

Enhanced screening in polymer melts with periodic boundary conditions

Nathan Clisby
Swinburne University of Technology
Melbourne, Australia
nclisby@swin.edu.au

AIP Congress
Adelaide
13 December, 2022

Dense polymer systems

- Joint work with Burkhard Dünweg of MPI for Polymer Research, Mainz.
- Polymer melt: very dense system of polymers where each polymer interacts with many other polymers.
- Two competing effects: self-repulsion causes the walk to spread out (like for the self-avoiding walk), while crowding from neighbouring polymers compresses the polymer.
- Remarkably, to leading order these effects cancel, and in a polymer melt each individual chain behaves like a simple random walk and obeys Gaussian statistics.¹ This is known as “Flory screening”.

¹de Gennes, P. G., *Scaling Concepts in Polymer Physics*, Cornell University Press: 1979.

Dense polymer systems

- We measure correlations in the chain via the bond correlation function:

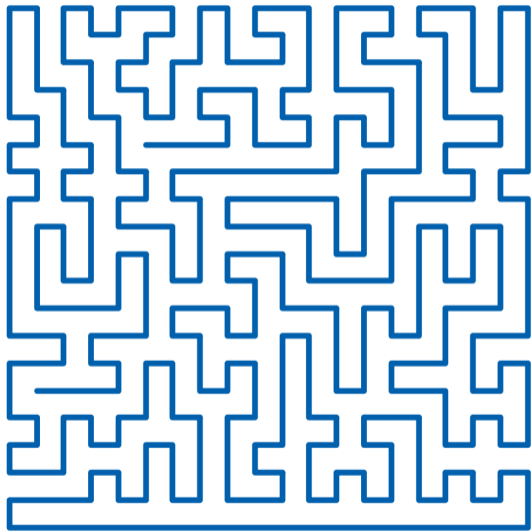
$$C(s) = \frac{1}{b^2} \langle \vec{l}_i \cdot \vec{l}_{i+s} \rangle$$

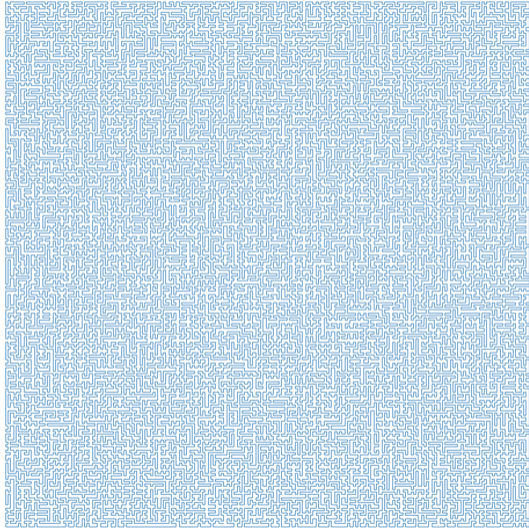
- For a random walk / Brownian motion, $C(s)$ decays exponentially rapidly.
- In a melt, the leading-order correction causes $C(s)$ to decay with a power law²:
 $C(s) \sim s^{-3/2}$.
- We wish to study within chain correlations and other phenomena, e.g. knotting.
- Difficult, because dynamics (including molecular dynamics) for long polymers very slow due to entanglement.

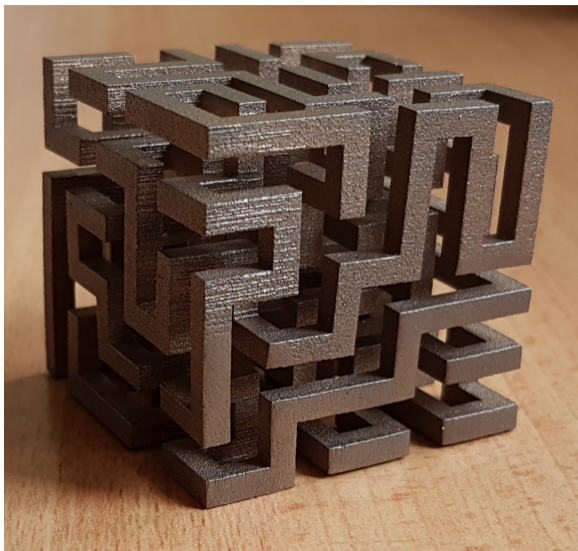
²Wittmer, J. P. et al. *EPL (Europhysics Letters)* **2007**, 77, 56003.

Hamiltonian paths

- Hamiltonian paths are self-avoiding walks which visit every vertex in a graph.
- Generally take the graph to be a region of the square or simple cubic lattices.
- Model of the crystal phase of polymers.
- Can extend to polymer melts which involve many paths.
- Universality implies that these lattice models capture essential physics of dense polymer systems.
- What do they look like?







Sampling dense polymer systems

- Connectivity changing Monte Carlo moves, in particular backbite moves, very effective.
- Due to slow equilibration of polymer melts, the quest for efficient Monte Carlo moves has been of interest for a long time.
- For system size N , equilibration in $O(N)$ Markov chain time steps.

Partial history of connectivity changing moves

- Early work in 1980s by Olaj and Lantschbauer³, Mansfield⁴.
- Later: Deutsch⁵, Theodorou and collaborators⁶, Jacobsen and collaborators⁷.

³Olaj, O. F.; Lantschbauer, W. *Macromolecular Rapid Communications* **1982**, *3*, 847–858.

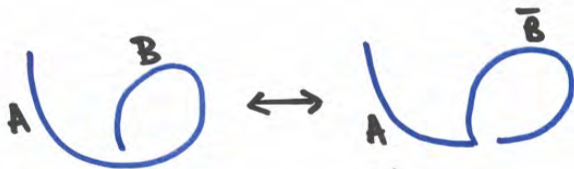
⁴Mansfield, M. L. *J. Chem. Phys.* **1982**, *77*, 1554–1559.

⁵Deutsch, J. M. *J. Chem. Phys.* **1997**, *106*, 8849–8854.

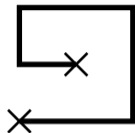
⁶Karayiannis, N. C. et al. *J. Chem. Phys.* **2002**, *117*, 5465–5479.

⁷Jacobsen, J. L. *Phys. Rev. Lett.* **2008**, *100*, 118102.

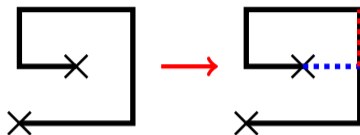
Backbite move: choose an end, extend by a single step which will form a loop, traverse loop in opposite direction and delete last bond.



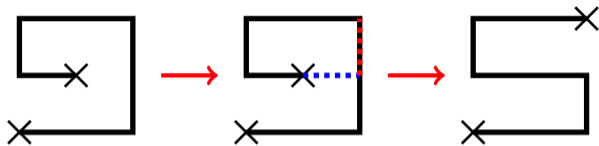
Backbite moves for sampling Hamiltonian paths.



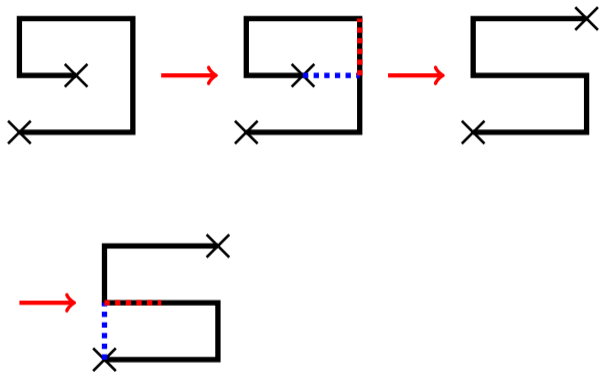
Backbite moves for sampling Hamiltonian paths.



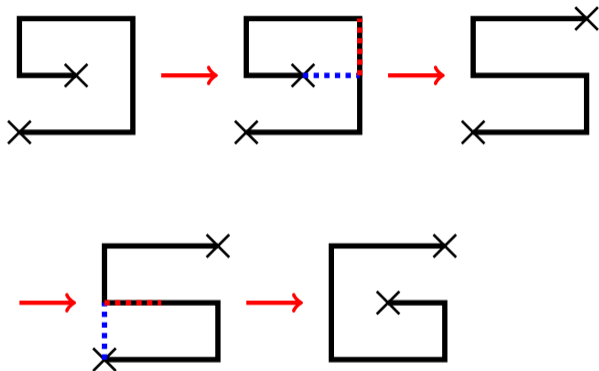
Backbite moves for sampling Hamiltonian paths.



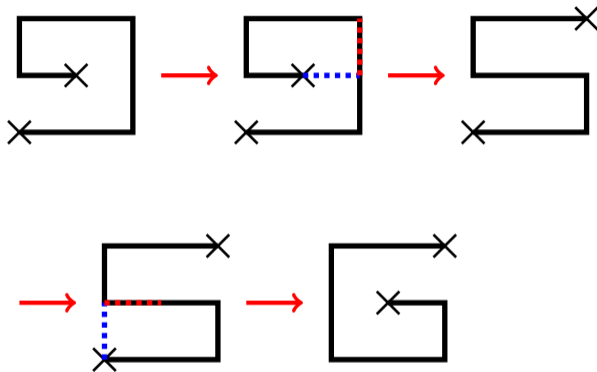
Backbite moves for sampling Hamiltonian paths.



Backbite moves for sampling Hamiltonian paths.



Backbite moves for sampling Hamiltonian paths.

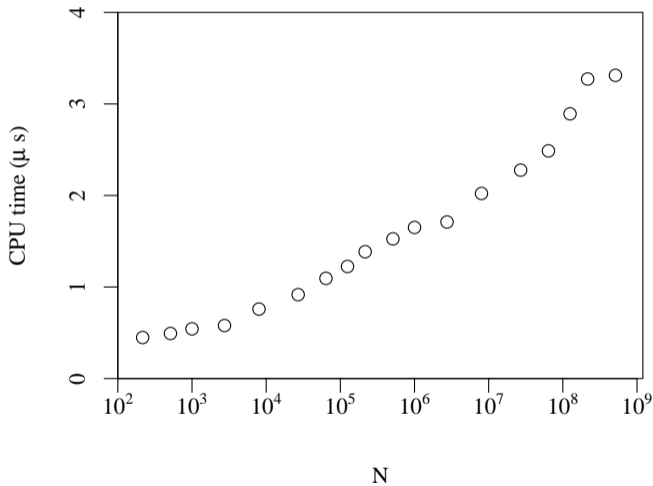


Each time we make a backbite move we create a loop, delete the edge that completes the loop, and *reverse* the orientation of the remaining edges of the loop.

Backbite implementation

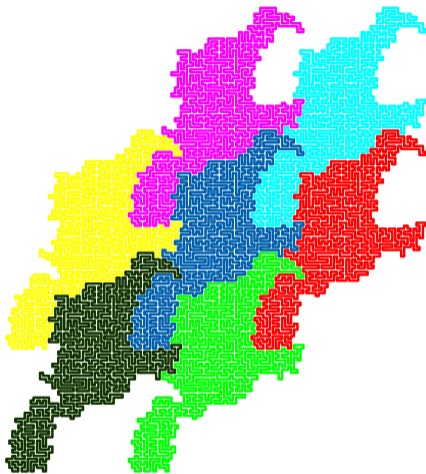
- For the simple cubic lattice, loops are of mean size $O(N)$.
- \Rightarrow mean CPU time per backbite move $O(N)$?
- Binary tree implementation: to reverse $O(N)$ steps requires $O(\log N)$ operations (“tree rotations”).
- For simple cubic lattice, mean size of loops is $O(N)$.
- $L = 800$, $N = 512$ million:
 - Reverse 178 million steps, ...
 - ... or perform 18.7 tree rotations.
- Very fast in practice.

CPU time per backbite move \mathbb{Z}^3

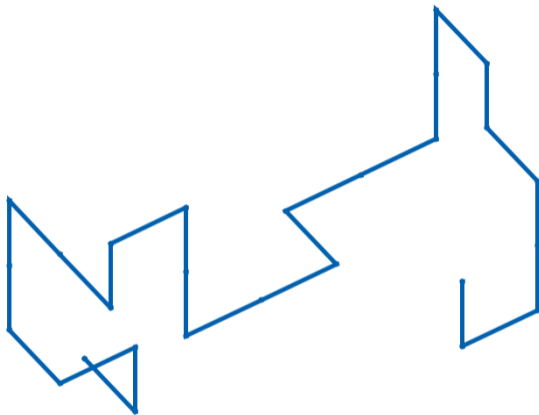


A single dense polymer with PBC

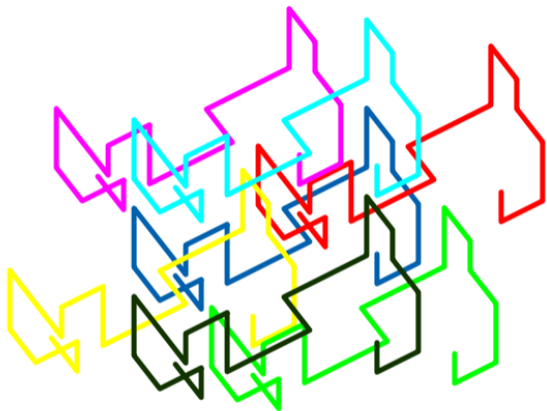
- Can a Hamiltonian path with periodic boundary conditions (PBC) reproduce behaviour of a polymer melt?
- Can explicitly see random walk behaviour for $d = 3$ when we unwind it.
- Multiple copies are space filling, because in reduced coordinates the walk must fill the original grid.
- In the large N limit, do we get the same behaviour as the polymer melt?



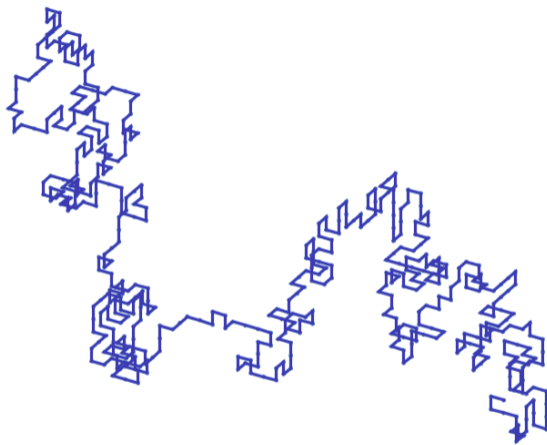
40×40 grid, with copies from winding.
Note that the walk is disc like.



$3 \times 3 \times 3$ grid.



$3 \times 3 \times 3$ grid, with copies from winding around.



$8 \times 8 \times 8$ grid; random walk behaviour clearly observable.

A single dense polymer with PBC

- $N = L^3$; random walk behaviour.
- Subchains of length s do not “feel” the boundary until they wind around the box, that is when

$$s^{1/2} = L = N^{1/3};$$
$$\Rightarrow s = L^2 = O(N^{2/3}).$$

- For $s \ll L^2$ we expect that the subchain will behave as in a melt.
- A priori unclear what will happen for $s \gg L^2$.

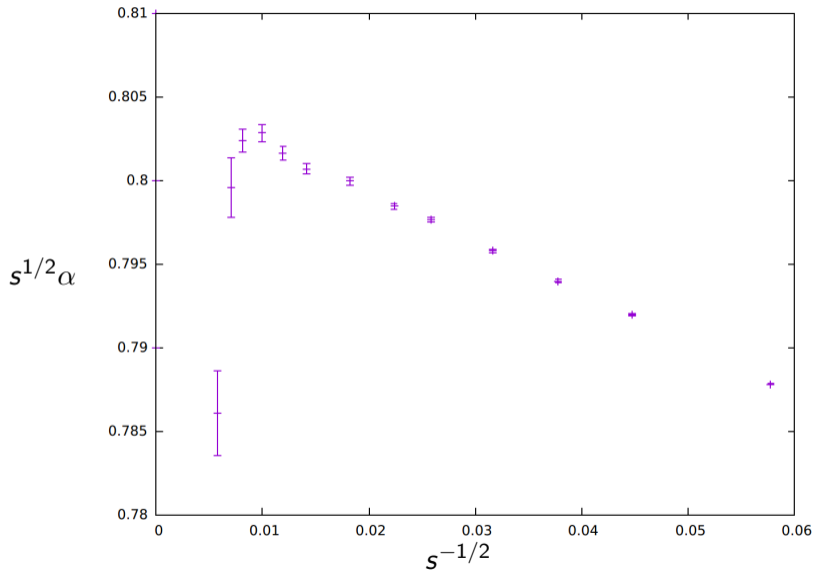
A single dense polymer with PBC

- Wittmer et al. predicted power-law within-chain correlations. This results in leading correction to scaling for $\langle R_E^2 \rangle$ to be $O(s^{-1/2})$ for a chain of length s .
- Expect that universal amplitude ratios assume random walk values.
- Together:

$$\frac{\langle R_E^4 \rangle}{\langle R_E^2 \rangle^2} = \frac{5}{3} \left(1 + \frac{a}{s^{1/2}} + \frac{b}{s} + \dots \right)$$

- We sample systems with $L = 300$ so $N = 27 \times 10^6$, and expect that subchains of length $s \lesssim L^2 = 9000$ will behave as if they are in a melt.
- Estimate:

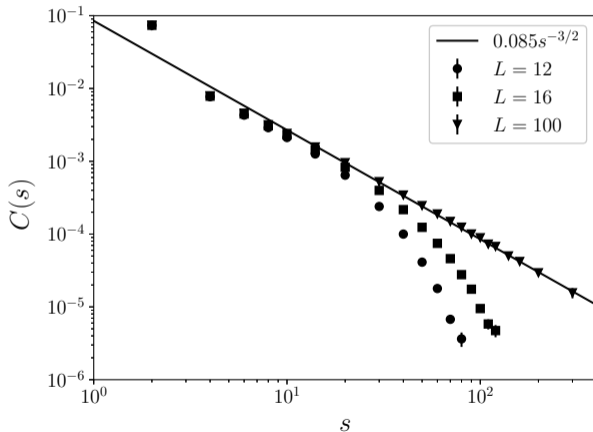
$$\alpha = \frac{\langle R_E^4 \rangle}{\langle R_E^2 \rangle^2} - \frac{5}{3}, \quad s^{1/2} \alpha = a' + \frac{b'}{s^{1/2}} + \dots$$



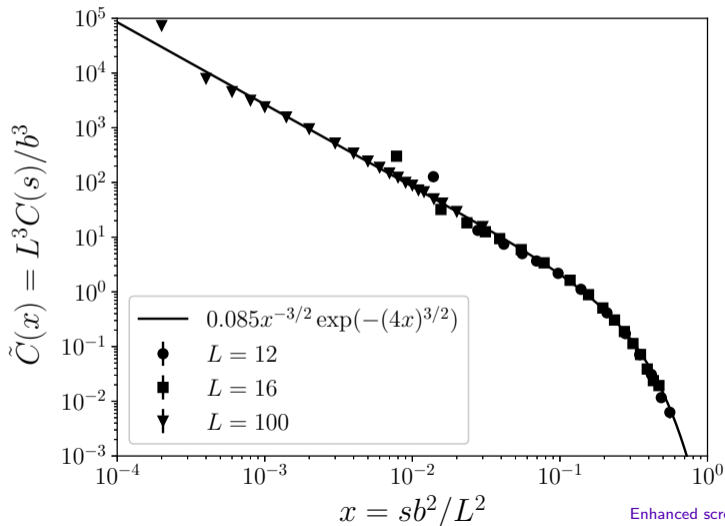
Bond-vector autocorrelation

We study the bond-vector autocorrelation function $C(s)$, where s is the separation along the chain.

- Expect $C(s)$ decays as $s^{-3/2}$; this leads to the $s^{-1/2}$ correction term for $\langle R_E^4 \rangle / \langle R_E^2 \rangle^2$.
- But, once $s \sim L^2$ decay is far more rapid! The autocorrelations are screened once the walk wraps around the box.
- Data collapse possible in terms of a scaling variable.



$\tilde{C}(x) = (L^3/b^3)C(s)$ as a function of the finite-size scaling variable $x = sb^2/L^2$.
(Note that the error bars are not visible at this scale.)



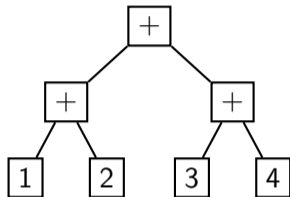
Conclusion

- Backbite moves can be implemented very efficiently via a binary tree.
- Working with subchains of single long chain with PBC seems like a viable way to understand melts.
- We verify Wittmer et al.'s prediction of the $s^{-3/2}$ decay in correlations and $s^{-1/2}$ correction to the universal amplitude ratio to high precision.
- Open questions regarding enhanced convergence / Flory screening.
- Numerically well understood, and we have a complete empirical description.
- Paper being written up now . . .

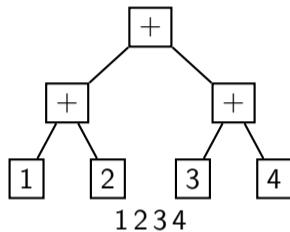
Conclusion

- Backbite moves can be implemented very efficiently via a binary tree.
- Working with subchains of single long chain with PBC seems like a viable way to understand melts.
- We verify Wittmer et al.'s prediction of the $s^{-3/2}$ decay in correlations and $s^{-1/2}$ correction to the universal amplitude ratio to high precision.
- Open questions regarding enhanced convergence / Flory screening.
- Numerically well understood, and we have a complete empirical description.
- Paper being written up now ...
- ... but we are in search of a theory from first principles!

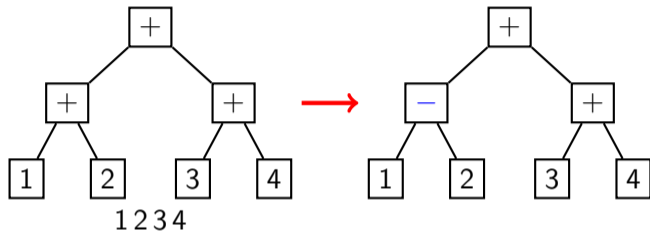
Time reversal symmetry elements in the binary tree nodes.



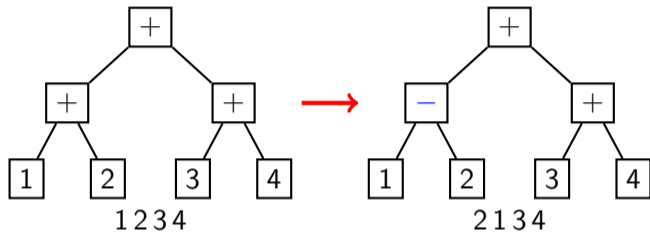
Time reversal symmetry elements in the binary tree nodes.



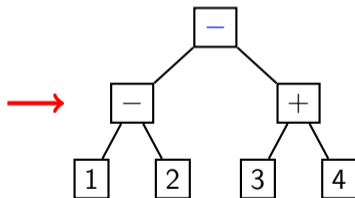
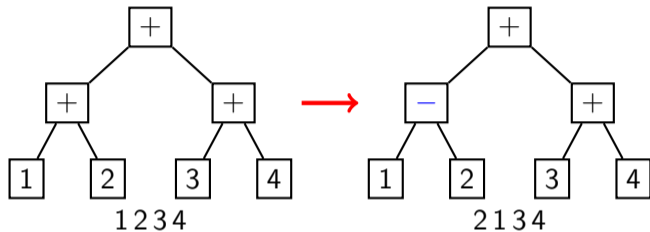
Time reversal symmetry elements in the binary tree nodes.



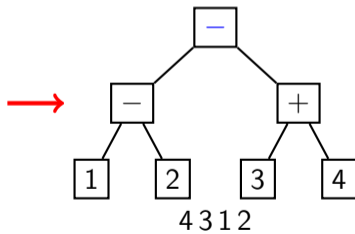
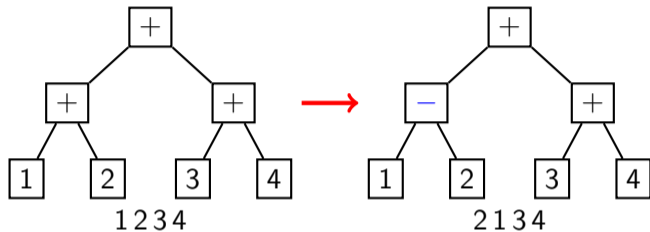
Time reversal symmetry elements in the binary tree nodes.



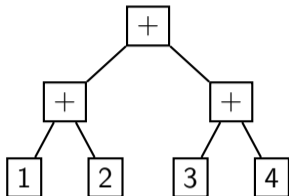
Time reversal symmetry elements in the binary tree nodes.



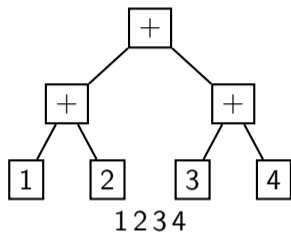
Time reversal symmetry elements in the binary tree nodes.



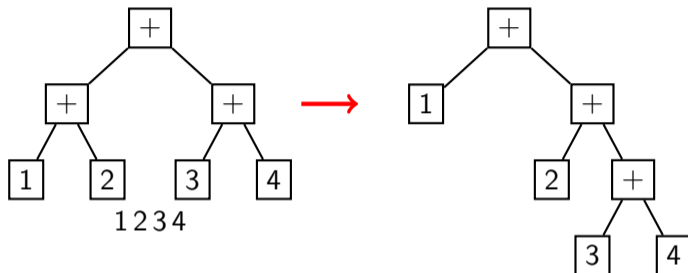
How do we reverse sequences of steps which don't align with the tree?



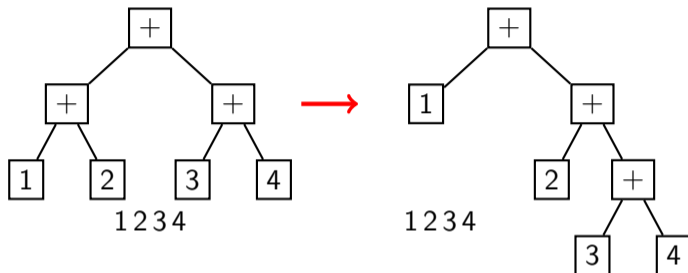
How do we reverse sequences of steps which don't align with the tree?



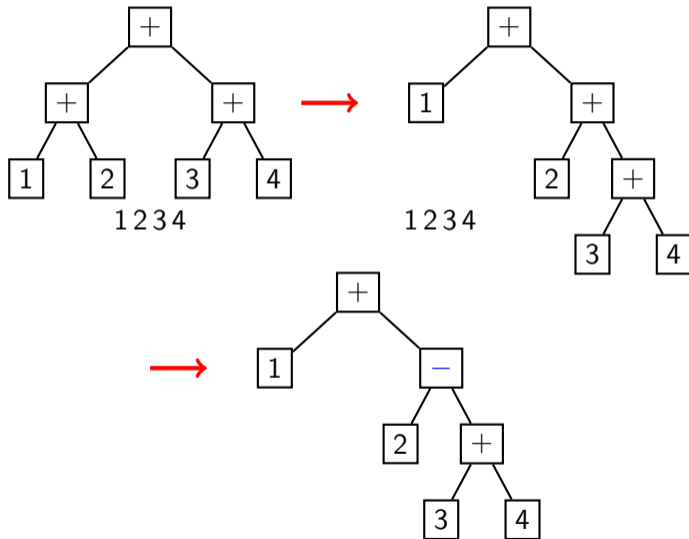
How do we reverse sequences of steps which don't align with the tree?



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



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



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

