2007 Summer School on Computational Materials Science Quantum Monte Carlo: From Minerals and Materials to Molecules July 9 –19, 2007 • University of Illinois at Urbana–Champaign http://www.mcc.uiuc.edu/summerschool/2007/qmc/



Reptation Monte Carlo and other topics

David Ceperley

University of Illinois

Reptation Monte Carlo and other topics

OUTLINE

- Review of Diffusion Monte Carlo and Path Integral Monte Carlo
- Path Integral representation of the projector Method
- What action to use?
- How to sample paths?
- Advantages and disadvantages
- Excited states and MaxEnt(?)

REFERENCES

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Diffusion Monte Carlo process

- Imaginary time SE.
- This is a diffusion + branching process.
- Justify in terms of Trotter's theorem.
- Requires interpretation of the wavefunction as a probability density.

$$-\frac{\partial \psi(R,t)}{\partial t} = (H - E_T)\psi(R,t)$$
$$H = -\sum_{i} \frac{\hbar^2}{2m_i} \nabla_i^2 + V(R)$$
$$\int_{-\frac{\partial \psi(R,t)}{\partial t}} = -\sum_{i} \frac{\hbar^2}{2m_i} \nabla_i^2 \psi(R,t)$$
$$-\frac{\partial \psi(R,t)}{\partial t} = (V(R) - E_T)\psi(R,t)$$

Trotter's theorem

- How do we find the solution of:
- The operator solution is:
- Trotter's theorem (1959):

$$\frac{d\hat{\rho}}{dt} = (A+B)\hat{\rho}$$
$$\hat{\rho} = e^{(A+B)t}$$

$$\hat{\rho} = \lim_{n \to \infty} \left[e^{\frac{t}{n}\hat{A}} e^{\frac{t}{n}\hat{B}} \right]^n$$

• Assumes that A,B and A+B are reasonable operators.

$$\left\langle R_{0}\left|\left[e^{\frac{t}{n}\hat{A}}e^{\frac{t}{n}\hat{B}}\right]^{n}\right|R_{n}\right\rangle = \left\langle R_{0}\left|e^{\frac{t}{n}\hat{A}}\right|R'_{1}\right\rangle\left\langle R'_{1}\left|e^{\frac{t}{n}\hat{B}}\right|R_{1}\right\rangle....\left\langle R_{n-1}\left|e^{\frac{t}{n}\hat{A}}\right|R'_{n}\right\rangle\left\langle R'_{n}\left|e^{\frac{t}{n}\hat{B}}\right|R_{n}\right\rangle\right\rangle$$

- This means we just have to figure out what each operator does independently and then alternate their effect. This is rigorous in the limit as $n \rightarrow \infty$.
- In the DMC case A is diffusion operator, B is a branching operator.
- Just like "molecular dynamics" At small time we evaluate each operator separately.

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Importance Sampling

Kalos 1970. Ceperlev 1979

- Why should we sample the wavefunction? The physically correct pdf is $|\phi|^2$.
- Importance sample (multiply)by trial wavefunction. ۲

$$f(R,t) \equiv \psi_T(R)\phi(R,t) \qquad \lim_{t \to \infty} f(R,t) \equiv \psi_T(R)\phi_0(R)$$
$$-\frac{\partial f(R,t)}{\partial t} = \psi_T(R)H[f(R,t)/\psi_T(R)]$$

 $-\frac{\partial f(R,t)}{\partial t} = -\lambda \nabla^2 f - \lambda \nabla \left(2f \nabla \ln \psi_T(R)\right) + \left(\psi_T^{-1} H \psi_T\right) f(R,t)$ Evolution = diffusion + drift + branching

- •
- Use accept/reject step for more accurate evolution. ٠ make acceptance ratio>99%. Determines time step.
- We have three terms in the evolution equation. Trotter's theorem still • applies.

- To the pure diffusion algorithm we have added a drift step that pushes the random walk in directions of increasing trial function: $R' = R + 2\lambda \tau \nabla \ln \psi_{\tau}(R)$
- Branching is now controlled by the local energy

$$E_L(R) - E_T = \psi^{-1}(R)\widehat{H}\psi(R) - E_T$$

- Because of zero variance principle, fluctuations are controlled.
- Cusp condition can limit infinities coming from singular potentials.
- We still determine E_T by keeping asymptotic population stable.

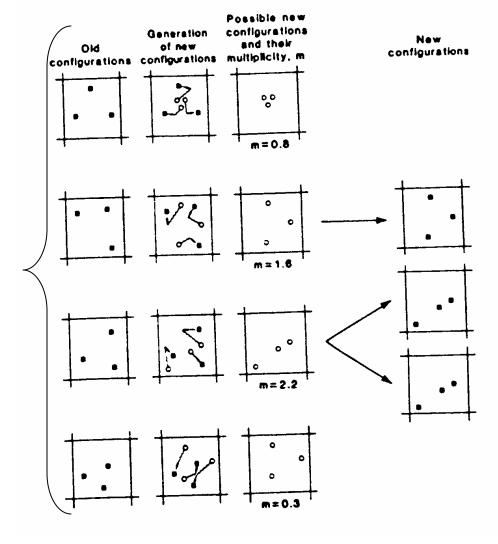
$$E_0 = \lim_{t \to \infty} \frac{\int dR\phi(R, t) H\psi_T(R)}{\int dRf(R, t)} \approx \left\langle E_{\psi}(R) \right\rangle_{f(\infty)}$$

Schematic of DMC

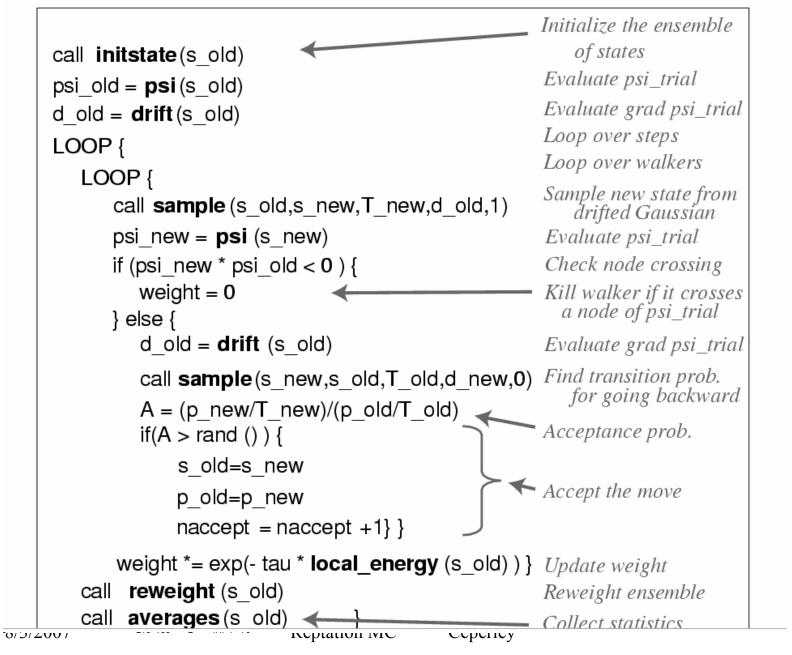
Ensemble evolves according to

- Diffusion
- Drift
- branching

ensemble



DIFFUSION MONTE CARLO CODE



Fixed-node method

- Initial distribution is a pdf. It comes from a VMC simulation.
- Drift term pushes walks away from the nodes.
- Impose the condition:
- This is the fixed-node BC
- Will give an upper bound to the exact energy, the best upper bound consistent with the FNBC.

$$f(R,0) = \left| \psi_T(R) \right|^2$$

$$\phi(R) = 0$$
 when $\psi_T(R) = 0$.

$$E_{FN} \ge E_0$$

$$E_{FN} = E_0 \text{ if } \phi_0(R)\psi(R) \ge 0 \text{ all } R$$

•f(R,t) has a discontinuous gradient at the nodal location.

- •Accurate method because Bose correlations are done exactly.
- •Scales well, like the VMC method, as N³. Classical complexity.
- •Can be generalized from the continuum to lattice finite temperature, magnetic fields, ...
- •One needs trial functions with accurate nodes. 8/3/2007 Reptation MC Ceperley

Fixed-Phase method

Ortiz, Martin, DMC 1993

Generalize the FN method to complex trial functions:

٠

 $\Psi(R) = e^{-U(R)}$ Since the Hamiltonian is Hermitian, the variational energy is real:

$$E_{V} = \frac{\int dR \ e^{-2\Re U(R)} \left[V(R) + \lambda \nabla^{2} U(R) - \lambda \left[\Re \nabla U(R) \right]^{2} + \lambda \left[\Im \nabla U(R) \right]^{2} \right]}{\int dR \ e^{-2\Re U(R)}}$$

- We see only one place where the energy depends on the phase of the wavefunction.
- If we fix the phase, then we add this term to the potential energy. In a magnetic field we get also the vector potential.

effective potential= $V(R) + \sum_{i} \lambda_i \left[A(r_i) + \Im \nabla_i U(R) \right]^2$

- We can now do VMC or DMC and get upper bounds as before.
- The imaginary part of the local energy will not be zero unless the right • phase is used.
- Used for twisted boundary conditions, magnetic fields, vortices, • phonons, spin states, ... Reptation MC Ceperley

The mixed estimator problem

- Problem is that PMC samples the wrong distribution.
- OK for the energy
- Linear extrapolation helps correct this systematic error

$$\left\langle A \right\rangle_{M} \equiv \frac{\int dR\psi^{*}(R) A\phi(R)}{\int dR\psi^{*}(R) \phi(R)}$$
$$\left\langle A \right\rangle_{o} \equiv \frac{\int dR\phi^{*}(R) A\phi(R)}{\int dR\phi^{*}(R) \phi(R)}$$
S
$$\left\langle A \right\rangle_{V} \equiv \frac{\int dR\psi^{*}(R) A\psi(R)}{\int dR\psi^{*}(R) \psi(R)}$$

$$\left\langle A \right\rangle_{0} \simeq 2 \left\langle A \right\rangle_{M} - \left\langle A \right\rangle_{V} + O\left(\left(\phi - \psi\right)^{2}\right)$$
$$\left\langle A \right\rangle_{0} \simeq \frac{\left\langle A \right\rangle_{M}^{2}}{\left\langle A \right\rangle_{V}} + O\left(\left(\phi - \psi\right)^{2}\right) \text{ for the density}$$

 $\langle A \rangle_{M} = \langle A \rangle_{V} \Rightarrow \int dR (\phi - \psi)^{2}$ minimized wrt A

- Other solutions:
 - Maximum overlap
 - Forward walking
 - Reptation/path integrals

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Path Integral Monte Carlo

• We sample the distribution:

$$e^{-\sum_{i=1}^{M} S(R_i, R_{i+1}; \tau)} / Z$$
 where $Z = \int dR_1 ... dR_M e^{-\sum_{i=1}^{M} S(R_i, R_{i+1}; \tau)}$

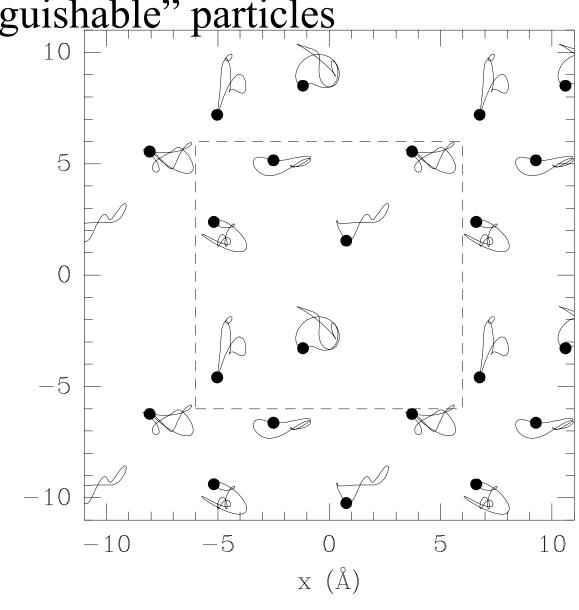
Where the "primitive" <u>link action</u> is:

$$S(R_0, R_1; \tau) = -\frac{3N}{2} \ln(4\pi\lambda\tau) + \frac{(R_0 - R_1)^2}{4\lambda\tau} + \frac{\tau}{2} \left[V(R_0) + V(R_1) \right]$$

- Similar to a classical integrand where each particle turns into a "polymer."
 - K.E. is spring term holding polymer together.
 - P.E. is inter-polymer potential.
- Trace implies $R_1 = R_{m+1} \Rightarrow$ closed or ring polymers ^{8/3/2007} Reptation MC Ceperley

"Distinguishable" particles

- Each atom is a ring polymer; an exact representation of a quantum wavepacket in imaginary time.
- Trace picture of 2D helium The dots represent the "start" of the path. (but all \succ points are equivalent)
- The lower the real • temperature, the longer the "string" and the more spread out the wavepacket.



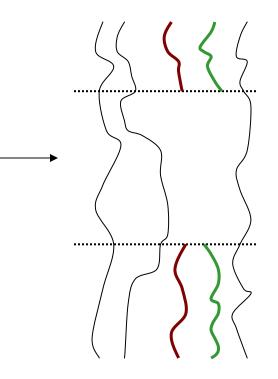
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PIMC Sampling considerations

- Metropolis Monte Carlo that moves a single variable is too slow and will not generate permutations.
- We need to move many time slices together
- Key concept of sampling is how to sample a "<u>bridge</u>": construct a path starting at R_0 and ending at R_t .
- How do we sample R_{t/2}? GUIDING RULE. Probability is:

$$P(R_{t/2}) = \frac{\left\langle R_0 \left| e^{-tH/2} \right| R_{t/2} \right\rangle \left\langle R_{t/2} \left| e^{-tH/2} \right| R_t \right\rangle}{\left\langle R_0 \left| e^{-tH} \right| R_t \right\rangle}$$



How to sample a single slice.

- pdf of the midpoint of the bridge:(a pdf because it is positive, and integrates to 1)
- For free particles this is easy-a Gaussian distribution
- PROVE: product of 2 Gaussians is a Gaussian.
- Interaction reduces P(R) in regions where spectator atoms are.
- Better is correlated sampling: we add a bias given by derivatives of the potential (for justification see RMP pg 326)
- Sampling potential U_s is a smoothed version of the pair action.

$$P(R_{t/2}) = \frac{\left\langle R_0 \left| e^{-tH/2} \right| R_{t/2} \right\rangle \left\langle R_{t/2} \left| e^{-tH/2} \right| R_t \right\rangle}{\left\langle R_0 \left| e^{-tH} \right| R_t \right\rangle}$$

$$R_{t/2} = \frac{1}{2} (R_0 + R_t) + \eta$$
$$\sigma^2 = \lambda t / 2 = \langle \eta^2 \rangle$$

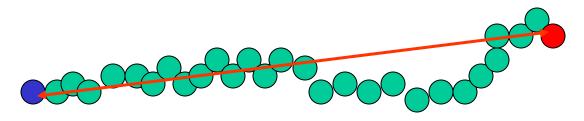
$$R_{t/2} = \frac{1}{2} \left(R_0 + R_t \right) + \lambda t \nabla U_s \left(R_{t/2}^0 \right) + \eta$$
$$= \frac{1}{2} \left(\frac{1}{2} - \frac{1}{2} \left(\frac{1}{2} - \frac{1}{2} - \frac{1}{2} - \frac{1}{2} \left(\frac{1}{2} - \frac{1}{2} - \frac{1}{2} - \frac{1}{2} \right) \right)$$
$$= \frac{1}{2} \left(\frac{1}{2} - \frac{1}$$

Reptation Monte Carlo (RQMC) Ground State Path Integral (PIGS or GSPI)

- Similar technique to Diffusion MC:
 - Instead of (imaginary time=computer time), keep entire path in memory
 - Update with a Metropolis based method instead of branching diffusing random walks
- Two key questions:
 - How to move the paths?
 - Reptation means move like a snake. This is how polymers can move.
 - Bisection since they are path integrals
 - What to use for the action
 - DMC action
 - Path Integral action
- Advantages
 - Get exact properties: no forward walking or mixed estimators
 - Good for energy differences.

Polymer Reptation (slithering snake)

- Polymers move very slowly because of entanglement.
- A good algorithm is "reptation."
 - Choose end at random.
 - Cut off one end and stick onto the other end.



- Sample directly the bonding interaction
- Acceptance probability is change in non-bonding potential.
- Simple moves go quickly through polymer space.
 - But Ergodic? Not always (what if both ends get trapped?)
- Decorrelation time is $O(N^2)$..
- Completely unphysical dynamics or is it?
 - This is how entangled polymers actually move. (theory of de Gennes)

Ground State Path Integrals

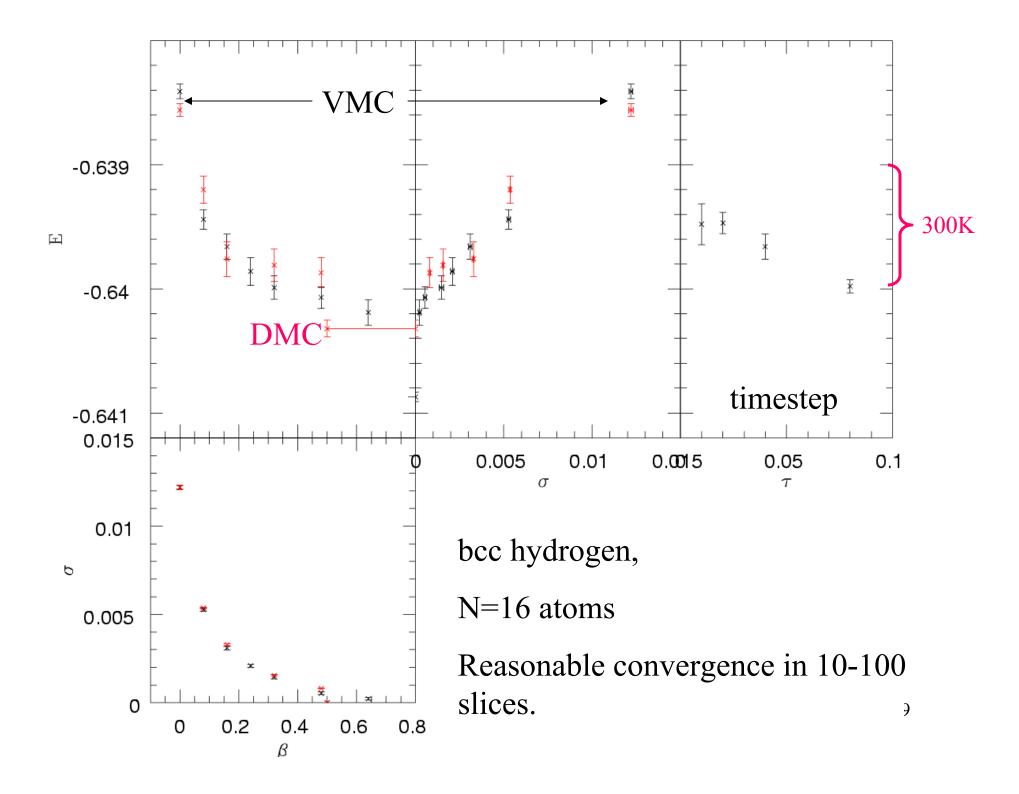
Project a trial function as in DMC.

 $\Psi(\beta) = e^{-\frac{\beta}{2}H}\Psi$ $\Psi(\beta) \text{ converges to the exact ground state as a function of imaginary time.}$ $E(\beta) = e^{-\frac{\beta}{2}H}\Psi$ $E(\beta) = \frac{\langle \Psi(\beta)H\Psi(\beta)\rangle}{\langle \Psi(\beta)\Psi(\beta)\rangle} = \langle E_L(R_0)\rangle_{\beta}$ $E(\beta) \text{ is an upper bound converging to the exact answer monotonically}$ $Z(\beta) = \langle \Psi(\beta)\Psi(\beta)\rangle = \langle \Psi e^{-\beta H}\Psi\rangle = \int dR_0 \dots dR_p\Psi(R_0)\langle R_0 e^{-\tau H}R_1\rangle \dots \langle R_{p-1}e^{-\tau H}R_p\rangle\Psi(R_p)$ $\tau = \frac{\beta}{p} = \text{timestep}$ $\sigma^2(\beta) = \langle \delta E_L(R_0)\delta E_L(R_p)\rangle = -\frac{dE(\beta)}{d\beta}$ R_0

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Metropolis algorithm

Three key concepts:

- 1. Sample by using an ergodic random walk.
- 2. Determine equilibrium state by using detailed balance
- 3. Achieve detailed balance by using rejections.

Detailed balance: $\pi(s) P(s \rightarrow s') = \pi(s')P(s' \rightarrow s)$. *Rate balance from s to s'*.

Put $\pi(s)$ into the master equation.

$$\sum_{s} \pi(s) P(s \to s') = \sum_{s} \pi(s') P(s' \to s) = \pi(s') \sum_{s} P(s' \to s) = \pi(s')$$

- Hence $\pi(s)$ is an eigenfunction.
- If $P(s \implies s')$ is ergodic then $\pi(s)$ is the unique steady state solution. ^{8/3/2007} Reptation MC Ceperley 20

General Metropolis MC

Metropolis achieves detailed balance by *rejecting* moves. Break up transition probability into sampling and acceptance:

$$P(s \to s') = T(s \to s')A(s \to s')$$
$$T(s \to s') = \text{sampling probability}$$
$$A(s \to s') = \text{acceptance probability}$$

The optimal acceptance probability that gives detailed balance is:

$$A(s \to s') = \min\left[1, \frac{T(s' \to s)\pi(s')}{T(s \to s')\pi(s)}\right]$$

Note that normalization of $\pi(s)$ is not needed or used!

Reptation moves

- Let d be the direction of the move
 - -1 tail move
 - +1 head move

$$T_d\left(s \to s'\right)$$

- Standard method.
 - Choose "d" at random:
 - Acceptance probability is:

$$s = (R_1 \quad R_2 \quad \dots \quad R_{p-1} \quad R_p)$$
$$s' = (R \quad R \quad R \quad R \quad R \quad R)$$

 r_{p+1}

$$T(s \to s') = \frac{1}{2} \Big[T_{-1}(s \to s') + T_1(s \to s') \Big] \qquad a = \frac{T(s' \to s)\pi(s')}{T(s \to s')\pi(s)} = \frac{T_{-d}(s' \to s)\pi(s')}{T_d(s \to s')\pi(s)}$$

- Sample the same Gaussian used in DMC!
- Change in action involves wavefunction at new point, and previously saved numbers Takes O(p²) steps to decorrelate..
- One way reptation gives the wrong answers.
- <u>Bounce method</u>:
 - add "d" to the state.
 - Change "d" only on rejections.
 - Use same acceptance formula!!
 - Does not satisfy detailed balance but still gives correct answer since it is an eigenfunction of T.
 - Moves are 1/(rejection rate) times more effective!

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Link action

- PIMC method: pair action plus nodal action ٠
- DMC method. Use importanced-sampled evolution to suggest action • (good for accurate trial functions)

$$\left\langle R \left| e^{-\tau H} \right| R' \right\rangle = \frac{\psi(R')}{\psi(R)} \exp\left[-\frac{\left(R' - R - \tau F \right)^2}{4\lambda\tau} - \tau E_L(R) \right]$$

Symmetrize with respect to R and R' to get higher accuracy.

- time step is longer in RQMC than in DMC because action is ٠ symmetric (Hermitian).
- For fixed-phase: add a potential to avoid the sign problem. Exact answer if potential is correct. $(\operatorname{Im}\nabla\ln\Psi)^2$
- Local energy enters through the acceptance rate and not through the • branching.

Averages

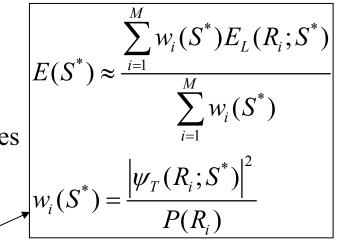
• Take them in the middle of the reptile.

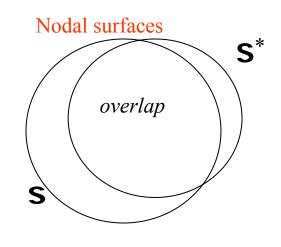
$$\langle O \rangle = \lim_{\beta \to \infty} \langle \Psi(\beta) O \Psi(\beta) \rangle = \langle O(R_{p/2}) \rangle$$

- But you need to make p twice as large for averages (energy always converges faster)
- Forward walking with DMC is inherently unstable for long projection times because of weight fluctuations.
- No instability in RQMC; perhaps an ergodic problem.
- Little loss of efficiency in taking the middle with bounce algorithm, since every point is the middle one time.

Energy difference methods

- We need a fast way of computing difference: [E(S)-E(S*)]
- Naïve (<u>direct</u>) method is to do separate (uncorrelated) samples of S and S*. Noise increases by √2.
- Correlated methods map S walks into S* walks.
- Simplest is "VMC re-weighting" (1-sided)
- With fixed-node fermions, we need to worry about changes in the nodal surfaces. 1-sided methods can give the wrong answer because the distributions are not defined in the same regions of path space.
- Reptation is convenient because we know the probability for a path.





"Reptile" space



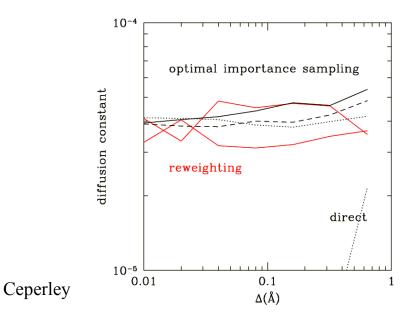
Optimal Importance Sampling

• What distribution has the lowest variance for the energy difference? (ignoring autocorrelation effects)

$$p(s) \propto \left| \Psi_1(s)^2 \Delta E_{L1} - \Psi_2(s)^2 \Delta E_{L2} \right|$$
$$p(s) \sim \left| \Psi_1(s) \right|^2 + \left| \Psi_2(s) \right|^2$$

Reptation MC

- Sum of squares is almost as good, and eliminates barriers which might be hard to cross.
- Symmetric in the two distributions.
- 2 orders of magnitude faster



COMPARISON OF METHODS

they are all based on thermal density matrix

they share features: the action, the sampling

DMC

- State space: P walkers
- Action/Dynamics determined by H
- Observables have mixed estimator problem-need to do forward walking
- No permutations
- Trial function & trial energy
- Population bias
- Energy is "zero variance""

RQMC

- State space: reptile & direction
- Action fixed/Dynamics arbitrary
- Single particle moves more difficult
- Observables from middle of path
- Trial function
- Projection bias
- Energy is "zero variance"

PIMC

- State space: closed path & permutation
- Action fixed/Dynamics arbitrary
- Observables anywhere
- Particle statistics=Permutations
- Temperature>0! T=0 expensive.

Calculation of excited-state energies

Correlation Function MC: J. Chem. Phys. 89, 6316 (1988).

- No fixed-node upper bound for all excited states.
- Construct a basis of trial functions spanning excited states ulletin question. $\{f_i(R)\}$ $1 \leq i \leq M$
- Using VMC, calculate all the matrix elements as a function of imaginary time
- Find lowest energy in this basis
- Solve the generalized eigenvalue problem:
- $N_{ii}(t) \equiv \langle f_i \mid f_i \rangle$ McDonald's theorem $H_{ii}(t)C_i^{\lambda} = E(t)^{\lambda}N_{ii}(t)C_i^{\lambda}$ $H_{ii}(t) \equiv \left\langle f_i \left| H \right| f_i \right\rangle$
- E_k approaches the exact eigenvalue from above. Then
- Use correlated sampling to calculate all energies together. $|\psi|^2 = \sum |f_n|^2$ Best guiding function:

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Properties of solution to GEP

• For a basis of size m, there exist "m" eigenvalues and orthonormal eigenfunctions:

$$\psi_n(R) = \sum_{k=1}^m a_{k,n} f_k(R)$$
$$\langle \psi_n \psi_m \rangle = a_n^* S_{nm} a_m = \delta_{nm}$$

• McDonald's theorem: the nth eigenvalue in a basis is an upper bound to the nth "exact eigenvalue.

$$E_0 \le E_1 \le E_2 \le \dots \le E_m$$
$$E_n^{ex} \le E_n$$

- We can always lower all the energies by augmenting the basis
- When basis is complete, we get exact answers!
- Orthogonality taken into account in the solution.

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Diffusion/Reptation Monte Carlo method

• The time-evolved basis approaches the exact eigenfunctions:

$$f_i(R, t) = e^{-tH/2}f_i(R)$$

• Using bosonic DMC (no nodes) or reptation calculate the N and H as a function of imaginary time. Note, H=dN/dt.

$$N_{ij}(t) \equiv \left\langle f_i \left| e^{-t\hat{H}} \right| f_j \right\rangle$$

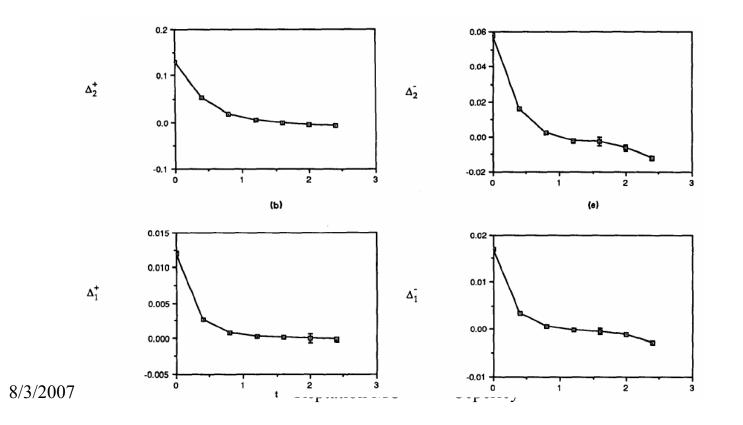
- In reptation it is the end-end correlation function
- Use same guiding function for importance sampling.
- Solve the generalized eigenvalue problem:

$$H_{ij}(t)a_i^{\lambda} = E(t)^{\lambda}N_{ij}(t)a_i^{\lambda}$$

• Then $E^{\lambda}(t)$ approaches the exact λ^{th} energy exponentially fast and from above.

Typical results

- Look for plateau in energy.
- Error bars grows exponentially in time (sign problem).
- Best results are for lower energy states
- Can use symmetry to reduce matrix size.



Remarks on CFMC

- Zero variance principle applies.
- Can treat a large basis and hence get a whole spectrum at once.
- Sign problem is still there. In practice "t" cannot be too large.
- If nodes in the DMC are present, excited state energies will be wrong.
- Maybe MaxEnt methods can do better. But problems working in energy space. Much better in effective Hamiltonian space.
- Difficult to make realistic basis for many-body systems.

Exciton-Exciton scattering

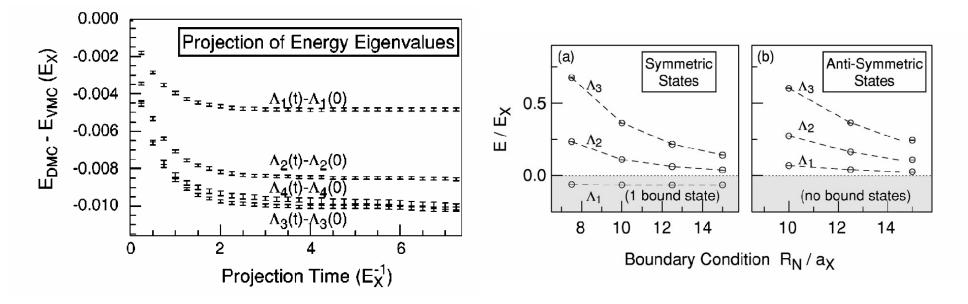
Shumway and DC, Phys. Rev. B 63, 165209-165215 (2001).

- 4-quantum particles
- Boundary conditions and energy determine phase shifts
- Use excited state method to get exact energies inside boundaries.



$$r_c \Rightarrow E_0, E_1, E_2, \dots \Rightarrow k_0, k_1, k_2, \dots$$

 $(r_c, k_n) \Rightarrow \delta(k_n) \Rightarrow \sigma(k)$



Imaginary time correlations

• With PIMC and DMC we can calculate imaginary time dynamics: $F_O(\tau) = Z^{-1} \left\langle Oe^{-\tau \hat{H}} Oe^{-(\beta - \tau)\hat{H}} \right\rangle$

(DMC corresponds to $\beta \rightarrow \infty$)

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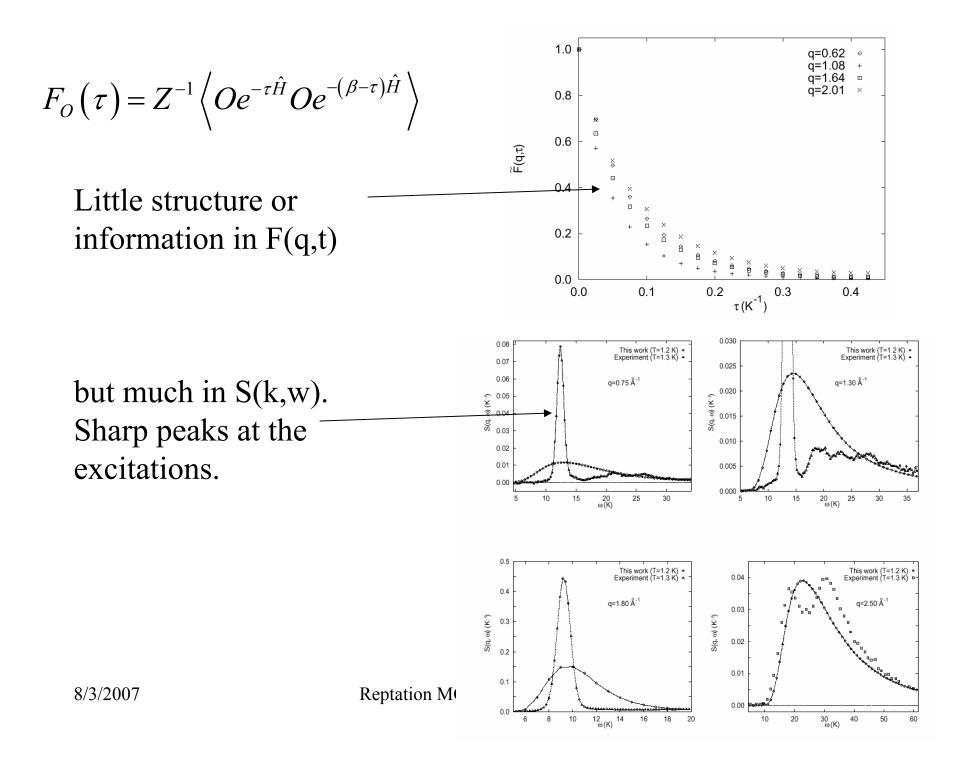
- If we could determine this analytically we could just substitute imaginary values of τ for real values.
- Dynamic structure function is the response to a density perturbation is (e.g. density-density response)

$$S_{k}(\omega) = \frac{1}{2\pi} \int_{-\infty}^{\infty} dt e^{i\omega t} F_{k}(t) \text{ where } O = \frac{1}{\sqrt{N}} \sum_{i=1}^{N} e^{i\vec{k}\cdot\vec{r_{i}}}$$
$$F_{k}(\tau) = \int_{-\infty}^{\infty} d\omega e^{-\tau\omega} S_{k}(\omega)$$

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Bayes' theorem

- What is the most probable value of $S_k(w)$ given:
 - The PIMC data
 - Prior knowledge of $S_k(w)$.
- Bayes' theorem (also used by Laplace)

 $\Pr(S(\omega)|F(t)) \propto P_L(F(t)|S(\omega))P_P(S(\omega))$

• Likelihood function follows from central limit theorem $P_{L}(F(t)|S(\omega)) \propto \exp\left[-\frac{1}{2}\sum_{\tau,\tau'}\delta F(\tau)\sigma(\tau,\tau')^{-1}\delta F(\tau')\right]$ $\delta F(\tau) = F(\tau) - \langle F(\tau) \rangle \text{ and } \sigma(\tau,\tau') = \langle \delta F(\tau)\delta F(\tau') \rangle$ • But what to choose for the prior P_p(S)? Typical choice is the "entropy." $P_{P}(S(\omega)) \propto \exp\left[\alpha \sum_{\omega} S(\omega) \ln(S(\omega) / m(\omega))\right]$ Now two routes to making the inversion:

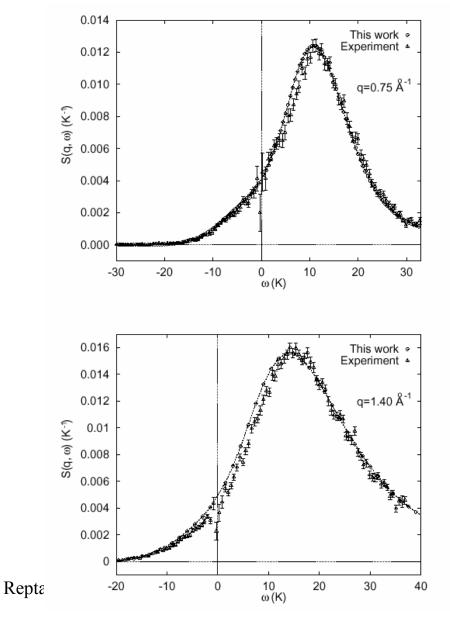
- 1. Sample $S_k(w)$. AvEnt Using MCMC make moves in $S_k(w)$ space. Take averages and also get idea of the allowed fluctuations. Model defined self consistently
- 2. Find most probable $S_k(w)$. MaxEnt Maximize function. Ok if the p.d.f. is highly peaked. Estimate errors by the curvature at the maximum. Fast to do numerically but makes more assumptions.
- How do we choose α ? Choose it from its own prior function so the strength of the likelhood function and the prior function are balanced. P(α)=1/ α .

Example: Liquid ⁴He Boninsegni and DMC

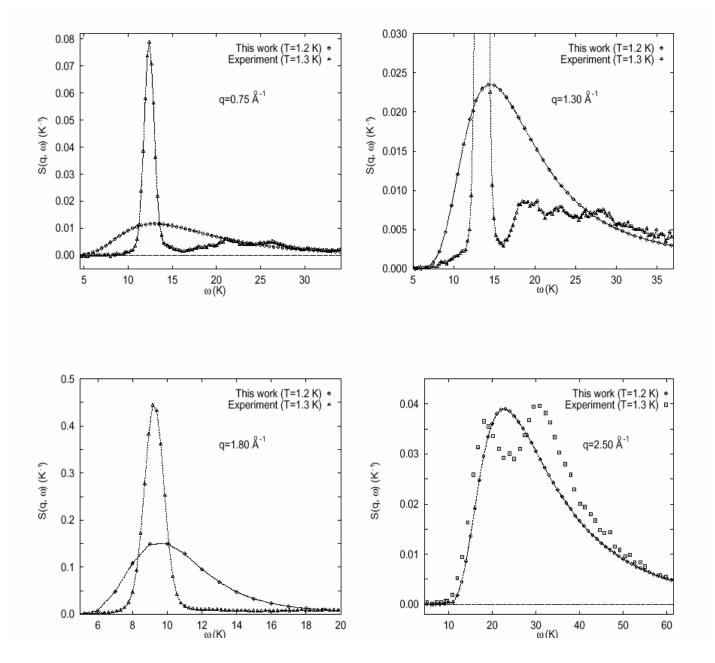
- Calculate $F_k(\tau)$ using PIMC (UPI). •
- AvEnt works beautifully in normal phase. •
- Gives peaks too broad in the superfluid phase. Failure of • the entropic prior.
- It makes the assumption that energy modes are uncoupled. ٠ This is false! Energy levels repel each other so that if there is energy at one level, it is unlikely at nearby values.
- Would require incredible precision to get sharp features. \bullet
- But good method for determining the excitation energy. •

Comparison in normal liquid He phase

- MaxEnt works well in normal phase (T=4K)
- Modes are quantum but independent of each other



Comparison in Superfluid



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Excitation energies

- Better PIMC data, more time values, smaller errors.
- Better to work in effective hamiltonian space, not energy space.
- Get more information, for example,
 - multiphonon correlation functions
 - Incorporate exchange values
 - Analytic information about response properties

Reasonable excitation energies

