

# Optimal spatial resolution for Monte-Carlo PET Simulation

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## 1. Introduction

Monte-Carlo simulation of the physics of the PET system allows for the generation of simulated PET data based on a radioactivity distribution defined on an anatomic template. Given the heavy computational burdens of Monte-Carlo simulation, the optimal spatial resolution for simulating PET images remains an open question. Stute, et al. [1] have shown that for a spherical source with homogenous radioactivity distribution, there is no advantage to using a radioactivity template with a finer spatial resolution than that of the PET scanner. However, it is not clear that these results extend to objects, such as the human brain, with more complex geometries and radiotracer distributions. Our aim was to determine if there is a potential advantage to using high-resolution templates for producing realistic simulated PET images.

## 2. Methods

Two anatomic templates were created based on a 0.1mm classified version of the BigBrain [2] (Fig.1.A) by downsampling the latter to 500um (Fig.1.C) and 1mm (Fig.1.D) using nearest-neighbor interpolation. Radioactivity values were assigned to the white matter (300Bq), cortical gray matter (1000Bq in layer 1 and 900Bq elsewhere). PET simulations of the HRRT [3] were performed with Gate (v. simulation7.0) [4]. 1000 simulations of 0.06s were performed for the 1mm template and 259 for the 0.5mm template. The simulated data were compared with the Welch two sample t-test for the total number of detected photon coincidences (counts), the deposition energy of the photons, and their respective sensitivities. The position of the annihilation events were also recorded for both 500um and 1mm simulations. These were grouped into 1mm bins and compared by calculating the normalized mutual information between both.

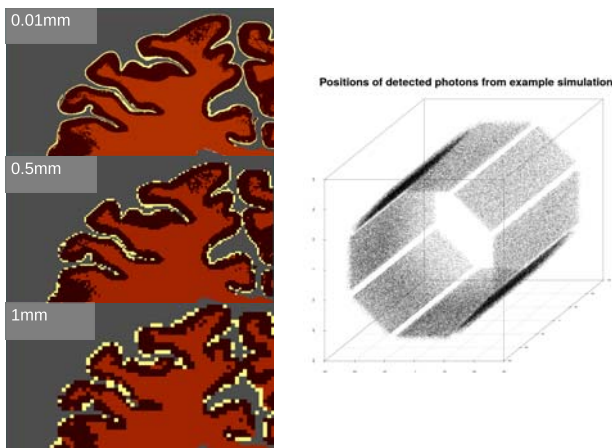


Fig 1. (Left) Two different anatomic templates were input into the Gate simulator. Both templates were downsampled from a 100um segmentation of the BigBrain, one to 500um and one to 1mm. (Right) Example of detected counts for simulated HRRT.

## 3. Results

The mean counts ( $p < 0.001$ ,  $t=7989.1$ ), sensitivity ( $p < 0.001$ ,  $t=9680.6$ ), and energy depositions ( $p < 0.001$ ,  $t=460.98$ ) were all significantly different between PET data generated with the the 0.5mm and 1mm templates. Whereas the effect size was large for the counts (1mm:  $228,383 \pm 501$ ; 0.5mm:  $65,1079 \pm 794$ ; see Fig.1) and sensitivity (1mm:  $0.23\% \pm 0.0005$ ; 0.5mm:  $0.016\% \pm 0.00006$ ), it was very small for the photon deposition energy (1mm:  $0.475 \pm 0.0001$ ; 0.5mm:  $0.472 \pm 0.00007$ ). The normalized mutual information between the binned positions of the annihilation events was 0.28.

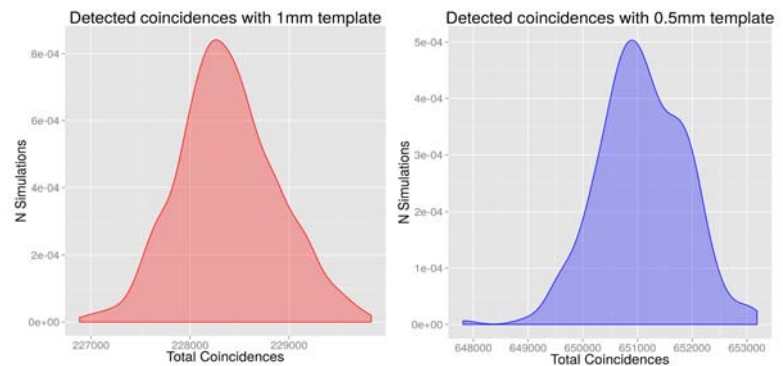


Fig 2. Histograms of detected coincidences between 1mm and 500um shows different distributions.

The simulation computational burden of both simulations is shown in Table.1 and indicate that 0.5mm simulation was 7 times longer than for the 1mm simulation.

Resolution	Simulated Time	Computation Time	Total Size
1mm	42s	447 hours	497G
0.5mm	60s	3462 hours	1.1T

Table 1. Computational burden was significantly larger in both computation time and size of the the output between 500um and 1mm PET simulations.

## 4. Conclusion

The statistical differences in the simulated data suggest that the spatial resolution of the anatomic template may have an important effect on PET simulation. The difference in total counts is attributable in part by artefacts induced by the use of nearest neighbour downsampling. The relatively low normalized mutual information score suggests that there may be important differences between the simulated images. Future work will use a wider range of resolutions for the template and reconstruct the count data into 3D images.

### References:

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