GMC ['gımık]: a one-variable Monte Carlo dose algorithm for proton therapy.

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Abstract. This work presents the CPU implementation of GMC ['gımık]: a fast yet accurate one-variable Monte Carlo dose algorithm for proton therapy to be incorporated into our in-house treatment planning system, Astroid. GMC is based on a simple mathematical model using the formulated proton scattering power and tabulated data of empirical depth-dose distributions. These Bragg peaks determine the energy deposited along the particle’s track. The polar scattering angle is based on the particle’s local energy and the voxel’s density, while the azimuthal component of that scattering angle is the single variable in GMC, uniformly distributed from 0 to $2\pi$. The halo effect of the beam, currently not implemented, will consider large scattering angles and secondary protons for a small percentage of the incident histories. GMC shows strong agreement with both the empirical data and GEANT4-based simulations. Its current CPU implementation runs at $\sim300$ m.s$^{-1}$, approximately ten times faster than GEANT4. Significant speed improvement is expected with the upcoming implementation of multi-threading and the portage to the GPU architecture. In conclusion, a one-variable Monte Carlo dose algorithm was produced for proton therapy dose computations. Its simplicity allows for fast dose computation while conserving accuracy against heterogeneities, hence drastically improving the current algorithms used in treatment planning systems.

1. Introduction
Proton therapy treatment planning systems (TPS) are all currently relying on a Pencil Beam Algorithm (PBA) for dose computation in patient. PBA, while relatively fast, fails to model heterogeneities’ effects which could be critical in Pencil Beam Scanning delivery (PBS)[1]. For accurate results it is necessary to turn towards full Monte Carlo (MC) systems such as GEANT4. The latter, however, present a large overhead and can be significantly time consuming. We therefore propose an extremely simplified MC algorithm for proton dose calculation. The latter, known as GMC ['gımık] (A unique or quirky special feature that makes something “stand out” from its contemporaries.), intends to be extremely fast yet accurate against tissue inhomogeneities. Moreover, GMC will be implemented at the lowest level as part of our in-house PBS TPS, Astroid, simply replacing the current PBA.

2. Materials and methods
Figure 1 shows a representation of the particle transport in GMC at the voxel level. A particle enters a voxel (density $\rho$, volume $V$) with certain input parameters: current energy $E_i$, relative position in the voxel $(x_i, y_i, z_i)$, direction $(u_i, v_i, w_i)$, and initial energy $E_0$ (energy
at the entrance of the phantom/patient). A cord length $L$ is computed from a non-scattered transport of the particle (straight line) through the voxel. The mean radial scattering angle is subsequently computed from the scattering power described by Gottschalk [2], as shown in equation 1:

$$
\langle \theta^2 \rangle = \int_0^L T_{dM} dx \approx T_{dM} \times L \quad \text{(rad}^2),
$$

with

$$
T_{dM} = f_{dM}(E_i, E_0) \times \left( \frac{E_i}{E_0} \right)^2 \times \frac{1}{X_s},
$$

where

$$
f_{dM} = 0.5244 + 0.1975 \times \log_{10}(1 - \left( \frac{E_i}{E_0} \right)^{2} ) + 0.2320 \times \log_{10}\left( \frac{E_i}{MeV} \right) - 0.0098 \times \log_{10}(\log_{10}(1 - \left( \frac{E_i}{E_0} \right)^{2} )) \quad \text{(MeV)}
$$

where $\theta$ is the average radial scattering angle, $x$ the distance already traveled along the track in cm, $E_s = 15.0$ MeV, and $X_s = 46.88$ cm.

The azimuthal scattering angle is the only random variable in GMC, between 0 and $2\pi$.

![Image of GMC model at the voxel level.](image)

**Figure 1.** GMC model at the voxel level.

The mean energy loss $\Delta E$ is based on the initial proton energy $E_0$ and the trapezoidal approximation of the integral under the curve of its corresponding Bragg Peak, TPS beam data as described in Clasie [3]. The local deposited dose $\Delta D$ is then computed from equation 4 assuming a mass stopping power ratio equal to unity. This integral is shown in figure 2.

$$
\Delta D = \frac{\Delta E}{\rho V} \quad \text{(Gy)},
$$

where,

$$
\Delta E = S_{\text{water}} \times L \times \left( \frac{dE}{dx} \right)_{\text{water}} = \int_{X_1}^{X_2} f(X) dX \quad \text{(MeV)},
$$

and,

$$
\int_{X_1}^{X_2} f(X) dX \approx \rho L \left( f(X_2) + f(X_1) \right) / 2
$$
where \( S_{\text{water}}^{\text{medium}} \) is the relative stopping power ratio, and \( \int_{X_1}^{X_2} f(X) dX \) the integral below the Bragg peak curve in which \( X_1 \) and \( X_2 \) are based on the current particle energy \( E_i \); \( f(X) \) is given in units of \( \text{Gy.cm}^2 \), and \( X_1 \) and \( X_2 \) in \( \text{g/cm}^2 \).)

![Figure 2. Dose deposition based on TPS beam data [3].](image)

Not currently taken into account, the Halo effect [3], characterized by larger scattering angles and secondary protons, will later be implemented based on further experimental results.

3. Results
The presented implementation of GMC ran at \( \sim 300 \text{ m.s}^{-1} \), approximately ten times faster than GEANT4.9.0 (a full MC system) for a similar setup.

Figure 3 shows two simulations in a water phantom that highlights the expected depth-dependence of an incident beam with a) zero lateral spread and b) uniform square distribution.

![Figure 3. GMC simulations: a) no initial spread nor entrance angle, b) a uniform field.](image)

Figure 4 stresses that the longitudinal dose algorithm was implemented correctly within
GMC[2]. Simulations were performed in water and compared to the original TPS (Astroid) Bragg peaks that were used to tune the model. Figure 4 is an example of such a Bragg peak comparison, zoomed in on the end of range.

![Figure 4](image-url)

**Figure 4.** Comparison of depth dose deposition between the original TPS Bragg peak data (Astroid) and a GMC simulation.

Finally, and most importantly, Figure 5 highlights GMC’s behavior against heterogeneities. In that simulation, a water phantom ($\rho = 1$) is considered with blocks of lung material ($\rho = 0.4$, white overlay) and bone material ($\rho = 1.71$, black overlay); two pencil beams go through the inhomogeneities in a different order. PBA would result in similar scattering and dose deposition for each pencil beam. GMC, however, properly models the expected physics and dissimilarities in shape and dose are observed after the heterogeneities.

![Figure 5](image-url)

**Figure 5.** GMC’s behavior against heterogeneities.

4. **Conclusion**

GMC, a fast yet accurate proton dose algorithm, has been successfully implemented. Expected dose distributions were obtained, and the algorithm exhibited appropriate behavior when dealing with heterogeneities. Future work will involve systematic comparison/analysis of beam scattering and dose deposition against expected results, as well as significant speed improvement by implementing multi-threading and portage to a GPU architecture.

5. **References**

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