

# Monte Carlo calculation of the hydrodynamic radius for self-avoiding walks

---

Nathan Clisby  
MASCOS, The University of Melbourne

Statistical mechanics of soft matter, (SM)<sup>2</sup>  
RMIT University, City Campus  
November 21, 2013



# Self-avoiding walk model

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



# Self-avoiding walk model

- A walk on a lattice, step to neighbouring site provided it has not already been visited.
- Models polymers in good solvent limit.



# Self-avoiding walk model

- A walk on a lattice, step to neighbouring site provided it has not already been visited.
- Models polymers in good solvent limit.
- Exactly captures universal properties such as critical exponents.





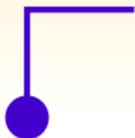
Simple random walk





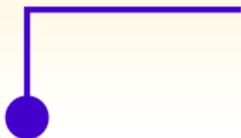
Simple random walk





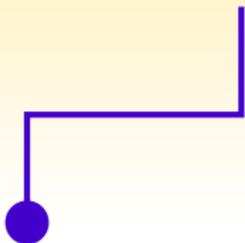
Simple random walk





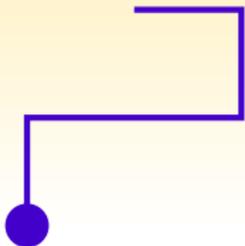
Simple random walk





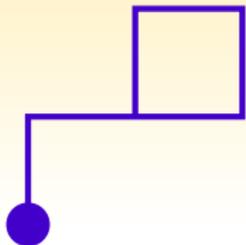
Simple random walk





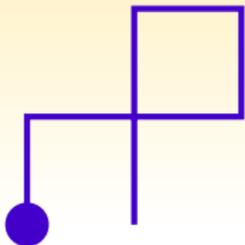
Simple random walk





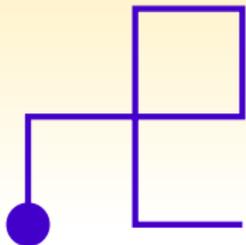
Simple random walk





Simple random walk



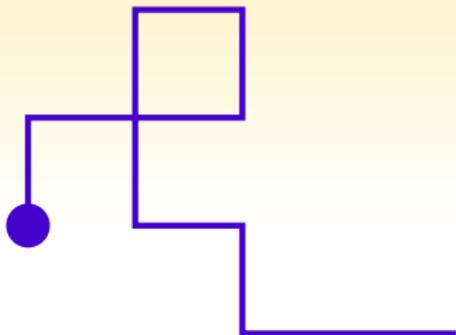


Simple random walk



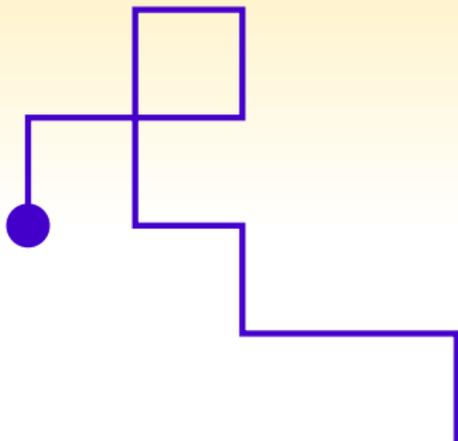






Simple random walk

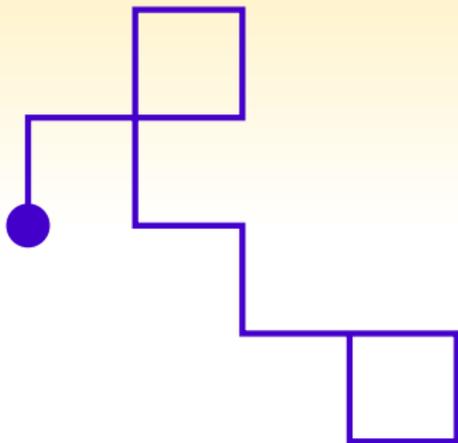




Simple random walk



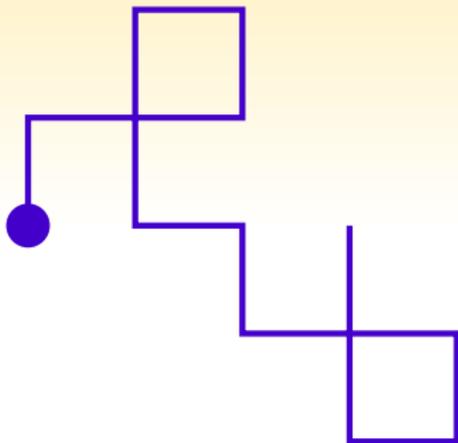




Simple random walk





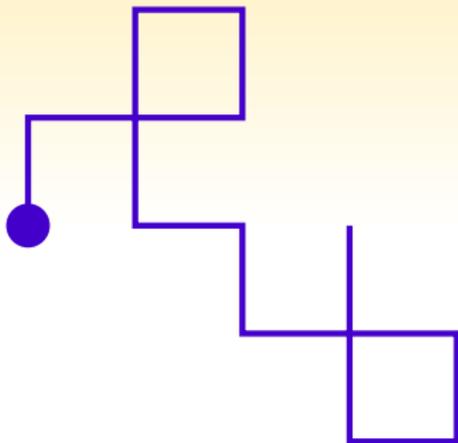


Simple random walk



Self-avoiding walk



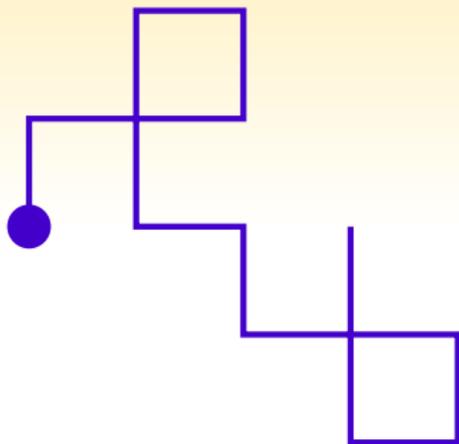


Simple random walk

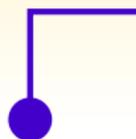


Self-avoiding walk



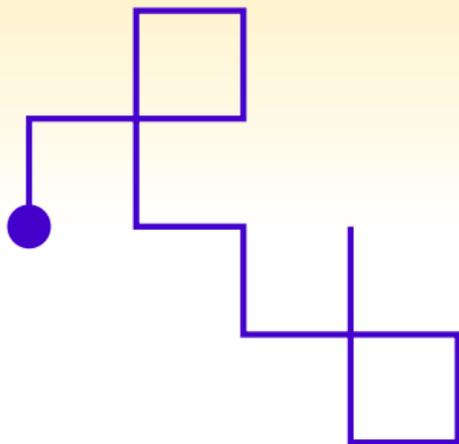


Simple random walk



Self-avoiding walk





Simple random walk



Self-avoiding walk

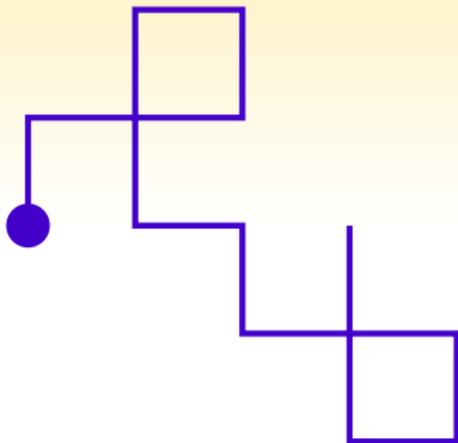




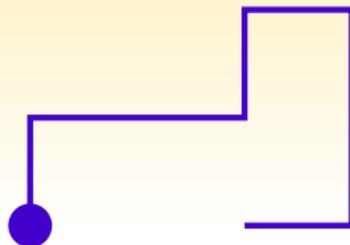






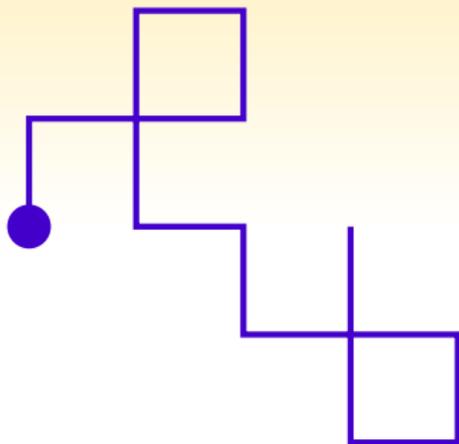


Simple random walk

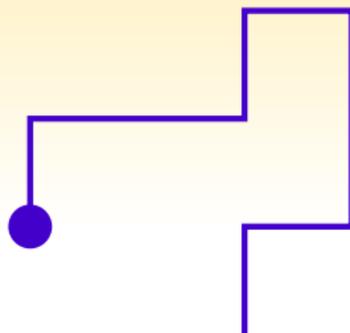


Self-avoiding walk



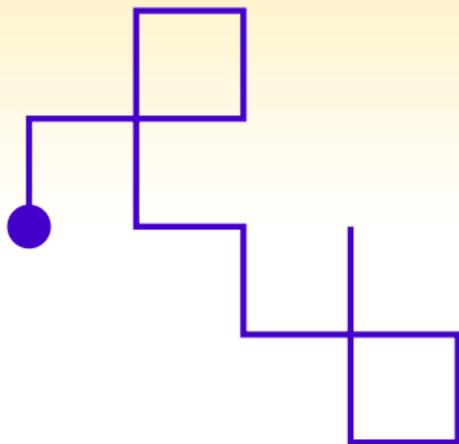


Simple random walk

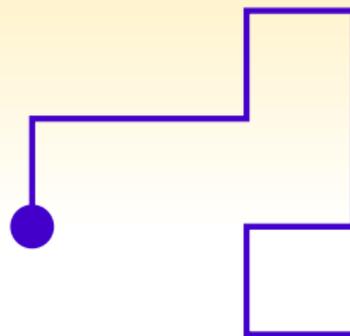


Self-avoiding walk





Simple random walk



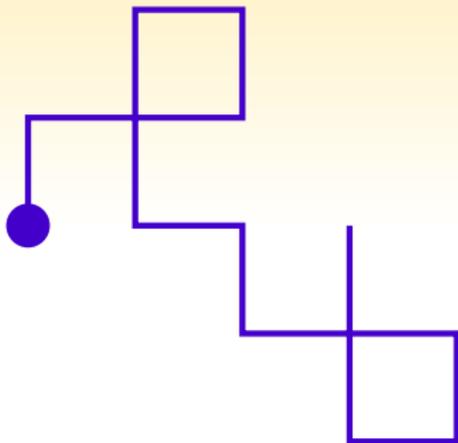
Self-avoiding walk



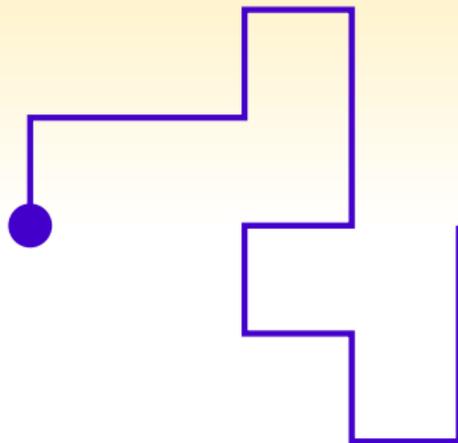








Simple random walk

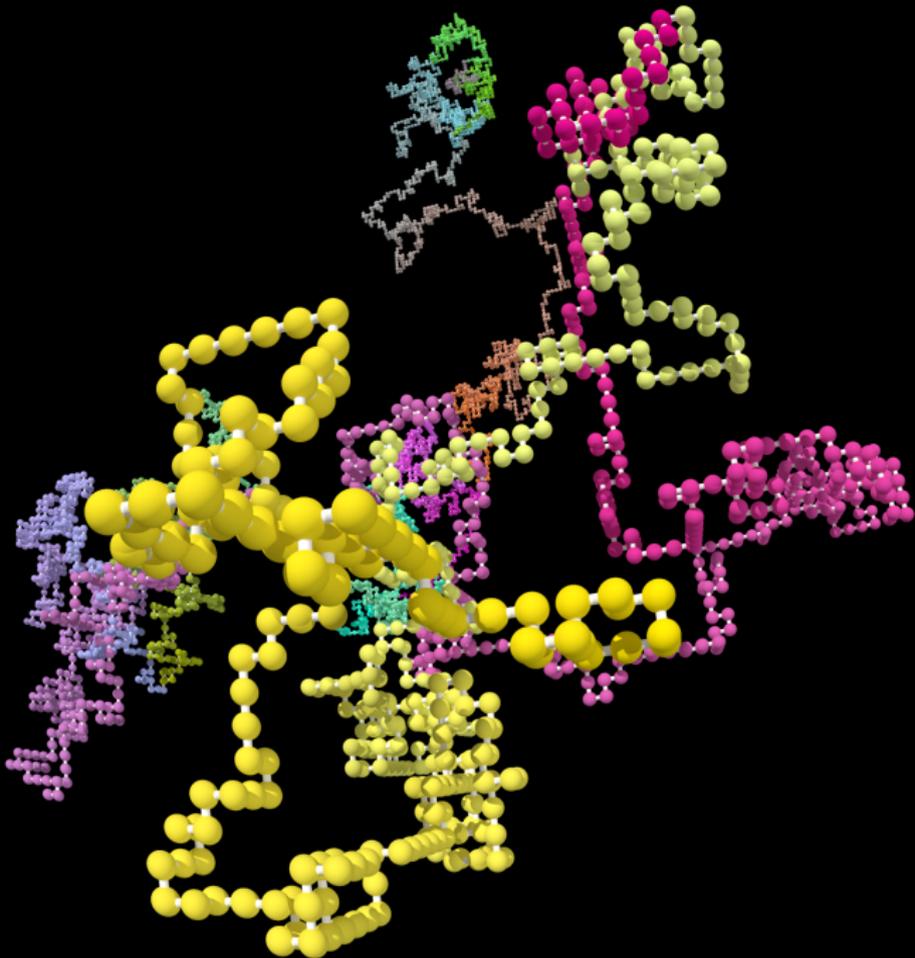


Self-avoiding walk



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





- Polymers can't have two monomers in the same place.



- Polymers can't have two monomers in the same place.
- This is *the* key property of polymers in a good solvent.



- Polymers can't have two monomers in the same place.
- This is *the* 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.
- This is *the* key property of polymers in a good solvent.
- SAW *exactly* captures universal properties of polymers.
- E.g. growth in size of a polymer grows as number of monomers increases.



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

$$R = DN^\nu$$



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

$$R = DN^\nu$$

- Size can be defined in various ways:



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

$$R = DN^\nu$$

- Size can be defined in various ways:
  - $\langle R_e^2 \rangle$ : mean square end-to-end distance



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

$$R = DN^\nu$$

- Size can be defined in various ways:
  - $\langle R_e^2 \rangle$ : mean square end-to-end distance
  - $\langle R_g^2 \rangle$ : mean square radius of gyration



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

$$R = DN^\nu$$

- Size can be defined in various ways:
  - $\langle R_e^2 \rangle$ : mean square end-to-end distance
  - $\langle R_g^2 \rangle$ : mean square radius of gyration
  - $\langle R_h \rangle$ : mean hydrodynamic radius



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

$$R = DN^\nu$$

- Size can be defined in various ways:
  - $\langle R_e^2 \rangle$ : mean square end-to-end distance
  - $\langle R_g^2 \rangle$ : mean square radius of gyration
  - $\langle R_h \rangle$ : mean hydrodynamic radius
- $D$  is non-universal, different for every kind of polymer molecule, or every choice of grid for SAW.



- Typical size of a SAW / polymer grows with the number of monomers,  $N$ , as:

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

- Size can be defined in various ways:
  - $\langle R_e^2 \rangle$ : mean square end-to-end distance
  - $\langle R_g^2 \rangle$ : mean square radius of gyration
  - $\langle R_h \rangle$ : mean hydrodynamic radius
- $D$  is non-universal, different for every kind of polymer molecule, or every choice of grid for SAW.
- Flory exponent  $\nu$  is universal! *Exactly* the same in each case.



# Pivot algorithm

- Markov chain Monte Carlo (MCMC) sampling very powerful for SAW, especially for  $d = 3$ .



# Pivot algorithm

- 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).



# Pivot algorithm

- 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

- How can we sample self-avoiding walks?



# Pivot algorithm

- How can we sample self-avoiding walks?
- Local moves make a small deformation, e.g. adding or removing a monomer,  $O(N^2)$  moves to get an “essentially new” configuration.



# Pivot algorithm

- How can we sample self-avoiding walks?
- 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 algorithm

- How can we sample self-avoiding walks?
- 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.



# Pivot algorithm

- Procedure:



# Pivot algorithm

- Procedure:
  - Choose a pivot site at random



# 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.

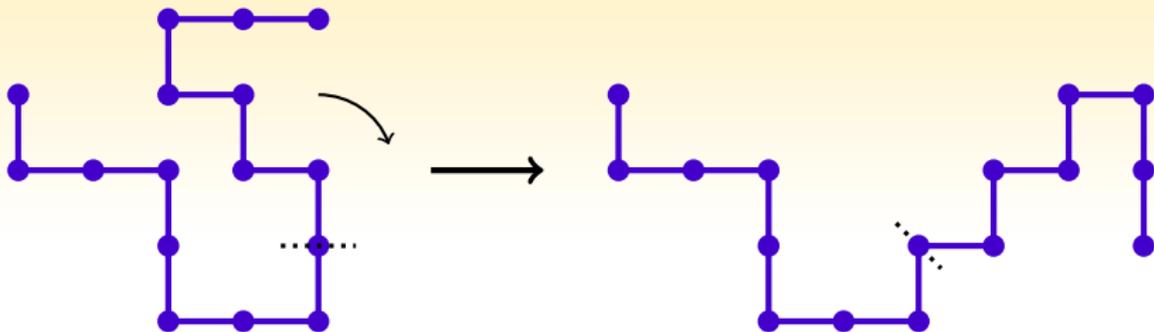


# Pivot algorithm

- 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.

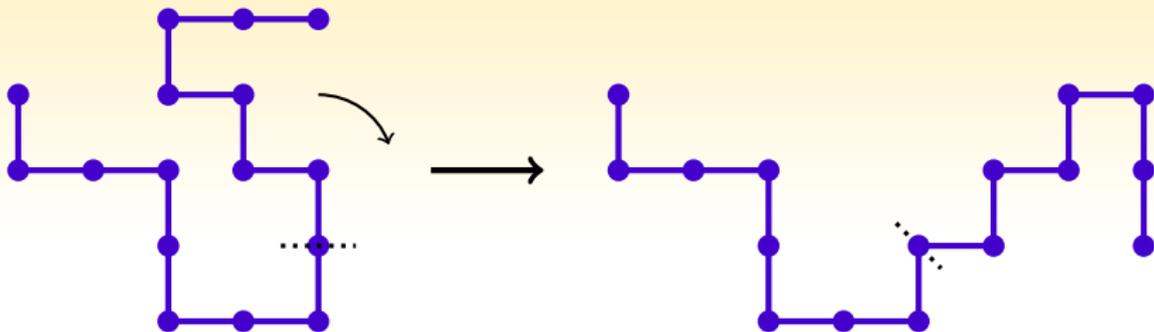






Example pivot move



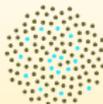


Example pivot move

Run simulation



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

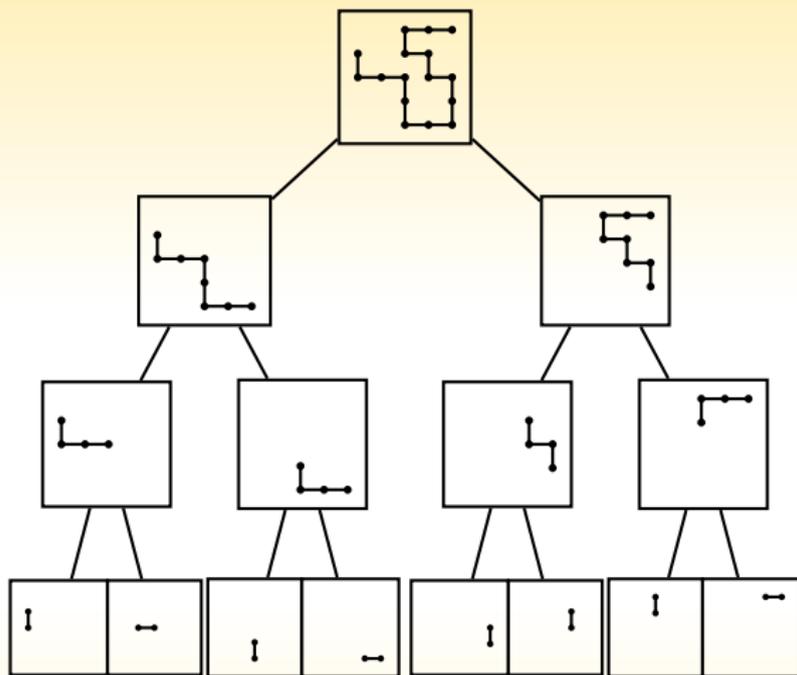


- Time  $O(N)$  to write down an  $N$ -step walk, so this must be best possible for pivot move?
- In fact, don't need to write down!



- 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!
- Bookkeeping can be handled efficiently in binary tree structure.





SAW-tree representation of a walk.



- 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.  
(Relies on the fact that monomers which are close on the chain are also close in space.)



- 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.  
(Relies on the fact that monomers which are close on the chain are also close in space.)
  - Calculating global observables such as  $R_e^2$  and  $R_g^2$ .



- 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.  
(Relies on the fact that monomers which are close on the chain are also close in space.)
  - Calculating global observables such as  $R_e^2$  and  $R_g^2$ .
- Very fast, can rapidly simulate SAW with many millions of steps.



- 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.  
(Relies on the fact that monomers which are close on the chain are also close in space.)
  - Calculating global observables such as  $R_e^2$  and  $R_g^2$ .
- Very fast, can rapidly simulate SAW with many millions of steps.
- Flory exponent:  $\nu = 0.587597 \pm 0.000009$  (Clisby, 2010).



# Hydrodynamic radius

- Calculating  $R_e^2$  easy - just need to keep track of ends.



# Hydrodynamic radius

- Calculating  $R_e^2$  easy - just need to keep track of ends.
- $R_g^2$  almost as easy.



# Hydrodynamic radius

- Calculating  $R_e^2$  easy - just need to keep track of ends.
- $R_g^2$  almost as easy.
- Burkhard (2010): Why not calculate  $R_h$ ?

$$R_h^{-1} = \frac{1}{N^2} \sum_{i \neq j} \frac{1}{r_{ij}}$$
$$\langle R_h \rangle \sim D_h N^\nu \left( 1 + \frac{a}{N^{1-\nu}} + \frac{b}{N^{0.53}} + \dots \right)$$



# Hydrodynamic radius

- Calculating  $R_e^2$  easy - just need to keep track of ends.
- $R_g^2$  almost as easy.
- Burkhard (2010): Why not calculate  $R_h$ ?

$$R_h^{-1} = \frac{1}{N^2} \sum_{i \neq j} \frac{1}{r_{ij}}$$
$$\langle R_h \rangle \sim D_h N^\nu \left( 1 + \frac{a}{N^{1-\nu}} + \frac{b}{N^{0.53}} + \dots \right)$$

- Relevant to experiments.



# Hydrodynamic radius

- Calculating  $R_e^2$  easy - just need to keep track of ends.
- $R_g^2$  almost as easy.
- Burkhard (2010): Why not calculate  $R_h$ ?

$$R_h^{-1} = \frac{1}{N^2} \sum_{i \neq j} \frac{1}{r_{ij}}$$
$$\langle R_h \rangle \sim D_h N^\nu \left( 1 + \frac{a}{N^{1-\nu}} + \frac{b}{N^{0.53}} + \dots \right)$$

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



# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.



# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.
- Answer #2 (2011): Estimate  $R_h$  instead!



# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.
- Answer #2 (2011): Estimate  $R_h$  instead!
- MCMC: Time average( $O$ ) = Ensemble average( $O$ ).



# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.
- Answer #2 (2011): 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( $O$ ).



# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.
- Answer #2 (2011): 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( $O$ ).
- This is "obvious", but identity is not commonly utilised.



# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.
- Answer #2 (2011): 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( $O$ ).
- This is "obvious", but identity is not commonly utilised.
- Our situation is unusual since calculation of the observable is the bottleneck!



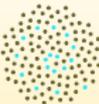
# Hydrodynamic radius

- Answer #1 (2010): Can't rapidly calculate  $R_h$ , as it depends non-linearly on all  $O(N^2)$  interparticle distances.
- Answer #2 (2011): 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( $O$ ).
- This is "obvious", but identity is not commonly utilised.
- Our situation is unusual since calculation of the observable is the bottleneck!
- Our estimator is a weighted version of  $1/r_{ij}$ , monomers  $i$  and  $j$  chosen at random.



# Results

- Estimated  $\langle R_h \rangle$  and  $\langle R_g \rangle / \langle R_h \rangle$  to extremely high precision, for SAW with lengths from 256 to 4194304.



# Results

- Estimated  $\langle R_h \rangle$  and  $\langle R_g \rangle / \langle R_h \rangle$  to extremely high precision, for SAW with lengths from 256 to 4194304.
- Clearly observed 2 competing corrections to scaling, with correct exponents.



# Results

- Estimated  $\langle R_h \rangle$  and  $\langle R_g \rangle / \langle R_h \rangle$  to extremely high precision, for SAW with lengths from 256 to 4194304.
- Clearly observed 2 competing corrections to scaling, with correct exponents.
- Estimated the universal amplitude ratio  $\langle R_g \rangle / \langle R_h \rangle$ :



# Results

- Estimated  $\langle R_h \rangle$  and  $\langle R_g \rangle / \langle R_h \rangle$  to extremely high precision, for SAW with lengths from 256 to 4194304.
- Clearly observed 2 competing corrections to scaling, with correct exponents.
- Estimated the universal amplitude ratio  $\langle R_g \rangle / \langle R_h \rangle$ :
  - $1.591 \pm 0.007$ , (Dünweg et al., 2002).



# Results

- Estimated  $\langle R_h \rangle$  and  $\langle R_g \rangle / \langle R_h \rangle$  to extremely high precision, for SAW with lengths from 256 to 4194304.
- Clearly observed 2 competing corrections to scaling, with correct exponents.
- Estimated the universal amplitude ratio  $\langle R_g \rangle / \langle R_h \rangle$ :
  - $1.591 \pm 0.007$ , (Dünweg et al., 2002).
  - $1.58040 \pm 0.00002$ .



# Conclusion

- Recently developed algorithms have radically improved our ability to sample SAW.



# Conclusion

- Recently developed algorithms have radically improved our ability to sample SAW.
- New approach allows us to calculate “difficult” observables such as  $R_h$ .



# Conclusion

- Recently developed algorithms have radically improved our ability to sample SAW.
- New approach allows us to calculate “difficult” observables such as  $R_h$ .
- Estimated  $\langle R_h \rangle$  with unprecedented accuracy.



# Conclusion

- Recently developed algorithms have radically improved our ability to sample SAW.
- New approach allows us to calculate “difficult” observables such as  $R_h$ .
- Estimated  $\langle R_h \rangle$  with unprecedented accuracy.
- Extend to dense polymers, off-lattice walks,  $\theta$ -polymers.



# Conclusion

- Recently developed algorithms have radically improved our ability to sample SAW.
- New approach allows us to calculate “difficult” observables such as  $R_h$ .
- Estimated  $\langle R_h \rangle$  with unprecedented accuracy.
- Extend to dense polymers, off-lattice walks,  $\theta$ -polymers.
- Release an open source software library for polymer simulation.



# Conclusion

- Recently developed algorithms have radically improved our ability to sample SAW.
- New approach allows us to calculate “difficult” observables such as  $R_h$ .
- Estimated  $\langle R_h \rangle$  with unprecedented accuracy.
- Extend to dense polymers, off-lattice walks,  $\theta$ -polymers.
- Release an open source software library for polymer simulation.
- Combine Monte Carlo and molecular dynamics?



