Purpose: In order to accurately model a tomosynthesis image acquisition for estimating organ and effective doses with PCXMC, we must consider each discrete projection angle of the x-ray tube separately, compute the dose in each case, and sum the results. This can be a time-consuming task that requires a considerable amount of data entry. We have developed two techniques that we can use to improve the user-friendliness and time-efficiency of obtaining dose estimates for a tomosynthesis sweep.

Methods: We developed a MATLAB program to automatically generate the definition files for each x-ray tube position and compared the resulting definition files and dose calculations to those that we created manually for two test cases. We also calculated the doses by simplifying the imaging geometry to neglect the motion of the x-ray tube during the tomosynthesis sweep. We applied the sum of the incident air kerma for the entire sweep to a single, central projection, and evaluated the impact of this simplification on the speed and accuracy of the dose calculations.

Results: Our program produced the same definition files and doses as our manual calculation in both cases, and using the program resulted in a dramatic reduction in the amount of time required to complete the calculations. When neglecting the motion of the x-ray tube, the doses to some organs were over- or underestimated but the effective doses still agreed with the values calculated using the more accurately modeled geometry.

Conclusions: Our MATLAB program allows us to accurately model the imaging geometry of a tomosynthesis exam in PCXMC in a time-efficient manner. For both test cases, a reasonable estimate of the effective dose can be achieved very quickly by neglecting the motion of the x-ray tube, but this also sacrifices the accuracy of individual organ dose calculations.