Machine Learning Based Multi-scale Modeling:

How can we construct interpretable and truly reliable models using concurrent learning?

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Outline

- Multi-scale multi-physics modeling
- 2 Concurrent learning
- Molecular modeling
- Reinforced dynamics for the exploration of very high dimensional spaces
- 5 Kinetic model for gas dynamics
- 6 Concluding remarks

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Objective: remove the ad hoc part of the modeling process and use only truly reliable models.



Sequential vs concurrent coupling

• sequential coupling: precompute the macro-scale model using the micro-scale model.

Multi-scale multi-physics modeling

• concurrent coupling: couple the macro-scale and the micro-scale models "on-the-fly".



Figure: schematic of the heterogeneous multi-scale method (E and Engquist 2003)

Difficulty: parametrizing the components needed in the macro-model, using data from the micro-scale model. For problems without separation of scales, this has been an essential obstacle.

Machine learning comes to the rescue

Two objectives:

- multi-scale modeling in situations without scale separation
- interpretable and truly reliable physical models with machine learning

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Sequential vs concurrent learning

Where are the data sets? (It is very expensive to get the data)

- sequential learning: first collect labeled data $\{x_j, y_j\}$, then perform learning
- **concurrent learning**: generate the data set on the fly as learning proceeds

compare with "active learning": having unlabeled data $\{x_j\}$, and decide which ones to label and use them to perform learning

concurrent learning: generate "**optimal data set**" (both unlabeled and labeled, representative enough yet as small as possible)

the latter is a more interactive process

The exploration-labeling-training procedure for concurrent learning

Zhang, Wang and E (2018), J. Chem. Phys.

Start out with no (macro-scale) model, no data; but with a micro-scale model. Repeat the following steps:

- exploration: explore the configuration space, and decide which configurations need to be labeled.
- Iabeling: compute the micro-scale solutions for the configurations that need to be labeled. This is our data set.

Training: train the macro-scale model, and use it to help the exploration Similar to "active learning" but more interactive.....

Concurrent learning

DP-GEN: concurrent learning for uniformly accurate model



Indicator: $\epsilon = \max_i \sqrt{\langle \| f_i - \bar{f}_i \|^2 \rangle}$, $\bar{f}_i = \langle f_i \rangle$ "Active Learning of Uniformly Accurate Inter-atomic Potentials for Materials Simulation." arXiv:1810.11890 (2018).

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Molecular modeling

Example 1: Molecular dynamics

Traditional dilemma: accuracy vs cost.

$$E = E(\boldsymbol{x}_1, \boldsymbol{x}_2, ..., \boldsymbol{x}_i, ..., \boldsymbol{x}_N),$$

$$m_i \frac{d^2 \boldsymbol{x}_i}{dt^2} = \boldsymbol{F}_i = -\nabla_{\boldsymbol{x}_i} E.$$

Two ways to calculate E and F:

• Computing the inter-atomic forces on the fly using QM, e.g. the Car-Parrinello MD. Accurate but expensive:

$$E = \langle \Psi_0 | H_e^{KS} | \Psi_0 \rangle, \ \mu \ddot{\phi}_i = H_e^{KS} \phi_i + \sum_j \Lambda_{ij} \phi_j.$$

• Empirical potentials: efficient but unreliable. The Lennard-Jones potential:

$$V_{ij} = 4\epsilon [(\frac{\sigma}{r_{ij}})^{12} - (\frac{\sigma}{r_{ij}})^6], \ E = \frac{1}{2} \sum_{i \neq j} V_{ij}.$$

Integrating ML with molecular modeling

New paradigm:

- quantum mechanics model data generator
- machine learning parametrize (represent) the model
- molecular dynamics simulator

Interaction potential between atoms in molecular dynamics

Consider a system of N atoms, $\boldsymbol{r} = \{\boldsymbol{r}_1, \boldsymbol{r}_2, ..., \boldsymbol{r}_N\}$.

the coordinate matrix $\mathcal{R} \in \mathbb{R}^{N \times 3}$:

$$\mathcal{R} = \{\boldsymbol{r}_1^T, \cdots, \boldsymbol{r}_i^T, \cdots, \boldsymbol{r}_N^T\}^T, \ \boldsymbol{r}_i = (x_i, y_i, z_i).$$

 r_c : a pre-defined cut-off radius.

For atom *i*, defined its neighbors $\mathcal{N}_{r_c}(i) = \{j | r_{ij} < r_c\}$, and $r_{ji} \equiv r_j - r_i$. Define *i*'s local environment matrix

$$\mathcal{R}^{i} = \{ \boldsymbol{r}_{1i}^{T}, \cdots, \boldsymbol{r}_{ji}^{T}, \cdots, \boldsymbol{r}_{N_{i},i}^{T} \}^{T}, \ \boldsymbol{r}_{ji} = (x_{ji}, y_{ji}, z_{ji}).$$

 $E(\mathcal{R}) \equiv E$: a map from the coordinate matrix to the potential energy;

Molecular modeling

Deep Potential: construction

Structure: composite neural networks (NNs). $E = \sum_{i} E^{i}$.



Models of this type are extensible, which implies linear scaling. Behler, J., Parrinello, M. (2007). Phys. Rev. Lett., 98(14), 146401. Deep Potential (Comm. Comp. Phys. 23.3 (2018): 629-639.), DPMD (Phys. Rev. Lett. 120 (2018), 143001)

Molecular modeling

The importance of preserving the symmetries



Preserving symmetry: Poor man's version

• remove translational and rotational symmetry by fixing a local frame of reference

Molecular modeling

• remove permutational symmetry by fixing an ordering of the atoms in the neighborhood

Creates small discontinuity when atoms switch their orders.



Preserving the symmetries

Translation, rotation, and permutation.

$$\hat{T}_{\boldsymbol{b}}f(\boldsymbol{r}) = f(\boldsymbol{r} + \boldsymbol{b}), \ \hat{R}_{\mathcal{U}}f(\boldsymbol{r}) = f(\boldsymbol{r}\mathcal{U}),$$
$$\hat{P}_{\sigma}f(\boldsymbol{r}) = f(\boldsymbol{r}_{\sigma(1)}, \boldsymbol{r}_{\sigma(2)}, ..., \boldsymbol{r}_{\sigma(N)})$$

• Translation and Rotation:

$$\Omega^i_{jk} = \boldsymbol{r}_{ji} \cdot \boldsymbol{r}_{ki}.$$

Lemma: Ω^i_{jk} is an overcomplete array of basic invariants with respect to rotation, reflection, and translation.

• Permutation:

$$\sum_{j\in\mathcal{N}(i)}g(oldsymbol{r}_{ji})oldsymbol{r}_{ji}.$$

Lemma: A function $f(r_{1i}, ..., r_{ji}, ..., r_{N_i i})$ is invariant to the permutation of instances in r_{ji} , if and only if it can be

decomposed in the form $\rho(\sum_{j \in \mathcal{N}(i)} g(\boldsymbol{r}_{ji}) \boldsymbol{r}_{ji})$, for suitable transformations g and ρ .

Deep potential: smooth version

The whole sub-network consists of an encoding net $\mathcal{D}^i(\mathcal{R}^i)$ and a fitting net $E^i(\mathcal{D}^i)$.

Molecular modeling



(Rotation: $\tilde{\mathcal{R}}^{i}(\tilde{\mathcal{R}}^{i})^{T}$, permutation: $(\mathcal{G}^{i1})^{T}\tilde{\mathcal{R}}^{i}$ and $(\tilde{\mathcal{R}}^{i})^{T}\mathcal{G}^{i2}$.) DeepPot-SE (arxiv: 1805.09003, NIPS 2018), see also Behler and Parrinello, PRL 2007. Molecular modeling

DP-GEN: Automatic generation of deep potentials using concurrent learning

The exploration-labeling-training procedure

- Exploration:
 - Sample the (T,p) space
 - For each value of (T, p), sample the canonical ensemble (using DPMD).
 - In addition, initialize the exploration with a variety of different initial configurations.
- Labeling: Using DFT (with periodic boundary condition)
- Training: Using "deep potential"

Molecular modeling

Systems		Al		Mg		Al-Mg alloy		
Type	Lattice	#atom	#Confs	#Data	#Confs	#Data	#Confs	#Data
Bulk	FCC	32	$15,\!174,\!000$	1,326	$15,\!174,\!000$	860	39,266,460	7,313
	HCP	16	$15,\!174,\!000$	908	$15,\!174,\!000$	760	$18,\!999,\!900$	2,461
	Diamond	16	5,058,000	1,026	5,058,000	543	$5,\!451,\!300$	2,607
	\mathbf{SC}	8	5,058,000	713	5,058,000	234	$2,\!543,\!940$	667
Surface	FCC (100)	12	$3,\!270,\!960$	728	$3,\!270,\!960$	251	$62,\!203,\!680$	1,131
	FCC (110)	$16^{a},\!20^{b}$	$3,\!270,\!960$	838	$3,\!270,\!960$	353	10,744,2720	$2,\!435$
	FCC (111)	12	$3,\!270,\!960$	544	$3,\!270,\!960$	230	$62,\!203,\!680$	1,160
	HCP (0001)	12	$3,\!270,\!960$	39	3,270,960	109	$62,\!203,\!680$	176
	HCP $(10\overline{1}0)$	12	$3,\!270,\!960$	74	3,270,960	167	$62,\!203,\!680$	203
	HCP $(11\overline{2}0)$	$16^{a},\!20^{b}$	$3,\!270,\!960$	293	$3,\!270,\!960$	182	$107,\!442,\!720$	501
sum			60,089,760	$6,\!489$	60,089,760	$3,\!689$	529,961,760	$18,\!654$

^aPure Al

 $^b\mathrm{Mg}$ and Al-Mg alloy

 ${\sim}0.005\%$ configurations explored by DPMD are selected for labeling.

Case 1: accuracy is comparable to the accuracy of the data



Case 2: structural information of DFT water

Radial and angular distribution function of liquid water (PI-AIMD):

Molecular modeling



Distribution of the Steinhardt order parameter \bar{Q}_6 :



Open-source softwares: DeePMD-kit





- TensorFlow: efficient network operators
- LAMMPS, i-PI; MPI/GPU support.

Free download from https://github.com/deepmodeling/deepmd-kit H. Wang,. et al, .Comp.Phys.Comm., 0010-4655 (2018). Molecular modeling

Open-source softwares: DP-GEN



Free download from https://github.com/deepmodeling/dpgen

Molecular modeling

Discussion group

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bbs.deepmd.org

Water phase diagram modeled by DP+SCAN

10

100 150 200 250 300 350 400 450

T (K)



10

150 200 250 300 350 400 450

T (K)

10

100 150 200 250 300 350 400 450

T (K)

Molecular modeling

DP-GEN for water



- **Reference model:** DFT at the classical SCAN level;
- Starting configurations: relaxed Ice I-XV at T = 0 K and equilibrated liquid at T = 330 K;
- Range of thermodynamic conditions: red dashed box;
- **number of MD snapshots:** DPMD exploration: 1.4 billion, DFT calculation: 32 thousand (~0.002% of the former).

Typical AIMD trajectory: 100 thousand snapshots (50-100 ps).

• number of DP-GEN iterations: 100.

Molecular modeling

Lithium diffusion in solid-state electrolyte

Ability to handle multi-component systems, here the LiGePS-type systems.



Jun Cheng's group at Xiamen U

physical/chemical problems

- understanding water (phase diagram of water, including reactive regions; phase transition: ice to water, ionic liquid to super-ionic ice; nuclear quantum effect: collective tunneling, isotope effect; reactive event: dissociation and recombination; water surface and water/TiO2 interface; spectra: infra-red; Raman; X-ray Absorption; exotic properties: dielectric constant; density anomaly, etc.
- physical understanding of different systems that require long-time large-scale simulation with high degrees of model fidelity (high-pressure iron: fractional defect; phase boundary; high-pressure hydrogen: exotic phases)
- catalysis (Pt cluster on MoS2 surface; CO molecules on gold surface, etc.)
- 2 materials science problems
 - battery materials (diffusion of lithium in LGePS, LSGeSiPS, etc.; diffusion of Se in Cu2Se alloy)
 - high entropy/high temperature alloy (CoCrFeMnNi alloy; Ni-based alloy)
- organic chemistry/bio problems
 - crystal structure prediction of molecular crystals;
 - protein-ligand interaction;
 - protein folding.

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Exploration of very high dimensional configuration spaces

Problems of interest:

- structural optimization (e.g. protein folding)
- free energy calculation
- coarse-grained molecular dynamics

Metadynamics (Laio and Parrinello, 2002)

- free energy is computed by adding up little Gaussians
- free energy is used to help exploration



Very effective when the number of collective variables is small.

Collective variables and free energies

Consider a pre-defined set of collective variables (CV) s. Free energy surface (FES) A(s):

$$A(\boldsymbol{s}) = -\frac{1}{\beta} \ln p(\boldsymbol{s}), \quad p(\boldsymbol{s}) = \frac{1}{Z} \int e^{-\beta U(\boldsymbol{r})} \delta(\boldsymbol{s}(\boldsymbol{r}) - \boldsymbol{s}) \, d\boldsymbol{r},$$

Mean forces

$$\boldsymbol{F}(\boldsymbol{s}) = -\nabla_{\boldsymbol{s}} A(\boldsymbol{s}).$$

Reinforced dynamics

- exploration:
 - biased molecular dynamics:

$$\tilde{\boldsymbol{f}}_i(\boldsymbol{r}) = -\nabla_{\boldsymbol{r}_i} U(\boldsymbol{r}) + \sigma(\boldsymbol{\epsilon}(\boldsymbol{s}(\boldsymbol{r}))) \nabla_{\boldsymbol{r}_i} \boldsymbol{A}(\boldsymbol{s}(\boldsymbol{r}))$$

 σ is an activation function that switches on and off the biasing term

• decide which ones to label: train an ensemble of networks ${m F}_j, j=1,\cdots,N$ and compute

$$\text{variance} = \langle | \boldsymbol{F}_j(\boldsymbol{s}) - \bar{\boldsymbol{F}}(\boldsymbol{s}) \|^2 \rangle, \quad \bar{\boldsymbol{F}}(\boldsymbol{s}) = \langle \boldsymbol{F}_j(\boldsymbol{s}) \rangle$$

- labeling: compute the mean force (using restrained MD)
- training: deep potential-like coarse-grained model

Can now handle many collective variables

Reinforced dynamics

- Left: Tripeptide: brute-force simulation (\sim 50 μ s) v.s. RiD (10 ns biased + 190 ns restrained):
- Right: higher dimensional FES: ala-10 and 20 CVs.





Reinforced dynamics

More recently: Trp-cage folded (20 amino acids, 38 CVs)



Now we are folding more.

Coarse graining (CG)

Given CG variables s. Free energy surface (FES), or CG potential, A(s):

$$A(\boldsymbol{s}) = -\frac{1}{\beta} \ln p(\boldsymbol{s}), \quad p(\boldsymbol{s}) = \frac{1}{Z} \int e^{-\beta U(\boldsymbol{r})} \delta(\boldsymbol{s}(\boldsymbol{r}) - \boldsymbol{s}) \, d\boldsymbol{r}.$$

Radial distribution functions (left) and angular distribution functions (right):



(J. Chem. Phys. 2018, 149(3): 034101.)

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Modeling gas dynamics



Boltzmann Equation

One-particle density function $f(\boldsymbol{x}, \boldsymbol{v}, t)$

$$\partial_t f + \boldsymbol{v} \cdot \nabla_{\boldsymbol{x}} f = \frac{1}{\varepsilon} Q(f), \quad \boldsymbol{v} \in \mathbb{R}^3, \quad \boldsymbol{x} \in \Omega \subset \mathbb{R}^3,$$

 $\varepsilon = \mathsf{Knudsen}$ number and Q is the collision operator.

Macroscopic state variables: ho, $oldsymbol{u}$ and T (density, bulk velocity and temperature)

$$\rho = \int f \,\mathrm{d}\boldsymbol{v}, \quad \boldsymbol{u} = \frac{1}{\rho} \int f\boldsymbol{v} \,\mathrm{d}\boldsymbol{v}, \quad T = \frac{1}{3\rho} \int f |\boldsymbol{v} - \boldsymbol{u}|^2 \,\mathrm{d}\boldsymbol{v}.$$

When $\varepsilon \ll 1$, Boltzmann can be approximated by Euler:

$$\partial_t \boldsymbol{U} + \nabla_{\boldsymbol{x}} \cdot \boldsymbol{F}(\boldsymbol{U}) = 0,$$

with $p=\rho T$, $E=\frac{1}{2}\rho {\bm u}^2+\frac{3}{2}\rho T$, ${\bm U}=(\rho,\rho {\bm u},E)^T$

$$\boldsymbol{F}(\boldsymbol{U}) = (\rho \boldsymbol{u}, \rho \boldsymbol{u} \otimes \boldsymbol{u} + pI, (E+p)\boldsymbol{u})^T$$

Conventional Moment Method

Proceed in 3 steps:

1. Start with the choice of a finite-dimensional linear subspace of functions of v (usually to be polynomials, e.g., Hermite polynomials).

2. Expand $f(\boldsymbol{x}, \boldsymbol{v}, t)$ using these functions as bases and take the coefficients as moments (including macroscopic variables ρ , \boldsymbol{u} , T, etc.).

3. Finally close the system with simplified assumptions, e.g., truncating moments of higher orders

$$\begin{cases} \partial_t \boldsymbol{U} + \nabla_{\boldsymbol{x}} \cdot \boldsymbol{F}(\boldsymbol{U}, \boldsymbol{W}) = 0, \\ \partial_t \boldsymbol{W} + \nabla_{\boldsymbol{x}} \cdot \boldsymbol{G}(\boldsymbol{U}, \boldsymbol{W}) = \frac{1}{\varepsilon} \mathbb{R}(\boldsymbol{U}, \boldsymbol{W}). \end{cases}$$

For instance, in Grad 13-moment system, (U, W) is constructed based on the moments of the bases $\{1, v, (v - u) \otimes (v - u), |v - u|^2 (v - u)\}$.

Machine learning-based moment method

Objective: construct an uniformly accurate (generalized) moment model using machine learning.

1: Learn the Moments through Autoencoder

Find an encoder Ψ that maps $f(\cdot, \boldsymbol{v})$ to generalized moments $\boldsymbol{W} \in \mathbb{R}^M$ and a decoder Φ that recovers the original f from $\boldsymbol{U}, \boldsymbol{W}$

$$\boldsymbol{W} = \Psi(f) = \int \boldsymbol{w} f \, \mathrm{d} \boldsymbol{v}, \quad \Phi(\boldsymbol{U}, \boldsymbol{W})(\boldsymbol{v}) = h(\boldsymbol{v}; \boldsymbol{U}, \boldsymbol{W}).$$

The goal is essentially to find optimal ${\bf w}$ and h parametrized by neural networks through minimizing

$$\mathbb{E}_{f\sim\mathcal{D}}\|f-\Phi(\Psi(f))\|^2+\lambda_\eta(\eta(f)-h_\eta(\boldsymbol{U},\boldsymbol{W}))^2.$$

 $\eta(f)$ denotes entropy.

2: Learn the Fluxes and Source Terms in the PDE

Recall the general conservative form of the moment system

$$\begin{cases} \partial_t \boldsymbol{U} + \nabla_{\boldsymbol{x}} \cdot \boldsymbol{F}(\boldsymbol{U}, \boldsymbol{W}; \varepsilon) = 0, \\ \partial_t \boldsymbol{W} + \nabla_{\boldsymbol{x}} \cdot \boldsymbol{G}(\boldsymbol{U}, \boldsymbol{W}; \varepsilon) = \mathbb{R}(\boldsymbol{U}, \boldsymbol{W}; \varepsilon). \end{cases}$$

Rewrite it into (variance reduction)

$$\begin{cases} \partial_t \boldsymbol{U} + \nabla_{\boldsymbol{x}} \cdot [\boldsymbol{F}_0(\boldsymbol{U}) + \tilde{\boldsymbol{F}}(\boldsymbol{U}, \boldsymbol{W}; \varepsilon)] = 0, \\ \partial_t \boldsymbol{W} + \nabla_{\boldsymbol{x}} \cdot [\boldsymbol{G}_0(\boldsymbol{U}) + \tilde{\boldsymbol{G}}(\boldsymbol{U}, \boldsymbol{W}; \varepsilon)] = \mathbb{R}(\boldsymbol{U}, \boldsymbol{W}; \varepsilon). \end{cases}$$

 $F_0(U), G_0(U)$ are the fluxes of the moments U, W under the Maxwellian distribution. Our goal is to obtain ML models for $\tilde{F}, \tilde{G}, \mathbb{R}$ from the original kinetic equation. Issues: (1) physical symmetries (e.g. Galilean invariance); (2) data generation (active learning algorithm); (3) locality vs. non-locality of the model



preparing the data finding the moments learning the closure exploring the data Figure: Schematic diagram of the machine learning-based moment method

- exploration: random initial conditions made up of waves and discontinuities
- labeling: solving kinetic equation (Boltzmann equation for Maxwell molecules)
- training: Galilean invariance

Galilean Invariant Moments

Galilean invariance of the Boltzmann equation:

$$f'(\boldsymbol{x}, \boldsymbol{u}, t) = f(\boldsymbol{x} - t\boldsymbol{u}', \boldsymbol{v} - \boldsymbol{u}', t).$$

Moments:

$$\boldsymbol{W}_{\mathsf{Gal}} = \Psi(f) = \int f(\boldsymbol{v}) \mathbf{w} \left(\frac{\boldsymbol{v} - \boldsymbol{u}}{\sqrt{T}} \right) \mathrm{d}\boldsymbol{v}.$$

Closure:

$$\partial_t \int_{\mathbb{R}^D} f(\boldsymbol{v}) \mathbf{w} \left(\frac{\boldsymbol{v} - \boldsymbol{u}_j}{\sqrt{T_j}} \right) \mathrm{d}\boldsymbol{v} + \nabla_{\boldsymbol{x}} \cdot \int_{\mathbb{R}^D} f(\boldsymbol{v}) \mathbf{w} \left(\frac{\boldsymbol{v} - \boldsymbol{u}_j}{\sqrt{T_j}} \right) \boldsymbol{v}^{\mathrm{T}} \mathrm{d}\boldsymbol{v} = \int_{\mathbb{R}^D} \frac{1}{\varepsilon} Q(f) \mathbf{w} \left(\frac{\boldsymbol{v} - \boldsymbol{u}_j}{\sqrt{T_j}} \right) \mathrm{d}\boldsymbol{v}$$

$$\partial_t \boldsymbol{W}_{\mathsf{Gal}} + \nabla_{\boldsymbol{x}} \cdot \boldsymbol{G}_{\mathsf{Gal}}(\boldsymbol{U}, \boldsymbol{W}_{\mathsf{Gal}}; \boldsymbol{U}_j) = \frac{1}{\varepsilon} \mathbb{R}_{\mathsf{Gal}}(\boldsymbol{U}, \boldsymbol{W}_{\mathsf{Gal}}).$$

The data efficiency is better than the previous one since it learns the dynamical system more intrinsically.

 $\varepsilon \sim \text{Log10-Uniform}(-3,1)$, constant across the domain; initial profiles consist of a combination of a few sin waves and shocks.

Size of dataset array: $200 \times 100 \times 48 \times 48 \times 100$. Specify $\boldsymbol{W} \in \mathbb{R}^9$.



Figure: Sample profiles of ρ , ρu , E (from left to right) at t = 0, 0.05, 0.1 (from top to bottom), $\varepsilon = 8.10$

 ε varies from 10^{-3} to 10 in the domain; initial profiles are the same as before



Figure: Profiles of ρ , ρu , E (from left to right) at t = 0, 0.05, 0.1 (from top to bottom)

Numerical results

Learned functions $\mathbf{w}(v)$ as generalized moments



Other possible applications of concurrent learning

- solving PDEs
- model-based reinforcement learning
- control

Essentially any time we have a code (or a simulator) to generate the states and the data.

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Concluding remarks

- Concurrent learning is a very powerful tool for multi-scale modeling.
 - DPMD allows us to perform MD simulation of large systems with quantum accuracy
 - RiD allows us to compute free energy function with many collective variables
 - ML based moment closure allows to obtain hydrodynamic models for the Boltzmann equation for Maxwell molecules that are uniformly accurate for a wide range of Knudsen numbers
- These are models, not just algorithms (sequential multi-scale modeling paradigm)
- The methodologies are quite general
- It is important to take into account symmetries and other physical constraints
- New paradigm for multi-scale models: analogy to Euler's equations for complex gases

A new annual conference:

Mathematical and Scientific Machine Learning (MSML)

First meeting:

- Program Chairman: Jianfeng Lu (Duke) and Rachel Ward (Univ Texas/Austin)
- Time: July 15-17, 2020
- Location: Princeton
- Submission deadline: November 30, 2019
- website: http://msml-conf.org