

Learning Everywhere: Pervasive Machine Learning for Effective High-Performance Computation

Geoffrey Fox¹, James A. Glazier¹, JCS Kadupitiya¹, Vikram Jadhao¹,
Minje Kim¹, Judy Qiu¹, James P. Sluka¹, Endre Somogyi¹, Madhav Marathe²,
Abhijin Adiga², Jiangzhuo Chen², Oliver Beckstein³, Shantenu Jha^{4,5}

¹ *Indiana University, Bloomington, IN*

² *University of Virginia, Charlottesville, VA*

³ *Arizona State University, Tempe, AZ*

⁴ *Rutgers, the State University of New Jersey, Piscataway, NJ 08854, USA*

⁵ *Brookhaven National Laboratory, Upton, New York, 11973*

Abstract—The convergence of HPC and data intensive methodologies provide a promising approach to major performance improvements. This paper provides a general description of the interaction between traditional HPC and ML approaches and motivates the "Learning Everywhere" paradigm for HPC. We introduce the concept of "effective performance" that one can achieve by combining learning methodologies with simulation based approaches, and distinguish between traditional performance as measured by benchmark scores. To support the promise of integrating HPC and learning methods, this paper examines specific examples and opportunities across a series of domains. It concludes with a series of open software systems, methods and infrastructure challenges that the Learning Everywhere paradigm presents.

I. INTRODUCTION

This paper explores opportunities at the interface between large-scale simulations, experiment design and control, machine learning (ML including deep learning DL) and High-Performance Computing (HPC). We describe both the current status and possible research opportunities in allowing machine learning to pervasively enhance high-performance computational science. How should one do this and where is it valuable? We focus on research challenges on computing for science and engineering (as opposed to commercial) use cases for both big data and big simulation problems. More details including further citations can be found at [1].

The convergence of HPC and learning methodologies provides a promising approach to major performance improvements. Traditional HPC simulations are reaching the limits of original progress. The end of Dennard scaling of transistor power usage, and the end of Moores Law as originally formulated has yielded fundamentally different processor architectures. The architectures continue to evolve, resulting in highly costly, if not damaging churn in scientific codes that need to be finely tuned to extract the last iota of parallelism and performance. This approach to high-performance scientific computing is simply unsustainable.

In domain sciences such as biomolecular sciences, advances in statistical algorithms and runtime systems have enabled extreme scale ensemble based applications [2] to overcome

limitations of traditional monolithic simulations. However, in spite of several orders of magnitude improvement in efficiency from these adaptive ensemble algorithms, the complexity of phase space and dynamics for modest physical systems, require additional orders of magnitude improvements and performance gains.

In many application domains, integrating traditional HPC approaches with machine learning methods arguably holds the greatest promise towards overcoming these barriers. The need for performance increase underlies the international efforts behind the exascale supercomputing initiatives. We believe that integration of ML into large scale computations (for both simulations and analytics) is a very promising way to get even larger performance gains. Further, it can enable paradigms such as control or steering, and provide a fundamental approach to coarse-graining which is a difficult but essential aspect of the many multi-scale application areas. Papers at two recent workshops BDEC2 [3] and NeurIPS [4] confirm our point of view and our approach is synergistic with the BDEC2 process with its emphasis on new application requirements and their implications for future scientific computing software platforms.

We would like to distinguish between traditional performance measured by operations per second or benchmark scores, from the effective performance that one gets by combining learning with simulation which gives increased performance as seen by the user without changing the traditional system characteristics. This is of particular interest in cases where there is a tight coupling between the learning and simulation components (as outlined below for MLforHPC). The need for significant enhancement in the effective performance of HPC motivates the introduction of a new paradigm in HPC: Learning Everywhere!

Different Interfaces of ML and HPC: We have identified [5], [3] several important distinctly different links between machine learning (ML) and HPC. We define two broad categories: HPCforML and MLforHPC,

- **HPCforML:** Using HPC to execute and enhance ML performance, or using HPC simulations to train ML

algorithms (theory guided machine learning), which are then used to understand experimental data or simulations.

- **MLforHPC:** Using ML to enhance HPC applications and systems

This categorization is related to Jeff Dean’s “Machine Learning for Systems and Systems for Machine Learning” [6] and Matsuoka’s convergence of AI and HPC [7]. We further subdivide **HPCforML** as

- **HPCrunsML:** Using HPC to execute ML with high performance
- **SimulationTrainedML:** Using HPC simulations to train ML algorithms, which are then used to understand experimental data or simulations.

We also subdivide **MLforHPC** as

- **MLautotuning:** Using ML to configure (autotune) ML or HPC simulations. Already, autotuning with systems like ATLAS is hugely successful and gives an initial view of MLautotuning. As well as choosing block sizes to improve cache use and vectorization, MLautotuning can also be used for simulation mesh sizes [8] and in big data problems for configuring databases and complex systems like Hadoop and Spark [9], [10].
- **MLafterHPC:** ML analyzing results of HPC as in trajectory analysis and structure identification in biomolecular simulations
- **MLaroundHPC:** Using ML to learn from simulations and produce learned surrogates for the simulations. The same ML wrapper can also learn configurations as well as results. This differs from SimulationTrainedML as there typically a learnt network is used to redirect observation whereas in MLaroundHPC we are using the ML to improve the HPC performance.
- **MLControl:** Using simulations (with HPC) in control of experiments and in objective driven computational campaigns [11]. Here the simulation surrogates are very valuable to allow real-time predictions.

All 6 topics above are important and pose many research issues. However, in this paper, we focus on topics in MLforHPC, with close coupling between ML, simulations, and HPC. We involve applications as a driver for the requirements and evaluation of the computer science and infrastructure. In researching **MLaroundHPC** we will consider ML wrappers for either HPC simulations or complex ML algorithms implemented with HPC. Our focus is on how to increase effective performance with the learning everywhere principle and how to build efficient learning everywhere parallel systems.

One can view the use of ML learned surrogates as a performance boost that can lead to huge speedups as calculation of a prediction from a trained network, can be many orders of magnitude faster than full execution of the simulation as shown in section III-D. One can reach Exa or even Zetta scale equivalent performance for simulations with existing hardware systems. These high-performance surrogates are valuable in education and control scenarios by just speeding existing simulations. Simple examples are the use of a surrogate to

represent a chemistry potential, or a larger grain size to solve the diffusion equation underlying cellular and tissue level simulations. Development of systematic ML-based coarse-graining techniques in both socio-technical simulations and nano-bio(cell)- tissue layering arises as an important area of research. In general, domain-specific expertise will be needed to understand the needed accuracy and the number of training simulation runs needed.

There are many groups working in MLaroundHPC but most of the work is just starting and not built around a systematic study of research issues as we propose. There is some deep work in building reduced dimension models to use in control scenarios [12]. We look at three distinct important areas: Networked systems with socio-technical simulations, multi-scale cell and tissue simulations, and at a finer scale biomolecular and nanoscale molecular systems.

Molecular sciences has had several successful examples of using ML for autotuning and ML for analyzing the output of HPC simulation data. Several fields have made progress in using MLaroundHPC, e.g., Cosmoflow and CosmoGAN [13] are amongst the better known projects; and the Materials community is actively exploring the uptake of MLControl for the design of materials [3].

This paper does not cover development of new ML algorithms. It advances the understanding of ML, including Deep Learning (DL) in support of MLaroundHPC. Of course, the usage experience is likely to suggest new ML approaches of value outside the MLaroundHPC arena. If one is to use an ML to replace a simulation, then an accuracy estimate is essential and as discussed in III-B there is a need to build on initial work on Uncertainty Quantification (UQ) with ML [14] such as that using dropout regularization to build ensembles for UQ. There are more sophisticated Bayesian methods to investigate. The research must also address ergodicity, viz., have we learned across the full phase space of initial values. Here methods taken from Monte-Carlo arena could be useful as reliable integration over a domain is related to reliable estimates of values defined across a domain. Further much of our learning is for analytic functions whereas much of the existing DL experience is for discrete-valued classifiers of commercial importance.

Section III discusses cyberinfrastructure and computer science questions, section III-B covers UQ for learnt results, while section III-C the infrastructure requirements needed to implement MLforHPC. Section III-D gives a general performance analysis method and applies to current cases, Section IV covers new opportunities and research issues.

II. SCIENCE EXEMPLARS

A. Machine learning for Networked Systems

In this section we describe a hybrid method that fuses machine learning and mechanistic models to overcome the challenges posed by scenarios where data is sparse and knowledge of underlying mechanism is inadequate. Across domains, the two approaches have been compared [15]. The machine learning approach usually needs a large amount of

observation data for training, and does not explicitly account for mechanisms that govern the complex phenomenon. On the other hand, mechanistic models (like agent-based models) result from a bottom-up approach; but they tend to have too many parameters, are compute intensive and hard to calibrate. In recent years, there have been several efforts to study physical processes under the umbrella of theory-guided data science (TGDS), with focus on artificial neural networks (ANN) as the primary learning tool. [16] provides a survey of these methods and their application to hydrology, climate science, turbulence modeling, etc. where the underlying theory can be used to reduce the variance in model parameters by introducing constraints or priors in the model space.

Here we consider a particular class of mechanistic models - network dynamical systems, which have been applied in diverse domains such as epidemiology and computational social science. A network dynamical system is composed of a network where nodes of the network are agents (representing population, computers, etc.) and the edges capture the interactions between them. A popular example of such systems is the SEIR model of disease spread in a social network [17]. The complexity of the dynamics in such a network, due to individual level heterogeneity and interactions, makes it difficult to train a machine learning model that can be generalized to patterns not yet presented in historical data. Completely data driven models cannot discover higher resolution details (e.g. county level incidence) from lower resolution ground truth data (e.g. state level incidence).

Learning from observational and simulation data: Data sparsity is often a challenge for applying machine learning, especially deep learning methods to forecasting problems in socio-technical systems. One example of such problems is to predict weekly incidence in future weeks in an influenza epidemic. In such socio-technical systems, we usually have only limited observational data, e.g. weekly incidence number reported to the Centers for Disease Control and Prevention (CDC). Such data is of low spatial temporal resolution (weekly at state level), not real time (at least one week delay), incomplete (reported cases are only a small fraction of actual ones), and noisy (adjusted several times after being published), thus necessitating a hybrid framework for forecasting by learning from observational and simulation data.

Observations need to be augmented with existing domain knowledge and behavior encapsulated in the agent-based model to inform the learning algorithm. In such hybrid framework, the network dynamical system is used to guide the learning algorithm so that it conforms to the principles (**consistency**). At the same time, the learning algorithm will facilitate model selection in a principled manner. Moreover, the synthetic data goes beyond the observation data, thus helps voiding over-fitting and makes the learned model capable of processing patterns unseen in the observation data (**generalizability**). When the dynamical system is more detailed (e.g. individual level) than the observation data, the hybrid framework allows detailed forecasting (**high resolution**).

Epidemic Forecasting: Simulation trained machine learn-

ing methods can be used for epidemic forecasting. An example of such a framework is DEFSI (Deep Learning Based Epidemic Forecasting with Synthetic Information) proposed in [18]. It consists of (i) a model configuration module that estimates a distribution for each parameter in an agent based epidemic model based on coarse surveillance data; (ii) simulation-generated synthetic training data module which generates high-resolution training data by running HPC simulations parameterized from distributions estimated in the previous module; (iii) a two-branch deep neural network trained on the synthetic training dataset and used to make details forecasts with coarse surveillance data as inputs.

Experimental results show that DEFSI performs comparably or better than the other methods for state level forecasting; and it outperforms the EpiFast method for county level forecasting. See Ref. [1] and citations therein for details.

B. ML for Virtual Tissue and Cellular Simulations

1) *Virtual Tissue Models:* Virtual Tissue (VT) simulations [19] are mechanism-based multi-scale spatial simulations of living tissues that address questions about development, maintenance, damage and repair. They also find application in the design of tissues (tissue engineering) and the development of medical therapies, especially personalized therapies. VT simulations are computationally challenging for a number of reasons: 1) VT simulations are agent-based, with the core agent often representing biological cells. The number of cells in a real tissue is often of the order of 10^8 or more. 2) Agents are often hierarchical, with agents composed of multiple agents at smaller scales. 3) Agents interact strongly with each other, often over significant ranges [20]. 3) Individual agents typically contain complex sub models that control their properties and behaviors. 4) Materials properties may be complex, like the shear thickening or thinning or swelling or contraction of fiber networks. 5) Modeling transport and diffusion is compute intensive. 6) Models are typically stochastic, so predictivity requires many replicas. 7) Simulations involve uncertainty both in model parameters and in model structure. 8) Biological and medical time-series data are often qualitative, semi-quantitative or differential, making their use in classical optimization difficult. 9) VT models often produce movies of configurations over time. 10) Finally, simulating populations can add several orders of magnitude to the computational challenge. It is possible that ML techniques can be used to short circuit implementations at and between scales.

2) *Virtual Tissue Modeling and AI + ML and HPC:* AI can directly benefit VT applications in a number of ways:

- 1) Short-circuiting: The replacement of computationally costly modules with learned analogues.
- 2) Parameter fitting in high dimensional parameter spaces.
- 3) Treating stochasticity in results as information rather than noise.
- 4) Prediction of bifurcations in models.
- 5) Design of maximally discriminatory experiments – predict the parameter sets by which two models can be differentiated.

- 6) Run time backwards, to determine initial conditions that lead to observed endpoints.
- 7) The elimination of short time scales, e.g., short-circuit the calculations of advection-diffusion.
- 8) Generating additional spatial data sets from experimental images.

Representative prior work by Karniadakis [12], Kevrekidis [21] and Nemenman [22] shows that neural networks can reproduce the temporal behaviors of biochemical regulatory and signaling networks. Ref. [23] has shown that networks can learn nonlinear biomechanics simulations of the aorta—being able to predict the stress and strain distribution in the human aorta from the morphology observable with MRI or CT.

C. Machine Learning and Molecular Simulations

1) *Nanoscale simulation:* Despite the employment of the optimal parallelization techniques suited for the size and complexity of the system, nanoscale simulations remain time consuming. In research settings, simulations can take up to several days and it is often desirable to foresee expected overall trends in key quantities; for example, how does the contact density vary as a function of ion concentration in nanoscale confinement or how the peak positions of the pair correlation functions characterizing nanoparticle assembly evolve as the environmental parameters are tuned. Given the dramatic rise in ML and HPC technologies, it is not the question of if, but when, ML can be integrated with HPC to enhance nanoscale simulation methods. Recent years have seen a surge in the use of ML to accelerate material simulation techniques: ML has been used to predict parameters, generate configurations in material simulations, and classify material properties (see Ref [1] and citations therein). At this time, it is critical to understand and develop the software frameworks to build ML layers around HPC to 1) enhance simulation performance 2) enable real-time and anytime engagement, and 3) broaden the applicability of simulations for both research and education (in-classroom) usage.

In the context of nanoscale simulation, an initial set of applications for the MLaroundHPC framework can be the prediction of the structure or correlation functions (outputs) characterizing the nanoscale system over a broad range of experimental control parameters (inputs). MLaroundHPC can enable the following outcomes:

- 1) Learn pre-identified critical features associated with the simulation output.
- 2) Generate accurate predictions for un-simulated state-points (by entirely bypassing simulations).
- 3) Exhibit auto-tunability (with new simulation runs, the ML layer gets better at making predictions).
- 4) Enable real-time, anytime, and anywhere access to simulation results (particularly important for education use).
- 5) No run is wasted. Training needs both successful and unsuccessful runs.

To illustrate these outcomes, we discuss nanoscale simulations aimed at the computation of the structure of ions confined

by surfaces that are nanometers apart which has been the focus of recent experiments and computational studies (see Ref [1] and citations therein). Typically, the entire ionic distribution averaged over sufficient number of independent samples generated during the simulation is a quantity of interest. However, in many important cases, average values of contact density or center density directly relate to important experimentally-measured quantities such as the osmotic pressure [24]. Further, often it is useful to visualize expected trends in the behavior of contact or mid-point density as a function of solution conditions or ionic attributes, before running simulations to explore specific system conditions. It is thus desirable that a “smart” simulation framework provide rapid estimates of these critical output features with high accuracy. MLaroundHPC can enable precisely this as we recently showed that an artificial neural network successfully learns from completed simulation results the desired features associated with the output ionic density profiles to rapidly generate predictions for contact, peak, and center densities in excellent agreement with the results from explicit simulations [25].

2) *Biomolecular simulations:* The use of ML and in particular DL approaches for biomolecular simulations [26] lags behind other areas such as nano-science and materials science [27]. This might be partly due to the difficulty to account for large heterogeneous systems with important interactions at short and long length scales. But it might also indicate that the commonly used classical empirical force fields are surprisingly successful [28] and it is not easy to outperform them at this level of approximation. Therefore, one primary direction of research in this area is to improve the accuracy of the simulation while maintaining the performance of empirical energy functions.

One promising approach is based on work by Behler and Parrinello [29] who devised a NN-based potential that was trained on quantum mechanical DFT energies; their key insight was to represent the total energy as a sum of atomic contributions and represent the chemical environment around each atom by an identically structured NN, which takes as input appropriate symmetry functions that are rotation and translation invariant as well as invariant to exchange of atoms while correctly reflecting the local environment that determines the energy [30]. Based on this work, Gastegger *et al.* [31] used ML to accelerate ab-initio MD (AIMD) to compute accurate IR spectra for organic molecules including the biological Ala_3^+ tripeptide in the gas phase. Interestingly, the ML model was able to reproduce anharmonicities and incorporate proton transfer reactions between different Ala_3^+ tautomers without having been explicitly trained on such a chemical event, highlighting the promise of such an approach to incorporate a wide range of physically relevant effects with the right training data. The ML model was >1000 faster than the traditional evaluation of the underlying quantum mechanical physical equations.

Roitberg *et al.* [32] trained a NN on QM DFT calculations, based on modified Behler-Parrinello symmetry functions. The resulting ANI-1 model was shown to be chemically accurate,

transferrable, with a performance similar to a classical force field, thus enabling ab-initio molecular dynamics (AIMD) at a fraction of the cost of "true" DFT AIMD. Extensions of their work with an active learning (AL) approach demonstrated that proteins in an explicit water environment can be simulated with a NN potential at DFT accuracy [33]. The AL approach reduced the amount of required training data to 10% of the original model [33] by iteratively adding training data calculations for regions of chemical space where the current ML model could not make good predictions. Using transfer learning, the ANI-1 potential was also extended to predict energies at the highest level of quantum chemistry calculations (coupled cluster CCSD(T)), with speedups in the billion.

In general the focus has been on achieving DFT-level accuracy because NN potentials are not cheaper to evaluate than most classical empirical potentials. However, replacing solvent-solvent and solvent-solute interactions, which typically make up 80%-90% of the computational effort in a classical all-atom, explicit solvent simulation, with a NN potential promises large performance gains at a fraction of the cost of traditional implicit solvent models and with an accuracy comparable to the explicit simulations [34], as also discussed above in the case of electrolyte solutions. Furthermore, inclusion of polarization, which is expensive (factor 3-10 in current classical polarizable force fields [35]) but of great interest when studying the interaction of multivalent ions with biomolecules might be easily achievable with appropriately trained ML potentials.

III. INTEGRATING ML AND HPC: BACKGROUND AND OPPORTUNITIES

A primary contribution of this paper is in the categorization, description and examples of the different ways in which ML can enhance HPC (MLforHPC). Before we expound upon MLforHPC and open research issues, we provide a summary status of HPC for ML (beyond the obvious and well-studied use of GPUs for ML).

A. HPC for Machine Learning

There has been substantial community progress here with the Industry supported MLPerf [36] machine learning benchmark activity and Ubers Horovod Open Source Distributed Deep Learning Framework for TensorFlow [37]. We have studied different parallel patterns (kernels) of machine learning applications, looking in particular at Gibbs Sampling, Stochastic Gradient Descent (SGD), Cyclic Coordinate Descent (CCD) and K-means clustering [38]. These algorithms are fundamental for large-scale data analysis and cover several important categories: Markov Chain Monte Carlo (MCMC), Gradient Descent and Expectation and Maximization (EM). We show that parallel iterative algorithms can be categorized into four types of computation models (a) Locking, (b) Rotation, (c) All-Reduce, (d) Asynchronous, based on the synchronization patterns and the effectiveness of the model parameter update. A major challenge of scaling is owing to the fact that computation is irregular and the model size can be huge. At the

meantime, parallel workers need to synchronize the model continually. By investigating collective vs. asynchronous methods of the model synchronization mechanisms, we discover that optimized collective communication can improve the model update speed, thus allowing the model to converge faster. The performance improvement derives not only from accelerated communication but also from reduced iteration computation time as the model size may change during the model convergence. To foster faster model convergence, we need to design new collective communication abstractions. We identify all 5 classes of data-intensive computation[39], from pleasingly parallel to machine learning and simulations. We are investigating how simulations and Big Data can use common programming environments with a runtime based on a rich set of collectives and libraries for a model-centric approach [40], [41].

Parallel Computing: We know that heterogeneity can lead to difficulty in parallel computing. This is extreme for MLaroundHPC as the ML learnt result can be huge factors (10^5 in our initial example[25]) faster than simulated answers. Further learning can be dynamic within a job and within different runs of a given job. One can address by load balancing the unlearned and learnt separately but this can lead to geometric issues as quite likely that ML learning works more efficiently (for more potential simulations) in particular regions of phase space.

B. Uncertainty Quantification for Deep Learning

An important aspect of the use of a learned ML model is that one must learn not just the result of a simulation but also the uncertainty of the prediction e.g. if the learned result is valid enough to be used. This can be explained in the sense of the bias-variance trade-off, which is based on the decomposition of the expected error into two parts: variance and bias. The variance part explains the uncertainty of the model training process due to the randomness in the training algorithms or the lack of representativeness of the training set. A regularization scheme can reduce the variance so that the model complexity is in control and can result in a *smoother* model. However, the regularization approach comes at the cost of an increased amount of bias, which is another term in the expected error decomposition that explains the fitness of the model—by regularizing the model the training algorithm can do only a limited effort to minimize the training error. On the contrary, an unregularized model with a higher model complexity than necessary can also result in a minimal training error, while it suffers from high variance.

Ideally, the bias-variance trade-off can be resolved to some degree by averaging trained instances of an originally complex model. Once these model instances are complex enough to fit the training data set, we can use the averaged predictions as the output of the model. However, averaging many different model instances implies a practical difficulty that one has to conduct multiple optimization tasks to secure a statistically meaningful sample distribution of the predictions. Given the assumption that the model might as well be a complex one

to minimize the bias component (e.g. a deep neural network), the model averaging strategy is computationally challenging.

Dropout has been extensively used in deep learning as a regularization technique [42], but recent researches revisit it as an uncertainty quantification (UQ) tool [43]. The dropout procedure can be seen as an efficient way to maintain a pool of multiple network instances for the same optimization task. It is an efficient ensemble technique as it applies a randomly sampled Bernoulli mask to a layer-wise input unit, thus exposing the optimization process to many differently structured instances of the network.

A set of differently thinned versions of the network can form a sample distribution of predictions to be used as a UQ metric. The dropout-based UQ scheme can provide an opportunity for the MLaroundHPC simulation experiments. As a data-driven model it is reasonable to assume that a better ML surrogate can be found once the training routine sees more examples generated from the simulation experiment. However, creating more examples to train a better ML model is a conflicting requirement as the purpose of training the ML surrogate is to avoid such computation. The UQ scheme can play a role here to provide the training routine with a way to quantify the uncertainty in the prediction—once it is low enough, the training routine might less likely need more data.

C. Machine Learning for HPC

Here we review the nature of the Machine Learning needed for MLforHPC in different application domains. The Machine Learning (ML) load depends on 1) Time interval between its invocations, which will translate into the number of training samples S and 2) size D of data set specifying each sample. This size could be as large as the number of degrees of freedom in simulation or could be (much) smaller if just a few parameters are needed to define simulation. We note two general issues

- There can be very important data transfer and storage issues in linking the Simulations and Machine Learning parts of system. This could need carefully designed architectures for both hardware and software.
- The Simulations and Machine Learning subsystems are likely to require different node optimizations as in different types and uses of accelerators.

D. Science Exemplar: Nanosimulations

In this subsection, using the example of Nanosimulations, we show progress in all areas at the intersection of HPC and ML are having an impact.

In each of two cases below, one is using scikit-learn, Tensorflow and the Keras wrapper for Tensorflow, as the ML subsystem. The papers [25], [8] are using ML to learn results (ionic density at a given location) of a complete simulation

- $D=5$ with the five specifying features as confinement length h , positive valency z_p , negative valency z_n , salt concentration c , and the diameter of the ions d .
- $S=4805$ which 70% of total 6864 runs with 30% of the total runs used for testing.

In [8], one is not asking ML to predict a result as in [25], but rather training an Artificial Neural Net (ANN) to ensure that the simulation runs at its optimal speed (using for example, the lowest allowable timestep dt and "good" simulation control parameters for high efficiency) while retaining the accuracy of the final result (e.g. density profile of ions). For this particular application, we could get away by dividing a 10 million time-step run (10 nanoseconds that is a typical timescale to reach equilibrium and get data in such systems) into 10 separate runs.

- Input data size $D=6$ (1 input uses 64 bits floats and 5 inputs use 32 bits integers - total 224 bits)
- Input number of samples (S) = 15640 (70% training 30% test)
- Hidden layer 1 = 30
- Hidden layer 2 = 48
- Output variables = 3

Creation of the training dataset took = 64 cores * 80 hrs * 5400 simulation runs = 28160000 or 28 million CPU hours on Indiana University's BigRed2 GPU compute nodes. Each run is 10 million steps long, and you use/learn/train ML every 1 million steps (so block size is a million), yielding 10 times more samples than runs.

Generalizing this, the hardware needs will depend on how often you block, to stop and train the network, and then either on-the-fly or post-simulation, use that training to accelerate simulation or evaluate structure respectively. Blocking every timestep will not improve the training as typically, it won't produce a statistically independent data point to evaluate any structure you desire. So you want to block at a timescale that is at least greater than the autocorrelation time dc ; this is, of course, dependent on example you are looking at – and so your blocking and learning will depend on the application. In [25], it is small and dc is 3-5 dt ; in glasses, it can be huge as the viscosity is high; and in biomolecular simulations, it will also depend on the level of coarse-graining and will be different in fully atomistic or very coarse-grained systems.

The training effort will also depend on the input data size D , and the complexity of the relationship you are trying to learn which change the number of hidden layers and nodes per layer. For example, suppose you are tracking a particle (a side atom on a molecule in a typical nanoscale simulation), in order to come up with a metric (e.g. distance between two side atoms on different molecules) to track the diversity of clusters of particles during the self-assembly process. This comes from expectation that correlations between side atoms may be critical to a macroscopic property (such as formation of these particles into a FCC crystal). In this case your D is huge, and your ML objectives may be looking for a deep relationship, and you may have to invoke an ensemble of ANN's and this will change hardware needs.

Scaling of Effective Performance: An initial approach to estimate speedup in a hybrid MLaroundHPC situation is given in [25] for a nano simulation. One can estimate the speedup in terms of four times T_{seq} the sequential execution time of simulation; T_{train} the time for the parallel

execution of simulation to give training data; T_{learn} is the time per sample to train the learning network; and T_{lookup} is the inference time to predict the results of the simulation by using the trained network. In the formula below, N_{lookup} is the number of trained neural net inferences and N_{train} the number of parallel simulations used in training.

$$EffectiveSpeedup S = \frac{T_{seq}(N_{lookup} + N_{train})}{T_{lookup}N_{lookup} + (T_{train} + T_{learn})N_{train}}$$

This formula reduces to the classic simple $\frac{T_{seq}}{T_{train}}$ when there is no machine learning and in the limit of large $\frac{N_{lookup}}{N_{train}}$ becomes $\frac{T_{seq}}{T_{lookup}}$ which can be huge!

There are many caveats and assumptions here. We are considering a simple case where one runs the N_{train} simulations, followed by the learning and then all the N_{lookup} inferences. Further we assume the training simulations are useful results and not just overhead. We also have not properly considered how to build in the likelihood that training, learning and lookup phases are probably using different hardware configurations with different node counts.

IV. OPPORTUNITIES AND RESEARCH ISSUES

Research Issues: In addition to the six categories at the interface of ML and HPC, the research issues we identify reflect the multiple interdisciplinary activities linked in our study of MLforHPC, including application domains described in sections II-A, II-B, II-C1 and II-C2, as well as coarse graining studied in our case for network science and nano-bio areas.

We have identified the following research areas, which can be categorized into Algorithms and Methods (1-5), Applied Math (10), Software Systems (6,7), Performance Measurement and Engineering (8,11).

- 1) Where can application domains use MLaroundHPC and MLautotuning effectively and what science is enabled by this
- 2) Which ML and DL approaches are most relevant and how can they be set up to enable broad user-friendly MLaroundHPC and MLautotuning in domain science
- 3) How can Uncertainty Quantification be enabled and separately study ergodicity (bias) and accuracy issues?
- 4) Is there a new area of algorithmic research focusing on finding algorithms that can be most effectively learnt?
- 5) Is there a general multi-scale approach using MLaroundHPC.
- 6) What are appropriate systems frameworks for MLaroundHPC and MLautotuning. For example, should we wrap micro-services invoked by a Function as a Service environment? Where and how should we enable learning systems? Is Dataflow useful?
- 7) The different characters of surrogate and real executions produce system challenges as surrogate execution is much faster and invokes distinct software and hardware. This heterogeneity gives challenges for parallel computing, workload management and resource scheduling

(heterogeneous and dynamic workflows). The implication for performance is briefly discussed in sections III-A and III-D.

- 8) Scaling applications that are composed of multiple heterogeneous computational (execution) units, and have distinct forms of parallelism that need balanced performance. Consider a workload comprised of N_L learning units, N_S simulation units. The relative number of learning units to simulation units will vary with application and problem type. The relative values will even vary over execution time of the application, as the amount of data generated as a ratio of training data will vary. This requires runtime systems that are capable of real-time performance tuning and adaptive execution for workloads comprised of multiple heterogeneous tasks.
- 9) The application of these ideas to statistical physics problems may need different techniques than those used in deterministic time evolutions.
- 10) The existing UQ frameworks based on the dropout technique can provide the level of certainty as a probabilistic distribution in the prediction space. However, it does not always mean that the quality of the distribution is dependent on the quality/quantity of data. For example, two models with different dropout rates can produce different UQ results. If the goal of UQ in MLaroundHPC context is to supply only an adequate amount of data, we need a more reliable UQ method tailored for this purpose rather than the dropout technique that tends to manipulate the architecture of the model.
- 11) Application agnostic description and definition of effective performance enhancement.

Conclusion: In traditional HPC the prevailing orthodoxy "Faster is Better" has driven the quest for hierarchical parallelism to speeding up single units of works. Relinquishing the orthodoxy of hierarchical parallelism as the primary route to performance is necessary. In fact, there is a need to carefully reconsider discredited approaches, while adopting the new paradigms. The "Learning Everywhere" paradigm in HPC — where the essential idea is that Machine Learning can dramatically improve effective performance by embedding learning methods and approaches in all aspects of the system execution — promises new performance gains.

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