

Parameterizing Complex Reactive Force Fields Using Multiple Objective Evolutionary Strategies (MOES). Part 1: ReaxFF Models for Cyclotrimethylene Trinitramine (RDX) and 1,1-Diamino-2,2-dinitroethene (FOX-7)

James P. Larentzos,[†] Betsy M. Rice,[‡] Edward F. C. Byrd,[‡] N. Scott Weingarten,^{*,‡} and James V. Lill[§]

[†]Engility Corporation, High Technology Services Group, U.S. Army Research Laboratory, Aberdeen Proving Ground, Maryland 21005, United States

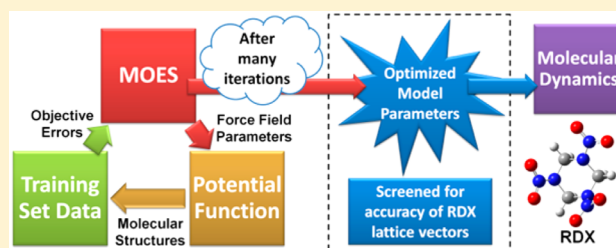
[‡]Energetic Materials Science Branch, Weapons and Materials Research Directorate, U.S. Army Research Laboratory, Aberdeen Proving Ground, Maryland 21005, United States

[§]Engility Corporation, High Technology Services Group, U.S. Air Force Research Laboratory, Wright-Patterson AFB, Ohio 45433, United States

J. Chem. Theory Comput. **2015** DOI: 10.1021/ct5007899

S Supporting Information

ABSTRACT: ReaxFF (van Duin, A.C.T.; Dasgupta, S.; Lorant, F.; Goddard, W.A. *J. Phys. Chem. A*, **2001**, *105*, 9396–9409) reactive potentials are parametrized for cyclotrimethylene trinitramine (RDX) and 1,1-diamino-2,2-dinitroethene (FOX-7) in a novel application combining data envelopment analysis and a modern self-adaptive evolutionary algorithm to optimize multiple objectives simultaneously and map the entire family of solutions. In order to correct the poor crystallographic parameters predicted by ReaxFF using its base parametrization (Strachan, A.; van Duin, A. C. T.; Chakraborty, D.; Dasgupta, S.; Goddard, W. A. *Phys. Rev. Lett.*, **2003**, *91*, 098301), we augmented the existing training set data used for parametrization with additional (SAPT)DFT calculations of RDX and FOX-7 dimer interactions. By adjusting a small subset of the ReaxFF parameters that govern long-range interactions, the evolutionary algorithm approach converges on a family of solutions that best describe crystallographic parameters through simultaneous optimization of the objective functions. Molecular dynamics calculations of RDX and FOX-7 are conducted to assess the quality of the force fields, resulting in parametrizations that improve the overall prediction of the crystal structures.



1. INTRODUCTION

Application of classical molecular dynamics (MD) to chemically reactive systems demands the development of highly accurate reactive force fields capable of reproducing the potential energy surfaces that describe the making and breaking of chemical bonds. While there are numerous reactive potentials of varying complexity that have been developed (e.g., Tersoff,^{1,2} Brenner,³ REBO,⁴ AIREBO⁵), ReaxFF is currently the most general reactive potential used in classical MD simulations of condensed phase materials^{6,7} and has been applied extensively in modeling molecular crystals consisting of carbon, hydrogen, oxygen, and nitrogen. The goal of the developers of ReaxFF was to create a transferable reactive potential that could be used to describe any chemical system composed of any element in the periodic table. ReaxFF was originally developed for hydrocarbon systems⁶ and later extended to systems containing numerous other atomic species,⁸ including oxygen and nitrogen.⁹

Modeling high energy explosive materials (many of which are composed of energetic molecular crystals) at extreme conditions

is of particular interest due to the difficulties of experimentally measuring ultrafast chemical events at high pressures and temperatures. Numerous studies have used ReaxFF to model high energy explosive materials, such as 1,3,5-trinitro-1,3,5-triazine (RDX),^{9–12} octahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine (HMX),¹³ nitromethane (NM),^{11,14} pentaerythritol tetranitrate (PETN),^{11,15} 1,3,5-triamino-2,4,6-trinitrobenzene (TATB),^{11,13} and triacetone triperoxide (TATP).¹⁶ In order to do this, however, the training set used for parametrization of ReaxFF¹⁷ has been extended, and many reparameterizations have resulted.⁸

While development of ReaxFF and other reactive force fields^{3–5} have demonstrated great potential in depicting complex chemical reactions in the condensed phase, the wide-scale adoption of reactive potentials has been hindered by their extremely complicated mathematical structures, the correspond-

Received: August 28, 2014

ingly large numbers of parameters, and the difficulties associated with obtaining suitable values for the parameters in order to simulate the simplest chemical systems. This results in the extreme difficulty of constructing optimized parameter sets for systems of interest that minimize the errors between various quantities predicted by the force fields and the corresponding *ab initio* or experimental values provided in a training set. For ReaxFF, there are >600 parameters for systems containing carbon, hydrogen, oxygen, and nitrogen, making parametrization of these a daunting task.

In order to fit complicated functional forms such as those used in ReaxFF, numerous optimization approaches have been employed including gradient-based approaches,⁶ genetic algorithms,^{18–22} and neural networks.^{23–26} In general, the first task in fitting force fields is to construct a “training set” that consists of sufficient *ab initio* or experimental data, against which calculations will be performed to test the ReaxFF formalism using the candidate parameter sets. These data can include bond energies, bond lengths, bond angles, vibrational frequencies, heats of formation, etc. To date, most parameter optimizations are performed by specifying a single penalty function that consists of a weighted sum of the errors obtained by evaluating the different (noncommensurate) quantities in the training set with the given parametrization. While some of these weights can be rationalized on chemical grounds—for example, giving more weight to barriers along reaction pathways or to equilibrium geometries or to the known crystal structure—any weights that are involved in combining quantities with different dimensions (e.g., bond lengths, configurational energies, partial charges, etc.) must be arbitrary and requires user intervention to tune the optimization. Further, optimization algorithms can obtain very different values for the “best” parameters by choosing different sets of weights.

By contrast, in multiple objective approaches based on the idea of *Pareto dominance*, no arbitrary weights multiplying the various (typically noncommensurate) objectives have to be specified.^{27,28} Rather, such algorithms naturally yield a family of solutions that in principle correspond to all the possible values of the various arbitrary weights. As the name suggests, the idea of *Pareto dominance* is a *relative* measure of the “goodness” of a solution to a multiple objective optimization problem. After evolving a population of solutions to a multiple objective optimization problem, a given solution—that is, a given parameter set—is said to dominate another solution, provided (in the case of minimization) that every objective of the dominant solution is less than or equal to the corresponding objective of the dominated solution, and further that there exists at least one objective of the dominant solution that is strictly less than the corresponding objective of the dominated solution. The set of all nondominated solutions forms the *Pareto Frontier* or *Pareto Optimal Set*^{27–30} and constitutes the “best” solutions (compared to all the dominated solutions) of the multiple objective optimization problem.

Mathematically, the idea of a *Pareto Frontier* is similar to, but more general than, the *Convex Hull*;^{27,31,32} in general the *Pareto Frontier* need not be convex. Because of the nonuniqueness of the weights, there might be several sets of weights that could be consistent with a given fitness as evaluated by *Data Envelopment Analysis*²⁹ (DEA). By construction, solutions on the *Pareto Frontier* express the best ways of balancing the satisfaction of all the objectives that is possible within the current population. Comparing each solution against all the others, the solutions on the frontier have the property that it is impossible to improve one

objective without making at least one other objective worse. However, this is not equivalent to treating all the objectives equally; assigning equal weights to each objective would result in a particular instance of a single objective optimization scheme and yield a single point on the *Pareto Frontier*. Convergence of a multiple objective algorithm therefore not only includes the minimization (for example) of each objective but also the coverage of the *Pareto Frontier*. There are, of course, algorithms for multiple objective optimization that are not based on the idea of *Pareto dominance*;³³ however, detailed comparisons of several methods^{34,35} suggest that the *Pareto-based* methods are superior.^{36,37}

Multiple objective optimization algorithms can also be grouped into *a priori* and *a posteriori* methods.^{38,39} In the former case, the user selects a weight for each objective and forms a weighted sum of the objectives, which is then minimized using a single objective algorithm. In effect, one evolves a population of solutions that samples a single point on the *Pareto Frontier* and yields the best solution at that point. In principal, the *Pareto Frontier* may be reconstructed by repeatedly performing evolutions using randomly varied weights, although multiple sets of weights can yield the same point on the *Pareto frontier*. By contrast, *a posteriori* methods attempt to evolve the entire *Pareto Frontier* at once, and no arbitrary weights for the objectives need ever be specified. A third class of multiple objective methods consist of *progressive* or *guided* algorithms in which the user intervenes in the calculation in order to direct the algorithm in a particular direction.^{38,39} An example of an *a priori* method—GARFField—has recently been applied to the optimization of ReaxFF parameters.²¹ An example of a *progressive* (but nonevolutionary) optimization algorithm is the original method used to parametrize ReaxFF.^{6,17} Here, the user selects one ReaxFF parameter at a time, performs a gradient-based minimization, and then repeats the process with another parameter. The order of the parameters to be optimized, including possible repetitions, is left up to the user. By contrast, the Multiple Objective Evolutionary Strategies (MOES) framework presented in this work is an *a posteriori* method and distinguishes itself from other *a posteriori* methods²² by the marriage of two algorithms: *Evolution Strategies* (ES)^{40–42} and *Data Envelopment Analysis* (DEA).²⁹ While there has been only very limited use of DEA in evolutionary algorithms previously,⁴³ this combination of ES with DEA is the most innovative aspect of our approach. This removes any user-defined selection of arbitrary weights and allows for the selection of a suitable force field for the problem at hand from the family of *Pareto optimal* force fields.

Evolution Strategies is a self-adaptive evolutionary algorithm; a set of strategy parameters evolve simultaneously with the physical parameters. In our problem, each ReaxFF parameter has a corresponding strategy parameter—essentially a standard deviation that gives the magnitude of the random mutations allowed. (If desired, covariances can also be employed to perform correlated mutations of the parameters.) As the population of solutions evolves and the algorithm settles onto some local minimum, all of these standard deviations are driven to zero because any random mutation takes the solution away from the local minimum. These standard deviations must be driven to zero to demonstrate conclusively that the algorithm has converged. One way of looking at ES is that it is similar to *Simulated Annealing*.⁴⁴ But each degree of freedom has its own temperature, and the algorithm determines its own annealing schedules during the course of the computation. In this manner, the ES

algorithm can “adapt itself” to each specific problem, altering the way it searches through parameter space as the solutions evolve.

Our multiple objective algorithm evaluates the fitness by using the so-called “efficiency” computed with DEA. DEA is a specialized application of linear programming^{45,46} that identifies the multiple points on the Pareto Frontier and assigns relative “efficiencies” to all the solutions based on the distance from the Pareto Frontier.²⁹ The typical time required for calculation of the DEA efficiencies is trivial compared with the time required for calculation of the objectives. There are in fact several versions of DEA models that could be applied, some of which assume that the Pareto Frontier is a convex hull. We compute efficiencies using the Free Disposal Hull (FDH) model, which makes no assumptions concerning convexity.²⁹ In testing a variety of DEA models, we found the “FDH efficiencies” are the same as “Pareto efficiencies” in the general case where the Pareto Frontier may or may not be convex.⁴⁷ We will continue to use “DEA” when referring to MOES, but it is understood that all calculations of fitness are performed using the FDH model. The combination of ES with DEA thus provides a natural framework for solving problems in multiple objective parameter optimization. The algorithm is also naturally parallel: First, the objectives of each individual solution in the evolving population can be computed independently. Second, computing the DEA efficiencies involves solving an independent linear problem for each solution in the evolving population.

The goal of this work is to apply MOES to develop force fields suitable for MD simulations of the energetic molecular crystals cyclotrimethylene trinitramine (RDX) and 1,1-diamino-2,2-dinitroethene (FOX-7). It is known that the original parametrization of ReaxFF poorly describes the equilibrium crystal structure of RDX; the developers published a modified form of ReaxFF (i.e., ReaxFF-*lg*¹¹) and parametrized it to dispersion-corrected DFT information to remedy this. However, it is of interest to know whether parameters can be obtained using the original ReaxFF function that would better describe the structure of energetic molecular crystals without the need for inclusion of the dispersion correction given in ReaxFF-*lg*. In this paper, we augment the training set to include highly accurate intermolecular interaction energies for use in the parametrization of the van der Waals terms and EEM terms in ReaxFF. The accompanying paper⁴⁸ will detail MOES parametrization of ReaxFF-*lg*. The general computational approach to fit parameters for the ReaxFF potential is described. This work demonstrates the utility of the MOES approach for fitting potentials by supplementing first-principles data into the training set to tune existing potentials for targeted systems.

2. COMPUTATIONAL APPROACH

2.1. Multiple Objective Evolutionary Strategies (MOES). The algorithm just described has been implemented in the massively parallel Multiple Objective Evolution Strategies (MOES) software package. The MOES program has been parallelized using MPI and runs efficiently on HPC architectures.⁴⁷ The code is constructed using a master–slave approach. The evolution itself (mutation and selection) is performed on the master processor, and all the objectives and DEA efficiencies are computed on the slaves using a “bag of tasks” paradigm.⁴⁹ We have written code to compute the DEA efficiencies using the freely available linear program solver *lpsolve*.⁵⁰

The MOES software was developed to parametrize reactive force fields for use in simulations of the dynamic response of materials involving chemistry. Pareto-based methods such as that

presented here provide a natural⁵¹ technique for balancing the errors of various noncommensurate quantities, such as bond energies, bond lengths, etc. Additional details of the software can be found elsewhere.⁴⁷

The process of optimizing a potential requires various components to communicate with each other in a parallel manner. The overall workflow of the parametrization process is illustrated in Figure 1. The software contains three main components: MOES optimization software, potential function evaluation engine, and training set data.

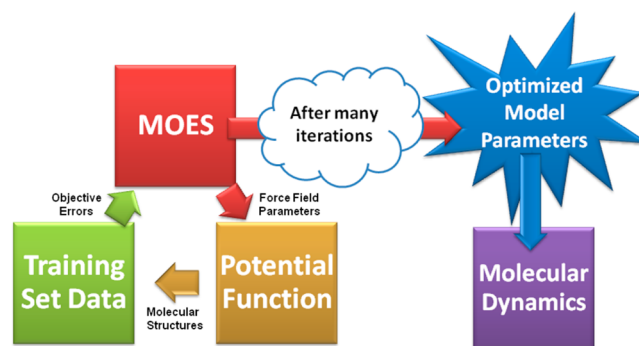


Figure 1. Relation between MOES, ReaxFF potential, training set data, and molecular dynamics simulations.

In general, the process is initiated by providing MOES with an initial parametrization of the potential function. The initial parametrization is typically chosen to be an existing parametrization in the literature and is hereafter referred to as the base parametrization. MOES manipulates the base parametrization according to a set of strategy parameters and creates the first generation of parent and child parametrizations. The energetic and structural properties calculated using ReaxFF and the parametrizations are then compared with the reference data contained within the training set, and the objective errors are computed and returned to MOES. MOES interprets the objective errors and determines how to best manipulate the parametrizations according to its evolving strategy parameters to create a new generation of parametrizations. The process is repeated until convergence is achieved. Once the optimized parametrizations are obtained, a final Pareto analysis is conducted to identify the solutions that lie on the Pareto Frontier. The Pareto efficient solutions are tested via molecular dynamics (MD) simulations to assess the quality of each candidate force field according to a user-defined set of criteria; in this case, crystallographic parameters at the ambient state. Additional details of each component of the parametrization process are provided in the subsections that follow.

2.2. The ReaxFF Force Field. ReaxFF is a general reactive force field used in classical MD simulations of condensed phase materials.^{6,7} The ReaxFF formalism is based on a bond order/bond distance relationship, where contributions to the sigma, pi, and double-pi bonds are computed from the interatomic distances. The bond order is subsequently used to compute various partial energy contributions to the overall system energy, as given by eq 1.

$$E_{\text{Reax}} = E_{\text{bond}} + E_{\text{lp}} + E_{\text{over}} + E_{\text{under}} + E_{\text{val}} + E_{\text{pen}} + E_{\text{coa}} + E_{\text{tors}} + E_{\text{conj}} + E_{\text{H-bond}} + E_{\text{vdW}} + E_{\text{Coulomb}} \quad (1)$$

Table 1. 46 ReaxFF Parameter Values and Bounds for Optimization via MOES

parameter	initial value	bounds
γ_w : vdW gamma; C, H, O, N (4 parameters)	100.0	0.501–100.0
r_{core} : vdW innerwall param; C, H, O, N (4 parameters) with the constraint that O > C > N > H	C: 1.6737	C: 1.3742–1.9684
	H: 1.2669	H: 0.6867–1.3525
	O: 1.7221	O: 1.3142–1.9741
	N: 1.5967	N: 1.2456–2.0437
e_{core} : vdW innerwall param; C, H, O, N (4 parameters)	C: 0.1421	0.005–0.2
	H: 0.0139	
	O: 0.1670	
	N: 0.1649	
a_{core} : vdW innerwall param; C, H, O, N (4 parameters)	C: 14.0707	10.0–20.0
	H: 12.4538	
	O: 13.9991	
	N: 13.9888	
D_{ij} : vdW dissociation energy; C–H, H–O, H–N, C–O, C–N, O–N (6 parameters)	C–H: 0.0464	$\pm 5\%$
	H–O: 0.0403	
	H–N: 0.0524	
	C–O: 0.1028	
	C–N: 0.2070	
	O–N: 0.0491	
r_{vdW} : vdW radius; C–H, H–O, H–N, C–O, C–N, O–N (6 parameters)	C–H: 1.8296	C–H: $\pm 5\%$
	H–O: 1.6913	H–O: $\pm 20\%$
	H–N: 1.7325	H–N: $\pm 10\%$
	C–O: 1.9277	C–O: $\pm 5\%$
	C–N: 1.7366	C–N: $\pm 5\%$
	O–N: 1.7025	O–N: $\pm 5\%$
γ_w : vdW gamma; C–H, H–O, H–N, C–O, C–N, O–N (6 parameters)	C–H: 9.9214	$\pm 5\%$
	H–O: 10.4801	
	H–N: 10.1306	
	C–O: 9.1521	
	C–N: 9.5916	
	O–N: 10.6101	
γ_{ij} : EEM gamma; C, H, O, N (4 parameters)	C, N, O: 0.8712	$\pm 25\%$
	H: 0.8910	
χ_{EEM} : EEM chi; C, H, O, N (4 parameters)	C: 5.7254	1.001–15.0
	H: 3.8446	
	O: 8.5000	
	N: 2.4419	
η_{EEM} : EEM eta; C, H, O, N (4 parameters)	C: 6.9235	1.001–15.0
	H: 10.0839	
	O: 7.1412	
	N: 6.8349	

The partial energy terms account for the bond energy, lone pair energy, corrections for atom overcoordination and undercoordination, valence angle energy including a penalty function, angle conjugation energy, torsion angle energy, torsion conjugation energy, hydrogen bond energy, van der Waals energy, and Coulomb energy. Additional details of the ReaxFF potential can be found in van Duin et al.⁶ and Chenoweth et al.⁵²

The equations for the entire ReaxFF potential are outlined in the Supporting Information of Chenoweth et al.⁵² In all, there are >600 parameters for a system containing carbon, hydrogen, oxygen, and nitrogen. In this work, we focus on varying only a subset of the parameters; specifically, the 46 van der Waals parameters and the charge equilibration (EEM) parameters are varied.

The energy of the vdW term is expressed as a function of r_{ij} , the separation distance between atoms i and j

$$E_{vdW} = \text{Tap}$$

$$\times \left\{ \begin{aligned} & D_{ij} \times \exp \left[\alpha_{ij} \times \left(1 - \frac{f_{13}(r_{ij})}{r_{vdW}} \right) \right] \\ & - 2 \times \exp \left[\frac{1}{2} \times \alpha_{ij} \times \left(1 - \frac{f_{13}(r_{ij})}{r_{vdW}} \right) \right] \\ & + e_{core} \times \exp \left[a_{core} \times \left(1 - \frac{r_{ij}}{r_{core}} \right) \right] \end{aligned} \right\} \quad (2)$$

$$f_{13}(r_{ij}) = \left[r_{ij} + \left(\frac{1}{\gamma_w} \right)^{p_{vdW1}} \right]^{1/p_{vdW1}} \quad (3)$$

where Tap is a taper function, D_{ij} , α_{ij} , r_{vdW} , γ_w and p_{vdW1} are the van der Waals energy, distance, and shielding parameters defined

in Chenoweth et al.⁵² The e_{core} , a_{core} , and r_{core} parameters are the inner wall energy and distance parameters.

The Coulomb energy is expressed as

$$E_{\text{Coulomb}} = \text{Tap} \times C \times \frac{q_i \times q_j}{[r_{ij}^3 + (1/\gamma_{ij})^3]^{1/3}} \quad (4)$$

where C is a unit conversion constant, q_i and q_j are the partial charges of atoms i and j , and γ_{ij} is a Coulomb energy parameter. Atomic charges are calculated using the Electron Equilibration Method (EEM),⁵³ which has an electronegativity parameter, χ_{EEM} , and a hardness parameter, η_{EEM} , associated with it.

MOES is applied to systematically adjust the ReaxFF parameters. During the optimization procedure, the ReaxFF parameters are adjusted to sample a normal distribution around the initial parameter values. The base parametrization was developed for modeling hydrocarbons⁶ and next extended to model nitrogen and oxygen chemistry.⁹ In general, ES algorithms are much less sensitive to the initial parameter values than sequential univariate optimization (i.e., optimizing one parameter at a time in a specified sequence), but the trade-off is that valid ranges for each parameter must be provided to define the size of searchable phase space. Thus, upper and lower bounds are specified, and in some cases, constraints are applied to maintain the physical nature of the parameters (e.g., r_{core} size parameters are constrained to obey the relation $r_{\text{core,O}} > r_{\text{core,C}} > r_{\text{core,N}} > r_{\text{core,H}}$). The upper and lower bounds were determined through a timing analysis in which each parameter was independently varied, while fixing all other parameters to their default values defined within the base parametrization. The wall clock time to evaluate the training set relates to the bonding environment computed by ReaxFF. If a single parameter caused a significant increase in the evaluation time—or in some case, caused the software to crash—it was considered to be an indication of an unphysical bonding environment and thus becomes defined as the upper (or lower) limit to which the parameter is permitted to sample. At a minimum, MOES requires only that each variable be given finite upper and lower bounds in order to start an evolution. The 46 ReaxFF base parametrization values and their optimization bounds are provided in Table 1. Any additional insight about the physical nature of the parameters that can be incorporated into the parameter bounds to further limit the search space would likely have a positive impact on the overall convergence of the algorithm. We have opted not to restrict the MOES search space in favor of enabling the algorithm to naturally evolve to the best solutions, acknowledging that further restriction of the search space is certainly warranted depending on the final system to be studied.

2.3. Description of Training Set. The ReaxFF formalism has been used in extremely large scale computations, but its complexity requires an unusually high degree of expertise in parametrization. ReaxFF has previously been parametrized by van Duin⁶ and Strachan⁹ using a training set of relevant structural and reaction pathway energetic data that encapsulates the various environments that carbon, hydrogen, oxygen, and nitrogen typically experience in the formation and breaking of bonds. The training set is composed of various chemical systems and includes molecular energies, geometries, heats of formation, partial charges, and vibrational frequencies obtained from first-principles quantum mechanical calculations. These are grouped into objectives and are described in Table 2. It is noted that the type of training set objective functions may include alternative

descriptions as described by van Duin¹⁷ and need not be limited to those reported in Table 2.

Table 2. Objectives Used in Parameterizations of ReaxFF with MOES

1	charges	atomic partial charges of various structures
2	geometry	bond lengths, angles and torsions of various structures
3	heat of formation	formation enthalpies of various chemical species
4	energy	reaction pathway and bond dissociation energies of chemical species
5	energy	relative SAPT(DFT) energies of RDX ⁵⁴ and FOX-7 ⁵⁵ dimers

The original training set for ReaxFF^{6,9} was augmented with highly accurate quantum mechanical information on two C–H–N–O energetic molecular crystals, specifically, single-point energy calculations for 1148 RDX dimer configurations⁵⁴ and 938 FOX-7 dimer configurations⁵⁵ using the SAPT (DFT)⁵⁶ description. The augmented training set consists of nearly 3600 reference data points composed of energies and structures (obtained via quantum mechanical calculations). The training set is provided in the Supporting Information (ct500788c_si_001.pdf). Associated with each reference data point is a corresponding weight, as defined in van Duin's *reac* program.¹⁷ Similar reference data points with commensurate dimensions are grouped together (e.g., energies in one group, geometrical data in another group) from which the corresponding objective function (i.e., error) is calculated by

$$\text{Obj}(j) = \sum_{i=1}^{N_{\text{Data}}(j)} \left(\frac{\text{calc}(i) - \text{ref}(i)}{\text{weight}(i)} \right)^2 \quad (5)$$

where j denotes the objective. From this equation, the measure of the fitness of each force field is determined. If a method based on minimizing a single objective had been chosen, an additional set of weights would be defined for each objective, where a single weighted objective would be formed by summing over the products of each objective value and weight. The use of a multiple objective optimization algorithm avoids defining these extra weights for the noncommensurate objectives in Table 2.

Solving the linear programs associated with DEA provides efficiencies for each parameter set in the evolving population; MOES then uses these efficiencies as fitness functions. In principle, one can obtain effective weights for the various objectives that are assigned by each parameter set; these are the “dual” solutions to the “envelopment” linear programs solved by DEA. However, because these linear programs are rectangular—there are many more parameter sets in the evolving population than objectives—the weights obtained are not unique (see the discussion by Cooper, Seiford, and Tone²⁹). After MOES has converged on a final Pareto frontier, we must examine these solutions—in this case using MD simulations—to see which ones offer the best trade-off in satisfying the various objectives.

2.4. Molecular Dynamics Simulations. After generating the Pareto efficient solutions (i.e., families of ReaxFF parameter sets) through MOES, the quality of each parametrization is assessed by performing MD simulations of crystalline α -RDX and crystalline α -FOX-7 under ambient conditions using the LAMMPS simulation software.⁵⁷ Experimental crystal structures for RDX⁵⁸ and FOX-7⁵⁹ were used as initial structures in the MD simulations. The α phase of RDX crystallizes in an orthorhombic lattice with *Pbca* space group symmetry and lattice constants $a =$

13.18 Å, $b = 11.57$ Å, $c = 10.71$ Å. The 3024-atom RDX MD simulations used a supercell composed of a $3 \times 3 \times 2$ array of unit cells, each of which contains eight RDX molecules. The α phase of FOX-7 crystallizes in a monoclinic lattice with $P2_1/n$ space group symmetry and lattice constants $a = 6.94$ Å, $b = 6.637$ Å, $c = 11.341$ Å, $\beta = 90.611^\circ$. The 2688-atom FOX-7 MD simulations used a supercell composed of a $4 \times 4 \times 3$ array of unit cells, each of which contains four $C_2H_4N_4O_4$ molecules. The MD simulations are conducted according to a two-phase protocol. In the first phase, all Pareto efficient solutions are tested by simulating the RDX and FOX-7 models under ambient conditions and comparing the crystal structure to the experimental values. The screening-phase consists of a 1.25 ps MD simulation in the NVE ensemble with velocity rescaling at every step to a temperature of 300 K, followed by a 1.25 ps NVT simulation and subsequent 7.5 ps anisotropic-NPT simulation (1 time step = 0.5 fs). Damping parameters are 0.5 ps for the barostat and 0.05 ps for the thermostat. At the conclusion of the 10.0 ps simulation, the lattice constants are compared to experimental values and a scoring function that sums the absolute percent error of each lattice constant, and the absolute error of each cell angle are evaluated. The Pareto solutions with the best scores for the RDX and FOX-7 structures are selected for further evaluation in the second MD “production” phase. Parameter sets that produce crystal structures that score worse than the base parametrization are rejected and not considered for any further analysis. It is assumed that these parametrizations are unable to produce the correct crystal structure at equilibrium (the achievement of which may take longer than 10.0 ps).

The second “production” phase MD simulations, in which thermodynamic averages are obtained, are conducted in the isothermal–isostress (N σ T) ensemble for 25.0 ps (1 time step = 0.25 fs) to allow volumetric and cell vector fluctuations of the simulation cell. The lattice constants and angles for RDX and FOX-7 are averaged over configurations recorded at 500 time-step intervals (0.125 ps) during the final 10.0 ps and compared to experiment and simulations using the base parametrization.

3. RESULTS

A total of 19 independent evolutions are spawned with MOES to optimize the 46 ReaxFF parameters that correspond to the nonbonded van der Waals energy and EEM (see eqs 2–4) with a training set that was augmented with SAPT(DFT) data describing the intermolecular interactions for RDX dimers and for FOX-7 dimers. The evolving population of each generation consists of $\mu = 100$ parent parametrizations and $\lambda = 400$ child parametrizations. For all parametrizations in the evolving population, DEA²⁹ is employed to assign a numerical score (efficiency), which is a measure of the fitness that is based on the distance between the solution and the Pareto Frontier. At the conclusion of a generation, the parametrizations in the evolving population are ordered according to fitness, and the best 100 parametrizations are retained as parents for the next generation. The maximum lifetime that a given parametrization in the evolving population can have is $\kappa = 10$ generations. In the notation of Evolutions Strategies, these evolutions⁴⁰ would be called $(\mu, \lambda, \kappa) = (100, 400, 10)$ strategies. Over the course of an evolution, a list of the 100 elite solutions with the best efficiencies is accumulated and used for the final Pareto analysis. In combining the 19 independent evolutions, a total of 1900 elite solutions are retained from a total population of 5.7 million and are subjected to the final Pareto analysis. Taking advantage of the explicit parallelization inherent in the MOES software, the

calculations performed in this study averaged 50,000 CPU hours on an average of 200 cores per evolution.

We employ a “mutation-only” strategy in which the child parametrizations are produced through mutation of the parent parametrizations without using any crossover operations. Mutation of the ReaxFF parameters is controlled by a set of MOES “strategy parameters”, which are the standard deviations of the normal distributions around the initial ReaxFF parameters. The standard deviations are initialized at 0.33% of the initial value and do not exceed the parameter boundaries specified in Table 1. The strategy parameters evolve along with the ReaxFF parameters and alter the manner in which the algorithm searches through the space of physical parameters, thus allowing the algorithm to adapt itself. Empirically, we have found that the average of the standard deviations for all the variables provides a convenient measure of convergence of an individual evolution. Commonly seen behavior is an increase in the initial standard deviations as the algorithm examines phase space and then decrease rapidly as the algorithm concentrates upon a local minimum (a representative example is given in Figure 2). As the

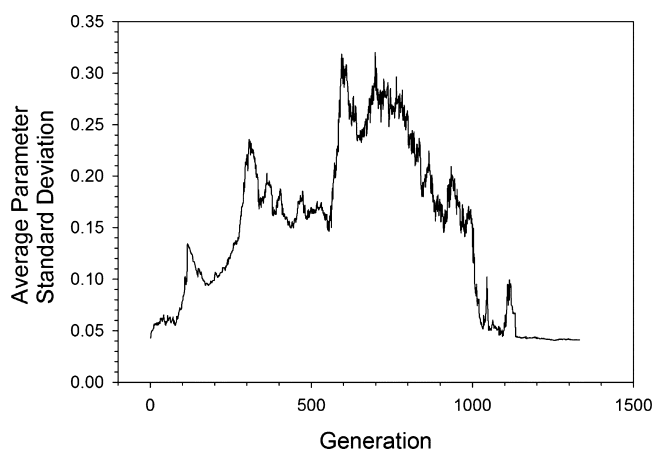


Figure 2. Representative example of the average of the standard deviations of the ReaxFF parameters as a function of generation. The standard deviations are themselves evolving parameters that are used by Evolution Strategies to control the size of the mutations applied to the ReaxFF parameters. We can rationalize the behavior of the average standard deviation in this graph by saying that the standard deviations start at some very small preassigned values and then grow as the evolutionary algorithm explores more and more of parameter space. When the algorithm settles upon some minimum, the standard deviations decrease rapidly—because any mutation then tends to increase the error—indicating convergence.

evolution converges, the standard deviations should approach zero. Convergence is achieved when each of the current best objectives averaged over the solutions on the DEA frontier differ from the corresponding averaged best objectives over the past 50 generations (again averaged over the solutions on the Pareto frontier) by an amount less than 0.001.

After convergence, a final Pareto analysis was performed over all 19 evolutions, and 604 solutions of the 1900 elite solutions were found to lie on the five-dimensional Pareto Frontier surface. For each Pareto efficient parametrization, the five objective values described in Table 2 were compared to the base parametrization objective values (Supporting Information, ct500788c_si_002.pdf). In general, the Pareto efficient parametrizations improved the fit to at least one of the geometry, heat of formation, or the RDX/FOX-7 SAPT(DFT) energy

Table 3. Average RDX and FOX-7 Lattice Constants of Parameterizations Obtained from Screening Objective Functions

		parameterization ID							
		17	202	203	246	392	602	base	expt ^{58,59}
RDX									
	<i>a</i>	13.78	12.85	13.44	13.78	12.77	13.37	13.30	13.18
	<i>b</i>	12.06	10.87	12.10	12.83	10.77	11.82	11.93	11.57
	<i>c</i>	11.94	13.58	11.89	11.25	13.58	12.41	12.43	10.71
	α	89.58	90.35	89.88	90.08	89.82	89.92	90.05	90.00
	β	89.76	89.69	90.04	84.68	89.62	89.91	90.05	90.00
	γ	89.76	89.69	90.04	84.68	89.62	89.91	90.22	90.00
	score	1.10	1.32	0.38	10.92	1.31	0.45	0.52	
density % error	−17.7	−13.9	−15.5	−16.5	−12.5	−16.7	−17.2		
FOX7									
	<i>a</i>	6.99	7.03	7.68	7.01	7.14	6.89	6.96	6.94
	<i>b</i>	6.39	6.26	8.21	6.36	7.75	6.26	6.44	6.64
	<i>c</i>	11.93	11.85	9.30	11.94	9.71	11.93	11.91	11.34
	α	99.00	81.49	89.64	81.02	90.08	90.12	90.19	90.00
	β	89.28	90.01	89.64	89.82	90.58	89.90	89.83	90.61
	γ	89.28	90.01	89.64	89.82	90.58	89.90	89.83	90.00
	score	11.15	9.24	2.21	10.06	1.03	1.05	1.22	
density % error	0.5	2.4	−10.9	0.6	−2.8	1.5	−2.2		

Table 4. Average RDX and FOX-7 Lattice Constants and Cell Angles for Best Performing Parameterizations from RDX Screening Procedure

		parameterization ID						
		48	134	251	366	421	base	expt ^{58,59}
RDX	<i>a</i>	13.28	13.48	13.35	13.74	13.54	13.30	13.18
	<i>b</i>	11.47	11.44	11.49	11.81	11.33	11.93	11.57
	<i>c</i>	11.19	10.61	11.02	10.67	10.54	12.43	10.71
	α	90.01	90.06	89.29	91.42	90.23	90.05	90.00
	β	89.72	90.28	90.04	89.95	89.33	90.05	90.00
	γ	90.68	90.03	89.62	89.10	89.69	90.22	90.00
	score	1.03	0.41	1.18	2.44	1.27	0.52	
	density % error	−4.2	−0.2	−3.4	−5.6	1.0	−17.2	
FOX7	<i>a</i>	7.02	6.33	6.99	6.45	6.94	6.96	6.94
	<i>b</i>	5.62	7.37	5.59	7.53	5.41	6.44	6.64
	<i>c</i>	11.32	10.95	11.33	10.85	11.46	11.91	11.34
	α	89.69	93.64	90.46	88.95	90.01	90.19	90.00
	β	90.33	89.04	89.48	90.94	90.01	89.83	90.61
	γ	90.33	89.04	89.48	90.94	90.01	89.83	90.00
	score	1.09	6.40	2.28	2.57	0.82	1.22	
	density % error	17.0	2.7	18.0	−0.8	21.4	−2.2	

objectives, while none were successful in improving the fit to the charge or reaction pathway energy objectives (objectives 1 and 4, respectively).

A variety of screening techniques are tested to reduce the Pareto efficient parametrizations to those that are most suitable for modeling crystalline RDX and FOX-7 structures. Ultimately, the goal is to find parametrizations that improve the crystal structures of RDX and FOX-7 as compared to the base parametrization. When modeling RDX with the base parametrization, a nearly orthorhombic volume is predicted with a density that is ~17.2% less than experiment. The *a* and *b* lattice constants deviate by less than 0.4 Å from the experiment, but the *c* lattice constant is greatly overpredicted by ~1.7 Å. For FOX-7, the base parametrization predicts a density that is 2.2% less than experiment. The *a* lattice constant is correctly predicted. The *b* lattice constant is 0.2 Å shorter than experiment. The *c* lattice

constant is overpredicted by 0.57 Å. The crystal structure is predicted to be triclinic rather than monoclinic, and the cell angles are observed to deviate by 0.17°–0.78°.

The first screening approach examines the objective functions of each Pareto efficient parametrization. A total of 81.1% (490/604) of the Pareto efficient parametrizations successfully improved the fit to at least one objective function, 28.1% (170/604) improved the fit of at least 2 objective functions and only 1% (6/604) improved the fit of 3 objective functions (Supporting Information, ct500788c_si_002.pdf). These six parametrizations are an obvious choice for further evaluation via NsT molecular dynamics simulations to assess their ability to predict the RDX and FOX-7 crystal structures. The average lattice constants and scores for RDX and FOX-7 are compared to the base parametrization and experimental measurements in Table 3.

Table 5. Average RDX and FOX-7 Lattice Constants and Cell Angles for Best Performing Parameterizations from FOX-7 Screening Procedure

		parameterization ID						
		60	85	130	396	477	base	expt ^{58,59}
RDX	<i>a</i>	12.77	13.05	13.90	13.17		13.30	13.18
	<i>b</i>	10.91	11.29	10.78	11.34		11.93	11.57
	<i>c</i>	13.50	12.36	12.43	12.49		12.43	10.71
	α	90.32	90.29	88.74	89.60		90.05	90.00
	β	90.18	90.82	90.30	89.86		90.05	90.00
	γ	90.18	90.10	90.30	89.86		90.22	90.00
	score	1.03	1.40	2.14	0.87		0.52	
	density % error	−13.2	−10.3	−12.3	−12.4		−17.2	
FOX7	<i>a</i>	6.77	6.67	6.88	6.79	6.80	6.96	6.94
	<i>b</i>	7.22	6.68	6.86	6.92	5.84	6.44	6.64
	<i>c</i>	11.33	11.45	11.44	11.48	11.74	11.91	11.34
	α	90.54	89.89	80.06	89.63	85.47	90.19	90.00
	β	91.87	90.38	91.61	89.87	95.80	89.83	90.61
	γ	91.87	89.70	91.61	89.87	95.80	89.83	90.00
	score	3.78	0.70	12.60	1.32	15.69	1.22	
	density % error	−5.5	2.4	−0.1	−3.2	15.1	−2.2	

According to the scoring function, two of the six parameterizations (parameterizations 203 and 602) are found to improve the RDX crystal structure as compared to the base parameterization. Parameterization 203 produces a nearly orthorhombic crystal structure with a density that is ~15.5% smaller than experiment and is a modest improvement over the base parameterization (17.2% smaller). However, it underpredicts the density for FOX-7 by 10.9% and is considerably worse than the base parameterization. Only parameterization 602 produces a better RDX crystal structure (16.7% smaller density) and FOX-7 crystal structure (1.5% larger density). Through the objective screening approach, modest improvements to the RDX and FOX-7 crystal structures are achieved, but the densities are found to deviate significantly from experiment.

A second screening approach involves testing each of the 604 Pareto efficient parameterizations with a short MD equilibration simulation and selecting those that most closely predict the experimental lattice constants of either of the RDX or FOX-7 target systems. After the equilibration simulations, 212 parameterizations (35.1%) are found to improve the RDX crystal structure and 28 parameterizations (4.6%) are found to improve the FOX-7 crystals structure relative to the equilibrated base parameterization structure (Supporting Information, ct500788c_si_003.pdf and ct500788c_si_004.pdf). It is also noted that 83/604 (13.7%) of the parameterizations are unstable and caused the premature termination of the RDX or the FOX-7 simulations at ambient conditions. This may be due to the conservative parameter bound limits defined in Table 1, where correlation effects between parameters have been neglected. The best five parameterizations that predict the RDX crystal structure and the best five parameterizations that predict the FOX-7 crystal structure after the short MD equilibration simulations are further investigated through NsT MD simulations (Supporting Information, ct500788c_si_005.pdf). The time-averaged lattice constants and cell angles of the best parameterizations obtained from the RDX and FOX-7 screening procedures are compared to the base parameterization and experimental measurements in Tables 4 and 5, respectively.

The best five parameterizations obtained from the RDX screening procedure produce crystal structures that are a significant improvement in terms of density over the base parameterization (Table 4). Parameterization 134 has the best overall score as it matches exceptionally well with experimental lattice constants and has a density that is 0.2% smaller than experiment. The crystal structure deviates slightly from the orthogonal unit cell measured through experiment, where $\beta = 90.28^\circ$. The lattice constants *a*, *b*, and *c* deviate by 0.30, 0.13, and 0.10 Å, respectively. However, this parameterization produces a worse FOX-7 crystal structure, where the *a* and *b* lattice constants deviate by more than 0.6 Å and the cell angles deviate by 1–3.6°. The remaining crystal structures obtained through the RDX screening procedure are all viable solutions, but none are successful in improving the FOX-7 structure relative to the base parameterization in terms of both the scoring function and density error metrics. The best five parameterizations obtained from the RDX screening procedure showed an improvement in the geometry objective, indicating the importance of the structural information in the training set in obtaining the proper crystal structure.

The best five crystal structures from the FOX-7 screening procedure were found to deviate by less than 0.23 Å in the *a*, *b*, and *c* unit cell lengths from the experimental values (Table 5). Parameterization 85 has the best overall score, where it improves the fit to SAPT(DFT) energy objective and predicts the FOX-7 density to within 2.4% of experiment. While the RDX density is within 10.3% of experiment, the RDX score reflects that the shape of the unit cell is worse than that produced by the base parameterization (i.e., β cell angle is 90.82°). Parameterizations 130 and 477 failed to produce viable FOX-7 crystal structures under isostress–isothermal simulation conditions. The remaining parameterizations produce FOX-7 crystal structures that are worse than the base parameterizations.

4. CONCLUSIONS

The MOES software package provides a novel means of fitting interatomic potentials based on evolutionary strategies and has been applied to improve parameterizations of the reactive force

field ReaxFF for use in classical MD simulations of C–H–N–O energetic materials. RDX and FOX-7 SAPT(DFT) data were added to the training set to improve the description of the intermolecular interactions of energetic molecular crystals. The base C–H–N–O parametrization of the ReaxFF potential was modified through the MOES procedure by adjusting a small subset of the parameters that govern nonbonded van der Waals interactions and the EEM.

The quality of the Pareto efficient parametrizations was tested via molecular dynamics simulations to model the crystal structures of RDX and FOX-7. Several screening procedures were applied to search the Pareto efficient solutions for those that give desirable properties of interest for a given target system. In this work, a scoring function composed of the lattice constant errors and cell angle deviations was used to compare the lattice constants and cell angles of the Pareto efficient parametrizations to the base parametrization. It should be noted that the metric used to judge the quality of the force field is completely arbitrary; other criteria than chosen for this study (e.g., molecular structure, molecular orientation, etc.) could just as readily be used to screen the quality of the force fields. Furthermore, depending on the metric, different objective functions will correlate with parametrization performance. It is to be expected that the best parametrizations will shift to different regions of the Pareto surface (i.e., different force field parameters) as alternative screening metrics are applied.

The best performing parametrizations using the imposed fitness criteria resulted in crystallographic parameters that were in outstanding agreement with experiment. However, the best performing force fields suffer from transferability issues for the two molecular systems examined in this work. Some parametrizations showed improvement for both RDX and FOX-7 in comparison with the base parametrization, but in these cases, only modest improvements were observed. As transferability of a model is always desirable, it was hoped that a parametrization would be found that accurately predicts the crystal structures of both RDX and FOX-7, as well as other energetic materials of interest. This aspect will be further examined in an accompanying paper.⁴⁸

While the MOES software has been shown to produce improved parametrizations for targeted systems of interest, there are a number of simulation settings that can be adjusted that may further improve the overall fit to objective functions, the quality of the force fields, and their transferability. For instance, there is no limit on the number of objectives that can be specified in the training set. This work grouped the training set data into five separate objectives that included a combined RDX/FOX-7 SAPT(DFT) energy objective. The second part to this study will examine the effects of separating the RDX/FOX-7 objective into two objectives or including additional objective functions (e.g., vibrational frequencies) to capture important physics of the molecular interactions.⁴⁸

Another MOES setting that warrants further investigation is the number of parameters that are adjusted simultaneously during the fitting process. In this work, 46 parameters were chosen based on what was thought to have the most influence on the intermolecular interactions. The parameter bounds were selected to limit the size of phase space around an initial C–H–N–O base parametrization.

MOES successfully produced Pareto efficient parametrizations that were found to improve the fit to the geometry, heat of formation, and RDX/FOX-7 SAPT(DFT) energy objectives, but none of the Pareto efficient parametrizations were successful in

improving the fit to the charge or reaction pathway energy objectives. Inclusion of different or perhaps additional parameters beyond the 46 adjustable long-range van der Waals and EEM parameters may be necessary to observe improvement in all objective functions and improve the overall transferability. We note that in comparing reaction pathway reference data, the MOES parametrizations were comparable to the base parametrization; this will be explored in further detail in the accompanying paper.⁴⁸

MOES is limited, however, in the number of parameters that can be optimized simultaneously. Experience with smaller test problems has suggested that the size of the evolving population should be approximately eight to ten times the number of evolving parameters, and we have followed that prescription in the larger ReaxFF evolutions. Optimizations of the entire ReaxFF parameter set of 600+ parameters within a multiple objective framework is not computationally feasible given the size of the evolving population and the number of generations required to achieve convergence. In current practice, MOES is limited to optimizing at most ~100 parameters. A parameter reduction technique has recently been proposed by Pahari²⁰ to explore the sensitivity of parameters and reduce the number of parameters to the subset that plays a significant role for the target systems. In their work, they were able to reduce the parameter set from 611 to 51 significant parameters for application of a single-objective genetic algorithm (GA) minimization technique for ReaxFF to nitromethane and its decomposition products. Future studies will be focused on understanding which parameters have the largest influence on the desired properties.

Finally, modifications to the training set data will influence the overall fit. In this work, the training set was supplemented with additional SAPT(DFT) data for dimer interactions of both RDX and FOX-7. However, improvement in the fit might result from inclusion of additional high energy state data to train the parametrization in avoiding unlikely configurations and interactions. Furthermore, additional first principles data of alternative energetic materials may be necessary to help with issues in transferability.

Overall, success has been demonstrated in applying the MOES technique to improve ReaxFF predictions of ambient-state crystal structures of RDX and FOX-7 by adjusting a small subset of the ReaxFF parameters with a modified training set. Ultimately, a good model should be able to improve the crystal structure as well as the orientation and structures of the molecules in the crystal and should be transferable to structures not included in the training or test sets. In the second part of this work (reported in the accompanying paper⁴⁸), the focus goes beyond the prediction of crystal structures and examines the molecular structures and orientations within the unit cell as well as the transferability to other energetic materials. Additional tests will be performed to investigate the influence of the number of objectives, number of parameters, and ReaxFF functional form.

■ ASSOCIATED CONTENT

📄 Supporting Information

Training set, parametrizations, objective values for Pareto efficient parametrizations, and scoring function values for Pareto efficient parametrizations of RDX and FOX-7. This material is available free of charge via the Internet at <http://pubs.acs.org>.

AUTHOR INFORMATION

Corresponding Author

*E-mail: neil.s.weingarten.civ@mail.mil. Phone: (410) 306-0718.

Notes

The authors declare no competing financial interest.

ACKNOWLEDGMENTS

The authors acknowledge Dr. Anthony Yau for insightful discussions regarding ReaxFF and his help in developing the MOES software. Additionally, the authors gratefully acknowledge Prof. Adri van Duin of Penn State University who generously provided a copy of his *reac* program that served as the basis for the ReaxFF training set used by MOES and who offered guidance through numerous insightful discussions. The authors also thank Dr. Shawn Brown of the Pittsburgh Supercomputing Center who performed the initial MPI parallelization of MOES. The authors acknowledge the computational resources and PETTT software support from the DoD High Performance Computing Modernization Program (HPCMP). The HPCMP provided the supercomputing resources under a Computing Challenge Project entitled, "Construction of Accurate Reactive Potentials for Large Scale Molecular Dynamics Simulations." This time was made available at the DoD Supercomputing Resource Centers at the U.S. Army Research Laboratory, Air Force Research Laboratory, and Engineer Research and Development Center. The authors acknowledge support by the Department of Defense HPCMP Software Application Institute for Multiscale Reactive Modeling of Insensitive Munitions.

REFERENCES

- (1) Tersoff, J. *Phys. Rev. Lett.* **1988**, *61*, 2879–2882.
- (2) Abell, G. C. *Phys. Rev. B* **1985**, *31*, 6184–6196.
- (3) Brenner, D. W. *Phys. Rev. B* **1990**, *42*, 9458–9471.
- (4) Brenner, D. W.; Shenderova, O. A.; Harrison, J. A.; Stuart, S. J.; Ni, B.; Sinnott, S. B. *J. Phys.: Condens. Matter* **2002**, *14*, 783–802.
- (5) Stuart, S. J.; Tutein, A. B.; Harrison, J. A. *J. Chem. Phys.* **2000**, *112*, 6472–6486.
- (6) van Duin, A. C. T.; Dasgupta, S.; Lorant, F.; Goddard, W. A. *J. Phys. Chem. A* **2001**, *105*, 9396–9409.
- (7) van Duin, A. C. T.; Strachan, A.; Stewman, S.; Zhang, Q.; Xu, X.; Goddard, W. A. *J. Phys. Chem. A* **2003**, *107*, 3803–3811.
- (8) Jensen, B. D. *Parametric Study of ReaxFF Simulation Parameters for Molecular Dynamics Modeling of Reactive Carbon Gases*. Master's Thesis, Michigan Technological University, 2013. <http://digitalcommons.mtu.edu/etds/643> (accessed June 10, 2014).
- (9) Strachan, A.; van Duin, A. C. T.; Chakraborty, D.; Dasgupta, S.; Goddard, W. A. *Phys. Rev. Lett.* **2003**, *91*, 098301.
- (10) Strachan, A.; Kober, E. M.; van Duin, A. C. T.; Oxgaard, J.; Goddard, W. A. *J. Chem. Phys.* **2005**, *122*, 054502.
- (11) Liu, L.; Liu, Y.; Zybin, S. V.; Sun, H.; Goddard, W. A. *J. Phys. Chem. A* **2011**, *115*, 11016–11022.
- (12) Nomura, K.; Kalia, R. K.; Nakano, A.; Vashishta, P.; van Duin, A. C. T.; Goddard, W. A. *Phys. Rev. Lett.* **2007**, *99*, 148303.
- (13) Zhang, L.; Zybin, S. V.; van Duin, A. C. T.; Dasgupta, S.; Goddard, W. A. *J. Phys. Chem. A* **2009**, *113*, 10619–10640.
- (14) Guo, F.; Cheng, X.; Zhang, H. *J. Phys. Chem. A* **2012**, *116*, 3514–3520.
- (15) Budzien, J.; Thompson, A. P.; Zybin, S. V. *J. Phys. Chem. B* **2009**, *113*, 13142–13151.
- (16) van Duin, A. C. T.; Zeiri, Y.; Dubnikova, F.; Kosloff, R.; Goddard, W. A. *J. Am. Chem. Soc.* **2005**, *127*, 11053–11062.
- (17) van Duin, A. C. T. *ReaxFF User Manual*, 2002. http://www.engr.psu.edu/ADRI/Upload/reax_um.pdf (accessed June 10, 2014).
- (18) Larsson, H. R.; van Duin, A. C. T.; Hartke, B. *J. Comput. Chem.* **2013**, *34*, 2178–2189.
- (19) Angibaud, L.; Briquet, L.; Philipp, P.; Wirtz, T.; Kieffer, J. *Nucl. Instrum. Methods Phys. Res., Sect. B* **2011**, *269*, 1559–1563.
- (20) Pahari, P.; Chaturvedi, S. *J. Mol. Model.* **2012**, *18*, 1049–1061.
- (21) Jaramillo-Botero, A.; Naserifar, S.; Goddard, W. A. *J. Chem. Theory Comput.* **2014**, *10*, 1426–1439.
- (22) Handley, C. M.; Deeth, R. J. *J. Chem. Theory Comput.* **2012**, *8*, 194–202.
- (23) Hunger, J.; Huttner, G. *J. Comput. Chem.* **1999**, *20*, 455–471.
- (24) Prudente, F. V.; Acioli, P. H.; Neto, J. J. S. *J. Chem. Phys.* **1998**, *109*, 8801–8808.
- (25) Skinner, A. J.; Broughton, J. Q. *Modelling Simul. Mater. Sci. Eng.* **1995**, *3*, 371–390.
- (26) Saad, D.; Rattray, M. *Phys. Rev. Lett.* **1997**, *79*, 2578–2581.
- (27) Deb, K. *Multi-Objective Optimization using Evolutionary Algorithms*; Wiley: New York, 2001.
- (28) Zitzler, E. *Evolutionary Algorithms for Multiobjective Optimization: Methods and Applications*. Ph.D. Dissertation, Swiss Federal Institute of Technology (ETH), Zurich, November 1999. <http://www.tik.ee.ethz.ch/~sop/publicationListFiles/zitz1999a.pdf> (accessed June 10, 2014).
- (29) Cooper, W. W.; Seiford, L. M.; Tone, K. *Data Envelopment Analysis: A Comprehensive Text with Models, Applications, References and DEA-Solver Software*; Kluwer: Boston, 2000.
- (30) Coello Coello, C. A.; Lamont, G. B.; van Veldhuizen, D. A. *Evolutionary Algorithms for Solving Multi-Objective Problems*, 2nd ed.; Springer: New York, 2007.
- (31) de Berg, M.; van Kreveld, M.; Overmars, M.; Schwarzkopf, O. *Computational Geometry: Algorithms and Applications*, 3rd ed.; Springer Verlag: Berlin, 2008.
- (32) Goel, T.; Vaidyanathan, R.; Haftka, R. T.; Shyy, W.; Queipo, N. V.; Tucker, K. *Comput. Methods Appl. Mech. Eng.* **2007**, *196*, 879–893.
- (33) Fonseca, C. M.; Fleming, P. J. *Evol. Comput.* **1995**, *3*, 1–16.
- (34) Zitzler, E.; Deb, K.; Thiele, L. *Evol. Comput.* **2000**, *8*, 173–195.
- (35) Zitzler, E.; Deb, K.; Thiele, L. Comparison of Multiobjective Evolutionary Algorithms on Test Functions of Different Difficulty. In *Proceedings of the GECCO-1999 Genetic and Evolutionary Computation Conference*; Banzhaf, W., Daida, J., Eiben, A. E., Garzon, M. H., Honavar, V., Jakiela, M., Smith, R. E., Eds.; Morgan Kaufmann: Orlando, FL, 1999.
- (36) Zitzler, E.; Thiele, L. *An Evolutionary Approach for Multiobjective Optimization: The Strength Pareto Approach*; Computer Engineering and Networks Laboratory (TIK) Report 43; Swiss Federal Institute of Technology (ETH): Zurich, 1998.
- (37) Zitzler, E.; Laumanns, M.; Thiele, L. *SPEA2: Improving the Strength Pareto Evolutionary Algorithm*; Computer Engineering and Networks Laboratory (TIK) Report 103; Swiss Federal Institute of Technology (ETH): Zurich, 2001.
- (38) Nicolaou, C. A.; Brown, N.; Pattichis, C. S. *Curr. Opin. Drug Discovery Dev.* **2007**, *10*, 316–324.
- (39) van Veldhuizen, D. A.; Lamont, G. B. *Evol. Comput.* **2000**, *8*, 125–147.
- (40) Bäck, T. *Evolutionary Algorithms in Theory and Practice: Evolution Strategies, Evolutionary Programming, Genetic Algorithms*; Oxford University Press: New York, 1996; p 314.
- (41) Bäck, T.; Schwefel, H. P. *Evol. Comput.* **1993**, *1*, 1–23.
- (42) Schwefel, H. P.; Rudolph, G. Contemporary Evolution Strategies. In *Proceedings of Advances in Artificial Life: Third European Conference on Artificial Life*; Granada, Spain, June 4–6, 1995; Morán, F., Moreno, A., Merelo, J. J., Chacón, P., Eds.; Lecture Notes in Computer Science 929; Springer: Berlin, 1995; pp 891–907.
- (43) Yun, Y.; Nakayama, H.; Tanino, T.; Arakawa, M. A Multi-Objective Optimization Method Combining Generalized Data Envelopment Analysis and Genetic Algorithms. In *IEEE SMC '99 Conference Proceedings*; IEEE: 1999; pp 671–677.
- (44) Kirkpatrick, S.; Gelatt, C. D.; Vecchi, M. P. *Science* **1983**, *220*, 671–680.
- (45) Chvátal, V. *Linear Programming*; W.H. Freeman and Company: New York, 1983.

- (46) Vanderbei, R. J. *Linear Programming: Foundations and Extensions*, 3rd ed.; Springer: New York, 2008.
- (47) Lill, J. V.; Yau, A., *Multiple Objective Evolution Strategies (MOES): A User's Guide to Running the Software*. ARL-CR-0753; Army Research Laboratory: Aberdeen Proving Ground, MD, US, 2014.
- (48) Rice, B. M.; Larentzos, J. P.; Byrd, E. F. C.; Weingarten, N. S.; J. *Chem. Theory Comput.*, 2015; DOI: 10.1021/ct5007899.
- (49) da Silva, F. A. B.; Senger, H. *Parallel Comput.* **2009**, 35, 57–71.
- (50) Berkelaar, M.; Eikland, K.; Notebaert, P. *Lpsolve5.5*, Open Source (Mixed-Integer) Linear Programming System, 2014. <http://sourceforge.net/projects/lpsolve/> (accessed June 10, 2014).
- (51) Zitzler, E.; Thiele, L.; Laumanns, M.; Fonseca, C. M.; Fonseca, V. G. *Performance Assessment of Multiobjective Optimizers: An Analysis and Review*; Computer Engineering and Networks Laboratory (TIK) Report 139; Swiss Federal Institute of Technology (ETH), Zurich, 2002.
- (52) Chenoweth, K.; van Duin, A. C. T.; Goddard, W. A. *J. Phys. Chem. A* **2008**, 112, 1040–1053.
- (53) Mortier, W. J.; Ghosh, S. K.; Shankar, S. *J. Am. Chem. Soc.* **1986**, 108, 4315–4320.
- (54) Podeszwa, R.; Bukowski, R.; Rice, B. M.; Szalewicz, K. *Phys. Chem. Chem. Phys.* **2011**, 13, 16629.
- (55) Taylor, D.; Rob, F.; Rice, B. M.; Podeszwa, R.; Szalewicz, K. *Phys. Chem. Chem. Phys.* **2011**, 13, 16629–16636.
- (56) Williams, H. L.; Chabalowski, C. F. *J. Phys. Chem. A* **2001**, 105, 646–659.
- (57) Plimpton, S. J. *Comput. Phys.* **1995**, 117, 1–19.
- (58) Choi, C. *Acta Crystallogr.* **1972**, B28, 2857–2862.
- (59) Gilardi, R. Cambridge Crystallographic Data Centre (CCDC), 1999, CSD Refcode 127539.