

Systematic Coarse-Grained Models for Molecular Systems Using Entropy

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Abstract: The development of systematic coarse-grained mesoscopic models for complex molecular systems is an intense research area. Here we first give an overview of different methods for obtaining optimal parametrized coarse-grained models, starting from detailed atomistic representation for high dimensional molecular systems. We focus on methods based on information theory, such as relative entropy, showing that they provide parameterizations of coarse-grained models at equilibrium by minimizing a fitting functional over a parameter space. We also connect them with structural-based (inverse Boltzmann) and force matching methods. All the methods mentioned in principle are employed to approximate a many-body potential, the (n-body) potential of mean force, describing the equilibrium distribution of coarse-grained sites observed in simulations of atomically detailed models. We also present in a mathematically consistent way the entropy and force matching methods and their equivalence, which we derive for general nonlinear coarse-graining maps. Finally, we apply, and compare, the above-described methodologies in several molecular systems: gas and fluid methane, water, and a polymer.

Keywords: coarse-graining; data-driven; relative entropy; path-space; uncertainty quantification



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Motivation

Simulating complex molecular systems: Enormous range of Length-Time scales

- Need to reduce complexity and system size.
- Dimensionality reduction: Coarse-graining
- Statistical equilibrium: Structural properties.
- Non-equilibrium: Dynamical properties.



K. Johnson, V. Harmandaris, Soft Matter, 2013, 9, 6696-6710



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Equilibrium Statistical Mechanics

A system of N >> 1 particles;

U(x), $x \in R^{3N}$ interaction potential, Gibbs configurational probability density

$$\mu(q) = Z^{-1} e^{-\beta U(q)}, \ q \in \mathbb{R}^{3N}$$

Coarse-graining (CG) as transformation operator

 $\boldsymbol{\Pi}: \mathsf{R}^{\mathsf{3N}} \rightarrow \mathsf{R}^{\mathsf{3M}} \text{ , } \boldsymbol{\mathsf{M}} < \mathsf{N}$

Examples:

- ✓ Linear map: Center of mass of groups
- ✓ Non-linear map: Bond angle, end-to-end vector





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Coarse-graining and Potential of Mean Force

□ Exact CG model at equilibrium $Q \in R^{3M}$

Potential of Mean Force (PMF)



$$U^{pmf}(Q) = -\frac{1}{\beta} \ln \int_{A(Q)} e^{-\beta U(q)} dq,$$

CG probability density

 $\mu^{pmf}(Q) \propto e^{-\beta U^{pmf}(Q)} \qquad A(Q) = \{q \in \mathbb{R}^{3N} : \Pi(q) = Q\}$

✓ Exact! But still High-dimensional!



□ Main goal: Derive effective CG models consistent with structure and dynamic properties of the microscopic system.



"Digital Twin"

Methods for optimal parametrization of mesoscopic models

 $\label{eq:how-to-find-optimal} \begin{array}{ll} \Theta \in \Theta \\ \text{ s.t. } \end{array}$

 $\overline{U}(Q;\theta) \sim U^{pmf}(Q)$

□ In what sense optimal?

Various Methodologies

Objective

Force matching

Forces

Voth et.al. J. Phys. Chem. B 2005, Noid et.a.l. 2008, J.F. Rudzinski and W.G. Noid (2012) , Kalligiannaki et. al. J. Chem. Phys. 2015

Variational inference: Relative entropy minimization

measures

M.S. Shell J. Chem. Phys. 2008, A. Chaimovich, M.S. Shell 2009

Inverse Boltzmann, Inverse Monte Carlo

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K. Soper Chem. Phys. 1996, F. Muller-Plathe Chem. Phys. Chem. 2002, P. Lyubartsev and A. Laaksonen, N. Meth. Soft Matter Sim., 2004 18–30 November 2019; Chaired by Prof. Geert Verdoolaege

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Gibbs

Relative Entropy minimization (Information theory).

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 $\min_{\theta} \mathcal{R}\left(\mu \mid \mid \bar{\mu}_{\theta}\right)$

 $\bar{\mu}_{\theta} \propto \exp\{-\beta \bar{U}(\cdot;\theta)\}$

 $\mathcal{R}\left(\mu \mid\mid \bar{\mu}_{\theta}\right) = \int \mu(x) \log \frac{\mu(x)}{\bar{\mu}_{\theta}(x)} dx$

 Relative Entropy measures the Information loss when using probability v instead of μ

> $\mathcal{R}(\mu|
> u) \ge 0$, $\mathcal{R}(\mu|
> u) = 0$ iff $\mu = \nu$ $\mathcal{R}(\mu|
> u) \ne \mathcal{R}(\nu|\mu)$

Thus, the optimal parameter set θ^* is the solution of the optimization problem:

$$\min_{\theta \in \Theta} \left\{ \beta \mathbb{E}_{\mu} \left[\bar{U}(\mathbf{\Pi}(\mathbf{q}); \theta) - U(\mathbf{q}) \right] - \left[\log Z^{\theta} - \log Z \right] \right\}$$



Dynamics: Path-space Relative Entropy minimization

Dynamics is described by stochastic processes:

- Microscopic (atomistic): $X_t = (q_t, p_t), \in \mathbb{R}^{6N}, t > 0$
- Mesoscopic (coarse-grained):

$$\overline{X}_t = (Q_t, P_t), \in \mathbb{R}^{6M}, \ t > 0$$

Back-mapped coarse-grained:

$$\widetilde{X}_t = (\widetilde{q}_t, \widetilde{p}_t), \in \mathbb{R}^{6N}, t > 0$$

✓ With path-space probabilities

$$P_X^{[0,T]} \qquad P_{\overline{X}}^{[0,T]} \qquad P_{\widetilde{X}}^{[0,T]}$$



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Dynamics: Path-space Relative Entropy minimization

Dynamics is described by stochastic processes

Path-space Relative Entropy

$$\mathcal{R}(P_{X}^{[0,T]}|P_{\tilde{X}}^{[0,T]}) = \mathbb{E}_{P_{X}^{[0,T]}} \left[\log \frac{dP_{X}^{[0,T]}}{dP_{\tilde{X}}^{[0,T]}} \right]$$

Relative Entropy Rate

$$\mathcal{H}(P_X|P_{\tilde{X}}) = \lim_{T \to \infty} \frac{1}{T} \mathcal{R}(P_X^{[0,T]}|P_{\tilde{X}}^{[0,T]})$$

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Coarse-graining Langevin dynamics

Microscopic (Atomistic) representation

position $q \in \mathbb{R}^{3N}$ momentum $p \in \mathbb{R}^{3N}$ Mesoscopic CG mapping

CG map:
$$\mathbf{\Pi}: \mathbb{R}^{6N} \to \mathbb{R}^{6M}$$
, $M < N$

Approximate dynamics model

Atomistic

Coarse-grained

$$\begin{cases} dq_t = M^{-1} p_t dt ,\\ dp_t = F(q_t) dt - \gamma M^{-1} p_t dt + \sigma dB_t , \end{cases}$$

$$\begin{cases} d\bar{q}_t = M^{-1}\bar{p}_t dt, \\ d\bar{p}_t = \bar{F}(\bar{q}_t; \theta) dt - \gamma M^{-1}\bar{p}_t dt + \sigma d\bar{B}_t. \end{cases}$$

CG Force/Potential

 $\bar{F}(\cdot;\theta) = -\nabla \bar{U}(\mathbf{Q};\theta)$



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Atomistic Force

 $F(q) = -\nabla_q U(q)$

Coarse-graining Langevin dynamics

Derivation of CG model: CG force/potential need to be parametrized

Path-space Relative Entropy minimization reduces to 'path-space force-matching'

$$\begin{aligned} \theta^* &= \operatorname{argmin}_{\theta} \mathcal{R}(P_X^{[0,T]} | P_{\tilde{X}}^{[0,T]}) \\ &= \operatorname{argmin}_{\theta} \mathbb{E}_{P^{[0,T]}} \left[\frac{1}{2\sigma^2} \int_0^T \left\| \mathbf{\Pi} F(q_s) - \bar{F}(\mathbf{\Pi} q_s; \theta) \right\|^2 ds \right] \end{aligned}$$

$$\mathbf{\Pi} F = \sum_{\{i \in \text{ CG particle } j\}} F_i(\mathbf{q})$$

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V. Harmandaris, E. Kalligiannaki, M. Katsoulakis, P. Plechac, J. Comp. Phys. 2016, M. Katsoulakis, P. Plechac, 2013,

on Entropy and Its Applications



In stationary (equilibrium) dynamics, path-space relative entropy minimization reduces to Relative Entropy Rate minimization which in turn reduces to the Force Matching method

$$egin{array}{rcl} eta^{*} &=& {
m argmin}_{ heta} \mathbb{E}_{\mu} \left[rac{1}{2\sigma^{2}} \left\| oldsymbol{\Pi} F(oldsymbol{q}) - ar{F}(oldsymbol{\Pi} oldsymbol{q}; heta)
ight\|^{2}
ight] \end{array}$$

For discrete time path observations
$$\mathcal{D}_{n_s,n_t} = \{\mathbf{X}_1^k, \dots, \mathbf{X}_{n_t}^k\}_{k=1}^{n_s}$$

Path-space Relative Entropy

$$\hat{\theta} = \operatorname*{argmax}_{\theta} \sum_{k=1}^{n_s} \log \frac{\bar{P}(\Pi X_1^k, \Pi X_2^k, ..., \Pi X_{n_t}^k)}{\bar{Q}^{\theta}(\Pi X_1^k, \Pi X_2^k, ..., \Pi X_{n_t}^k)}$$

Relative Entropy Rate

$$\hat{\theta} = \operatorname{argmax}_{\theta} \sum_{i=1}^{n_t-1} \log q^{\theta}(\mathbf{\Pi} X_i, \mathbf{\Pi} X_{i+1})$$

 $q^{\theta}(\bar{\mathbf{X}}, \bar{\mathbf{X}}')$

Parametric transition probability density

Goal: Provide confidence sets for the derived optimal CG model

• Large number of observations $n_s >> 1$

Point-estimates: Asymptotic standard error

Small number of observations n_s

Frequentist statistics tools: Bootstrap, jackknife

Bayesian statistics tools



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Example: Simple fluid - Bulk methane CH₄



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Study at Equilibrium and Transient Time Regimes

Data are generated from Molecular dynamics simulations for M = 666 methane molecules at temperature 100K (density is 0.3825 gr/cm³), and initial positions of molecules are at a FCC (Face Centered Cubic) crystal structure.





Equilibrated configuration:



System	Paths (n_p)	time step dt (ps)	Time interval (ps)	Configurations (n_t) per path
tFCC	10	0.1	[0,100]	1000
EQm	10	0.1	[900,1000]	1000
EQs	1	1	[1000,10000]	9000



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Results at Equilibrium Regime



- ✓ Forces of the equilibrium data set (Eqm), obtained through the PSFM method.
- ✓ In the inset is the derived CG pair effective potential.



Comparison of Equilibrium Methods



Effective pair interaction potential $u(R;\theta)$

Pair correlation function

 \checkmark E. Kalligiannaki., A. Chazirakis, A. Tsourtis, M. Katsoulakis, P. Plechac, V. Harmandaris, EPJ ST, 225, 1347-1372, 2016



Results at Transient Time Regime





 Evolution of the RDF g(r) of the data set tFCC with initial FCC crystal structure, for different time sub-intervals from the all-atom simulation

 Evolution of the effective CG potential with cubic splines, for different time sub-intervals of the all-atom simulation.



Water, one-site CG representation

- □ Simulated all-atom water, using the SPC/E force field. The model system consists of 1192 molecules at ambient conditions , T = 300 K, P = 1 atm. All-atom configurations were recorded every 10 ps.
- CG effective interactions for CG water molecules by analyzing the all-atom data, using force matching and relative entropy techniques







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Polymer Bulk System: Polyethylene

□ Atomistic simulated system: 96 PE chains with 99 monomers each, $N = 96 \times 99$, temperature = 450K

✤ CG map 3:1, i.e., CG system size M = 96×33

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$$\overline{U}(Q; \theta) = \overline{U}_{b}(Q; \theta) + \overline{U}_{bb}(Q; \theta)$$



- CG Bonded (Bonds; Angles; Dihedrals) interactions: Estimated with the Iterative Inverse Boltzmann method in tabulated form.
- CG Non-bonded interaction potential: Two-body pair potential: u(R ; θ) cubic B-splines.
 Estimated with the Force-Matching method.





Effective interaction between CG "Angles"





Non-bonded potentials: Large & small number of observations

□ Accuracy of the CG non-bonded effective interaction depends on the dataset.

 ✓ Point estimates for a large data et (2000 configurations): Linear versus cubic B-splines, pair potential representation





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Non-bonded potentials: Large & small number of observations

✓ Estimates for a small dataset (200 configurations): Bootstrap results for the cubic Bspline representation





Conclusion and Discussion

- Variational inference for mesoscopic models; continuous and discrete time observations;
- Hybrid data driven physics-based coarse-graining approach;
- Systems out of equilibrium;
- Quantify uncertainties;
- Transferability;
- Challenging: dependencies and correlations in space/time and between model elements (molecules, parameters, and mechanisms), regions of sparse data



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✤ Links:

MACOMMS: Mathematical and Computational Modeling of Complex Molecular Systems.

<u>SISDECS</u>: Statistical Inference with Stochastic Differential Equations and applications in Complex Stochastic systems.

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