE	Force RMSE
n10	8.83E-02	7.88E-01
n20	9.40E-02	3.79E-01
n50	1.51E-02	1.51E-01
n100	6.05E-03	4.91E-01
n200	1.96E-03	6.95E-02
n500	1.40E-03	1.15E-01
n1000	1.41E-03	1.60E-01
n2000	1.31E-03	1.04E-01
n5000	1.23E-03	9.65E-02

Table 10.5: Number of images

are now numerous implementations available such as PLUMED ⁴. In general, though sampling has not been studied closely in this thesis, an increase in high quality data is an obvious increase in neural network performance, both for electronic structure calculations and for other similar applications.

Neural networks are known as data-hungry, and typically require a large amount of data to perform well and also scale well with the number of data points. In order to test this we train a neural network on progressively larger sets of images generated from molecular dynamics, and evaluate them on a test set. The results are shown in table 10.5.

From these results we see that the energy RMSE scales favorably as the number of images available increase, and the force RMSE decreases as well, though not as systematically, due to stochasticity and the fact that the networks have not been trained on force. Since these images are sampled directly from molecular dynamics at constant intervals, this suggests that we can in fact increase the performance of the neural networks by simply increasing the simulation length, though obviously more efficient sampling algorithms should be considered eventually.

⁴<https://www.plumed.org/>

Chapter 11

Empirical potentials

In order to test the validity of using neural networks sampled from molecular dynamics trajectories to generate new trajectories we train neural networks on systems of copper and silicon atoms using the Effective Medium Theory and Stillinger-Weber potentials respectively. These potentials have efficient implementations through ASE and their ASAP interface, which makes it ideal for our purposes. Additionally these potentials have an intermediate complexity, with Stillinger-Weber explicitly including threebody interactions, which makes them ideal for testing whether the Behler-Parrinello method can replicate this. At temperatures which are not too large these potentials describe atoms in a crystalline structure in equilibrium, and we test whether the neural network can reproduce the correct potential energy, forces, radial distribution and mean squared displacement.

11.0.1 Effective Medium Theory

The Effective Medium Theory (EMT) potential gives a good description of the late transition metals in a Face-Centered Cubic (FCC) crystal lattice, and has a very efficient implementation in ASE, which makes it ideal for producing large amounts of data. We will use a rather small system of $4 \times 2^3 = 32$ atoms for training, since this means a larger amount of labels available for atoms when we are only using the potential energy. We train with only the energy for $8 \cdot 10^5$ steps with a timestep of $\Delta t = 5.0$ fs writing to file every 100 steps and then subsequently train using both energy and forces for $5 \cdot 10^4$ steps for a total of 500 configurations. We train on both sets of images for 2000 steps, where the BFGS optimizer has generally converged. After the calculator is

Table 11.1: Hyperparameters used in fitting.

Hyperparameter	Value
Symmetry functions	16 radial, 24 angular
Hidden layers	(10, 10)
Activation	Hyperbolic tangent
Timesteps (fs)	$8 \cdot 10^5$
Sampling intervall (fs)	100
Max epochs	4000
Optimizer	BFGS
Energy coefficient	1.0
Force coefficient	0.1

trained we compare the performance of the neural network with the EMT potential on a system of 32 atoms with a temperature of 300 Kelvin for 5000 steps.

11.0.2 Stillinger-Weber

The Stillinger-Weber is a potential which describes accurately Silicon atoms in the diamond lattice structure, and was one of the first potentials used to describe a realistic atomic-scale model of Silicon. It is also one of the most common examples of a potential with a threebody interaction, and its intermediate complexity makes it ideal for verification with for example quantum calculations or in our case machine learning methods. As in the previous section we integrate the system over $8 \cdot 10^5$ steps using a timestep of $\Delta t = 5.0$ fs (suitable for most metals in a crystalline structure) for a total of 8000 images for energy learning and 500 images used to train forces. We train for 4000 epochs, since the loss function is then usually suitably converged. We generate a test set with identical positions and velocities using the Stillinger-Weber potential and assess whether the neural network can accurately reproduce the potential energy, radial distribution function and more.

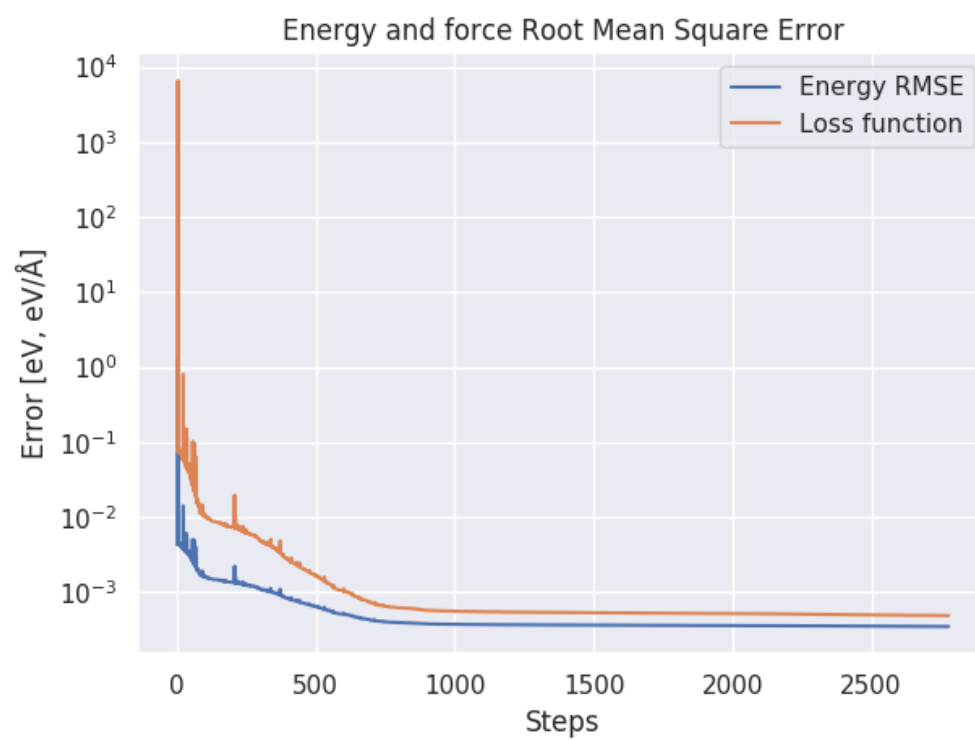


Figure 11.1: Placeholder

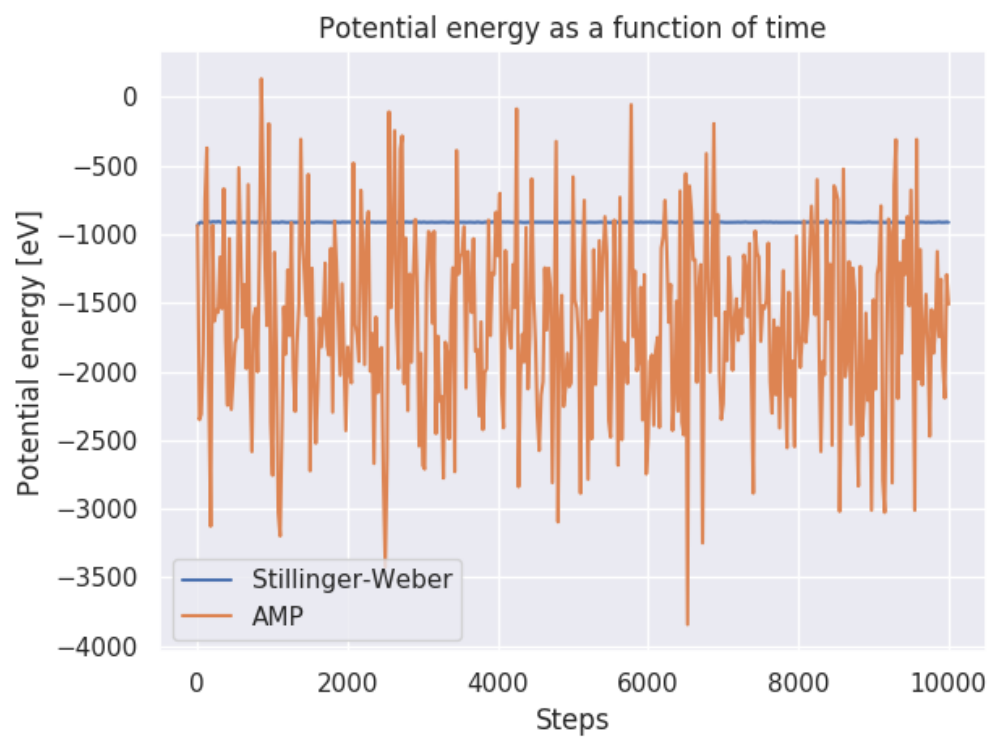


Figure 11.2: Placeholder

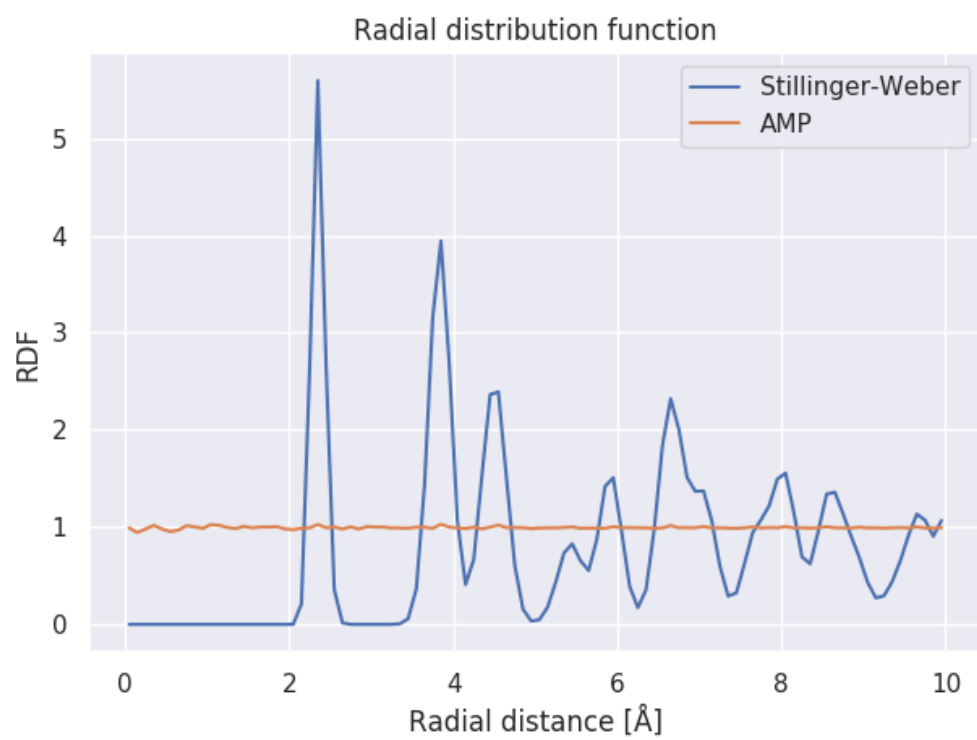


Figure 11.3: Placeholder



Figure 11.4: Placeholder

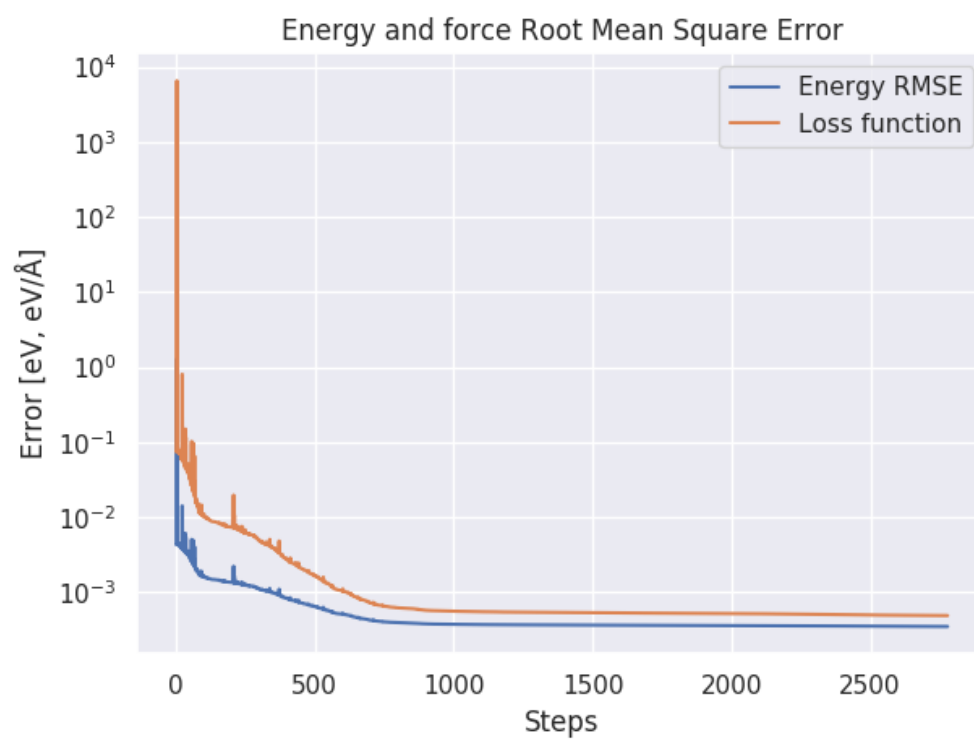


Figure 11.5: Placeholder

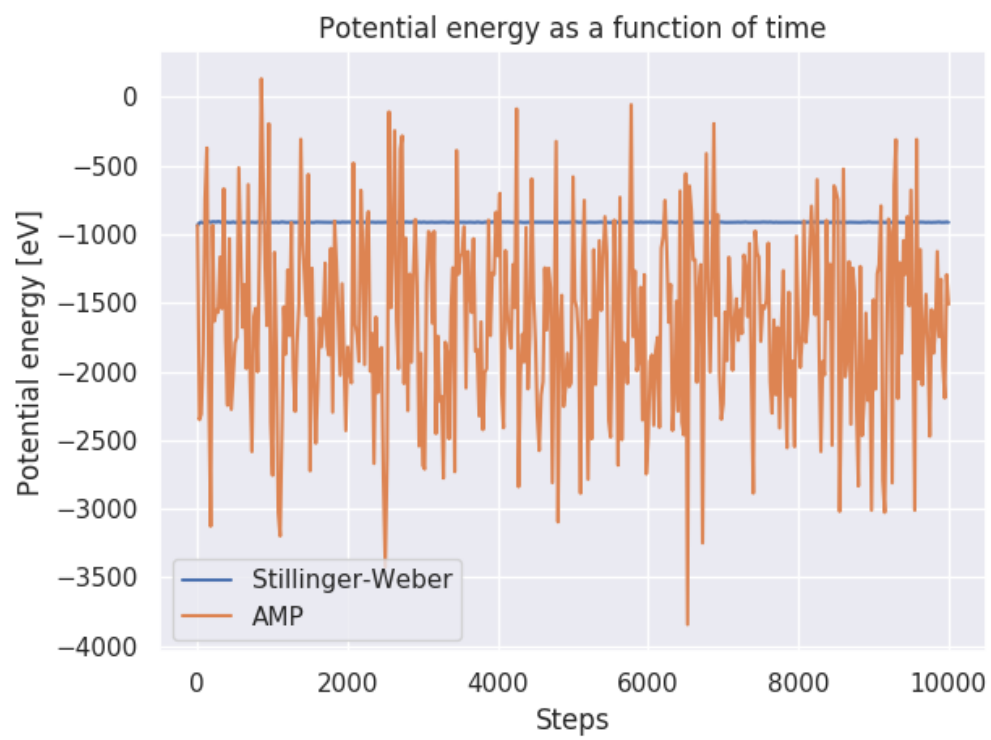


Figure 11.6: Placeholder

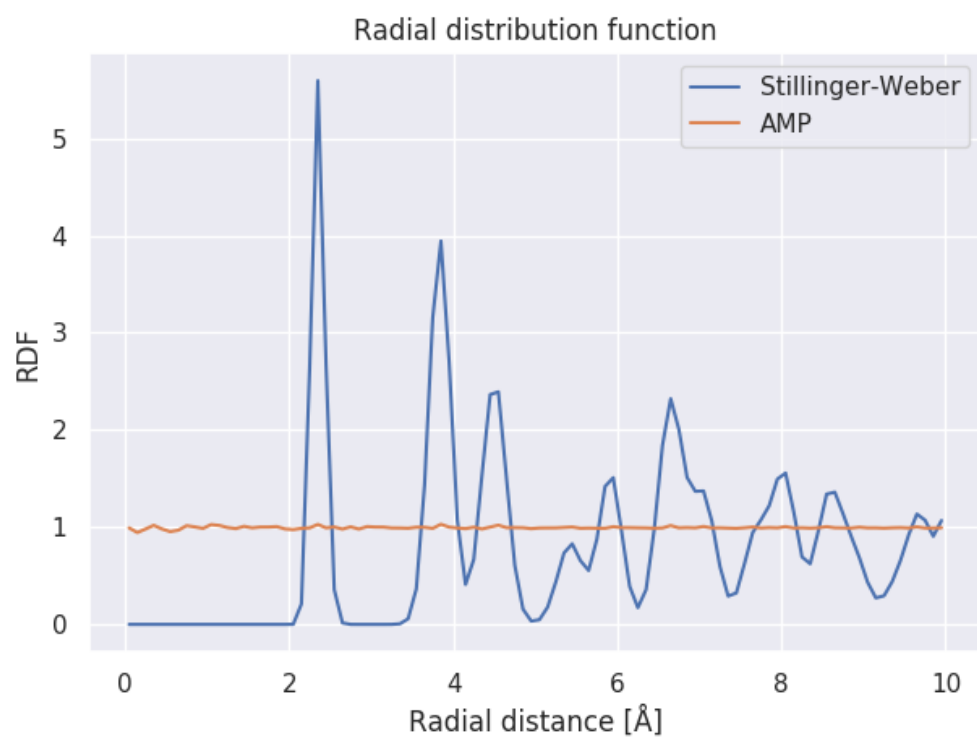


Figure 11.7: Placeholder

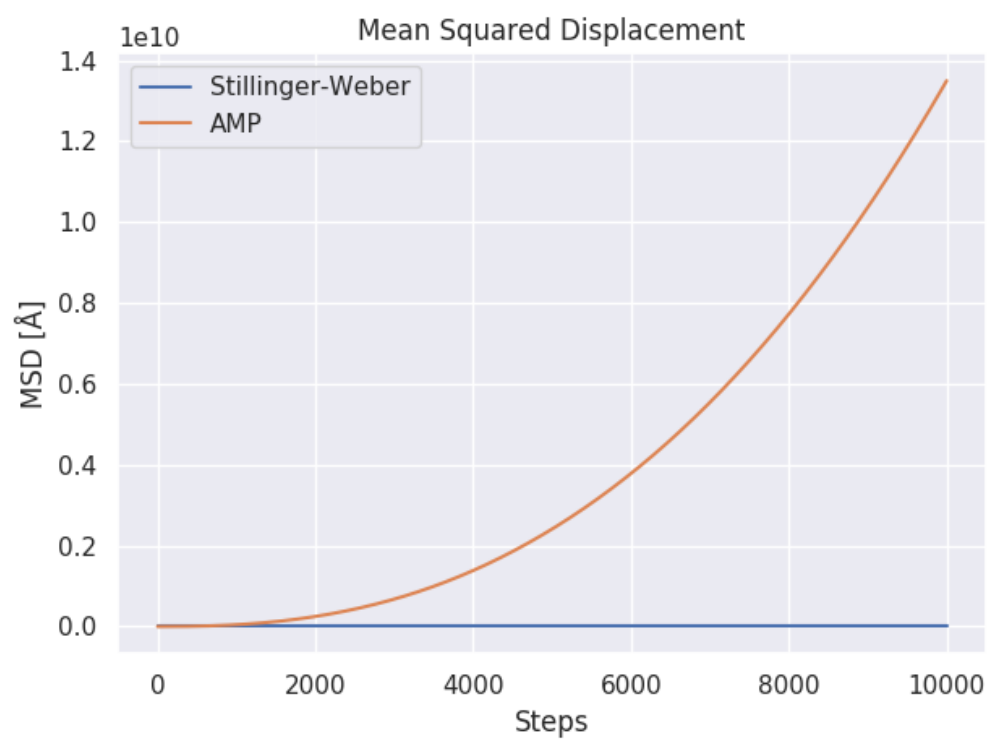


Figure 11.8: Placeholder

Chapter 12

Ab-Initio Molecular Dynamics

12.0.1 Silicon system

12.0.2 Copper system

Chapter 13

Conclusion

Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like “Huardest gefburn”? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

This is the second paragraph. Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like “Huardest gefburn”? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

And after the second paragraph follows the third paragraph. Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like “Huardest gefburn”? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the

alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

After this fourth paragraph, we start a new paragraph sequence. Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like “Huardest gefburn”? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like “Huardest gefburn”? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

Appendices

Appendix A

Title 1

Appendix B

Title 2

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