Purpose: In Positron Emission Tomography (PET) imaging, an early therapeutic response can be assessed based on variations of semi-quantitative parameters such as maximum standardized uptake values (SUV max) measured in PET scans carried out before and during the treatment. However, these measurements do not reflect tumor volume or radiotracer uptake distribution variations.

Methods: The proposed approach is based on multi-observation image statistical analysis for merging several PET acquisitions to assess tumour metabolic volume and uptake variations. The parameters defining the mixture distribution are estimated using the stochastic expectation maximization (SEM) method combined with adaptive spatial correlation estimation (ASEM). The proposed fusion process (ASEM) has been applied to simulated and clinical follow-up PET images of patients classified as partial responders (PR). We have compared the multi-observation fusion with threshold-based (TB) used in clinical practice for the assessment of the therapeutic response, applied independently to each follow-up scans. Volume errors (VE) and quantitative variations of SUV measurements and tumour volume (dV) were considered on simulated and clinical datasets respectively.

Results: : On simulated datasets, the adaptive threshold applied independently on both images led to significantly ($p<0.05$) higher errors than the ASEM fusion in the first follow-up scan (VE ASEM = -1±7%, VE TB = 21±8%), and higher for the second follow-up scan (VE ASEM = -22±19%, VE TB = 28±9%). This trend was enhanced with the clinical datasets, for which the adaptive threshold exhibited incoherent volume variations of +14±167% due to large overevaluation of tumor volumes in the second scan due to challenging conditions of contrast and noise. On the other hand, dV ASEM was -65±11% which is more appropriate since patients are PR.

Conclusions: The ASEM method demonstrated more accurate tumor volume evolution estimation than threshold-based independent segmentations. Future work will consist in applying the method to clinical multi-tracers datasets.