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A MONTE CARLO SYNTHETIC ACCELERATION METHOD FOR THE NON-LINEAR,TIME-DEPENDENT DIFFUSION EQUATION

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ABSTRACT

We present a Monte Carlo synthetic-acceleration method for solving the time-dependent, nonlinear, equilibrium diffusion equation in three-dimensions. The new scheme uses the adjoint Monte Carlo method as a relaxation step that accelerates standard Jacobi iteration. Results show that this method is 40% faster than regular Jacobi iteration and is competitive with Jacobi-preconditioned Conjugate Gradient methods. Furthermore, the new method is not limited to symmetric, positive-definite systems, and therefore, it can be used for non-symmetric systems. Such systems arise in fully coupled, nonlinear-consistent (Newton) solvers.

Key Words: Monte Carlo, synthetic acceleration, linear solvers, radiation diffusion

1. INTRODUCTION

In Ref. [1], we developed a residual Monte Carlo method that was an application of Halton's Sequential Monte Carlo method [2, 3] to the 1D equilibrium (1T) thermal radiation diffusion equation. At that time, Halton's method was not widely known in computational physics. While extending our method to 3D, we have discovered that the Sequential Monte Carlo method is actually a variant of iterative refinement cast as a residual method. Using Monte Carlo to accelerate fixed-point (Richardson) iteration, our new method surpasses our previous 1D method and allows for extension to more general solution techniques.

The purpose of this study is to demonstrate an efficient Monte Carlo solution method for 3D, time-dependent discrete systems. In this note, we extend our previous work in the following manner:

- We develop a rigorous synthetic-acceleration Monte Carlo method for solving sparse matrix systems.
- We apply this solver to the 1T thermal radiation diffusion equation in 3D.

In § 2 we review Monte Carlo methods for solving matrix systems and discuss our new synthetic-acceleration scheme and connect with previous work by Halton [3] and others [1]. We discuss using Synthetic-Accleration Monte Carlo to solve the time-dependent, nonlinear, equilibrium (1T) diffusion equation in § 4. We finish with conclusions and ideas for future work in § 5.

2. MONTE CARLO SYNTHETIC ACCELERATION

Monte Carlo methods for solving linear systems of equations have been in existence for many decades [4]. Briefly, the linear system

$$\mathbf{A}\mathbf{x} = \mathbf{b} \,, \tag{1}$$

can be expanded in the *Neumann* series,

$$\mathbf{x} = (\mathbf{I} - \mathbf{H})^{-1}\mathbf{b} = \mathbf{b} + \mathbf{H}\mathbf{b} + \mathbf{H}^2\mathbf{b} + \mathbf{H}^3\mathbf{b} + \dots \,, \tag{2}$$

where $\mathbf{H} = (\mathbf{I} - \mathbf{A})$. The Neumann series will converge when $\rho(\mathbf{H}) < 1 \; \forall \; \mathbf{b} \in \mathcal{R}^N$ [5].

Monte Carlo methods solve Eq. (1) by estimating the terms in the Neumann series through random walks. Two methods are used to estimate the terms, *direct* and *adjoint*. We begin a description of the direct method by rewriting Eq. (2) in order to calculate a component of $\mathbf{x}$,

$$\begin{aligned} x_i &= (\mathbf{b})_i + (\mathbf{H}\mathbf{b})_i + (\mathbf{H}^2\mathbf{b})_i + (\mathbf{H}^3\mathbf{b})_i + \dots \\ &= \sum_{k=0}^{\infty} \sum_{i_1}^{N} \sum_{i_2}^{N} \dots \sum_{i_k}^{N} h_{i,i_1} h_{i_1,i_2} \dots h_{i_{k-1},i_k} b_{i_k} \,. \end{aligned} \tag{3}$$

This series can be interpreted as a series of transitions from $i_{m-1} \rightarrow i_m$ that can be simulated by a random walk. Let X be a random variable sampled from a random walk with k events that initiates in state i,

$$\begin{aligned} X(i_0 = i) &= \sum_{m=0}^{k} W_m b_{i_m} \\ &= \sum_{m=0}^{k} w_{i,i_1} w_{i_1,i_2} \dots w_{i_{m-1},i_m} b_{i_m} \,. \end{aligned} \tag{4}$$

Here, the particle weight on the m^{th} step is denoted W_m, and each particle starts with unit weight. When the particle transitions between states, for example $i \rightarrow j$, the weight is multiplied by the factor

$$w_{ij} = \frac{h_{ij}}{p_{ij}} \,. \tag{5}$$

Then, the expected value of X is

$$\begin{aligned} E[X(i_0 = i)] &= \sum_{\nu} P_\nu X_\nu \\ &= \sum_{k=0}^{\infty} \sum_{i_1}^{N} \sum_{i_2}^{N} \dots \sum_{i_k}^{N} p_{i,i_1} p_{i_1,i_2} \dots p_{i_{k-1},i_k} w_{i,i_1} w_{i_1,i_2} \dots w_{i_{k-1},i_k} b_{i_k} \\ &= x_i \,, \end{aligned} \tag{6}$$

where ν denotes a particular random walk permutation. Therefore, the estimator in Eq. (4) is an unbiased estimator of the components of $\mathbf{x}$ provided $\rho(\mathbf{H}) < 1$.

We are left to define the transition probabilities, p_{ij}. The most straightforward approach is to set

$$p_{ij} = \frac{|h_{ij}|}{\sum_j |h_{ij}|} \,. \tag{7}$$

Each row of the transition probability matrix, $\mathbf{P}$, represents a discrete probability density function for selecting a new state j, given that the current state is i. Random walks can be terminated in two ways: the matrix can be augmented with a terminating event equation that describes the probability that a particle ends its walk, or the random walk can be terminated by weight cutoff. Generally, we choose to terminate random walks using a weight cutoff as opposed to augmenting the matrix.

An alternative approach to the one just described is to calculate contributions to every component of $\mathbf{x}$ during the random walk. In the mathematical literature this is referred to as an adjoint method; however, to transport practitioners this approach more closely resembles a traditional forward method. In this method, the weight change from state $i \rightarrow j$ is

$$w_{ij} = \frac{h_{ji}}{p_{ij}} \,. \tag{8}$$

The transition probabilities may be calculated as

$$p_{ij} = \frac{|h_{ji}|}{\sum_j |h_{ji}|} \,. \tag{9}$$

Note that the indices are reversed so that the probabilities are normalized over a column, as opposed to the forward method in which the probabilities are normalized over a row. This is equivalent to forming the Neumann series in reverse order. Correspondingly, the estimator for this method is

$$\begin{aligned} X &= \sum_{m=0}^{k} W_m \delta_{i_m,i} \\ &= \sum_{m=0}^{k} \hat{b}_{i_0} w_{i_0,i_1} w_{i_1,i_2} \ldots w_{i_{m-1},i_m} \delta_{i_m,i} \,. \end{aligned} \tag{10}$$

Here, $\hat{b}_{i_0}$ is the sampled source in cell/state i_0. The Kronecker delta implies that tallies are only made in the cell/state where the random walk currently resides. This is the common approach in standard Monte Carlo transport simulations. We will investigate this approach as applied to the 1T thermal radiation diffusion problem in § 3.

Similar to the direct Method, the adjoint method random walk process requires a terminating condition. In all of the work that follows we utilize a relative weight cutoff. The weight cutoff is defined as a fraction of the starting weight such that

$$W_f = W_c \hat{b}_{i_0} \,, \tag{11}$$

where W_f is the terminating weight of the random walk, W_c is the input relative weight cutoff, and $\hat{b}_{i_0}$ is the initial weight of the source particle. The random walk ends on the m^{th} step if $W_m < W_f$.

Both of these methods are characterized by very slow convergence rates that make them impractical for realistic applications. Halton [2, 3] proposed a staged residual scheme called Sequential Monte Carlo to

speed up the convergence of these methods. A variant of this scheme has been successfully applied to the 1D nonlinear thermal radiation diffusion equation in Ref. [1]. In this scheme, the adjoint method is used to estimate the solution to $\mathbf{A}\delta\mathbf{x}^{l+1} = \mathbf{r}^{l+1}$, and the residual is iterated to convergence.

We propose a modification of this scheme that uses Monte Carlo as a synthetic-acceleration scheme for fixed-point iteration. The Fixed-Point Monte Carlo Synthetic-Acceleration (MCSA) method is defined as follows:

$$\mathbf{x}^{l+1/2} = (\mathbf{I} - \mathbf{A})\mathbf{x}^{l} + \mathbf{b}\,, \tag{12a}$$

$$\mathbf{r}^{l+1/2} = \mathbf{b} - \mathbf{A}\mathbf{x}^{l+1/2}\,, \tag{12b}$$

$$\hat{\mathbf{A}}\delta\mathbf{x}^{l+1/2} = \mathbf{r}^{l+1/2}\,, \tag{12c}$$

$$\mathbf{x}^{l+1} = \mathbf{x}^{l+1/2} + \delta\mathbf{x}^{l+1/2}\,. \tag{12d}$$

The hat on $\mathbf{A}$ in Eq. (12c) indicates that the Monte Carlo solution only approximately inverts this operator. Thus, we have defined a scheme in which the initial estimate of $\mathbf{x}$ in each iteration is updated using a single fixed-point iteration. The residual is calculated and is used as a source to estimate the error, $\delta\mathbf{x}^{l+1/2}$, by solving Eq. (12c) via the Monte Carlo adjoint method.

3 Discrete Form of the Radiation Diffusion Equation

The nonlinear, thermal diffusion equation is [1]

$$(\rho C_v + 4aT^3)\frac{\partial T}{\partial t} - \nabla\cdot\Big(\frac{4acT^3}{3\sigma_{\mathrm{R}}}\Big)\nabla T = Q\,, \tag{13}$$

where $C_v \equiv C_v(\mathbf{r}, T(\mathbf{r},t))$ [GJ $\cdot$ g^{-1} $\cdot$ keV^{-1}] is the specific heat capacity of the material, $\rho \equiv \rho(\mathbf{r})$ [g $\cdot$ cm^{-3}] is the density of the material, $a = 0.01372$ [GJ $\cdot$ cm^{-3} $\cdot$ keV^{-4}] is the radiation constant, $c = 29.979$ [cm $\cdot$ ns^{-1}] is the vacuum light speed, and $T \equiv T(\mathbf{r},t)$ [keV] is the temperature that characterizes both the radiation and the material. The opacity, $\sigma_{\mathrm{R}} \equiv \sigma_{\mathrm{R}}$(**r**,T(**r**,t)) [cm^{-1}], is the Rosseland Mean opacity. The source, $Q \equiv Q(\mathbf{r},t)$ [GJ $\cdot$ cm^{-3} $\cdot$ ns^{-1}], is assumed to be independent of T.

We chose to use the angle-energy integrated radiation intensity, $\phi \equiv \phi(\mathbf{r},t)$ [GJ $\cdot$ cm^{-2} $\cdot$ ns^{-1}], as the primary state variable. The intensity is defined,

$$\begin{aligned}\phi(\mathbf{r},t) &= \int_{4\pi} d\mathbf{\Omega} \int_{\nu} d\nu\; \psi(\mathbf{r},\nu,\hat{\mathbf{\Omega}},t) \\ &= \int_{\nu} d\nu\; 4\pi B(\nu,T) \\ &= acT^4\,,\end{aligned} \tag{14}$$

where ψ is the angular radiation intensity. The Planck function (or Planckian) is defined as,

$$B(\nu,T) = \frac{2h\nu^3}{c^2}\big(e^{\frac{h\nu}{kT}} - 1\big)^{-1}\,, \tag{15}$$

where h is Planck's constant and k is the Boltzmann constant. Utilizing this definition of ϕ we can write

$$\partial T = \frac{1}{4acT^3}\partial\phi \,. \tag{16}$$

Inserting (16) into (13) yields

$$\Big(\frac{C_v}{4acT^3} + \frac{1}{c}\Big)\frac{\partial\phi}{\partial t} - \nabla\cdot D\nabla\phi = Q \,, \tag{17}$$

where D is the diffusion coefficient, $D \equiv D(\mathbf{r}, T(\mathbf{r},t))$ [cm], and is defined

$$D = \frac{1}{3\sigma_{\mathrm{R}}} \,. \tag{18}$$

Applying backward-Euler time differencing to Eq. (17) and lagging the temperature-dependent coefficients at t^n gives

$$-\nabla\cdot D^n\nabla\phi + \tilde{\sigma}^n\phi = q^n \,, \tag{19}$$

where we have suppressed the $n+1$ indices on ϕ and

$$\tilde{\sigma}^n = \frac{\rho C_v^n}{4ac(T^n)^3\Delta t} + \frac{1}{c\Delta t} \,, \tag{20}$$

$$q^n = \tilde{\sigma}^n\phi^n + Q^n \,, \tag{21}$$

$$\phi^n = ac(T^n)^4 \,. \tag{22}$$

Applying Fick's Law,

$$\mathbf{F} = -D\nabla\phi \,, \tag{23}$$

where $\mathbf{F}$ is the radiation flux, we define a flux-balance equation,

$$\nabla\cdot\mathbf{F} + \tilde{\sigma}^n\phi = q^n \,. \tag{24}$$

This equation is discretized in three-dimensional space using a finite volume method,

$$\begin{aligned}(F_{i+1/2} - F_{i-1/2})\Delta_j\Delta_k + (F_{j+1/2} - F_{j-1/2})\Delta_i\Delta_k \\ + (F_{k+1/2} - F_{k-1/2})\Delta_i\Delta_j + \tilde{\sigma}^n_{ijk}\phi_{ijk}V_{ijk} = q^n_{ijk}V_{ijk} \,.\end{aligned} \tag{25}$$

Using Fick's Law, Eq. (23), we can write $O(\Delta^2)$ expressions for the face-centered fluxes. Defining $l \in \{i,j,k\}$, the face-centered fluxes are

$$F_{l+1/2} = -D_{l+1/2}\frac{\phi_{l+1} - \phi_l}{\Delta_{l+1/2}} \,, \tag{26}$$

$$F_{l-1/2} = -D_{l-1/2}\frac{\phi_l - \phi_{l-1}}{\Delta_{l-1/2}} \,, \tag{27}$$

where

$$\Delta_{l+1/2} = \frac{\Delta_{l+1} + \Delta_l}{2} \,, \tag{28}$$

$$\Delta_{l-1/2} = \frac{\Delta_l + \Delta_{l-1}}{2} \,. \tag{29}$$

In order to be conservative, the flux must be continuous across a face. Thus, the face-centered flux evaluated from either side of the face must be equivalent,

$$\begin{aligned} F^{+}_{l+1/2} &= F^{-}_{l+1/2}\,, \\ 2D_{l+1}\frac{\phi_{l+1}-\phi_{l+1/2}}{\Delta_{l+1}} &= 2D_{l}\frac{\phi_{l+1/2}-\phi_{l}}{\Delta_{l}}\,, \\ \frac{1}{3\sigma_{l+1}}\frac{\phi_{l+1}-\phi_{l+1/2}}{\Delta_{l+1}} &= \frac{1}{3\sigma_{l}}\frac{\phi_{l+1/2}-\phi_{l}}{\Delta_{l}}\,, \end{aligned} \tag{30}$$

where we have dropped the subscript R from σ for clarity. Solving this system for $\phi_{l+1/2}$ and plugging into either $F^{+}_{l+1/2}$ or $F^{-}_{l+1/2}$ and setting the resulting expression equal to Eq. (26), one finds the face-centered diffusion coefficient,

$$D_{l+1/2} = \frac{2\Delta_{l+1/2}}{3\sigma_{l}\Delta_{l}+3\sigma_{l+1}\Delta_{l+1}}\,. \tag{31}$$

Following the same procedure at the $l-1/2$ face gives the diffusion coefficient on the low-side face,

$$D_{l-1/2} = \frac{2\Delta_{l-1/2}}{3\sigma_{l}\Delta_{l}+3\sigma_{l-1}\Delta_{l-1}}\,. \tag{32}$$

Using Eqs. (26), (27), (31), and (32) in the discrete flux-balance equation, (25), we obtain

$$\begin{aligned} &\sigma_{T\,ijk}\phi_{ijk} - \sigma^{-}_{i+1}\frac{\Delta_{i+1}}{\Delta_{i}}\phi_{i+1\,jk} - \sigma^{+}_{i-1}\frac{\Delta_{i-1}}{\Delta_{i}}\phi_{i-1\,jk} - \sigma^{-}_{j+1}\frac{\Delta_{j+1}}{\Delta_{j}}\phi_{i\,j+1\,k} \\ &\quad - \sigma^{+}_{j-1}\frac{\Delta_{j-1}}{\Delta_{j}}\phi_{i\,j-1\,k} - \sigma^{-}_{k+1}\frac{\Delta_{k+1}}{\Delta_{k}}\phi_{ij\,k+1} - \sigma^{+}_{k-1}\frac{\Delta_{k-1}}{\Delta_{k}}\phi_{ij\,k-1} = q^{n}_{ijk}\,. \end{aligned} \tag{33}$$

Here,

$$\sigma_{T\,ijk} = \sigma^{+}_{i} + \sigma^{-}_{i} + \sigma^{+}_{j} + \sigma^{-}_{j} + \sigma^{+}_{k} + \sigma^{-}_{k} + \tilde{\sigma}^{n}_{ijk}\,, \tag{34}$$

and

$$\sigma^{+}_{i} = \frac{1}{\Delta_{i}}\frac{2}{3\sigma_{ijk}\Delta_{i}+3\sigma_{i+1\,jk}\Delta_{i+1}}\,, \tag{35a}$$

$$\sigma^{-}_{i} = \frac{1}{\Delta_{i}}\frac{2}{3\sigma_{ijk}\Delta_{i}+3\sigma_{i-1\,jk}\Delta_{i-1}}\,, \tag{35b}$$

$$\sigma^{+}_{j} = \frac{1}{\Delta_{j}}\frac{2}{3\sigma_{ijk}\Delta_{j}+3\sigma_{i\,j+1\,k}\Delta_{j+1}}\,, \tag{35c}$$

$$\sigma^{-}_{j} = \frac{1}{\Delta_{j}}\frac{2}{3\sigma_{ijk}\Delta_{j}+3\sigma_{i\,j-1\,k}\Delta_{j-1}}\,, \tag{35d}$$

$$\sigma^{+}_{k} = \frac{1}{\Delta_{k}}\frac{2}{3\sigma_{ijk}\Delta_{k}+3\sigma_{ij\,k+1}\Delta_{k+1}}\,, \tag{35e}$$

$$\sigma^{-}_{k} = \frac{1}{\Delta_{k}}\frac{2}{3\sigma_{ijk}\Delta_{k}+3\sigma_{ij\,k-1}\Delta_{k-1}}\,. \tag{35f}$$

Also, note that

$$\sigma_{i-1}^{+} = \frac{1}{\Delta_{i-1}} \frac{2}{3\sigma_{ijk}\Delta_i + 3\sigma_{i-1\,jk}\Delta_{i-1}} ,$$
$$\sigma_{i+1}^{-} = \frac{1}{\Delta_{i+1}} \frac{2}{3\sigma_{ijk}\Delta_i + 3\sigma_{i+1\,jk}\Delta_{i+1}} ,$$
$$\ldots .$$

Equations (33) through (35) represent the discretized, 1T diffusion equation on an orthogonal 3D grid.

Equations (33) through (35) have been written in a manner that is amenable to Monte Carlo interpretation. One can envision the terms in Eq. (35) representing leakage out of each face of a cell. The off-diagonal terms then represent sources into the cell, or, equivalently, these terms are leakage out of the neighboring cells. A limitation of this interpretation is that it requires a symmetric system to implement the Monte Carlo scheme. More specifically, the operator $\mathbf{D}$ must be an H-matrix [5] such that the off-diagonal elements are negative and symmetric. In other words, the leakage out of a cell must be equivalent to the source into the adjacent cell. The methods described in § 2 do not suffer this limitation. Thus, we will interpret the solution via MCSA as a transport-like process, but we do not require any constraints on the system other than the spectral radius must be less than 1.

The discrete diffusion equation in (33) can be written in matrix-operator form as follows,

$$\mathbf{D}\boldsymbol{\phi} = \mathbf{q} \,, \tag{36}$$

where $\mathbf{D}$ is a symmetric, positive-definite (SPD) operator. Unfortunately, for many problems $\rho(\mathbf{D}) > 1$. Therefore, we must precondition Eq. (36) in order to use the MCSA method. Preconditioning accomplishes two purposes: it reduces the spectral radius of $\mathbf{D}$ so that Monte Carlo solution methods are applicable, and it reduces the number of iterations required for convergence. We apply left-preconditioning and write

$$\mathbf{M}^{-1}\mathbf{D}\boldsymbol{\phi} = \mathbf{M}^{-1}\mathbf{q} \,. \tag{37}$$

A good choice for the preconditioner, $\mathbf{M}$, is

$$\mathbf{M} = \mathrm{diag}(\mathbf{D}) \,. \tag{38}$$

Setting $\mathbf{M}$ equal to the diagonal elements of $\mathbf{D}$ accomplishes several objectives:

- It reduces the spectral radius such that $\rho(\mathbf{M}^{-1}\mathbf{D}) < \rho(\mathbf{D})$ and $\rho(\mathbf{M}^{-1}\mathbf{D}) < 1$. Thus, convergence is guaranteed and fewer iterations are required resulting in accelerated convergence.
- Makes the diagonal elements of the iteration matrix zero, $\mathrm{diag}(\mathbf{I} - \mathbf{M}^{-1}\mathbf{D}) = 0$. Thus, there will be no time wasted in transitions $i \rightarrow i$ during the random walk process.

The second item is quite important for Monte Carlo solutions of linear systems, and this type of scaling should be performed regardless of any additional preconditioner choices.

As discussed in § 2, the MCSA method requires two relaxation steps:

1. A fixed-point iteration to estimate $\boldsymbol{\phi}^{l+1/2}$. This is a matrix-vector multiply operation.
2. An adjoint Monte Carlo solve to estimate $\delta\boldsymbol{\phi}^{l+1/2}$.

The adjoint Monte Carlo method is used to estimate

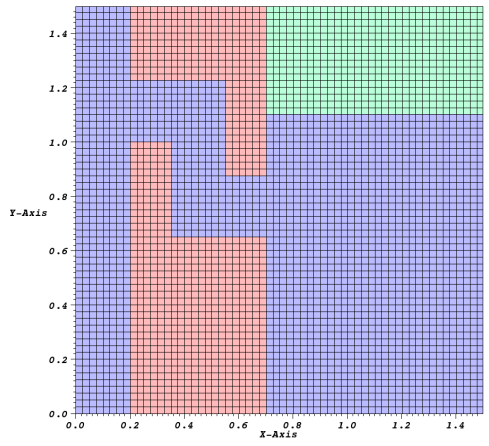
$$\mathbf{M}^{-1}\mathbf{D}\delta\boldsymbol{\phi}^{l+1/2} = \mathbf{r}^{l+1/2} \,. \tag{39}$$

As noted above, the residual acts as the source for this simulation. There are two Monte Carlo interpretations that can be applied to this system. The first follows the mathematical presentation given in § 2. Namely, we form probabilities from the iteration matrix and perform random walks to generate unbiased estimates of the solution vector, $\delta\boldsymbol{\phi}^{l+1/2}$, using the estimator in Eq. (10).

However, a more natural interpretation for Monte Carlo transport practitioners is to use the machinery described in § 2 to define Probability Distribution Functions (PDFs) that describe the transport of particles between cells. We then do a Monte Carlo transport calculation using Eq. (8) to calculate the weight change at each collision. Equation (9) gives the probability of scattering to an adjacent cell. We tally the contribution of ϕ in each cell using Eq. (10). The transport is terminated using a relative weight cutoff that is defined in Eq. (11).

4. RESULTS

We now test the performance of the MCSA method on a large multi-material problem. The multi-material problem has a dog-legged duct through a thick wall where the radiation flows into a thin region bound by a foil on one side. The mesh and geometry are illustrated in Fig. 1. A blackbody boundary flux is defined on



B.C.	$f_b^+(x=0, T=0.5) = \frac{ac}{4}T^4$
	$\mathbf{F} = 0 \quad \partial\Gamma \in \{x^+, y^-, y^+, z^-, z^+\}$
material properties	$\rho = 1.5\,\mathrm{g}\cdot\mathrm{cm}^{-3}$ (duct)
	$\rho = 8.0\,\mathrm{g}\cdot\mathrm{cm}^{-3}$ (wall)
	$\rho = 4.0\,\mathrm{g}\cdot\mathrm{cm}^{-3}$ (foil)
	$C_v = 0.1\,\mathrm{GJ}\cdot\mathrm{g}^{-1}\cdot\mathrm{keV}^{-1}$
	$T(t=0) = 1\times10^{-4}\,\mathrm{keV}$
opacity	$\sigma = T^{-3}\,\mathrm{cm}^2\cdot\mathrm{g}^{-1}$ (duct)
	$\sigma = 1000T^{-1}\,\mathrm{cm}^2\cdot\mathrm{g}^{-1}$ (wall)
	$\sigma = 5T^{-2}\,\mathrm{cm}^2\cdot\mathrm{g}^{-1}$ (foil)
mesh	$\Delta_i = \Delta_j = \Delta_k = 0.025\,\mathrm{cm}$
	$N_i = N_j = N_k = 60$

Figure 1. Multi-material problem mesh. The duct region is blue. The wall is red. The foil is green. The mesh is $60 \times 60 \times 60$.

the low-x face at $T = 0.5$ keV. We test three methods, Jacobi-preconditioned Conjugate Gradient (PCG),

Jacobi iteration (JACOBI), and MCSA. All three methods, give numerically identical answers when using a stopping criterion of 1×10^{-8}.

Table I shows the timing results for the multi-material problem using PCG, JACOBI, and MCSA. The

Table I. Comparison of solution methods for the multi-material problem. All methods were run with a stopping criterion of 1×10^{-8}. The MCSA method used $N_p = 1000$ and $W_c = 1 \times 10^{-3}$. The problem was run to an elapsed time of 10 sh. The MCSA method required 3.4 hours on a 3.6 GHz Xeon.

Method	Max Iterations	Relative CPU Time
PCG	18	1.03
JACOBI	38	1.43
MCSA	20	1.0

results correspond roughly with the results from the Marshak problem. The MCSA is marginally faster than PCG and 43% faster than JACOBI.

5. CONCLUSIONS

We have presented a new Monte Carlo solution method for solving the discrete, time-dependent diffusion equation in 3D. The MCSA method has been shown to match results using standard solution techniques to arbitrary precision. Also, the new method is faster than preconditioned CG and Jacobi iteration.

While we have demonstrated marginal improvements over standard solution schemes in this study, significant improvements could be realized in fully nonlinear-consistent solutions. In these cases, the MCSA method competes with GMRES, which is more costly in memory and time than CG. Another area where the MCSA scheme may have advantages over traditional solution methods is on dentritic, or adaptive, meshes. These meshes yield matrices with poor condition numbers because of the changing cell volumes at different refinement levels. A smart transport algorithm could be developed that more efficiently solves the residual on these types of meshes. These topics will be the focus of future study.

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