

# Reactive Molecular Dynamics: From Small Molecules to Proteins

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## **Abstract**

The current status of reactive molecular dynamics (MD) simulations is summarized. Both, methodological aspects and applications to problems ranging from gas phase reaction dynamics to ligand-binding in solvated proteins are discussed, focusing on extracting information from simulations that can not easily be obtained from experiments alone. One specific example is the structural interpretation of the ligand rebinding time scales extracted from state-of-the art time resolved experiments. Atomistic simulations employing validated reactive interaction potentials are capable of providing structural information about the time scales involved. Both, merits and shortcomings of the various methods are discussed and the outlook summarizes possible future avenues such as reactive potentials based on machine learning techniques.

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# GRAPHICAL TABLE OF CONTENTS

## INTRODUCTION

Understanding atomistic and molecular details of chemical reactions is one of the cornerstones in chemistry and biology. Characterizing reactions in time and space is challenging because the nuclear motion on various length- and time-scales needs to be followed.(El Hage et al., 2017) As an example, typical reaction times in the Claisen rearrangement(Claisen, 1912) are on the order of seconds (in aqueous solution)(Andrews, Smith, & Young, 1973) or milliseconds (in the protein).(Kast, Asif-Ullah, & Hilvert, 1996) However, the actual chemical step (i.e. C-C bond formation and C-O bond breaking) occurs on the femtosecond time scale. In other words, during  $10^9$  to  $10^{15}$  vibrational periods energy is redistributed in the system until sufficient energy has accumulated along the preferred “progression coordinate” for the reaction to occur. Because the “chemical step” is so rapid and the concentration of systems at the transition state is tiny, direct experimental characterization of a chemical reaction between reactant, transition state and product is extremely challenging even with current state-of-the art methods, including NMR,(D. Li, Keresztes, Hopson, & Williard, 2009) IR,(Helbing et al., 2004) or X-ray(Schotte et al., 2003; Kern et al., 2014) spectroscopic techniques or combinations thereof.

Atomistic simulations have shown their value in providing molecular-level insights into the energetics and dynamics of chemical reactions for systems ranging from small (triatomic) molecules to proteins in the condensed phase. An essential requirement for a meaningful contribution of computer-based work to understand and characterize chemical reactions is the quantitatively correct description of the intermolecular interactions along the entire reaction path. This involves regions around the reactants, products and the transition state(s). Intermolecular interactions in molecular systems are often represented as Born-Oppenheimer potential energy surfaces (BO-PESs or PESs). As such, these are  $3N - 6$  dimensional hypersurfaces, where  $N$  is the number of atoms. This already makes clear that a realistic representation of this object  $V(\vec{x})$ , where  $\vec{x}$  is a  $3N$  dimensional vector con-

taining all Cartesian coordinates, is a formidable undertaking. Following the dynamics on the PES is either done based on Newtonian mechanics (Brooks et al., 2009; Hess, Kutzner, van der Spoel, & Lindahl, 2008) (“molecular dynamics simulations”) or by solving the time-independent (Skouteris, Castillo, & Manolopoulos, 2000) or time-dependent (Peng, Zhang, Wang, Li, & Zhang, 2000; Mayneris, Gonzalez, & Gray, 2008) Schrödinger equation for a quantum mechanical approach. In recent years, path-integral-based approaches and variants thereof (Beyer, Richardson, Knowles, Rommel, & Althorpe, 2016) have also been explored.

Broadly speaking, there are two possible approaches for following chemical reactions using molecular dynamics (MD) simulations: those using quantum mechanics (QM)-based methods and those employing empirical force fields. Empirical energy functions represent the PES in one way or another as a computable function (see below) whereas QM-based methods solve the electronic Schrödinger equation directly for every configuration  $\vec{x}$  of the system for which it is required, for a review see Ref. (Cui, 2016) This is a very powerful technique as it provides a general framework for investigating the dynamics of chemical reactivity without preconceived reaction mechanisms. However, there are certain limitations which are due to the computational approach *per se* (such as the speed and efficiency of the method) or due to practical aspects of quantum chemistry (e.g. basis set superposition error, the convergence of the Hartree-Fock wavefunction to the desired electronic state for arbitrary geometries, or the choice of a suitable active space irrespective of molecular geometry). Improvements and future avenues for making QM-based approaches even more broadly applicable have been recently discussed. (Cui, 2016)

A particularly promising use of QM-based methods are mixed quantum mechanics/molecular mechanics (QM/MM) treatments which are popular for biophysical and biochemical applications. (Senn & Thiel, 2009) Using a decomposition into a “reactive region” which is treated with a quantum chemical (or semiempirical) method and an environment described by an empirical force field can considerably speed up simulations such that even free energy simulations in multiple dimensions can be computed. (Roston, Demapan, & Cui, 2016) One of the current open questions in such QM/MM simulations is that of the size of the QM region required for

converged results which was recently considered for Catechol O-Methyltransferase.(Kulik, Zhang, Klinman, & Martinez, 2016)

The focus of the present review is on the use of empirical energy functions to follow chemical reactions in the gas- and condensed phase. The motivation for this is twofold: first, due to their computational efficiency formulations based on empirical energy functions are expected to be suitable for situations where extensive sampling of the conformational space is required. Secondly, force fields fitted to electronic structure data, experimental observables or both can be systematically improved. However, most of the available approaches are not unbiased as they have to make assumptions about the bonding pattern for the states involved in the chemical transformation considered. In the following, several techniques to investigate chemical reactivity suitable for exploration through MD simulations are presented. This is done by adopting a historical perspective to highlight how the field has developed. Next, topical examples are discussed with a particular focus on relating the reactive dynamics with the time scales of elementary processes and the underlying conformational dynamics.

## Computational Techniques

Already in the 50s Linus Pauling - based on earlier work by Penney(Penney, 1937) - suggested that bond order and bond length are related.(Pauling, 1947) It was also recognized that the (fractional) bond order is related to the strength of the bond considered, i.e. to the interaction energy.(Penney, 1937) Following this, Johnston and Parr proposed a “bond energy bond order” (BEBO) potential.(Johnston & Parr, 1963) It was found that a) there exists a nearly linear relationship between bond order and bond length (Pauling, 1947) and b) a log-log plot of dissociation energies versus bond order is also almost linear. This approach yielded activation energies within  $\approx 2$  kcal/mol and chemical rates within an order of magnitude for well-known bond energies. One of the essential assumptions underlying this approach is that - at least for hydrogen-atom transfer reactions - the sum of the bond orders  $n_1$  of the breaking and the newly formed bond  $n_2$  fulfills  $n_1 + n_2 = 1$ . In other words: ”At

all stages of the reaction the formation of the second bond must be 'paying for' the breaking of the first bond".(Johnston & Parr, 1963)

## ReaxFF

An extension of the concept (and observation) that bond order, bond length and bond energy are related is the ReaxFF force field.(van Duin, Dasgupta, Lorant, & Goddard III, 2001) Here, van der Waals and Coulomb terms are included at the outset of the development and the dissociation and reaction curves are derived from electronic structure calculations. The total energy in ReaxFF is(van Duin et al., 2001; Chenoweth, van Duin, & Goddard, 2008)

$$E = E_{\text{bond}} + E_{\text{over}} + E_{\text{under}} + E_{\text{conj}} + E_{\text{val}} + E_{\text{pen}} + E_{\text{dihe}} + E_{\text{VDW}} + E_{\text{coul}} \quad (1)$$

Here,  $E_{\text{val}}$ ,  $E_{\text{dihe}}$ ,  $E_{\text{VDW}}$  and  $E_{\text{coul}}$  are the well-known valence-angle, dihedral, Van der Waals, and electrostatic terms. Central to ReaxFF is that the bond order can be calculated from the distance between two atoms. For a CC-bond this expresses the fact that two carbon atoms can be found to form anything between "no bond" (bond order = 0) to a triple bond. The energy term  $E_{\text{bond}}$  in the force field is calculated from the value of the bond order. To correct for over-coordination, a penalty term  $E_{\text{over}}$  is added to ReaxFF and for under-coordinated atoms additional favorable energy terms  $E_{\text{under}}$  reflecting resonance energies between  $\pi$ -electrons are introduced. The conjugation energy  $E_{\text{conj}}$  changes between a maximum value if successive bonds have bond-order values of 1.5 (e.g. benzene) to zero. Finally,  $E_{\text{pen}}$  reproduces the stability of systems with two double bonds sharing an atom in a valence angle. A recent review discusses the current status and future directions.(Senftle et al., 2016).

ReaxFF has been applied to a wide array of reactive chemical systems, including hydrocarbons(van Duin et al., 2001), the thermal decomposition of a zinc-oxide nanowire.(Russo & van Duin, 2011), shock-induced chemistry in high energy materials (Strachan, van Duin, Chakraborty, Dasgupta, & Goddard III, 2003), the activation and dissociation of  $\text{H}_2$  on platinum surfaces (Ludwig, Vlachos, van Duin, & Goddard III, 2006) or the oxidation of nanoparticles on aluminum surfaces (Vashishta, Kalia, & Nakano, 2006). Using ReaxFF and nonequilibrium

MD simulations it was found that depending on the impact velocities cyclic- $[\text{CH}_2\text{N}(\text{NO}_2)]_3$  decomposes into a variety of small molecules on the picosecond time scale or only into  $\text{NO}_2$ , both of which are consistent with experiments (Strachan et al., 2003). Such simulations provide valuable insight into the time dependence of concentration changes of particular species. As such they can complement studies such as the “nanoreactor” (Wang et al., 2014) which follows a similar logic - namely characterizing the time-dependent concentration of species given a particular initial distribution of reactants and corresponding thermodynamic conditions.

Contrary to empirical force field-based methods (see below), ReaxFF does not build on the concept of atom types. While the functional form of ReaxFF is universal, its application to concrete problems always involves more or less extensive fitting to reference calculations. (Senftle et al., 2016) Also, with respect to actual parametrizations, it is noted that several “branches” exist (e.g. the aqueous or combustion branch). The parametrizations for one chemical element in two different branches do not necessarily transfer. (Senftle et al., 2016)

## Empirical Valence Bond

A natural starting point to formulate a model for chemical reactivity in complex environments (e.g. in solution or a protein) is valence bond theory. This has been done within the framework of the empirical valence bond (EVB) approach. (Duarte & Kamerlin, 2017) As noted in the original EVB publication “The user[...] must choose, on the basis of experience and intuition, a set of bonding arrangements or “resonance structures” [...]”. (Warshel & Weiss, 1980; Hong, Rosta, & Warshel, 2006). Since the reactive species and its environment primarily interact through electrostatic interactions, empirical force fields can be used to describe the resonant forms of the reactant and product states. For ionic bond cleavage  $\text{AB} \rightarrow \text{A}^- + \text{B}^+$ , three resonance forms are considered:  $\psi_1 = \text{AB}$ ,  $\psi_2 = \text{A}^- \text{B}^+$ , and  $\psi_3 = \text{A}^+ \text{B}^-$ . (Warshel & Weiss, 1980) If A is more electronegative than B (i.e. formation  $\text{B}^-$  is unlikely in the presence of A), resonance structure  $\psi_3$  is largely irrelevant and the process

can be described by  $\psi_1$  and  $\psi_2$  alone. The choice of the necessary states in EVB is not always obvious *a priori* but may also need to be based, e.g., on the requirement to best reproduce the reference electronic structure calculations. (Glowacki, Orr-Ewing, & Harvey, 2015)

For a collection of covalent and ionic states, matrix elements for the EVB Hamiltonian have to be determined. They include diagonal elements  $H_{ii}$  for the covalent and ionic states, and off-diagonal elements that couple configurations (bonding patterns) that differ by the location of an electron pair. All other off-diagonal matrix elements  $H_{ij}$  are zero. The justification for this is that such matrix elements are proportional to the square or higher powers of the overlap between atomic orbitals, but they may also be retained (Coulson & Danielsson, 1954; Warshel & Weiss, 1980). The covalent diagonal matrix elements  $H_{ii}$  correspond essentially to an empirical force field, whereas for the ionic diagonal matrix elements the bonded terms are replaced by electrostatic interactions between the charged fragments and the formation energy of  $A^-B^+$  from  $AB$  has also to be added. For the two-fragment system  $AB$  the matrix elements are  $H_{11} = D_e(1 - \exp[-\beta(r - r_e)])^2$  and  $H_{22} = \Delta - \frac{e^2}{r} + V_{nb}$  where  $\Delta$  is the gas-phase formation energy of  $A^-B^+$  from  $AB$  at infinite separation, and  $V_{nb}$  is the nonbonded interaction potential such that the minimum of  $(\frac{-e^2}{r} + V_{nb})$  is given by the sums of the ionic radii of  $A^+$  and  $B^-$ . In the original version of EVB (Warshel & Weiss, 1980) the off-diagonal element  $H_{12} = H_{21}$  is determined through the requirement that the eigenvalues of the Hamiltonian  $E$  satisfy the relation  $H_{12} = \sqrt{(H_{11} - E)(H_{22} - E)}$  and  $E$  is the experimentally determined ground-state bond energy. In a later and slightly more general approach, the off-diagonal elements are parametrized functions depending on a pre-defined reaction coordinate of the form  $H_{ij} = A \exp(-\mu(r - r_0))$  (Hong et al., 2006), where  $A$ ,  $\mu$  and  $r_0$  are fitting parameters.

The definition of the off-diagonal terms has been a source of considerable discussion, in particular the assumption that upon transfer of the reaction from the gas phase to the solution phase these elements do not change significantly. (Hong et al., 2006). Alternative forms which also capture the shape and energetics of the potential energy surface around the transition state use generalized Gaussians (Chang & Miller, 1990). A comparison of different diabatic

models provides a notion of the common features and the differences between various approaches (Valero, Song, Gao, & Truhlar, 2009b, 2009a; Kamerlin, Cao, Rosta, & Warshel, 2009). A useful comparison of the similarities and differences between the various methods can be found in Ref. (Florian, 2002). Applications of EVB include enzymatic reactions (for which it was originally developed (Warshel, 1984)), proton transfer processes, and the autodissociation of water (Strajbl, Hong, & Warshel, 2002). More recently, this has been extended to other types of reactions, including bimolecular reactions (Greaves et al., 2011; Glowacki, Rose, Greaves, Orr-Ewing, & Harvey, 2011) or the association and dissociation of  $\text{CH}_3$  from diamond surfaces (Glowacki, Rodgers, Shannon, Robertson, & Harvey, 2017). Furthermore, several extensions have been suggested to the original EVB method allowing its application to a wider class of problems (Chang & Miller, 1990; Schmitt & Voth, 1998; Schlegel & Sonnenberg, 2006).

## **Reactive Molecular Dynamics: Mixing PESs in Time and Energy**

Time resolved experiments have contributed heavily to our understanding of chemical reactivity over the past 20 years. With the advent of short laser pulses (“femtochemistry”) it became possible to follow chemical transformations on the relevant time scale on which the actual chemical step (bond breaking or bond formation) occurs (see Introduction). Typical examples are the time resolved studies of ligand (re)binding in myoglobin (Mb) (Petrich et al., 1991; Nutt & Meuwly, 2006; Danielsson & Meuwly, 2008; Kruglik et al., 2010; J. Kim, Park, Lee, & Lim, 2012; Yoo, Kruglik, Lamarre, Martin, & Negrerie, 2012) or vibrationally induced reactivity (Crim, 1993; Vaida, Kjaergaard, Hintze, & Donaldson, 2003; Y. Miller & Gerber, 2006; Yosa Reyes, Brickel, Unke, Nagy, & Meuwly, 2016; Brickel & Meuwly, 2017).

This prompted the development of computational techniques that allow following chemical reactions in time which is the natural progression coordinate in a time resolved experiment. Reactive MD (Nutt & Meuwly, 2006) was based on earlier efforts to study ligand re-binding kinetics of nitric oxide to Mb (H. Li, Elber, & Straub, 1993; Meuwly, Becker, Stote, & Karplus, 2002). The underlying concept is to first introduce relevant “states” of the system,

i.e. bonding patterns in the language of empirical force fields. Along the MD simulation the system is then propagated on the lowest adiabatic energy  $V_R(\vec{x})$  (“electronic ground state”) while monitoring the energy gaps to all higher lying states for the same configuration. Once a crossing between  $V_R(\vec{x})$  and any other state  $V_P(\vec{x})$  higher in energy occurs the simulation is stopped, back propagated by a time  $t_s$  (half the switching time) and the two PESs involved in the crossing are mixed according to  $V_{\text{eff}}(\vec{x}) = f(t)V_R(\vec{x}) + (1 - f(t))V_P(\vec{x})$  where  $f(t)$  is a sigmoid switching function which changes from 1 to 0 between  $t = -t_s/2$  and  $t = t_s/2$ . At the beginning of the mixing the system is fully in the R-state ( $f(t = -t_s/s) = 1$ ), while at the end it is fully in the P-state ( $f(t > t_s/s) = 0$ ). The algorithm of ARMD is schematically shown for a collinear atom transfer reaction in Figure 1a.

Time-based ARMD(Nutt & Meuwly, 2006; Danielsson & Meuwly, 2008) does not explicitly couple the PESs describing the different states considered. The only free variable is the switching time  $t_s$  over which two (or several) crossing PESs are mixed. However, no control over the crossing region is possible which may be a disadvantage of the method.

During the mixing the system is propagated under a time-dependent Hamiltonian which does not strictly conserve total energy.(Yosa & Meuwly, 2011; Nagy, Yosa Reyes, & Meuwly, 2014) The magnitude of this effect can be shown to scale with  $1/m$  where  $m$  is the reduced mass involved in the reaction(Nagy et al., 2014) which is inconsequential for heavy systems such as NO rebounding to Mb but affects the dynamics in the product channel for proton transfer processes. This led to the development of multi state adiabatic reactive MD (MS-ARMD) which mixes the PESs with energy dependent weights and strictly conserves energy.(Nagy et al., 2014)

In MS-ARMD the PESs are mixed in energy-space according to

$$V_{\text{MS-ARMD}}(\vec{x}) = \sum_{i=1}^n w_i(\vec{x})V_i(\vec{x}) \tag{2}$$

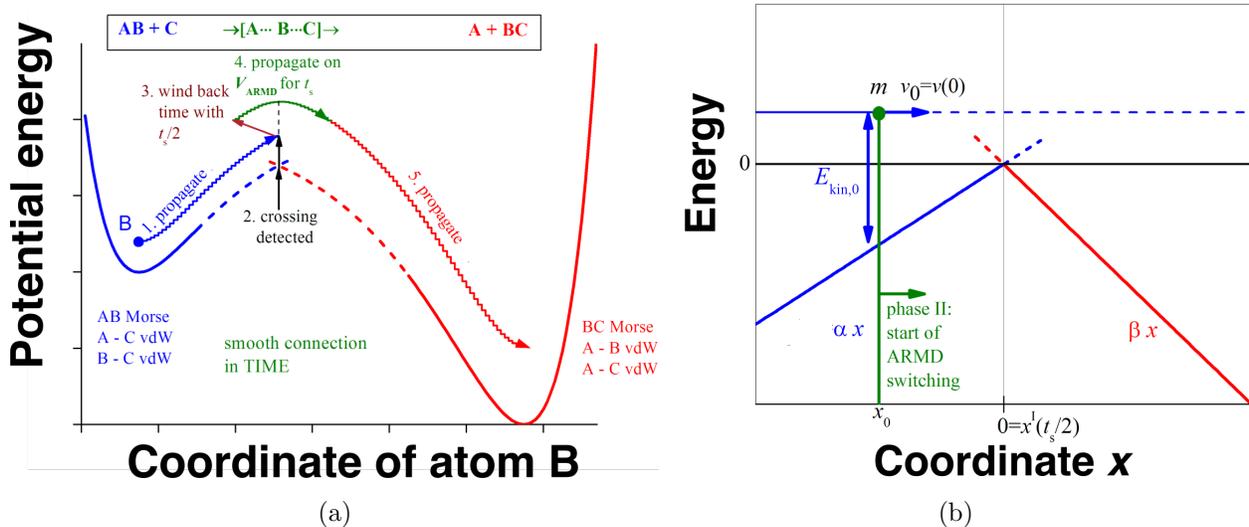


Figure 1: a) Schematic illustrating the ARMD method for a collinear reaction, where atom B is transferred from donor atom A to acceptor atom C. During crossing the surfaces are switched in time and the Morse bond is replaced by van der Waals (vdW) interactions and vice versa. b) Simple model for estimating energy violation in ARMD simulations. The system with mass  $m$  approaches from the left on PES  $V_R(x) = \alpha x$  (phase I). At time  $t = 0$  it is at  $x_0$  with velocity  $v_0$  and kinetic energy  $E_{\text{kin},0}$ . After crossing is detected at  $x = 0$  the time is rewound by  $t_s/2$  and the dynamics is re-simulated while  $V_R(x)$  is being switched to  $V_P(x) = \beta x$  in  $t_s$  (phase II).

The weights (see Figure 2)  $w_i(\vec{x})$  are obtained by renormalizing the raw weights  $w_{i,0}(\vec{x})$

$$w_i(\vec{x}) = \frac{w_{i,0}(\vec{x})}{\sum_{i=1}^n w_{i,0}(\vec{x})} \quad \text{where} \quad w_{i,0}(\vec{x}) = \exp\left(-\frac{V_i(\vec{x})}{\Delta V}\right) \quad (3)$$

The raw weights (Eq. 3) depend exponentially on the energy difference between surface  $i$  and the minimum energy surface over a characteristic energy scale  $\Delta V$  (switching parameter). Only those surfaces will have significant weights, whose energy is within a few times of  $\Delta V$  from the lowest energy surface. The performance of MS-ARMD is demonstrated for crossings of 1D and 2D surfaces in Figure 2. Finally, ARMD with energy-dependent weights mixes the different PESs by using Gaussian and polynomial functions (GAPOs) in the neighborhood of crossing points between the states. The parameters of these GAPOs need to be determined through fitting to reference data (e.g. from a calculation along the intrinsic reaction

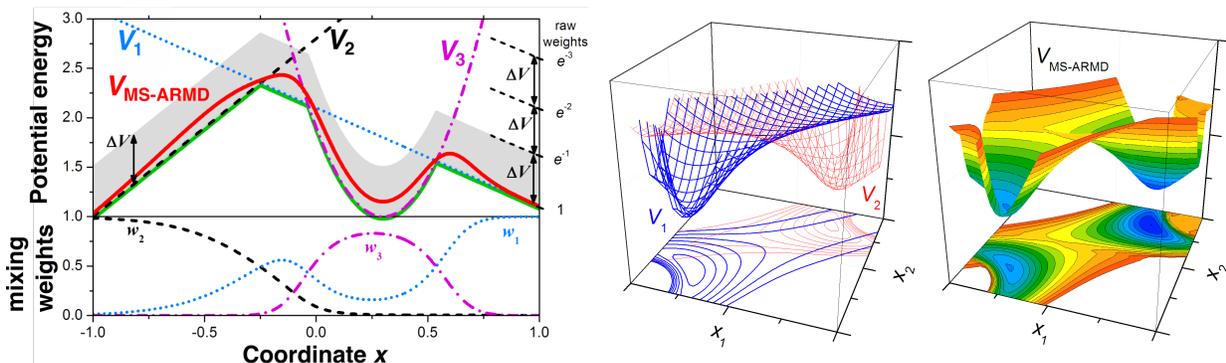


Figure 2: The MS-ARMD switching method applied in one and two dimensions to 3 and 2 surfaces ( $V_{1,2,3}$ ). The effective surface is ( $V_{\text{MS-ARMD}}$ ) always close to the lowest-energy surface ( $V_{\text{min}}$ ), except for regions where other surfaces are within a few times  $\Delta V$  (here = 0.5) in energy. Here, the algorithm switches smoothly among them by varying their weights ( $w_{1,2,3}$ ; lower left panel)

coordinate (IRC)). This step is the most demanding part in MS-ARMD.(Nagy et al., 2014) A smooth global surface is obtained everywhere, even for energies where more than two surfaces approach one another. Because the mixed PES  $V_{\text{MS-ARMD}}(\vec{x})$  depends on the energies of the different states through the weights  $w_i$  which in turn are analytical functions of the coordinates  $\vec{x}$  the derivatives can be readily determined which leads to energy conservation in MD simulations.

A recent extension(Schmid, Das, Landis, & Meuwly, 2018) of MS-ARMD is its combination with VALBOND, a force field that allows to describe the geometries and dynamics of metal complexes.(Landis, Cleveland, & Firman, 1998; Firman & Landis, 2001; Tubert-Brohman, Schmid, & Meuwly, 2009) Here, the formulation is reminiscent of EVB whereby the diagonal terms are VALBOND descriptions of the states involved and the off-diagonal elements describe the orbital overlap. Furthermore, MS-ARMD can also be combined with molecular mechanics with proton transfer (MMPT)(Lammers, Lutz, & Meuwly, 2008) to follow proton transfer in the gas- and condensed phase.(Mackeprang, Xu, Maroun, Meuwly, & Kjaergaard, 2016; Xu & Meuwly, 2017; Karandashev, Xu, Meuwly, Vanicek, & Richardson, 2017; Xu & Meuwly, 2018)

It is instructive to briefly compare EVB and the two ARMD approaches. While all three methods start from an empirical force field perspective, the EVB constructs an  $n \times n$  Hamiltonian with the force fields  $V_{nn}$  for the pure states on the diagonal and mixing elements  $V_{mn}$  ( $m \neq n$ ) as off-diagonal elements. This Hamiltonian needs to be diagonalized at every time step of an MD simulation and the forces can be determined from the Hellmann-Feynman theorem.(Glowacki et al., 2015) The parametrization of the off-diagonal elements is the most demanding part in a concrete EVB-application. First it has to be decided, whether or not elements  $V_{mn}$  should be constants or depend on one or several explicit coordinates. If they depend on (usually internal) coordinates, one or several reaction coordinates are chosen. Such choices can sometimes be justified but determining meaningful reaction coordinates remains a challenge. The second choice is that of a functional form. Typically, exponentially decaying or Gaussian functions(Schlegel & Sonnenberg, 2006) are used. Fitting the free parameters to reference energies is the final step in this procedure.

For ARMD the challenge is to fit the Gaussian polynomials (GAPO) to describe the barrier region. Usually, the force fields for the asymptotic reactant and product states can be fitted using standard steepest descent techniques. However, for the GAPOs more advanced fitting tools are required, e.g. differential evolution.(Storn & Price, 1997) Also, as the GAPOs are formulated in “energy space” it is not straightforward to provide simple and transparent guesses for the initial parameters for the fit.

## Global Potential Energy Surfaces

The most rigorous approach to reactive chemical dynamics is to use fully dimensional, reactive PESs, which are usually only available for low-dimensional systems. Specifically in the field of small molecule reactions involving processes such as  $A+BC \rightarrow AB+C$  or  $AB+CD \rightarrow A+BCD$  (or permutations thereof) involving a total number of 3 to 8 atoms the construction of globally valid potential energy surfaces is essential to make direct contact between computations and experiments. The limitation on up to 8 atoms is primarily owed to the fact that ac-

curately solving the nuclear Schrödinger equation for systems involving a larger number of nuclei remains an unsolved problem although considerable progress has been made over the past several years.(W. Zhang et al., 2010; Zhao, Zhang, Liu, & Zhang, 2017)

One of the earliest efforts to determine outcomes of chemical reactions is the H+H<sub>2</sub> atom exchange reaction. Using classical molecular dynamics (MD) and a modified London-Eyring-Polanyi-Sato (LEPS) surface,(Porter & Karplus, 1964) the differential cross sections for the D+H<sub>2</sub> reaction were calculated.(Karplus, Sharma, & Porter, 1964) It is of interest to note that some 10 years later the results of these quasi-classical simulations were almost quantitatively confirmed at room temperature by a full quantum treatment.(Schatz & Kuppermann, 1976) The LEPS surface(Porter & Karplus, 1964; Sato, 1955a, 1955b) was based on London's work on the H+H<sub>2</sub> reaction for which he used a 2 × 2 valence bond treatment (London, 1929) which is akin to an EVB-like treatment (see above). Subsequent work on fully-dimensional PESs for more complex systems further explored the use of valence bond theory and led to the diatomics-in-molecules (DIM) theory (Ellison, 1963; Olson & Garrison, 1984; Belyaev, Tiukanov, & Domcke, 2002).

A different approach was taken when determining reliable intermolecular potential energy surfaces was cast as an inversion problem from experimental - largely spectroscopic and scattering - data.(Hutson, 1990) For the special class of van der Waals complexes (AB+C, where AB is a di- or triatomic and C is a rare gas atom) the long-range part of the PES can be well described by inductive and dispersion interactions. Their functional forms are known and constrain the long-range, asymptotic region of the intermolecular interactions. For the short range part, a parametrized form was assumed (typically a damped Buckingham or a Lennard-Jones potential).(Hutson, 1990) By fitting the free parameters (usually some 10 to 20 parameters) to best reproduce the experimental observables quite accurate potential energy surfaces could be derived in this fashion for a wide range of systems, including the HF-, HCl-, and H<sub>2</sub>-rare gas series.(LeRoy & Hutson, 1987; Hutson, 1992) However, such an "inversion scheme" is only informative about the shape of the PES in regions which are also sampled by experiment.(Meuwly & Hutson, 1999a) This "dependence" on experi-

mental data vanished when high-level (at least Moller-Plesset MP2 but better CCSD(T) or multireference-configuration interaction) electronic structure calculations became possible to provide energies for arbitrary geometries for such systems.

High-level *ab initio* calculations have become more accurate and more efficient.(White, Johnson, Gill, & Head-Gordon, 1996; Adler, Knizia, & Werner, 2007; Knizia, Adler, & Werner, 2009) Along with the ever-increasing computational power it is now possible to compute thousands of energies at various geometries for small polyatomic systems within chemical accuracy (0.5 kcal/mol).(Bokhan, Ten-No, & Noga, 2008) With the availability of routine electronic structure calculations using large basis sets and accurate ways for approximately solving the electronic Schrödinger equation the problem shifted to *representing* the computed, discrete points on the PES. This is in particular needed when running MD simulations (classical or quasiclassical trajectory (QCT) simulations) where the total energy and the derivatives at arbitrary points are required. Similarly, quantum wavepacket calculations require analytical forms of the PES whereas for collocation methods it is sometimes sufficient to work with a discrete, precomputed set of energies. Nevertheless, it is nowadays standard to represent nonreactive and reactive PESs in a manner that allows to evaluate it at arbitrary points, given pointwise information from *ab initio* calculations only. In addition, the final representation should be computationally efficient in order to run statistically significant numbers of (reactive) trajectories in QCT simulations.(Yosa & Meuwly, 2011; Tong et al., 2012; Castro-Palacio, Nagy, Bemish, & Meuwly, 2014)

A direct way for obtaining an analytical representation of a PES is to use a parametrized functional form(Hutson, 1990; Aguado & Paniagua, 1992) and fit the parameters to a set of *ab initio* data using linear or non-linear least squares procedures.(Law & Hutson, 1997) For the specific case of van der Waals molecules such an approach has been very successful, in particular for applications in spectroscopy.(Hutson, 1990; Roche, Ernesti, Hutson, & Dickinson, 1996) Although such approaches have demonstrated to achieve root mean squared errors (RMSEs) within chemical accuracy,(Boothroyd, Keogh, Martin, & Peterson, 1996) choosing a functional form requires human intuition and the fitting itself can be tedious and

time-intensive.(Meuwly & Hutson, 1999b; Mas et al., 2000)

Over the past years alternative interpolation techniques including the modified Shepard interpolation(Franke & Nielson, 1980; Nguyen, Rossi, & Truhlar, 1995; Bettens & Collins, 1999), the moving least squares method(Lancaster & Salkauskas, 1981; Ischtwan & Collins, 1994; Dawes, Thompson, Wagner, & Minkoff, 2008), permutation invariant polynomials(Cassam-Chenai & Patras, 2008; Braams & Bowman, 2009; Paukku, Yang, Varga, & Truhlar, 2013) or neural network approaches(Sumpter & Noid, 1992; Bowman et al., 2010; Jiang, Li, & Guo, 2016) have been used to obtain multi-dimensional reactive PESs.(Jordan, Thompson, & Collins, 1995b, 1995a; Skokov, Peterson, & Bowman, 1998; Collins, 2002; Duchovic et al., 2002; X. Zhang, Braams, & Bowman, 2006; J. Li et al., 2012) As an example, the most general expression for a global PES involving 4 atoms using permutation invariant polynomials is(Braams & Bowman, 2009)

$$V(\vec{x}) = \sum_{m=0}^M D_{abcdef} \mathcal{S} \left[ y_{12}^a y_{13}^b y_{14}^c y_{23}^d y_{24}^e y_{34}^f \right] \quad (4)$$

where the  $y_{ij}^p$  are monomials which can, e.g., be Morse-type functions elevated to the power  $p$  and the coefficients  $D_{abcdef}$  need to be fitted to reference data. The operator  $\mathcal{S}[\dots]$  symmetrizes the monomials. For an  $A_2B$  molecule the two possible monomials are  $r_{12}^a r_{13}^b r_{23}^c$  and  $r_{12}^a r_{23}^b r_{13}^c$  which become  $r_{12}^a r_{13}^b r_{23}^c + r_{12}^a r_{23}^b r_{13}^c$  in symmetrized form. The total number of coefficients  $D_{a_1 \dots a_m}$  grows rapidly with the number of atoms. For total polynomial order of 5 and 4 atoms (molecule ABCD with 4 different atoms) there are 462 such coefficients and for 5 atoms (molecule ABCDE) there are 3003 of them. With increasing symmetry (e.g. molecule  $A_2BCD$ ) the number of distinct polynomials - and hence the number of unique coefficients - decreases. Thus, the number of reference energies that need to be determined depends on the number of distinct coefficients for the fitting problem to be well-defined. Common to all these approaches is the fact that they primarily minimize the RMSE with respect to the training data. In this respect they are similar to parametrized fits which may be acceptable for many cases. As will be discussed next, using reproducing kernel Hilbert space (RKHS) techniques it is possible to reproduce *all* training data *exactly* by construction.

## Reproducing Kernel Hilbert Space (RKHS) PES

Machine-learning (ML) methods allow to estimate an unknown function value using a model that was “trained” with a set of known data.(Rupp, 2015) For intermolecular interactions, Rabitz and coworkers(Ho & Rabitz, 1996; Hollebeek, Ho, & Rabitz, 1997, 1999) have popularized the use of reproducing kernel Hilbert space (RKHS) theory,(Aronszajn, 1950) that allows to construct a PES from a training set based on *ab initio* data. Such an approach is typically referred to as kernel ridge regression (KRR) in the ML community.(Hofmann, Schölkopf, & Smola, 2008; Rupp, 2015) The RKHS method has been successfully applied e.g. for constructing PESs for NO+O(Castro-Palacio et al., 2014),  $N_2^+ + Ar$ (Unke, Castro-Palacio, Bemish, & Meuwly, 2016) or  $H_2O$ .(Ho, Hollebeek, Rabitz, Harding, & Schatz, 1996) A combination of expanding the PES in spherical harmonics for the angular coordinates and reproducing kernels for the radial coordinates has been explored for  $H_2^+ - He$ (Meuwly & Hutson, 1999b) and is now also used for larger systems.(Dhont, van Lenthe, Groenenboom, & van der Avoird, 2005; van der Avoird, Pedersen, Dhont, Fernandez, & Koch, 2006)

It would be considerably more convenient to supply only a set of *ab initio* data to a toolkit that generates the interpolation (and meaningful extrapolation) of the PES along with all required parameters automatically. One step in this direction has been taken recently by introducing a toolkit for automatically constructing a RKHS of a multidimensional PES from gridded *ab initio* data.(Unke & Meuwly, 2017) A “reproducing kernel Hilbert space” (RKHS) consists of continuous evaluation functionals.(Weinert, 1982) Reproducing kernel Hilbert spaces arise in a number of areas, including approximation theory, statistics, or machine learning.(Hollebeek et al., 1999) In particular, if the values  $f_i$  of a function  $f(\mathbf{x})$  are known for a set of  $N$  training points  $\mathbf{x}_i$ , it can be shown(Schölkopf, Herbrich, & Smola, 2001) that  $f(\mathbf{x})$  can always be approximated as a linear combination of kernel products

$$\tilde{f}(\mathbf{x}) = \sum_{i=1}^N c_i K(\mathbf{x}, \mathbf{x}_i) \quad (5)$$

Here, the  $c_i$  are coefficients and  $K(\mathbf{x}, \mathbf{x}')$  is the reproducing kernel of the RKHS. The coeffi-

icients  $c_i$  satisfy the linear relation

$$f_j = \sum_{i=1}^N c_i K_{ij} \quad (6)$$

with  $K_{ij} = K(\mathbf{x}_i, \mathbf{x}_j)$  and can therefore be calculated from the known values  $f_i$  in the training set by solving

$$\begin{bmatrix} K_{11} & K_{12} & \dots & K_{1N} \\ K_{21} & K_{22} & \dots & K_{2N} \\ \vdots & \vdots & \ddots & \vdots \\ K_{N1} & K_{N2} & \dots & K_{NN} \end{bmatrix} \begin{bmatrix} c_1 \\ c_2 \\ \vdots \\ c_N \end{bmatrix} = \begin{bmatrix} f_1 \\ f_2 \\ \vdots \\ f_N \end{bmatrix} \quad (7)$$

Since the kernel matrix  $\mathbf{K} = [K_{ij}]$  is symmetric and positive-definite by construction, Cholesky decomposition (Golub & Van Loan, 2012) can be used to solve Eq. 7. Once the coefficients  $c_i$  have been determined, the function value at an arbitrary position  $\mathbf{x}$  can be calculated using Eq. 5.

Derivatives of  $\tilde{f}(\mathbf{x})$  of any order can be calculated analytically by replacing the kernel function  $K(\mathbf{x}, \mathbf{x}')$  in Eq. 5 with its corresponding derivative. As long as  $\tilde{f}(\mathbf{x})$  approximates  $f(\mathbf{x})$  reasonably well, derivatives of  $\tilde{f}(\mathbf{x})$  can be expected to be good approximations of derivatives of  $f(\mathbf{x})$ .

The explicit form of the multi-dimensional kernel function  $K(\mathbf{x}, \mathbf{x}')$  is chosen depending on the problem to be solved. In general, it is possible to construct  $D$ -dimensional kernels as tensor products of one-dimensional kernels  $k(x, x')$

$$K(\mathbf{x}, \mathbf{x}') = \prod_{d=1}^D k^{(d)}(x^{(d)}, x'^{(d)}) \quad (8)$$

where  $k^{(d)}$  is the one-dimensional kernel of dimension  $d$  and  $x^{(d)}$  and  $x'^{(d)}$  are the  $d$ -th components of the  $D$ -vectors  $\mathbf{x} = \{x^{(d)}\}$  and  $\mathbf{x}' = \{x'^{(d)}\}$ , respectively.

If the training set is constructed by scanning through combinations of sets of  $N^{(d)}$  points in each dimension, as is usually the case when computing energies from electronic structure methods, the training set is a multi-dimensional grid with a total number  $N$  of training

points

$$N = \prod_{d=1}^D N^{(d)} \tag{9}$$

Here,  $N^{(d)}$  can have a different values for each dimension  $d$ .

For practical applications in chemical physics it is also of interest to mention that it is possible to handle incomplete grids with an RKHS interpolation.(Hollebeek et al., 1999) This is important because even for triatomic systems it may happen that converging quantum chemical calculations turns out to be difficult for certain geometries. Under these circumstances the grid of target energies contains a “hole”.

In order to put RKHS into practical use, kernel functions  $k(x, x')$  have to be chosen. One particular advantage is that physical knowledge (e.g. appropriate asymptotic - long range - decay) can be encoded in a radial kernel function. This sets them apart from permutation-invariant polynomials(Cassam-Chenaï & Patras, 2008; Bowman et al., 2010), Gaussian approximated potentials (GAP)(Bartok & Csanyi, 2015), or PES constructed from Gaussian processes.(Kolb, Marshall, Zhao, Jiang, & Guo, 2017) Permutational invariance for RKHS interpolations can be achieved because any symmetry in the data is preserved by the symmetry of the kernels.

Explicit radial kernels include the reciprocal power decay kernel

$$k_{n,m}(x, x') = n^2 x_{>}^{-(m+1)} B(m + 1, n) {}_2F_1 \left( -n + 1, m + 1; n + m + 1; \frac{x_{<}}{x_{>}} \right) \tag{10}$$

or the exponential decay kernel

$$k_n(x, x') = \frac{n \cdot n!}{\beta^{2n-1}} e^{-\beta x_{>}} \sum_{k=0}^{n-1} \frac{(2n - 2 - k)!}{(n - 1 - k)! k!} [\beta(x_{>} - x_{<})]^k \tag{11}$$

where  $x_{>}$  and  $x_{<}$  are the larger and smaller of  $x$  and  $x'$  and the integer  $n$  determines the smoothness. In Eq. 10 the parameter  $m$  is the long-range decay of the dominant intermolecular interaction (e.g.  $m = 6$  for dispersion),  $B(a, b)$  is the beta function and  ${}_2F_1(a, b; c; d)$  is the Gauss hypergeometric function.

Recently, RKHS-interpolated PES have not only been used for spectroscopy (Meuwly & Hutson, 1999b) but also for reactive (bond-breaking/bond-formation) processes ranging from triatomics to ligand binding in proteins. (Castro-Palacio et al., 2014; Soloviov & Meuwly, 2014, 2015) For low-dimensional systems it is now possible to obtain RKHS representations (Unke & Meuwly, 2017) for thousands of reference *ab initio* calculations which can be used in running statistically significant numbers of QCT trajectories (Castro-Palacio et al., 2014; Unke et al., 2016; Yosa Reyes et al., 2016; Brickel & Meuwly, 2017) or to solve the nuclear Schrödinger equation. (Denis-Alpizar, Unke, Bemish, & Meuwly, 2017) In fact, the toolkit was applied to the interpolation of a six-dimensional function based on more than  $7 \times 10^6$  points. (Unke & Meuwly, 2017) For high-dimensional problems the total energy is decomposed into a part described by a RKHS PES and an environmental part describe by an empirical force field (Soloviov & Meuwly, 2014, 2015) akin to mixed quantum mechanical (QM)/molecular mechanics (MM) simulations.

In summary, representing gridded data from electronic structure calculations using RKHS approaches has the advantage that the interpolant *exactly* reproduces the reference energies and has guaranteed (and smooth) behaviour at long and short distances as built-in features in the kernel function.

## Existing Implementations

An EVB implementation is available within the MOLARIS package. (Warshel et al., 2012) More recently, EVB has also been made available in CHARMM (Glowacki et al., 2015), TINKER (Carpenter, Harvey, & Glowacki, 2015) and Q6. (Bauer et al., n.d.). Temporal MS-ARMD (Nutt & Meuwly, 2006; Danielsson & Meuwly, 2008) and MS-ARMD based on energy mixing (Nagy et al., 2014) have been implemented in CHARMM. Molecular mechanics with proton transfer (Lammers et al., 2008) and MS-ARMD with VALBOND (Tubert-Brohman et al., 2009; Schmid et al., 2018) (for metal force fields) are also available within CHARMM. In all these cases the essential step is fitting the force fields together with the features connecting them (off-diagonal elements or GAPOs, respectively) which is, as yet, not automated.

## Applications

Dynamics studies of chemical reactions date back more than 50 years.(Karplus et al., 1964) Since then the sophistication of the PESs and the accuracy with which the nuclear dynamics can be followed have continuously increased.(Bowman, Czako, & Fu, 2011) In the following a number of recent attempts primarily aimed at quantitative studies of chemical reactions in the gas- and condensed-phase are summarized.

### Small Molecule Reactions

*Reaction Dynamics in the Hypersonic Regime:* Particularly interesting applications of reactive MD simulation concern physical conditions that are difficult to achieve in laboratory experiments, such as extremely high ( $T \geq 10000$  K) temperatures as they occur in explosions or in hypersonics.(Millikan & White, 1963) The  $O(^3P) + NO(^2\Pi) \rightarrow O_2(X^3\Sigma_g^-) + N(^4S)$  reaction(Gilibert, Aguilar, Gonzalez, & Sayos, 1993; Gilibert, Gimenez, Gonzalez, Sayos, & Aguilar, 1995; Bose & Candler, 1997; Balakrishnan & Dalgarno, 1999; Defazio, Petrongolo, Gray, & Oliva, 2001; Defazio, Petrongolo, Oliva, Gonzalez, & Sayos, 2002; Gonzalez, Oliva, & Sayos, 2002; Caridade & Varandas, 2004; J.-J. Ma, Chen, Cong, & Han, 2006; Castro-Palacio et al., 2014; Castro-Palacio, Bemish, & Meuwly, 2015) is one such example which plays an important role for the energetics of the reactive air flow around spacecraft during hypersonic atmospheric reentry. This process is also known as the Zeldovich reaction which produces active nitrogen from molecular nitrogen ( $N_2$ ) in the gas phase(Zeldovich, 1946) which becomes important above  $\sim 2000$  K.

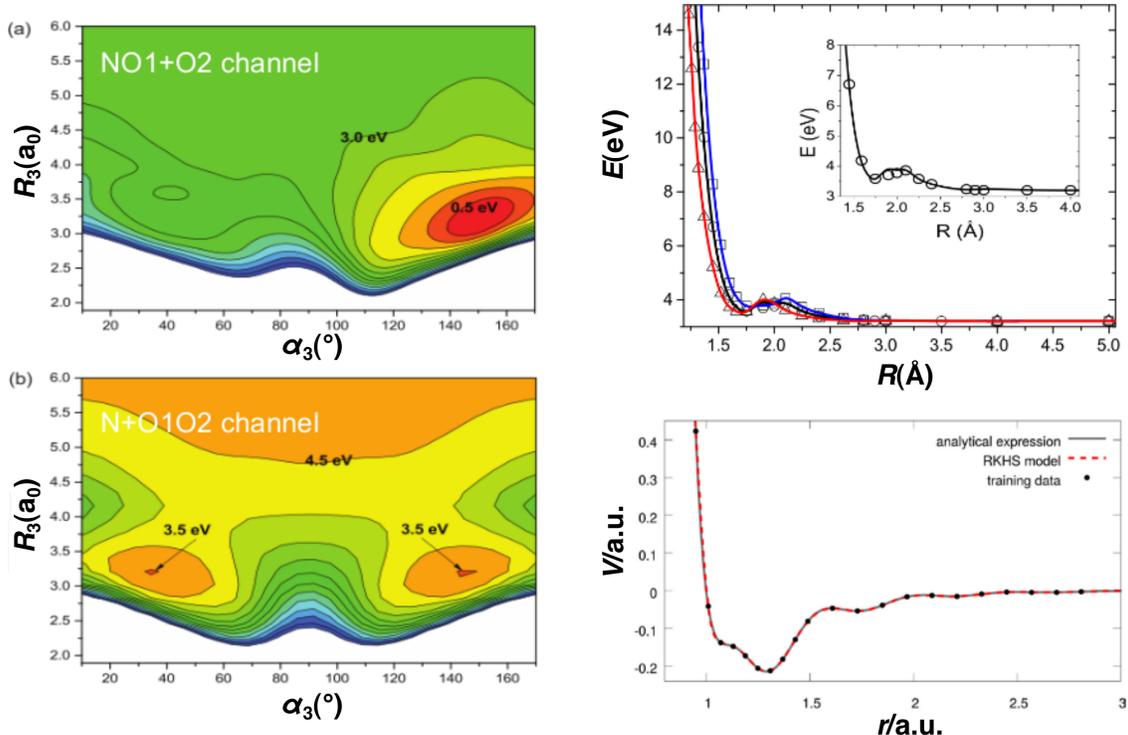


Figure 3: Contour plots for the NO1+O2 (panel a) and O2O1+N (panel b) grids in  $R_1$ ,  $\alpha_1$  and  $R_3$ ,  $\alpha_3$  Jacobi coordinates, respectively. The N-O1 ( $r_1$ ) and O2-O1 ( $r_3$ ) distances are  $2.25 a_0$  and the contour levels are separated by 0.5 eV. Panel c: MRCI+Q/cc-pVQZ energies along the  $R$  coordinate for  $r = 1.21 \text{ \AA}$  (N-O1 distance) and  $\alpha = 27.5$ ,  $34.0$  and  $43.1^\circ$  (squares, circles and triangles, respectively). The solid lines are RKHS interpolants. The inset in the graph represents a close-up of the cut for  $\alpha = 34.0^\circ$  which is not used for the RKHS interpolation. Panel d: Performance of the RKHS method for the function  $V(r) = \left(\frac{1}{r^9} - \frac{1}{r^6}\right) (\cos^2(7r) + 1)$ . The RKHS interpolant  $\tilde{f}(\mathbf{x})$  (red dashed line) constructed from the training samples (black dots) is virtually identical to the analytical expression (grey line). Panels a to c and d adapted from Refs.(Castro-Palacio et al., 2014; Unke & Meuwly, 2017).

The potential energy surfaces for this reaction range from Sorbie-Murrell potentials using contracted configuration interaction (CCI) calculations(Gilibert et al., 1993; Bose & Candler, 1997) to an RKHS-interpolated PES (see Figure 3) based on MRCI+Q calculation with large basis sets.(Castro-Palacio et al., 2014) The Sorbie-Murrell potential is based on a diatomics-

in-molecule expansion combined with a many body expansion.(Sorbie & Murrell, 1975; Gilibert et al., 1993) Further along these lines, a DIM-based double many body expansion (DMBE) PES has been developed(Varandas, 2003) and used in QCT simulations.(Caridade & Varandas, 2004) Using this DMBE PES the rate  $k_+(T)$  for the forward reaction ( $\text{N}+\text{O}_2 \rightarrow \text{NO}+\text{N}$ ) was determined from QCT simulations and that for the reverse reaction ( $k_-(T)$  from statistical mechanics. Combining the two, the equilibrium rate  $K(T) = \frac{k_+(T)}{k_-(T)}$  was found to be in good agreement with reference data.(Chase et al., 1985) A shortcoming of this approach is that the forward and reverse rate coefficients were determined using different methods which was done because the low reaction probability requires extensive sampling.

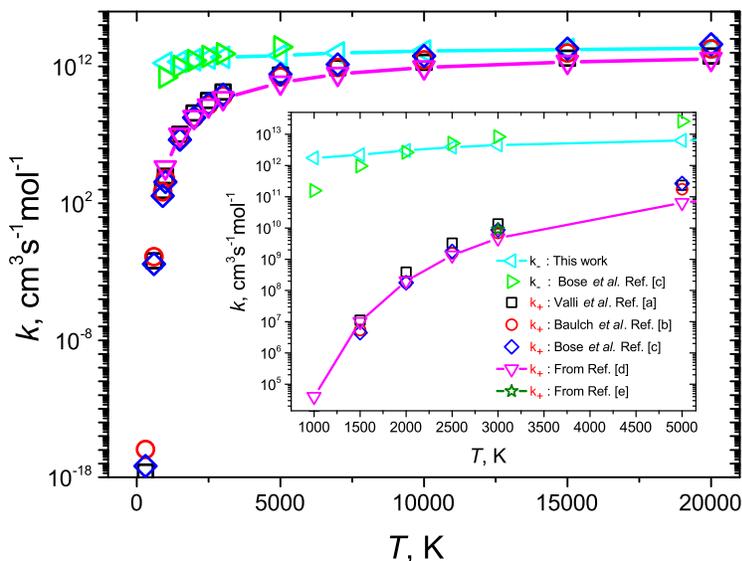


Figure 4: Rate coefficients  $k_-(T)$  (blue open triangles) and  $k_+(T)$  (red open triangles) for the  $\text{NO}(X^2\Pi)+\text{N}(^4S) \leftrightarrow \text{N}_2(X^1\Sigma)+\text{O}(^3P)$  reaction for  $300 \leq T \leq 20000$  K. The inset shows results for  $1000 \leq T \leq 5000$  K. The labels correspond to references: [a]=Ref.(Valli et al., 1995), [b]=Ref.(Baulch et al., 1994), [c]=Ref.(Bose & Candler, 1997), [d]=Ref.(Castro-Palacio et al., 2014), and [e]=Ref.(T. Clark et al., 1969). Figure adapted from Ref.(Castro-Palacio et al., 2015)

Using the fully reactive RKHS-PES,  $k_+(T)$  and  $k_-(T)$  were determined from explicit QCT simulations (Castro-Palacio et al., 2015) and compared with experimental data. A comparison of the forward and reverse rates is provided in Figure 4. For  $k_+(T)$  it is found that an experimentally measured data point at 3000 K (green star) agrees very favorably with the atomistic simulations (magenta) which provide a benchmark for the computations. Comparison of the equilibrium rate  $K(T)$  with those from the CEA database (Gordon & McBride, 1996; McBride, Zehe, & Gordon, 2002) shows very favourable agreement for temperatures  $T > 5000$  K.

For the related  $\text{NO}(X^2\Pi)+\text{N}(^4S) \leftrightarrow \text{N}_2(X^1\Sigma)+\text{O}(^3P)$  reaction fully-dimensional, global potential energy surfaces have also been computed. (Gamallo, Gonzalez, & Sayos, 2003; Lin, Varga, Song, Paukku, & Truhlar, 2016; Denis-Alpizar, Bemish, & Meuwly, 2017) Based on CASPT2 calculations a many-body expansion was fitted and used for variational transition state calculations (Gamallo et al., 2003) and QCT simulations. (Esposito & Armenise, 2017) A more recent effort used a least-squares fit of permutationally invariant polynomials to dynamically scaled MRCI energies. (Lin, Varga, et al., 2016) These PESs have then been used in subsequent QCT simulations. (Lin, Meana-Paneda, Varga, & Truhlar, 2016) This work focused on the scattering process and found that the fraction of NO deflected in the forward direction decreases with increasing collision energy. Complementary to this, RKHS-interpolated PESs based on MRCI+Q calculations were used to determine rate coefficients for different reaction channels for temperatures up to 20000 K, see Figure 4. (Denis-Alpizar, Bemish, & Meuwly, 2017) From the QCT simulations the rates  $k(T)$  for  $5000 \leq T \leq 20000$  can be fit to an Arrhenius expression

$$k^{\text{exch}}(T) = 1.475 \times 10^{-10} \exp(-20907.67/T) \quad (12)$$

and

$$k^{\text{form}}(T) = 1.712 \times 10^{-10} \exp(-7423.430/T) \quad (13)$$

for the exchange and  $\text{N}_2$  formation processes, respectively.

The QCT simulations and quantum wavepacket simulations reveal the non-equilibrium char-

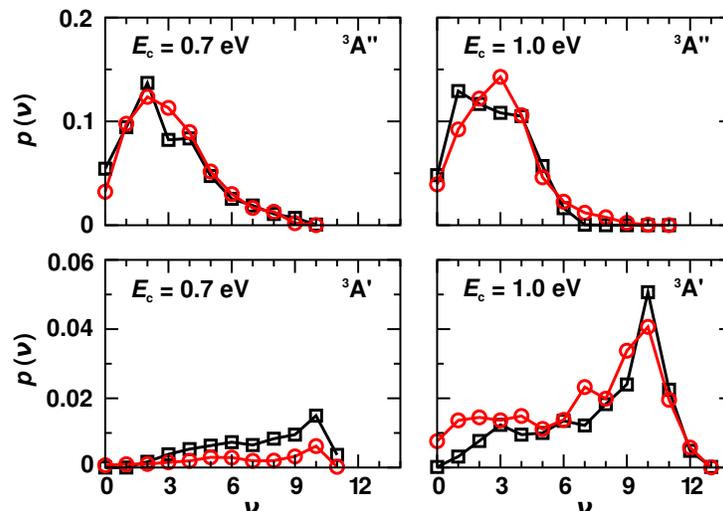


Figure 5: Vibrational energy distribution  $p(\nu)$  for the  $\text{N}_2$  product following the  $\text{NO}(\nu = j = 0) + \text{N} \rightarrow \text{N}_2 + \text{O}$  reaction with  $J = 0$  from time independent (red lines with circles) and QCT (black line with squares) simulations on both PESs,  ${}^3\text{A}'$  and  ${}^3\text{A}''$ . Figure adapted from Ref.(Denis-Alpizar, Bemish, & Meuwly, 2017).

acter of the  $\text{N}_2$ -product state distributions for the vibrational degree of freedom for collisional processes at high temperature. It is also found that quantum effects at such high temperatures are moderate (see Figure 5) and lead to differences in the percent range for product state distributions. Microscopic information about  $k(T)$  and  $p(\nu)$  is essential for the macroscopic modeling of the reactive flow around objects in the hypersonic flight regime.(Martin & Boyd, 2011) More generally, the results on  $\text{N} + \text{NO}$  and  $\text{O} + \text{NO}$  reactive scattering based on RKHS-interpolated PESs from high-level (MRCI+Q or similar) electronic structure calculations together with QCT or quantum dynamics simulations suggest that this is a generic framework to obtain reliable microscopic information under conditions that are difficult or even impossible to probe in a controlled laboratory environment.

*Vibrationally induced reactivity:* Reactions following the excitation of vibrational overtones are potentially relevant in atmospheric chemistry. Experimentally, such processes are challenging to study because preparing molecules in the gas phase with sufficient energy in one of the vibrations is difficult due to the small excitation cross sections for higher excited

states.(Crim, 1993) Hence, computations provide a meaningful complement to such studies.

A particularly topical example is the decomposition of  $\text{HSO}_3\text{X}$  ( $\text{X} = \text{OH}, \text{F}, \text{Cl}$ ) which is of considerable relevance in atmospheric chemistry(Rosen & Hofmann, 1983; Burkholder, Mills, & McKeen, 2000; Hintze, Kjaergaard, Vaida, & Burkholder, 2003; Vaida et al., 2003). It had been assumed that photodissociation of  $\text{H}_2\text{SO}_4$  would proceed via ultraviolet (UV) radiation. However, the electronic absorption spectrum of  $\text{H}_2\text{SO}_4$  above 140 nm could not be found(Burkholder et al., 2000; Hintze et al., 2003; Vaida et al., 2003; Wrenn, Butler, Rowland, Knox, & Phillips, 1999; Robinson, Schofield, & Kjaergaard, 2003) and UV photons with wavelengths shorter than 179 nm are efficiently absorbed at higher altitudes which makes UV photodissociation unlikely to occur at lower altitudes.(Burkholder et al., 2000) This lead to the proposal that vibrational overtone excitation of the OH stretch mode could drive photodissociation of  $\text{H}_2\text{SO}_4$ .(Donaldson, Frost, Rosenlof, & Tuck, 1997; Vaida & Donaldson, 2014)

In a first computational study, the photodissociation dynamics following excitation with  $\nu_9 = 4$  to 6 quanta in the OH-stretching vibration was investigated by semiempirical (PM3) classical trajectory simulations.(Y. Miller & Gerber, 2006) This was followed by extensive MS-ARMD simulations using separate force field parametrizations for the reactant ( $\text{H}_2\text{SO}_4$ ) and product ( $\text{SO}_3 + \text{H}_2\text{O}$ ) states.(Yosa Reyes et al., 2014) The quality of this parametrization, based on MP2/6-311G++(2d,2p) calculations, is reported in Figure 6. From several 1000 independent trajectories with excitations of  $\nu_9 = 4$  to 6 quanta the probability distribution for the reaction time for photodissociation were determined. With increasing excitation of the OH stretch the average reaction times decrease from 19.5 ns for  $\nu_9 = 4$  to 31 ps for  $\nu_9 = 6$ .(Yosa Reyes et al., 2014) Here it is important to note that water elimination from this nonequilibrium ensemble is characterized by a *distribution* of reaction times  $p(\tau)$  which can only be characterized if a statistically significant number of MD trajectories is run.(Yosa & Meuwly, 2011) For this system, 1 ns of *ab initio* MD simulations at the MP2/6-311G++(2d,2p) level of theory would be extremely challenging ( $\sim$  years), depending on the hardware available which is clearly impractical.

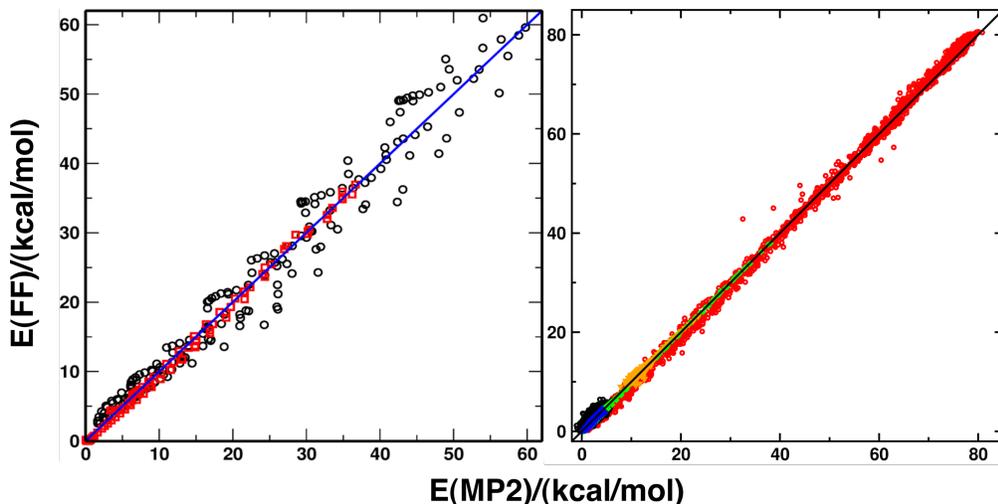


Figure 6: Quality of the reactive force fields for the photodissociation of  $\text{H}_2\text{SO}_4$  (left) and  $\text{HSO}_3\text{F}$  (right). In the left panel, points along the minimum energy paths are red squares and the remaining training points from finite-temperature MD simulations are black circles. In the right panel, the red, black, green, blue and yellow symbols correspond to sampling the  $\nu_{\text{OH}} = 6$  overtone,  $\text{HSO}_3\text{Cl}$  at 300 K, the minimum energy path, the dihedral dynamics, and the  $\text{HCl} + \text{SO}_3$  complex, respectively. Adapted from Refs. (Yosa Reyes et al., 2014, 2016)

## Condensed-Phase Reactions

Originally, (MS-)ARMD has been developed for ligand rebinding reactions in proteins, such as NO- rebinding to Myoglobin (Mb) (Nutt & Meuwly, 2006; Danielsson & Meuwly, 2008) or Histidine binding and unbinding in neuroglobin (Nienhaus, Lutz, Meuwly, & Nienhaus, 2013) using empirical force fields. The purpose was to directly follow the dynamics across the (high-dimensional) transition seam and to avoid treating the ligand-bound and ligand-unbound states separately. (Meuwly et al., 2002) Such a protocol also allows recrossing to take place which is one of the more serious deficiencies of transition state theory. Following the introduction of MS-ARMD (Nagy et al., 2014), the protocol was also combined with RKHS-interpolated PESs for the most important degrees of freedom involved in the reaction. (Soloviov & Meuwly, 2014, 2015) This not only provided the functionality of bond-

breaking and bond-formation but also the necessary accuracy to make direct contact with experiment.(Soloviov, Das, & Meuwly, 2016) Used in this fashion, MS-ARMD with RKHS is akin to a mixed quantum mechanical (QM)/molecular mechanics (MM) approach which treats part of the system with a “high accuracy” method (QM) whereas the remaining degrees of freedom are represented as an empirical force field (MM)(van der Kamp & Mulholland, 2013) The advantage, however, is that the energies and forces in MS-ARMD are evaluated at MM-speed and a statistically significant number of explicit MD simulations can be run due to the dramatically increased speed.

*Nitric Oxide Rebinding in Myoglobin:* A topical application of MS-ARMD/RKHS-simulations is the rebinding of nitric oxide to myoglobin. Nitric oxide is a physiologically relevant ligand(Pacher, Beckman, & Liaudet, 2007; Lundberg et al., 2009; Traylor & Sharma, 1992) which binds reversibly to the heme-active site of Mb. Experimentally, the rebinding kinetics of NO to the heme-group involving the bound  $^2A$  and unbound  $^4A$  states has been studied extensively, including UV/visible(Cornelius, Hochstrasser, & Steele, 1983; Petrich et al., 1991; Ionascu et al., 2005), mid-IR(Kruglik et al., 2010; J. Kim et al., 2012; Yoo et al., 2012; S. Kim, Jin, & Lim, 2004) and resonance Raman(Kruglik et al., 2010) techniques. In all cases the rebinding kinetics is multi-exponential with time constants on the 10 ps time scale and those on the 100 ps time scale.(Petrich et al., 1991; Kruglik et al., 2010; J. Kim et al., 2012; Yoo et al., 2012; Nutt & Meuwly, 2006; Danielsson & Meuwly, 2008)

One of the important protein degrees of freedom in this process is the Fe-out of plane (Fe-oop) motion. Upon ligand dissociation, which changes the iron coordination from octahedral to pyramidal, the iron moves below the plane towards the proximal histidine, His93 in WT Mb. Using a 3-dimensional RKHS-based PES  $V(R, \theta, \phi)$  for the ligand ( $R$  and  $\theta$ ) and Fe-oop ( $\phi$ ) degrees of freedom, the  $^2A$  and  $^4A$  PESs are represented as

$$V(R, \theta, \phi) = \sum_{\lambda=0}^{10} V_{\lambda}(R, \phi)P_{\lambda}(\cos(\theta)) + V_{\text{r}}(\phi) \quad (14)$$

where  $P_{\lambda}$  are Legendre polynomials,  $V_{\lambda}$  are radial strength functions, and  $V_{\text{r}}$  describes the doming in the asymptotic, long range region  $R \rightarrow \infty$  and is represented as a harmonic

potential:

$$V_{\text{lr}}(\phi) = \frac{1}{2}k(\phi - \phi_e)^2 \quad (15)$$

$k$  is the force constant and  $\phi_e$  is the equilibrium position. The radial strength functions  $V_\lambda(R, \phi)$  are represented as a reproducing kernel

$$V_\lambda(R, \phi) = \sum_{i,j} \alpha_{\lambda,i,j} \cdot \mathcal{K}(R, R_i) \cdot \mathcal{G}(\phi, \phi_j) \quad (16)$$

where  $\mathcal{K}(R, R_i)$  is a radial kernel (Ho & Rabitz, 1996; Hollebeek et al., 1999) and  $\mathcal{G}(\phi, \phi_j)$  is a Gaussian kernel. (Hangelbroek & Ron, 2010) The  $\alpha_{\lambda,i,j}$  are coefficients which follow from a singular value decomposition. (Hestenes, 1958; Golub & Kahan, 1965) In parametrized form, the radial reproducing kernels are

$$\mathcal{K}(R, R_i) = \frac{1}{14} r_{>}^{-7} \left( 1 - \frac{7 R_{<}}{9 R_{>}} \right) \quad (17)$$

where  $R_{>}$  and  $R_{<}$  are the greater and smaller distance, respectively, for any pair of  $R$ -values. The Gaussian kernel is defined as

$$\mathcal{G}(\phi, \phi_j) = \exp \left( -\frac{(\phi - \phi_j)^2}{2\sigma} \right) \quad (18)$$

where  $\sigma$  is the width of the kernel.

The force field for the bound and unbound state was validated (Soloviov & Meuwly, 2015) vis-a-vis experimental data from optical spectroscopy. (Lim et al., 1993) After breaking the Fe-NO bond the Fe immediately starts to move below the heme-plane on a  $\sim 100$  fs time scale and the relaxation dynamics extends over several 10 ps. Using the RKHS PES for the unligated state the decay follows a double exponential  $ae^{-t/\tau_1} + be^{-t/\tau_2}$  with  $\tau_1 = 3.5$  ps and  $\tau_2 = 64.4$  ps, as shown in Figure 7. This compares with time constants of  $\tau_1 = 3.5$  ps and  $\tau_2 = 83.0$  ps from the experiments. (Lim et al., 1993) Starting from a thermal ensemble of the ligated MbNO state, a statistically significant number of MS-ARMD rebinding trajectories for the fully hydrated system was run. Each trajectory for which the photodissociated ligand rebinds provides an individual rebinding time from which the fraction of rebound systems,  $N(t)$ , can be determined. The rebinding kinetics on the sub-nanosecond time scale follows a multiexponential decay with two time constants  $\tau_1 \approx 10$  ps and  $\tau_2 \approx 150$  ps, depending on the

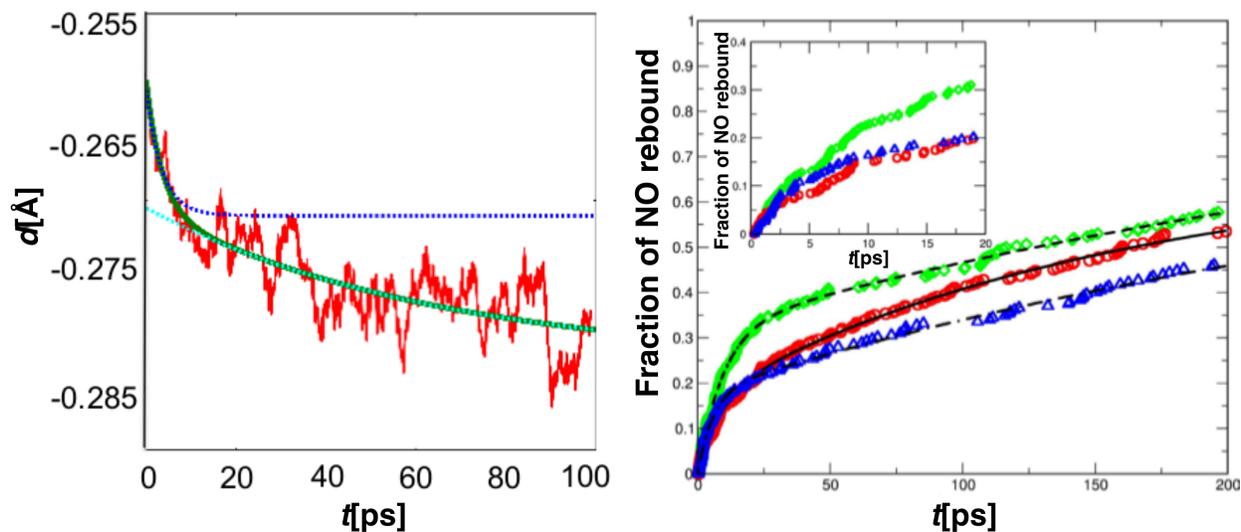


Figure 7: Left: Time dependence of the Fe-oop motion after photodissociation of the ligand and subsequent dynamics on the  $^4A$  PES. The black line is the fit to  $d(t) = ae^{-t/\tau_1} + be^{-t/\tau_2}$  and the blue and green lines are the experimentally determined exponential decays. (Lim et al., 1993) Right: NO-rebinding kinetics depending on the value of the asymptotic separation  $\Delta$ . Adapted from Refs. (Soloviov & Meuwly, 2015; Soloviov et al., 2016)

asymptotic separation  $\Delta$  of the two states which is a conformationally averaged quantity that relates the total energies of the two MS-ARMD/RKHS force fields. (Danielsson & Meuwly, 2008) The value for  $\Delta$  can be approximately calculated from electronic structure calculations but will eventually have to be fitted to reproduce experimental observables. (Danielsson & Meuwly, 2008) For a value of  $\Delta = -6.12$  kcal/mol the rebinding efficiency within 200 ps is  $\sim 55\%$  which compares with a value of 75% from recent XAS measurements on the same time scale. (Soloviov et al., 2016; Silatani et al., 2015) Decreasing the value to  $\Delta = -3.12$  kcal/mol yields quantitative agreement for the rebinding times and the rebound fraction.

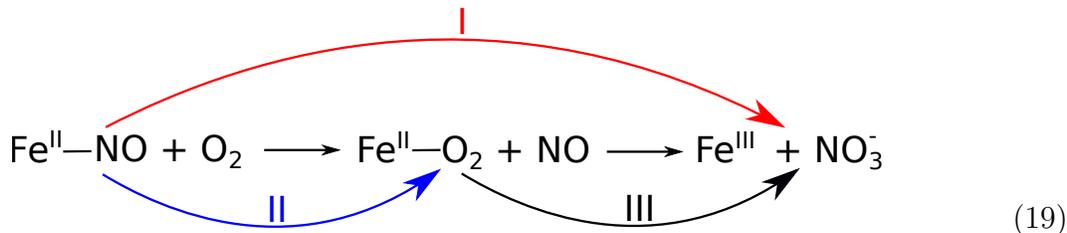
Additional information about structural changes accompanying the ligand binding and unbinding process has been obtained from X-Ray absorption (XAS) experiments. (Silatani et al., 2015) For an ensemble of structures from equilibrium simulations in the bound and unbound states the conformationally averaged XANES spectra and their difference spectrum has been determined. The computed difference spectrum almost quantitatively agrees with the ex-

perimentally measured transient after 50 ps. It had been suggested that such experiments are sensitive to the photodissociated ligand being “close to” or “far away” from the heme-Fe in the active site.(Silatani et al., 2015) However, the simulations demonstrate that such details can not be quantified from the experiments within the signal-to-noise of the experiment.

The real value of such validated MS-ARMD/RKHS-MD simulations is the fact that all structural and dynamical information is available from the aggregate simulations and can be analyzed in view of very specific questions. One of the unresolved points in NO-rebinding to myoglobin was the structural interpretation of the two observed rebinding times on the 10 ps and 100 ps time scale, respectively. Because the transition state of a chemical reaction is metastable with very short lifetime it can usually not be characterized directly using experiments. In the simulations it is, however, possible to cluster trajectories that rebound on particular time scales and investigate common and distinguishing features between them. This was done for NO rebinding to Mb by separately analyzing the ensemble of trajectories that rebound on the 10 ps and 100 ps time scale.(Soloviov et al., 2016) Such an analysis demonstrates that on the short time scale the His64 residue occupies a region away from the heme-iron which leaves the Fe-atom available for NO-rebinding. Contrary to that, for longer rebinding times (100 ps) the entire histidine side chain pushes towards the heme-iron and occludes it. For NO-rebinding to take place the His64 side chain needs to move away from this position. The two discrete states available to the His64 side chain are separated by a free energy barrier of  $\approx 2$  kcal/mol which is consistent with interconversion times of a few hundred picoseconds, observed previously.(Merchant et al., 2003; J. Ma, Huo, & Straub, 1997)

The combination of validated MS-ARMD/RKHS force fields for the  $^2A$  and  $^4A$  states of MbNO with statistically significant sampling of the rebinding dynamics provides a molecularly refined picture of the reactive process and a structural interpretation of the two experimentally known time scales.(Petrich et al., 1991) Directly linking rebinding time scales and structural dynamics from experiment alone appears extremely difficult and quantitative atomistic simulations provide the missing link for this.

*Competitive Ligand Binding in Truncated Hemoglobin N*: MS-ARMD with conventional force fields was recently also applied to the competitive rebinding of NO and O<sub>2</sub> in the active site of truncated Hemoglobin N (trHbN). (Das & Meuwly, 2018) The dioxygenation reaction converts harmful nitric oxide to benign nitrate in bacteria (Poole & Hughes, 2000) and is relevant for NO-detoxification in blood. (Bang et al., 2006; Tinajero-Trejo et al., 2014; Kollau et al., 2016; Carabet, Guertin, Lague, & Lamoureux, 2017) The reaction was first studied for Myoglobin (Mb) (Doyle & Hoekstra, 1981) followed by studies focusing on nitrate formation in other globins using experimental and computational approaches (Eich et al., 1996; Herold, Exner, & Nauser, 2001; Gladwin, Lancaster, Freeman, & Schechter, 2003; Mishra & Meuwly, 2010). From stopped flow experiments, the second order rate constants for the reaction of NO with oxyHb and oxyMb (process III, see equation 19) are  $4.36 \times 10^7$  and  $8.9 \times 10^7$  M<sup>-1</sup> s<sup>-1</sup>, respectively (Eich et al., 1996; Herold et al., 2001; Gladwin et al., 2003).



Because electronic structure calculations for Fe-O<sub>2</sub> complexes are notoriously difficult (Jensen & Ryde, 2004; Franzen, 2002; Kepp, 2013; Siegbahn, Blomberg, & Chen, 2010; Ali, Sanyal, & Oppeneer, 2012) the Fe-NO and Fe-O<sub>2</sub> interactions were parametrized solely on experimental data. (Das & Meuwly, 2018) Based on such a parametrization of the system MS-ARMD and umbrella sampling simulations for the free energy of ligand exchange were carried out. The free energy barrier associated with the  $\text{Fe}^{\text{II}} - \text{NO} + \text{O}_2 \rightarrow \text{Fe}^{\text{II}} - \text{O}_2 + \text{NO}$  reaction is 19.7 kcal/mol, see Figure 8. Using transition state theory, such a barrier corresponds to a rate of  $4.5 \times 10^{-3}$  s<sup>-1</sup> which agrees well with rates from experiments (Process I, see equation 19) ranging from  $1.0 \times 10^{-4}$  to  $4.4 \times 10^{-3}$  s<sup>-1</sup> depending on the protein considered and confirms that the ligand exchange reaction (process II, see equation 19) is the rate limiting step (Ascenzi, Bolognesi, & Visca, 2007; Ascenzi, Gullotta, Gioia, Coletta, & Fasano, 2011).

This is also consistent with the fact that process III ( $\text{Fe-O}_2 + \text{NO} \rightarrow \text{Fe(III)} + \text{NO}_3^-$ ) is fast as it occurs on the 10 to 100 ps time scale (Mishra & Meuwly, 2010).

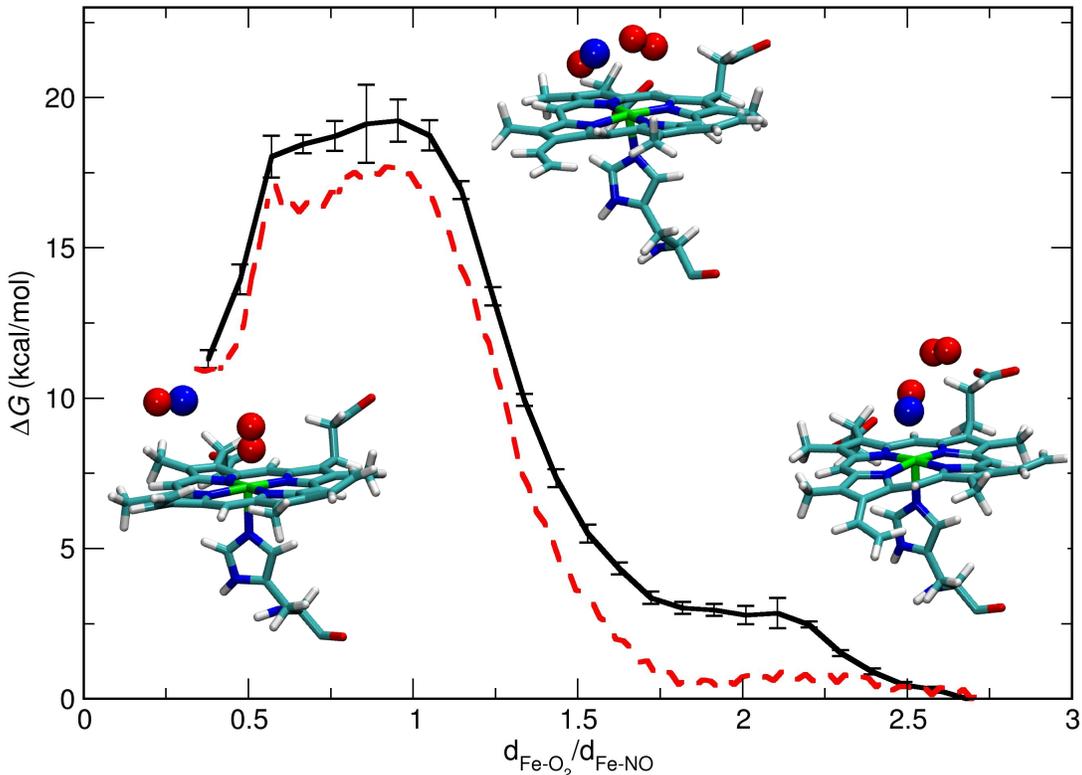


Figure 8: Free energy profile including error bars for the ligand exchange reaction in WT trHbN from umbrella sampling (black trace) along the reaction coordinate  $\rho = \frac{d_{\text{Fe-O}_2}}{d_{\text{Fe-NO}}}$ . The structures of  $\text{O}_2$ -bound ( $\rho = 0.25$ ),  $\text{NO}$ -bound ( $\rho = 2.5$ ) and the transition state ( $\rho \sim 1.0$ ) are also shown. The TS region is broad and involves a distributed structural ensemble. The red dashed line shows the free energy profile for the ligand exchange reaction for the Y33A mutant. Adapted from Ref. (Das & Meuwly, 2018)

Analysis of the structural dynamics of the Gln58 residue between the reactant and the TS suggests that this residue does not participate appreciably in the reaction and hence the overall rate should depend little on mutating this residue. Indeed, experiments find only an insignificant rate increase from  $(2.2 \pm 0.3) \times 10^8 \text{ M}^{-1}\text{s}^{-1}$  (WT) to  $(2.6 \pm 0.4) \times 10^8 \text{ M}^{-1}\text{s}^{-1}$  (Q58A) for nitrate formation. (Koebke, Waletzko, & Pacheco, 2016) Conversely, probability distribution functions for Tyr33 and Val80 differ appreciably between reactant and TS. Con-

comitantly, the rate coefficients increase by more than a factor of two (and hence the free energy barrier decreases by  $\approx 1.7$  kcal/mol based on transition state theory) upon Alanine mutation of these two residues, to  $(4.6 \pm 0.9) \times 10^8 \text{ M}^{-1}\text{s}^{-1}$  and  $(4.7 \pm 0.6) \times 10^8 \text{ M}^{-1}\text{s}^{-1}$ , for the Y33A and V80A mutants, respectively.(Koebke et al., 2016).

Umbrella sampling of the free energy surface and reaction barrier height for ligand exchange in the Y33A mutant find that the barrier height for the  $\text{Fe}^{\text{II}} - \text{NO} + \text{O}_2 \rightarrow \text{Fe}^{\text{II}} - \text{O}_2 + \text{NO}$  reaction is lowered by  $\Delta\Delta G = 1.5$  kcal/mol compared to WT. This result is in quantitative agreement with the value determined from experiment ( $\sim 1.7$  kcal/mol). Hence, the difference between WT and the Y33A mutant can be traced back to the stabilizing interaction between the ligands and the -OH group of the Tyrosine at position 33 in the WT protein which is absent in the Alanine-mutant.

Analysis of the pocket volumes in the TS indicates an expansion by more than 10 % in pocket volume between the WT ( $197 \text{ \AA}^3$ ) and Y33A mutant ( $234 \text{ \AA}^3$ ). This increases entropy and hence reduces the free energy and the barrier for rebinding. The decreased barrier for Y33A may be due to favorable entropic contributions. An enthalpic origin of that magnitude is unlikely due to the small dipole moments of both ligands. This was explicitly verified by computing average interaction energies (over 500 structures from 1 ns simulation in the TS) between the ligand and the surrounding protein which are  $-3.83$  kcal/mol for the WT compared with  $-3.40$  kcal/mol for the Y33A mutant i.e only a difference of  $\Delta H = 0.4$  kcal/mol compared to  $\Delta G = 1.5$  kcal/mol, leaving  $-T\Delta S = 1.1$  kcal/mol for the entropic contribution of the overall process. It is also of interest to note that the interaction energies of the free ligands in the WT reactant (Fe-NO) and product (Fe-O<sub>2</sub>) states are  $-2.7$  and  $-2.8$  kcal/mol, respectively, which suggests that in moving to the transition state a certain amount of entropic penalty is to be paid due to spatial constraints.

## OUTLOOK

Reactive force fields provide molecularly refined interpretations of chemical reactions in the gas and condensed phase. This concerns both, thermodynamic and kinetic aspects of chemical transformations. Despite the successes, the representation and fitting of such FFs is still a laborious process. For routine and broader application in the area of atomistic simulations, improved fitting strategies are required. In the following, a few novel developments based on machine learning (ML) are outlined.

In 1929 Paul Dirac (Dirac, 1929) noted that the (electronic and nuclear) Schrödinger equation (SE) contains all that is necessary to describe chemical phenomena and processes. As the underlying equation (SE) is too complicated to be solved in closed form but for the simplest systems, computational and numerical methods have been devised to find approximate solutions such that meaningful information about a system and/or a process can be obtained. Instead of approximating solutions either by resorting to “mean-field” or “perturbative” solutions within a Density functional Theory (DFT) or *ab initio* electronic structure framework or entirely empirical, parametrized energy functions it may also be possible to exploit the fact that the electronic Hamiltonian  $\hat{H}$  is uniquely determined by the external potential, which in turn depends only on the set of nuclear charges  $\{Z_i\}$  and atomic positions  $\{\mathbf{r}_i\}$  of the system. Providing a sufficiently large number of precomputed data (typically energies) to estimate properties for unknown compounds or structures (Rupp, Tkatchenko, Müller, & Von Lilienfeld, 2012; Montavon et al., 2013; Hansen et al., 2013, 2015) it has become possible to avoid to explicitly but only approximately solving the electronic Schrödinger equation. Instead, a computer system learns to predict energies based on an increasing amount of data.

Artificial neural networks (NNs) (McCulloch & Pitts, 1943; Kohonen, 1988; Abdi, 1994; Bishop, 1995; J. W. Clark, 1999; Ripley, 2007; Haykin, 2009) are a popular class of ML algorithms to tackle computationally demanding problems. (Hinton et al., 2012; Lawrence, Giles, Tsoi, & Back, 1997). Specifically, NNs have been used previously to fit PESs for molecular systems in the spirit of many-body expansions (Manzhos & Carrington Jr, 2006,

2007; Malshe et al., 2009; Handley & Popelier, 2010). While being accurate, they typically involve a large number of individual NNs (one for each term in the many-body expansion), making the method scale poorly for large systems. An alternative approach, known as high-dimensional NN (HDNN) first applied to bulk silicon,(Behler & Parrinello, 2007; Behler, 2011) decomposes the total energy of a system into atomic contributions, which is appealing, because “energy” is an extensive property and it allows to apply the same network to systems of different size.

A conceptually different approach, the deep tensor NN (DTNN)(Schütt, Arbabzadah, Chmiela, Müller, & Tkatchenko, 2017), allows to reuse the same NN to predict energies of systems with different composition across chemical space. Similar to HDNNs, DTNN accumulates atomic energy contributions to predict the total energy  $E_{\text{tot}}$ . More recently, the SchNet architecture was proposed(Schütt, Kindermans, et al., 2017), which improves upon the DTNN. When trained on 100k reference structures, SchNet predicts the energy of structures in the QM9 dataset(Ramakrishnan, Dral, Rupp, & Von Lilienfeld, 2014) with a mean average error (MAE) of 0.34 kcal mol<sup>-1</sup>.

Using a strictly local chemical descriptor, a NN-based method tailored for accurate energy evaluations, which can be applied to construct PESs for nonreactive and reactive dynamics of chemically heterogeneous systems in the condensed phase, has been introduced.(Unke & Meuwly, 2018) Such a NN trained on 100k reference structures can learn to accurately predict energies of structures in the QM9 dataset(Ramakrishnan et al., 2014) across chemical space with a MAE of 0.41 kcal/mol which is only slightly worse than that of the SchNet architecture(Schütt, Kindermans, et al., 2017) (MAE of 0.34 kcal/mol). Contrary to SchNet, this NN is considerably more efficient because a local descriptor is used and the network architecture is much simpler. In addition, the approach was also applied to 100k reference structures from a reactive MD simulation of malonaldehyde. It was found that they can be reproduced with mean average errors between 0.1 and 0.4 kcal/mol. As forces can also be evaluated it will be possible to train NN for reactive MD simulations. However, it should be remembered that developing NN-based energy functions depends on the availability of

massive amounts of training data (typically  $10^5$  or more reference energies are required).

Similar to a combination of RKHS-based and empirical FFs together with MS-ARMD to combine accurate representations of intermolecular interactions and the possibility to follow chemical reactions it may be possible to combine NN-based techniques with empirical FFs. Further applications of reactive FFs include the study of electron or proton transfer reactions. Both processes can be cast within the framework of MS-ARMD (Huang, Buchowiecki, Nagy, Vanicek, & Meuwly, 2014; Karandashev et al., 2017) but alternative techniques have also been employed. Typical applications are the investigation of the change in the solvent structure around metal-complexes (Szymczak, Hofmann, & Meuwly, 2013; Das, Solomon, Hofmann, & Meuwly, 2016; Jin et al., 2016; Das & Meuwly, 2017; Worner et al., 2017) or the spectroscopic signatures accompanying proton transfer (Vendrell, Gatti, & Meyer, 2007; Bowman, Carrington, & Meyer, 2008; Vendrell, Gatti, & Meyer, 2009; Yang & Meuwly, 2010; Huang et al., 2012; Howard, Kjaergaard, Huang, & Meuwly, 2015; Mackeprang et al., 2016; Xu & Meuwly, 2017), or the energetics of proton transfer in proteins (Lutz, Tubert-Brohman, Yang, & Meuwly, 2011). A field by itself is the investigation of proton transfer in bulk water for which a myriad of FF-based techniques have been developed (Schmitt & Voth, 1999; Day, Schmitt, & Voth, 2000; J. Kim, Schmitt, Gruetzmacher, Voth, & Scherer, 2002; Day, Soudackov, Cuma, Schmitt, & Voth, 2002; Voth, 2006; Wolf & Groenhof, 2014; Wiedemair, Hitzenberger, & Hofer, 2015). Finally, modern electronic structure methods may pave the way for *ab initio* MD simulations of large systems on extended time scales. They include hypertextor contractions (Hohenstein, Parrish, & Martinez, 2012) or density renormalization group techniques (Chan & Sharma, 2011). This may allow to study complex systems in explicit solvent akin to what is currently possible with semiempirical methods such as DFTB3 (Gaus, Cui, & Elstner, 2011).

In summary, using empirical force fields or energies represented using novel numerical tools (RKHS, permutationally invariant polynomials) in reactive MD simulations provides valuable molecular-level insights into a range of physico-chemical processes of practical relevance. An essential aspect of such studies is the validation of the computational model in view of

available experimental data. Based on this, the field of reactive molecular dynamics simulations will continue to make fundamental contributions to elucidating energetic and structural aspects of reactive processes in the gas- and condensed phase.

## **SIDEBAR: Structural Interpretation of Time Scales**

State-of-the art time resolved experiments (Schotte et al., 2003; Hamm, Helbing, & Bredenbeck, 2008; Ghosh, Ostrander, & Zanni, 2017; R. J. D. Miller, 2014; Ischenko, Weber, & Miller, 2017) provide a wealth of information concerning the time scale and, depending on the analysis, the number of elementary steps involved in a physico-chemical process. However, linking different time scales to distinct spatial processes remains a big challenge. Conversely, atomistic simulations contain the full information concerning the spatio-temporal changes in a system. From this time scales and spatial/structural changes of a process can be related. This has been done, e.g., for 2-dimensional infrared spectroscopy (Lee, Carr, Goellner, Hamm, & Meuwly, 2013) or ligand rebinding to a protein. (Soloviov et al., 2016) As such, quantitatively accurate simulations on an ensemble can provide molecular-level insight that is difficult to obtain from experiment alone. However, for non-equilibrium systems (e.g. highly vibrationally excited  $\text{HSO}_2\text{X}$ ) a structural interpretation of different time scales observed from the reaction kinetics is complicated. This is because here all elementary processes are characterized by distributions of reaction times.

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