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Worm algorithm for continuous-space Path Integral Monte Carlo simulations MASSIMO BONINSEGNI, University of Alberta, NIKOLAY PROKOF'EV, BORIS SVISTUNOV, University of Massachusetts — We present a new approach to Path Integral Monte Carlo (PIMC) simulations based on the "worm" algorithm, originally developed for lattice models,[1] and recently extended to continuous-space many-body systems.[2] The scheme allows for efficient computation of thermodynamic properties, including winding numbers and off-diagonal correlations, for systems of much greater size than that accessible to conventional PIMC. We present results for the superfluid transition of Helium-four in two and three dimensions. Using systems comprising several thousand particles, a very accurate determination of the superfluid transition temperature is feasible.

[1]N. V. Prokof'ev, B. V. Svistunov, and I. S. Tupitsyn, Phys. Lett. **238**, 253 (1998)
[2]M. Boninsegni, N. Prokof'ev and B. Svistunov, cond-mat/0510214

Massimo Boninsegni
University of Alberta

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