Bringing the Power of Monte Carlo methods to Long-Range-Interacting Molecular Systems

Philipp Höllmer (AG Monien)



Structure

- 1. Non-Reversible Event-Chain Monte Carlo (ECMC) for the Hard-Disk Model.
- 2. Generalization of ECMC to Molecular Systems.
- 3. ECMC Variants and Simulation Results.

Hard-Disk Model





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• Probability density of configuration $c = \{\mathbf{r}_1, \mathbf{r}_2, ..., \mathbf{r}_N\}$: $\pi(c) \propto \begin{cases} 1 & \text{if } c \text{ legal,} \\ 0 & \text{otherwise.} \end{cases}$



$$\pi(a) = \pi(b) \propto 1$$
$$\pi(c) = 0$$

W. Krauth, Statistical Mechanics: Algorithms and Computations (Oxford University Press, 2006)

Hard-Disk Model



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Hard-disk model has a phase transition when hard-disk density is changed:



E. Bernard, Algorithms and applications of the Monte Carlo method: Two-dimensional melting and perfect sampling (PhD thesis, 2011)

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Markov-Chain Monte Carlo (MCMC)

• Idea: Change configuration from c to c' with transition probability $p(c \rightarrow c')$. \rightarrow Only converges to probability distribution π if:

$$\sum_{c'} \pi(c') p(c' \to c)$$

• **Reversible** Markov chains obey global balance by satisfying a weaker condition:

$$\pi(c') p(c' \to c) = \pi(c)$$



Michel et al., J. Chem. Phys. **140**, 054116 (2014)

 $= \pi(c)$ (global balance)

 $p(c \rightarrow c')$ (detailed balance)



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1. Choose random disk i and propose random displacement in square around \mathbf{r}_i :

$$\mathbf{r}_i = (x_i, y_i) \to \mathbf{r}_i$$

$$\Delta_x \leftarrow \operatorname{ran}(-\delta, \delta)$$

2. Accept proposed configuration c' if no overlap is introduced (or more generally with probability $p(c \rightarrow c') = \min[1, \pi(c')/\pi(c)]$).



- $\mathbf{y}'_i = (x_i + \Delta_x, y_i + \Delta_y),$
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- **3.** Transfer velocity **v** from disk *i* to disk *t*.
- 4. Repeat steps 2. and 3. for chain time τ_{chain} .





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Phase Transition in the Hard-Disk Model

orders of magnitude faster than reversible Metropolis algorithm (LMC).



Li, Nishikawa, PH, Carillo, Maggs, and Krauth, arXiv:2207.07715 (2022, manuscript submitted for publication)

Philipp Höllmer (AG Monien), 09. November 2022, Journal Club on Condensed Matter Theory

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Required (single-core) CPU time for coalescence:

ECMC: \sim 1 week.

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$$\Rightarrow$$
 LMC: ~ 10 years.

Phase Transition in the Hard-Disk Model

PRL 107, 155704 (2011)

Two-Step Melting in Two Dimensions: First-Order Liquid-Hexatic Transition

Etienne P. Bernard^{*} and Werner Krauth[†]

Laboratoire de Physique Statistique Ecole Normale Supérieure, UPMC, CNRS 24 rue Lhomond, 75231 Paris Cedex 05, France (Received 6 July 2011; published 7 October 2011)

Melting in two spatial dimensions, as realized in thin films or at interfaces, represents one of the most fascinating phase transitions in nature, but it remains poorly understood. Even for the fundamental harddisk model, the melting mechanism has not been agreed upon after 50 years of studies. A recent Monte Carlo algorithm allows us to thermalize systems large enough to access the thermodynamic regime. We show that melting in hard disks proceeds in two steps with a liquid phase, a hexatic phase, and a solid. The hexatic-solid transition is continuous while, surprisingly, the liquid-hexatic transition is of first order. This melting scenario solves one of the fundamental statistical-physics models, which is at the root of a large body of theoretical, computational, and experimental research.



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PHYSICAL REVIEW LETTERS

week ending 7 OCTOBER 2011

Molecular Simulations

Molecular Dynamics (MD)

- Physical time evolution based on Newton's equations of motion.
- Discretizes time (and possibly space).

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MCMC

- Unphysical time evolution only restricted by global-balance condition.
- Directly samples Boltzmann distribution.

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- Superior computational complexity per MD time step: $\mathcal{O}(N \log N)$.
- Superior (Newtonian) exploration of configuration space.

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Reversible MCMC

- Inferior computational complexity per MCMC sweep: $\mathcal{O}(N^{3/2})$.
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Both disadvantages are overcome by non-reversible ECMC.

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Generalization of ECMC

- Conceived for systems described by continuous variables. \rightarrow Here: N point-like atoms with positions $\{\mathbf{r}_1, \dots, \mathbf{r}_N\}, \mathbf{r}_i \in \mathbb{R}^d$.
- Exploits translational symmetry of interaction potentials in molecular systems.



ECMC constructs a non-reversible rejection-free continuous-time Markov chain.

- Faulkner et al., J. Chem. Phys. **149**, 064113 (2018)
- Philipp Höllmer (AG Monien), 09. November 2022, Journal Club on Condensed Matter Theory



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- ECMC relies on three concepts:
 - 1. Factorized Metropolis filter accepts/rejects proposed configurations.
 - 2. Lifting framework proposes new configurations and solves rejections.
 - **3. Event-driven implementation.**

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Factorized Metropolis Filter

$$U(c = \{\mathbf{r}_1, \dots, \mathbf{r}_N\}) = \sum_M U_M(c_M = \{\mathbf{r}_i : i \in M\}) \longrightarrow \pi_B(c) = \frac{1}{Z} \prod_M e^{-\beta U_M(c_M)}$$

SPC/Fw water model:



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Decompose total potential U into sum over factor potentials U_M of factors M:

Faulkner et al., J. Chem. Phys. **149**, 064113 (2018)



Factorized Metropolis Filter

$$U(c = \{\mathbf{r}_1, ..., \mathbf{r}_N\}) = \sum_M U_M(c_M) = \{\mathbf{r}_M\}$$

Replace original Metropolis filter that $A^{\text{Met}}(c \to c') = \min\left[1, \prod e^{-\beta \Delta U_M(c_M \to c'_M)}\right] -$

Original Metropolis filter.

independently:

$$X^{\text{Fact}}(c \to c') = \bigwedge X_M(c_M \to c'_M)$$

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Whether the new configuration is accepted by factor M

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accepts a change of configuration
$$c \rightarrow c'$$
:

$$\rightarrow A^{\text{Fact}}(c \rightarrow c') = \prod_{M} \min \left[1, e^{-\beta \Delta U_M(c_M \rightarrow c'_M)} \right]$$

Factorized Metropolis filter.

Formulates consensus principle, new configuration is accepted from all factors

$$M \rightarrow c'_{M} = \begin{cases} \text{True} & \text{if } \operatorname{ran}_{M}(0,1) < e^{-\beta \Delta U_{M}(c_{M} \rightarrow c'_{M})} \\ \text{False} & \text{otherwise} \end{cases}$$

Lifting Framework

- Lift configuration $c \rightarrow (c, \mathbf{v}, a)$ to include active atom a and its velocity \mathbf{v} .
- Atom *a* moves with **v** until a factor breaks consensus.
- If a translationally symmetric pair potential between *a* and *t* breaks consensus:
 - \rightarrow Change active atom from *a* to *t* in a lifting move.





Event-Driven Implementation

- For every factor M containing a, sample a candidate event time Δt_M .
 - \rightarrow Proposed configuration c'_M : $c_M = \{\mathbf{r}_a, \mathbf{r}_t\} \rightarrow c'_M = \{\mathbf{r}_a + \Delta t_M \mathbf{v}, \mathbf{r}_t\}$.
 - \rightarrow Invert equation for Δt_M : $-\ln [ran_M(0,1)] = \beta \Delta U_M^+(c_M \rightarrow c'_M).$



<u>PH</u>, All-Atom Event-Chain Monte Carlo — Designing a General-Purpose Python Application (Master's thesis, 2019) Philipp Höllmer (AG Monien), 09. November 2022, Journal Club on Condensed Matter Theory

ECMC for SPC/Fw Water Model



PH, Maggs, and Krauth, *Bringing the Power of Monte Carlo methods to Long-Range-Interacting Molecular Systems* (2022, manuscript in preparation)

ECMC for SPC/Fw Water Model



- Integration and inversion of event rate can be tedious.
- In long-range-interacting N-body systems, consensus considers $\mathcal{O}(N)$ factors per event.



PH, Maggs, and Krauth, *Bringing the Power of Monte Carlo methods to Long-Range-Interacting Molecular Systems* (2022, manuscript in preparation)

Problems



Bounding Potentials

 Bounding potentials bound the event rate of their factor potential. \rightarrow Events of bounding potentials have to be confirmed.





Cell-Veto Algorithm

• Cell-based bounding potentials can be precomputed.



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• Cell-veto algorithm considers all non-nearby interactions at once with $\mathcal{O}(1)$ complexity

ECMC for Molecular Systems

- - \rightarrow ... without ever knowing U.
 - \rightarrow ...numerically exact without discretizing time (or space).
 - \rightarrow ...using non-equilibrium dynamics.

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• ECMC with cell-veto algorithm samples the Boltzmann distribution $\exp(-\beta U)$...

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- General-purpose open-source ECMC application JeLLyFysh for molecular simulations available [PH et al., Comput. Phys. Commun. 253, 107168 (2020)].
- Factors involving more than three atoms can be treated in a variety of ways (e.g., have most liftings within a water molecule).
- ECMC advances N SPC/Fw water molecules with $\mathcal{O}(N \log N)$ complexity.

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- Computational complexity per MD time step: $\mathcal{O}(N \log N)$.
- Superior (Newtonian) exploration of configuration space.

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ECMC

Computational complexity per MCMC sweep: $\mathcal{O}(N \log N)$.

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- - \rightarrow Consider both involved velocities in an event.

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PH et al., J. Chem. Phys. **156**, 084108 (2022)

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<u>PH</u> et al., J. Stat. Phys. **187**, 31 (2022)

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- Strongly improves rotation dynamics of dense tethered hard-disk dipoles.
- Entirely different escape behavior from locally stable hard-disk Böröczky packings.
- Trivial choice of the optimal chain time (very large or even infinite). \rightarrow No fine-tuning of internal parameters required.

Conclusion

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 - \rightarrow ... without ever knowing U.
 - \rightarrow ...numerically exact without discretizing time (or space).
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 - \rightarrow Decorrelate N water molecules in $\mathcal{O}(N \log N)$ computational complexity.

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Outlook

- Direct comparison with MD that considers the precision in the MD algorithm. Improve dynamics beyond Newtonian dynamics (e.g., with factor fields).
- Efficiently parallelize ECMC.