Conclusion

Assorted Topics in the Monte Carlo Simulation of Polymers

Nathan Clisby MASCOS / Department of Mathematics and Statistics The University of Melbourne

> SIAM Conference on Discrete Mathematics Minneapolis June 19, 2014



.

μ

Conclusion





μ

Conclusion



- Self-avoiding walks
- Pivot algorithm

Assorted Monte Carlo 2 / 32



- Self-avoiding walks
- Pivot algorithm
- SAW-tree, a data structure for fast pivot moves



- Self-avoiding walks
- Pivot algorithm
- SAW-tree, a data structure for fast pivot moves
- How can we extend this idea?

- Self-avoiding walks
- Pivot algorithm
- SAW-tree, a data structure for fast pivot moves
- How can we extend this idea?
 - Dense polymers new symmetries

- Self-avoiding walks
- Pivot algorithm
- SAW-tree, a data structure for fast pivot moves
- How can we extend this idea?
 - Dense polymers new symmetries
 - *R*_h estimate observables

- Self-avoiding walks
- Pivot algorithm
- SAW-tree, a data structure for fast pivot moves
- How can we extend this idea?
 - Dense polymers new symmetries
 - *R*_h estimate observables
 - μ neither local nor global

- Self-avoiding walks
- Pivot algorithm
- SAW-tree, a data structure for fast pivot moves
- How can we extend this idea?
 - Dense polymers new symmetries
 - *R*_h estimate observables
 - μ neither local nor global
- Conclusion



Self-avoiding walk model

• A walk on a lattice, step to neighbouring site provided it has not already been visited.

(SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion
_					

(SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion

Assorted Monte Carlo 4 / 32

(SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion
<u> </u>					

Assorted Monte Carlo 4 / 32

(SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion



(SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion









SAW	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion
_					
		_			

SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion
Г					



SAVV	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion



SAW)	Pivot algorithm	Dense polymers	Hydrodynamic radius	μ	Conclusion
































A typical SAW of 5000 steps on the simple cubic lattice:

.





• Polymers can't have two monomers in the same place key property of polymers in a good solvent.





- Polymers can't have two monomers in the same place key property of polymers in a good solvent.
- SAW *exactly* captures universal properties of polymers.





- Polymers can't have two monomers in the same place key property of polymers in a good solvent.
- SAW *exactly* captures universal properties of polymers.
- E.g. typical size of a SAW / polymer grows with the number of monomers, *N*, as:

$$\mathbf{R}=D\mathbf{N}^{\nu}$$



- Polymers can't have two monomers in the same place key property of polymers in a good solvent.
- SAW *exactly* captures universal properties of polymers.
- E.g. typical size of a SAW / polymer grows with the number of monomers, *N*, as:

$$\mathbf{R} = DN^{\nu}$$

 D is model dependent, but the critical exponent ν is a universal quantity.

 μ

Conclusion

Pivot algorithm

• No exact solution for SAW.

μ

Conclusion

- No exact solution for SAW.
- Markov chain Monte Carlo (MCMC) sampling very powerful for SAW, especially for d = 3.

____A

Conclusion

μ

- No exact solution for SAW.
- Markov chain Monte Carlo (MCMC) sampling very powerful for SAW, especially for d = 3.
- Estimate physical properties of system by sampling from all possible configurations (state space).

Conclusion

- No exact solution for SAW.
- Markov chain Monte Carlo (MCMC) sampling very powerful for SAW, especially for d = 3.
- Estimate physical properties of system by sampling from all possible configurations (state space).
- Basic idea: generate new configurations by deforming current configuration via a "move".

Pivot algorithm

 Local moves make a small deformation, e.g. adding or removing a monomer, O(N²) moves to get an "essentially new" configuration.

μ

- Local moves make a small deformation, e.g. adding or removing a monomer, $O(N^2)$ moves to get an "essentially new" configuration.
- Global moves can do much better.

μ

- Local moves make a small deformation, e.g. adding or removing a monomer, O(N²) moves to get an "essentially new" configuration.
- Global moves can do much better.
- Pivot move: O(1) successful moves for an essentially new configuration.

- Local moves make a small deformation, e.g. adding or removing a monomer, $O(N^2)$ moves to get an "essentially new" configuration.
- Global moves can do much better.
- Pivot move: O(1) successful moves for an essentially new configuration.
- Lal (1969) invented pivot algorithm, but key paper is by Madras and Sokal (1988).

Conclusion

Pivot algorithm

• Procedure:

.

Assorted Monte Carlo 10 / 32

 μ

Conclusion

Pivot algorithm

Procedure:

Choose a pivot site at random

Assorted Monte Carlo 10 / 32

Conclusion

Pivot algorithm

Procedure:

- Choose a pivot site at random
- Then rotate or reflect one of the two parts of the walk.



Pivot algorithm

Procedure:

.

- Choose a pivot site at random
- Then rotate or reflect one of the two parts of the walk.
- Retain new walk if it is self-avoiding, otherwise restore original walk.

Pivot algorithm

Procedure:

- Choose a pivot site at random
- Then rotate or reflect one of the two parts of the walk.
- Retain new walk if it is self-avoiding, otherwise restore original walk.
- "Global" because on average half of the monomers are moved.

Pivot algorithm

Procedure:

- Choose a pivot site at random
- Then rotate or reflect one of the two parts of the walk.
- Retain new walk if it is self-avoiding, otherwise restore original walk.
- "Global" because on average half of the monomers are moved.
- Ergodic, samples SAWs uniformly at random.



Example pivot move



Example pivot move



Example pivot move

Run simulation



• Time O(N) to write down an N-step walk, so this must be best possible for pivot move?

.



- Time O(N) to write down an N-step walk, so this must be best possible for pivot move?
- In fact, don't need to write down! $\Rightarrow o(N)$ (Kennedy, 2002)



- Time O(N) to write down an N-step walk, so this must be best possible for pivot move?
- In fact, don't need to write down! $\Rightarrow o(N)$ (Kennedy, 2002)
- Bookkeeping can be handled efficiently in binary tree structure. ⇒ O(log N) (C., 2010)

_ A

SAW



SAW-tree representation of a walk.

.

Key properties of the SAW-tree data structure.

• Each node contains:

Key properties of the SAW-tree data structure.

- Each node contains:
 - Symmetry information (for rotations / reflections);

Key properties of the SAW-tree data structure.

- Each node contains:
 - Symmetry information (for rotations / reflections);
 - "Bounding box" information (for intersection testing);

Key properties of the SAW-tree data structure.

- Each node contains:
 - Symmetry information (for rotations / reflections);
 - "Bounding box" information (for intersection testing);
 - Information about moments of positions, allowing for exact calculation of $R_{\rm e}^2$ and $R_{\rm g}^2$.
Key properties of the SAW-tree data structure.

- Each node contains:
 - Symmetry information (for rotations / reflections);
 - "Bounding box" information (for intersection testing);
 Information about moments of positions, allowing for
 - exact calculation of R_e^2 and R_g^2 .
- Tree structure can be altered via "tree rotations", so that symmetry operations can be applied to any section of the walk.

μ

Key properties of the SAW-tree data structure.

- Each node contains:
 - Symmetry information (for rotations / reflections);
 - "Bounding box" information (for intersection testing); Information about moments of positions, allowing for
 - exact calculation of $R_{\rm e}^2$ and $R_{\rm g}^2$.
- Tree structure can be altered via "tree rotations", so that symmetry operations can be applied to any section of the walk.
- Binary tree has typical height $O(\log N)$.

 μ

Conclusion

Example SAW-tree moves.



 μ

Conclusion

Example SAW-tree moves.



Example SAW-tree moves.





 μ

Conclusion

Example SAW-tree moves.



Example SAW-tree moves.



 μ

Example SAW-tree moves.



Conclusion

 μ

How do we apply symmetry to steps 2,3,4? Restructure the binary tree via a "tree rotation".



Conclusion

 μ

How do we apply symmetry to steps 2,3,4? Restructure the binary tree via a "tree rotation".



How do we apply symmetry to steps 2,3,4? Restructure the binary tree via a "tree rotation".



How do we apply symmetry to steps 2,3,4? Restructure the binary tree via a "tree rotation".



How do we apply symmetry to steps 2,3,4? Restructure the binary tree via a "tree rotation".



How do we apply symmetry to steps 2,3,4? Restructure the binary tree via a "tree rotation".





• With a binary tree implementation, pivot move has *global effect* for *local cost*.



- With a binary tree implementation, pivot move has *global effect* for *local cost*.
- *O*(log *N*) for:

- With a binary tree implementation, pivot move has *global effect* for *local cost*.
- *O*(log *N*) for:
 - Rotating part of the walk.

- With a binary tree implementation, pivot move has *global effect* for *local cost*.
- *O*(log *N*) for:
 - Rotating part of the walk.
 - Checking for self-intersections between two pieces.

- With a binary tree implementation, pivot move has *global effect* for *local cost*.
- *O*(log *N*) for:
 - Rotating part of the walk.
 - Checking for self-intersections between two pieces.
 - Calculating global observables such as $R_{\rm e}^2$ and $R_{\rm g}^2$.

- With a binary tree implementation, pivot move has *global effect* for *local cost*.
- *O*(log *N*) for:
 - Rotating part of the walk.
 - Checking for self-intersections between two pieces.
 - Calculating global observables such as $R_{\rm e}^2$ and $R_{\rm g}^2$.
- Very fast, can rapidly simulate SAW with many millions of steps.

μ

- With a binary tree implementation, pivot move has global effect for local cost.
- $O(\log N)$ for:
 - Rotating part of the walk.
 - Checking for self-intersections between two pieces.
 - Calculating global observables such as R_{e}^{2} and R_{g}^{2} .
- Very fast, can rapidly simulate SAW with many millions of steps.
- How can we extend this key idea fast global moves to other models?

μ

Conclusion

Hamiltonian paths

 Hamiltonian paths are self-avoiding walks which visit every site in a graph.

Conclusion

μ

Hamiltonian paths

- Hamiltonian paths are self-avoiding walks which visit every site in a graph.
- Models crystal phase of polymers.

Conclusion

μ

Hamiltonian paths

- Hamiltonian paths are self-avoiding walks which visit every site in a graph.
- Models crystal phase of polymers.
- Examples on 20×20 and 200×200 lattice (from generator at:

http://lattice.complex.unimelb.edu.au/hamiltonian_path)



μ

Conclusion

Hamiltonian paths

• Some effective MCMC moves for sampling dense polymers are based on changing the topology of configurations.



μ

Hamiltonian paths

- Some effective MCMC moves for sampling dense polymers are based on changing the topology of configurations.
- One example: backbite move, which is likely to be ergodic for the simple cubic lattice.

 μ

Conclusion





 μ

Conclusion



 μ



 μ





 μ

Backbite moves for sampling Hamiltonian paths.





Assorted Monte Carlo 22 / 32

μ

Backbite moves for sampling Hamiltonian paths.



Each time we make a backbite move we create a loop, delete the edge which completes the loop, and *reverse* the orientation of the remaining edges of the loop.

μ

Backbite move

• For the simple cubic lattice, loops are of mean size O(N).

μ

Backbite move

- For the simple cubic lattice, loops are of mean size O(N).
- This suggests time O(N) to perform a backbite move.
_ A

μ

Backbite move

- For the simple cubic lattice, loops are of mean size O(N).
- This suggests time O(N) to perform a backbite move.
- However, can use binary tree data structure with *time reversal* as our symmetry operation.

μ

Backbite move

- For the simple cubic lattice, loops are of mean size O(N).
- This suggests time O(N) to perform a backbite move.
- However, can use binary tree data structure with *time reversal* as our symmetry operation.
- Only trick required is bookkeeping for determining neighbours.

 μ

This time binary tree has time reversal symmetry elements in the nodes.



 μ

This time binary tree has time reversal symmetry elements in the nodes.



 μ

This time binary tree has time reversal symmetry elements in the nodes.



 μ

This time binary tree has time reversal symmetry elements in the nodes.



 μ

This time binary tree has time reversal symmetry elements in the nodes.





Assorted Monte Carlo 24 / 32

 μ

This time binary tree has time reversal symmetry elements in the nodes.



 μ

How do we reverse sequences of steps which don't align with the tree?



Assorted Monte Carlo 25 / 32

.

 μ

How do we reverse sequences of steps which don't align with the tree?



μ

How do we reverse sequences of steps which don't align with the tree?



Assorted Monte Carlo 25 / 32

 μ

How do we reverse sequences of steps which don't align with the tree?





.

Assorted Monte Carlo 25 / 32

' 1



Conclusion

 μ

+

3

.

4

How do we reverse sequences of steps which don't align with the tree?



' 1



Conclusion

 μ

+

3

.

4

How do we reverse sequences of steps which don't align with the tree?



Assorted Monte Carlo 26 / 32

.

Conclusion









• Moves have mean size $O(N^{\approx 0.75})$.

Conclusion

 μ

Assorted Monte Carlo 26 / 32





- Moves have mean size $O(N^{\approx 0.75})$.
- *L* = 8192, *N* = 67 108 864: 360 000 steps, versus 6.77 tree rotations.

μ



- Z²:
 - Moves have mean size $O(N^{\approx 0.75})$.
 - *L* = 8192, *N* = 67 108 864: 360 000 steps, versus 6.77 tree rotations.





Assorted Monte Carlo 26 / 32

.

μ



- \mathbb{Z}^2 :
 - Moves have mean size $O(N^{\approx 0.75})$.
 - *L* = 8192, *N* = 67 108 864: 360 000 steps, versus 6.77 tree rotations.
- Z³:
 - Moves have mean size O(N).

Assorted Monte Carlo 26 / 32

μ



- Z²:
 - Moves have mean size $O(N^{\approx 0.75})$.
 - *L* = 8192, *N* = 67 108 864: 360 000 steps, versus 6.77 tree rotations.
- Z³:
 - Moves have mean size O(N).
 - *L* = 512, *N* = 134 217 728: 46 million steps, versus 20.6 tree rotations.

Assorted Monte Carlo 27 / 32

_ A

 μ

Hydrodynamic radius

• Calculating $R_{\rm e}^2$ easy, just keep track of ends. $R_{\rm g}^2$ almost as easy.

Assorted Monte Carlo 27 / 32

_ A

μ

- Calculating $R_{\rm e}^2$ easy, just keep track of ends. $R_{\rm g}^2$ almost as easy.
- Why not $R_{
 m h}?$

$$egin{aligned} &\mathcal{R}_{\mathrm{h}}^{-1} = rac{1}{\mathcal{N}^2} \sum_{i
eq j} rac{1}{r_{ij}} \ &\langle \mathcal{R}_{\mathrm{h}}
angle \sim \mathcal{D}_{\mathrm{h}} \mathcal{N}^
u \left(1 + rac{a}{\mathcal{N}^{1-
u}} + rac{b}{\mathcal{N}^{0.53}} + \cdots
ight) \end{aligned}$$

 μ

Hydrodynamic radius

- Calculating $R_{\rm e}^2$ easy, just keep track of ends. $R_{\rm g}^2$ almost as easy.
- Why not $R_{\rm h}$?

$$egin{aligned} & R_{
m h}^{-1} = rac{1}{\mathcal{N}^2} \sum_{i
eq j} rac{1}{r_{ij}} \ & \langle R_{
m h}
angle \sim D_{
m h} \mathcal{N}^
u \left(1 + rac{a}{\mathcal{N}^{1-
u}} + rac{b}{\mathcal{N}^{0.53}} + \cdots
ight) \end{aligned}$$

Relevant to experiments.

Assorted Monte Carlo 27 / 32

μ

Hydrodynamic radius

- Calculating $R_{\rm e}^2$ easy, just keep track of ends. $R_{\rm g}^2$ almost as easy.
- Why not *R*_h?

$$egin{aligned} & R_{
m h}^{-1} = rac{1}{\mathcal{N}^2} \sum_{i
eq j} rac{1}{r_{ij}} \ & \langle R_{
m h}
angle \sim D_{
m h} \mathcal{N}^
u \left(1 + rac{a}{\mathcal{N}^{1-
u}} + rac{b}{\mathcal{N}^{0.53}} + \cdots
ight) \end{aligned}$$

- Relevant to experiments.
- Strong corrections to scaling, large N should make a big difference.

Assorted Monte Carlo 27 / 32

μ

Hydrodynamic radius

 Can't rapidly calculate R_h, as it depends non-linearly on all O(N²) interparticle distances, c.f. O(log N) to perform a pivot.

Assorted Monte Carlo 28 / 32

μ

- Can't rapidly calculate R_h, as it depends non-linearly on all O(N²) interparticle distances, c.f. O(log N) to perform a pivot.
- So estimate *R*_h instead!

Assorted Monte Carlo 28 / 32

μ

- Can't rapidly calculate R_h, as it depends non-linearly on all O(N²) interparticle distances, c.f. O(log N) to perform a pivot.
- So estimate *R*_h instead!
- MCMC: Time average(O) = Ensemble average(O).

Assorted Monte Carlo 28 / 32

μ

- Can't rapidly calculate R_h, as it depends non-linearly on all O(N²) interparticle distances, c.f. O(log N) to perform a pivot.
- So estimate *R*_h instead!
- MCMC: Time average(O) = Ensemble average(O).
- Key insight: for an unbiased estimator E(O),
 Time average(E(O)) = Ensemble average(O).

μ

- Can't rapidly calculate R_h, as it depends non-linearly on all O(N²) interparticle distances, c.f. O(log N) to perform a pivot.
- So estimate *R*_h instead!
- MCMC: Time average(*O*) = Ensemble average(*O*).
- Key insight: for an unbiased estimator E(O), Time average(E(O)) = Ensemble average(O).
- Our estimator is a weighted version of $1/r_{ij}$, monomers *i* and *j* chosen at random.

μ

- Can't rapidly calculate R_h, as it depends non-linearly on all O(N²) interparticle distances, c.f. O(log N) to perform a pivot.
- So estimate *R*_h instead!
- MCMC: Time average(O) = Ensemble average(O).
- Key insight: for an unbiased estimator E(O), Time average(E(O)) = Ensemble average(O).
- Our estimator is a weighted version of $1/r_{ij}$, monomers *i* and *j* chosen at random.
- 1.591 ± 0.007, (Dünweg et al., 2002), vs 1.58040 ± 0.00002.

 (μ)

Counting SAW

 Number of SAW of length N, c_N, tells us about how many conformations are available to SAW of a particular length:

$$c_N \sim A \ N^{\gamma-1} \mu^N \left[1 + ext{corrections}
ight]$$

Assorted Monte Carlo 29 / 32

Assorted Monte Carlo 29 / 32

 (μ)

Counting SAW

 Number of SAW of length N, c_N, tells us about how many conformations are available to SAW of a particular length:

$$c_N \sim A \, N^{\gamma-1} \mu^N \, [1 + ext{corrections}]$$

• We wish to count c_N , and estimate μ .

 (μ)

Counting SAW

 Number of SAW of length N, c_N, tells us about how many conformations are available to SAW of a particular length:

$$c_N \sim A \, N^{\gamma-1} \mu^N \left[1 + ext{corrections}
ight]$$

- We wish to count c_N , and estimate μ .
- Can estimate $c_N/(c_{N/2})^2$ via pivot algorithm probability that when two SAW are concatenated the result is self-avoiding.

 (μ)

Counting SAW

 Number of SAW of length N, c_N, tells us about how many conformations are available to SAW of a particular length:

$$c_N \sim A \, N^{\gamma-1} \mu^N \left[1 + ext{corrections}
ight]$$

- We wish to count c_N , and estimate μ .
- Can estimate $c_N/(c_{N/2})^2$ via pivot algorithm probability that when two SAW are concatenated the result is self-avoiding.
- Then use

$$c_N = \frac{c_N}{c_{N/2}^2} \left(\frac{c_{N/2}}{c_{N/4}^2}\right)^2 \cdots c_k^{N/k}.$$

Assorted Monte Carlo 29 / 32



μ

Conclusion









 (μ)

Counting SAW

 Sites of the walk which are close to the concatenation point have a much greater influence on the probability, than sites which are far away.




Assorted Monte Carlo 31 / 32

 (μ)

- Sites of the walk which are close to the concatenation point have a much greater influence on the probability, than sites which are far away.
- Pivot sites chosen uniformly: τ̃_{int} = Ω(N) (due to trapped configurations).

Assorted Monte Carlo 31 / 32

 (μ)

- Sites of the walk which are close to the concatenation point have a much greater influence on the probability, than sites which are far away.
- Pivot sites chosen uniformly: τ̃_{int} = Ω(N) (due to trapped configurations).
- Instead, choose distance from joint uniformly from all distance scales.

Assorted Monte Carlo 31 / 32

 (μ)

- Sites of the walk which are close to the concatenation point have a much greater influence on the probability, than sites which are far away.
- Pivot sites chosen uniformly: τ̃_{int} = Ω(N) (due to trapped configurations).
- Instead, choose distance from joint uniformly from all distance scales.
- $\Rightarrow \mu = 4.684\,039\,931(27)$ (C., 2013)

 (μ)

- Sites of the walk which are close to the concatenation point have a much greater influence on the probability, than sites which are far away.
- Pivot sites chosen uniformly: $\tilde{\tau}_{int} = \Omega(N)$ (due to trapped configurations).
- Instead, choose distance from joint uniformly from all distance scales.
- $\Rightarrow \mu = 4.684\,039\,931(27)$ (C., 2013)
- This idea can be applied to other systems with additional length scales: confined polymers, bridges, star polymers, perhaps θ-polymers.

μ

Conclusion

Conclusion

 Many opportunities to look for fast algorithms for polymer systems.

μ

Conclusion

Conclusion

- Many opportunities to look for fast algorithms for polymer systems.
- Confined polymers, novel observables, dense polymers, θ-polymers, bridges, co-polymers, ···?

μ

Conclusion

Conclusion

- Many opportunities to look for fast algorithms for polymer systems.
- Confined polymers, novel observables, dense polymers, θ-polymers, bridges, co-polymers, ···?
- Pivot algorithm only part of the story.