Adaptive error control for diffusion Monte Carlo

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- Typical DMC has a single time step for all electrons and moves
- Some electron configurations are problematic for fixed time steps
 - Near nodes, the drift vector must diverge
 - Local energy near nuclei is badly behaved
 - Core electrons have different time scales than valence electrons
- Time step should adapt based on the region of simulation space

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Continuous-time DMC

- Generate paths of length τ from a random walk with a drift velocity ν = ∇ log Ψ_T
- Weight each path R(t) by $w(R) = \exp\left[-\int_0^{\tau} (E_{loc}(R(t)) - E_{ref})dt\right]$
- Standard DMC is one discretization of this method
- Non-constant drift vector and local energy causes time step bias

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- Position error is approximately $\frac{\tau}{2} |v(R_1) v(R_0)|$
- Weight error is approximately $\frac{\tau}{2} |E_{loc}(R_1) E_{loc}(R_0)|$
- These quantities are available for free in a DMC simulation

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- What if drift vector or local energy varies significantly over a move?
- Rejection enforces detailed balance but does not eliminate bias
- Poor moves should be split in two by a Brownian bridge

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- Midpoint of a random walk with known ends is a Gaussian centered at the average of the ends with 1/4 the variance
- Drifted random walks are improved by refining the underlying random walk
- Refinement is recursive

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- Time step bias goes to zero as error tolerances go to zero, but only for whole-configuration moves
- Unrefined moves have no time penalty over nonadaptive moves
- Refinement has a 50% time penalty
- Whole-configuration moves are inefficient for refining drift vectors
- Analogue of single-electron moves is needed for efficiency

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- Exact detailed balance lost
- Needs Heun propagator to retain approximate detailed balance
- Algorithm is useful only if time step error is dominated by relatively few configurations
- Whole-configuration refinement will scale poorly

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- Exact single-electron propagation does not eliminate time step bias
- Single-electron move bias goes to zero as the time step goes to zero
- Can determine if electrons interact from wavefunction cross-derivatives

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- ► Two electrons e₁ and e₂ are connected in configuration R if ∂_{e1}v_{e2}(R) is large
- Connected electrons should be moved together to avoid single-electron move bias
- Connectedness is symmetric
- Connectedness divides the electrons in a given configuration into *clusters*
- Cluster moves avoid single-electron move bias

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Adaptive cluster moves

- 1. Move all electrons
- 2. Look at magnitude of drift vector change for each electron
- 3. Mark electron for refinement if drift vector change is above threshold
- 4. Refine moves of all marked electrons
- Clusters are not explicitly determined but are always moved together
- All time step related bias should go to zero as error tolerance goes to zero

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- Poor DMC moves can be systematically improved
- Adaptive moves should speed simulations when a variety of time scales is needed
- Cluster moves are needed to avoid single-electron move bias
- Future work
 - Testing algorithmic efficiency
 - Investigate optimum tolerances
 - Reincorporate detailed balance
 - Predict correct time step to reduce refinement penalty

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