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MaMiCo: Two-Way Coupled Parallel-in-Time Molecular-Continuum Flow Simulation?

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Overview: Topics of this talk

Outline

- Mol-cont
- Filtering Wh
- MaMiCo
- Parareal / SPASD
- Outlook: PinT in MaMiCo
- Summary

What we already have:

1)Coupled molecular-continuum flow simulations

2)Filtering system for molecular dynamics (MD) data

MaMiCo coupling tool

What we want to do in the future:

4) From Parareal to SPASD

5)Our new concept: modified SPASD variant for molecularcontinuum flow in MaMiCo

Main idea of this talk: Re-use existing continuum solver and various coupling methods for time parallelization of MD

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Molecular-Continuum Coupling:

Lennard-Jones particle system (explicit time integration)

MD Domain and inner cells



3D transient flow simulation, Lattice-Boltzmann Method, on a GPU



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Molecular-Continuum Coupling: A Coupling Cycle





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Molecular-Continuum Coupling: Cell Meshes and Overlap Regions



- MD boundary: Zhou boundary force [Zhou et al. '14]
- Mass flux: Particle insertion with USHER [Delgado-Buscalioni et al. '03]
- Velocity imposition: Nie transfer strategy [Nie et al. '04]

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MD Quantity Sampling

- 1)Velocity, density, or other values for the coupling are sampled cell-wise from the particle system and then averaged:
 - 1) over all particles in a cell and
 - 2) over all (i.e. ca 50 100) MD time steps corresponding to a continuum time step (= coupling cycle)

2)Resulting quantities still fluctuate with high thermal noise:









Multi-Instance Sampling

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- Averaging over ensemble of MD systems
- Enables short coupling time intervals => transient simulation
- Computationally very expensive (N instances reduce standard deviation of noise only by a factor of N^{1/2})
- We can modify N at runtime: 'dynamic MD'



Noise Filtering with POD / PCA

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• View flow quantities, e.g. a velocity component u(t, **x**), as matrix



- Compute temporal auto-correlation covariance matrix $C = A A^{T}$
- Perform EVD of C
- Temporal modes $a_k(t)$ are eigenvectors of C
- Compute spatial modes $\varphi_k(x) = \sum A(t,x) + a_k(t)$
- Obtain filtered smooth $\overline{u}(t, \mathbf{x})$ as sum over $\varphi_k(x) a_k(t)$ for a few k

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$$NLM[v](i) = \frac{1}{\sum_{j \in I} w(i,j)} \sum_{j \in I} w(i,j)v(j)$$

$$w(i, j) = \exp(-\frac{max(dist(i, j)-2\sigma^2, 0)}{h^2})*\frac{1}{1-t}$$
• We define a similar dist(i,j) to compare neighborhoods i.e. time windows are space x.

- We define a similarity metric dist(i,j) to compare local neighborhoods i.e. 4D spacetime windows around i and j
- NLM computes weighted average of input data, weighted by similarity
- Exploits redundancy of given information to remove noise



Noise Filtering with Non-Local Means (NLM)

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ML based Filtering, RNN + U-Net

- Current WIP: Hybrid ML model based on RNN + U-Net
- Can learn and predict MD data, so that computationally expensive MD computations can be skipped





MaMiCo Coupling Tool / C++ Framework

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Algorithm 1 Traditional Parareal algorithm

1: Initialization:

Compute initial iteration with Coarse propagator: $U_0^{n+1} = \mathcal{G}(U_0^n)$ for all $0 \le n \le N$. 2: Assume sequence $\{U_k^n\}$ is known for some $0 \le n \le N$ and $k \ge 0$:

Correction:

(a) Advance with Coarse propagator in serial: $\mathcal{G}(U_k^n)$ for all $0 \le n \le N - 1$.

(b) Advance with Fine propagator in parallel: $\mathcal{F}(U_k^n)$ for all $0 \le n \le N - 1$.

(c) Compute correction: $\delta_k^n = \mathcal{F}(U_k^n) - \mathcal{G}(U_k^n)$ for all $0 \le n \le N - 1$.

Prediction:

Advance with Coarse propagator in serial: $\mathcal{G}(U_{k+1}^n)$ for all $0 \le n \le N - 1$. Refinement:

Combine the correction and prediction terms: $U_{k+1}^{n+1} = \mathcal{G}(U_{k+1}^n) + \mathcal{F}(U_k^n) - \mathcal{G}(U_k^n)$ 3: Repeat *Step 2* to compute U_{k+2}^n for all $1 \le n \le N$ until a termination-condition is satisfied.

[Blumers et al. '19]



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- 1)'SPASD' = 'Supervised PinT algorithm for long-time Lagrangian simulations of stochastic dynamics' [Blumers et al. '19]
- 2)Basic idea: Use a low-dimensional macroscopic system as a coarse predictor to supervise state of particle simulator
- 3)Results of particle system correct the mean-field flow prediction and provide microscopic details
- 4)Unlike traditional Parareal: Macro-model can be inconsistent with microscale description, but the deviation is corrected by SPASD algorithm



Algorithm 2 SPASD 1: Initialization: Compute initial iteration with Coarse propagator: $U_0^{n+1} = \mathcal{G}(U_0^0)$ for all $0 \le n \le N$. 2: Assume sequence $\{U_k^n\}$ is known for some $0 \le n \le N$ and $k \ge 0$: Correction: (a) Filter solution to remove noise: $\mathscr{F}{U_k^n}$ (b) Advance with Coarse propagator in serial: $\mathcal{G}(\mathscr{F}\{U_k^n\})$ for all $0 \le n \le N-1$. (c) Map the macroscopic state to microscopic space: $\hat{\mathscr{R}}\{U_k^n\}$ (d) Advance with Fine propagator in parallel: $\mathcal{F}(\mathscr{R}\{U_k^n\})$ for all $0 \le n \le N-1$. (e) Project the microscopic state to macroscopic state: $\mathscr{P}{\mathcal{F}(\mathscr{R}{U_k^n})}$ (f) Compute the correction: $\delta_k^n \equiv \mathscr{P}\{\mathscr{F}(\mathscr{R}\{U_k^n\})\} - \mathscr{G}(\mathscr{F}\{U_k^n\}) \text{ for all } 0 \le n \le N-1.$ Prediction: Advance with Coarse propagator in serial: $\mathcal{G}(\mathscr{F}\{U_{k+1}^n\})$ for all $0 \le n \le N-1$ Refinement: Combine the correction and the prediction terms: $U_{k+1}^{n+1} = \mathcal{G}(\mathcal{F}\{U_{k+1}^n\}) + \mathcal{P}\{\mathcal{F}(\mathcal{R}\{U_k^n\})\} - \mathcal{G}(\mathcal{F}\{U_k^n\}) \text{ for all } 0 \le n \le N-1.$ 3: Repeat Step 2 to compute U_{k+2}^n for all $1 \le n \le N$ until a termination-condition is satisfied.

[Blumers et al. '19]

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1)Unlike traditional Parareal: fine and coarse propagator encompass other operations now:

1) Mapping operator \mathscr{R} (Macro \rightarrow MD)

2) Projection operator \mathscr{P} (MD \rightarrow Macro)

3) Filtering operator \mathcal{F} (to remove stochastic noise)

2)These operators link the two scales, i.e. translate between microscopic and macroscopic model



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[Blumers et al. '19]



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Our new concept: modified SPASD variant for molecular-continuum flow

- 1)In original SPASD, the continuum solver is introduced only as a coarse predictor to enable time parallelization of the particle system
- 2)For coupled molecular-continuum flow, we already have a continuum solver, but for a different purpose: To span larger spatial scales / extend the simulation domain

3)Idea: Use continuum solver for **both** now

4) Mapping operation to DPD is cheap (use flow quantity directly), mapping operation to MD requires interpolation, velocityrelaxation, equilibration of particle system etc

New concept: SPASD in MaMiCo



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Idea: Re-use the existing feature implementation, which were made for molecular-continuum coupling, to enable parallel-intime computations, examples:

1) Mapping operation *R* to MD requires to initialize a new particle simulation instance (at a 'future' state), but we have this already: Multi-instance MD handling, dynamic MD + checkpoints, etc ...

2) Projection \mathscr{P} (MD \rightarrow Macro) can be complex (quantity sampling, shift-timestep etc.) but we also have this already :-)

New concept: SPASD in MaMiCo



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Idea: Re-use the existing feature implementation, which were made for molecular-continuum coupling, to enable parallel-intime computations, examples:

3) Mapping operation \mathscr{R} to MD requires interpolation, velocityrelaxation, equilibration of particle system etc, but we have this already: USHER, Nie coupling, momentuminsertion, transfer strategy ...

4) Filtering F between propagators can be complex (transient 3D data), but we have this already: MaMiCo filtering subsystem, POD, NLM, ML module :-)

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- 1)Molecular-Continuum simulations extend the applicability of MD to larger simulation domains and time scales
- 2)MaMiCo: open-source C++ mol-cont coupling framework
- https://github.com/HSU-HPC/MaMiCo

Summary

- 3)SPASD: Extended Parareal with additional mapping, projection, filtering operations, for supervised PinT particle method
- 4) Future idea: Re-use the existing feature implementations, which were made for molecular-continuum coupling, to enable parallel-in-time computations in MaMiCo