1 Introduction

Global illumination (GI) is essential for photorealistic image synthesis, and is formalized by the light transport problem. Among hundreds of algorithms proposed to solve this problem, algorithms based on ray tracing and numerical integration are most promising and they are categorized as “consistent” or “unbiased” algorithms. The consistent algorithms (e.g., photon mapping) use (ir)radiance caching and interpolation to connect paths from light sources to a camera, and results always include statistical biases. On the other hand, in the unbiased algorithms, although artifacts appear only as results of estimation variance, they are inherently time-consuming. For example, Metropolis Light Transport (MLT) algorithm, which is one of the unbiased algorithms, solves the light transport problem efficiently, however, it has slow mixing (start-up bias) problem.

We propose a novel GI algorithm by using Replica-Exchange Monte-Carlo (RE-MC) method. The RE-MC method is a family of extended ensemble MC algorithms and have been used to solve the slow mixing problem especially in the field of computational physics or statistical information processing [Iba 2001]. Our algorithm has better convergence properties than both the MLT algorithm [Csaba et al. 2002] and the Bidirectional Path Tracing (BPT) algorithm.

2 Method

2.1 Replica-exchange Monte-Carlo method

The RE-MC method considers a set of distributions (systems/replicas) \{p(x_k|\theta_k)\} with different parameters \{\theta_k\}, k = 1,\ldots,K and those parameters are ordered as \theta_1 \geq \cdots \geq \theta_K. The method samples a simultaneous distribution \hat{p}(\{x_k\}) of \{x_k\} as stationary distribution \hat{p}(x_1)=\prod_{k=1}^{K} p(x_k|\theta_k) by Markov-chain Monte-Carlo method.

The method uses conventional and replica exchange update. The conventional update is defined in each replica k independently, and it has to satisfy the detailed balance condition for \hat{p}(x_k|\theta_k). The replica exchange update exchanges replicas which have neighboring parameters \theta_k and \theta_{k+1} according to acceptance probability \max\{1, r\}.

\[
r = \frac{p(x_{k+1}|\theta_k)p(x_k|\theta_{k+1})}{p(x_{k}|\theta_k)p(x_{k+1}|\theta_{k+1})}
\]  

(1)

The simultaneous distribution is invariant under the exchange and the detailed balance condition for the simultaneous distribution is satisfied.

2.2 Proposing method

We define an extended probabilistic density function for the RE-MC method in GI as \hat{p}(u_k|\beta_k) = \frac{\hat{f}\beta_k(u_k)}{\int_{0}^{1} \hat{f}\beta_k(u_k) du_k}, where u_k is a point in the primary sample space U which is introduced by [Csaba et al. 2002], \hat{f} is an integrand of light transport integration, and \{\beta_k\} = \{\theta_k\} (0 \leq \beta_k \leq 1) are hyper-parameters.

We choose the number of replicas K = 2^L + 1 (L = 0, 1, \ldots), and the parameters \beta_k = \frac{k-K}{k-1}. Then we can express the equation 1 as

\[
r = \frac{f^{(L)}(u_{k+1})}{f^{(L)}(u_k)}
\]

Note that MLT is L = 0 case of above definition.

The detail of our method is shown as following three steps: The first step estimates each normalizing term \beta_k by evaluating the large number of seed samples and choose initial u_k according to \hat{p}(u_k|\beta_k) by re-sampling from their samples. The second step determines mutation widths of each replica by several short simulations. To select the mutation widths based on an average of acceptance probability in the conventional update, our method searches the mutation widths by binary search algorithm because we assume a small/large mutation widths provide the high/low acceptance probability. The third step runs over the replica exchange and the conventional update. Our method exchanges the neighboring replicas \lfloor \frac{K}{2} \rfloor times in the replica exchange update and runs the metropolis sampling for each replica to generate samples according to \hat{p}(u_k|\beta_k) in the conventional update. Obtained samples from each replica are combined by the Multiple Importance Sampling (MIS) and are deposited onto the image plane by a filter function for a pixel.

3 Result and Discussion

Figure 1 shows results rendered by three different methods at a 300^2 resolution in one hour respectively. We represent BRDFs and light sources as point-sampled spectra, and the spectrum is evenly sampled with thirty-one points in the visible range. We use the balance/power heuristic for the MIS as the combination strategy, and use a box filter as the filter function. The rendered scene includes a yellow box covered by a glass box and the boxes are illuminated by two light sources placed above the box, and illuminate the box through a lens. BPT in Figure 1a produces a very noisy image. MLT algorithm in Figure 1b produces a splotchy appearance because if the algorithm found caustic paths, the algorithm would lose the paths by large-step mutation [Csaba et al. 2002]. On the other hand, our method which uses nine replicas produces the smoothest result compared with the other two results as shown in Figure 1c.

Figure 1: Comparison of BPT, MLT and our method.

4 Summary and Conclusion

We proposed an unbiased GI algorithm by using the RE-MC method. It is easy to implement and improved sampling efficiency. Experimental results show that our algorithm has better convergence properties than both BPT and MLT. Future work includes an extension of the algorithm for multi-thread architecture, the modification to effective spectral rendering, and so on.

References
