Documents

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Denoising proton therapy Monte Carlo dose distributions in multiple tumor sites: A comparative neural networks architecture study
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Abstract
Introduction: Monte Carlo (MC) algorithms provide accurate modeling of dose calculation by simulating the delivery and interaction of many particles through patient geometry. Fast MC simulations using large number of particles are desirable as they can lead to reliable clinical decisions. In this work, we assume that faster simulations with fewer particles can approximate slower ones by denoising them with deep learning. Materials and methods: We use mean squared error (MSE) as loss function to train networks (sNet and dUNet), with 2.5D and 3D setups considering volumes of 7 and 24 slices. Our models are trained on proton therapy MC dose distributions of six different tumor sites acquired from 50 patients. We provide networks with input MC dose distributions simulated using 1 × 106 particles while keeping 1 × 109 particles as reference. Results: On average over 10 new patients with different tumor sites, in 2.5D and 3D, our models recover relative residual error on target volume, ΔD95TV of 0.67 ± 0.43% and 1.32 ± 0.87% for sNet vs. 0.83 ± 0.53% and 1.66 ± 0.98% for dUNet, compared to the noisy input at 12.40 ± 4.06%. Moreover, the denoising time for a dose distribution is: < 9s and < 1s for sNet vs. < 16s and < 1.5s for dUNet in 2.5D and 3D, in comparison to about 100 min (MC simulation using 1 × 109 particles). Conclusion: We propose a fast framework that can successfully denoise MC dose distributions. Starting from MC doses with 1 × 106 particles only, the networks provide comparable results as MC doses with1 × 109 particles, reducing simulation time significantly. © 2021 Associazione Italiana di Fisica Medica

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Artificial intelligence; Convolutional neural networks; Dose denoising; Monte Carlo; Proton therapy

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