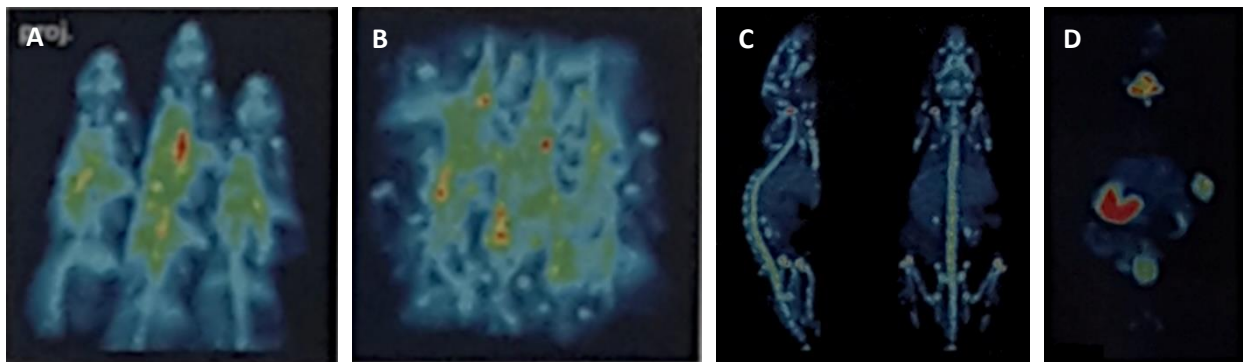


Multi-Target Regression of Radio Pharmaceuticals in Animal Models using Deep Learning on Multi-Pinhole Tomography Images.

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Motivation: High-resolution pinhole SPECT can be very useful in tracer development and pre-clinical research where new radio pharmaceuticals have to be tested in small animal studies. Multi-pinhole tomography is an extension of conventional single-pinhole tomography to more than one pinhole per collimator (typically 7 to 15), which achieves a higher sensitivity. The pinholes are arranged in a way that each pinhole of the multi-pinhole aperture only views a certain part of the object. This allows the imaging of non-spherical objects which can be very useful in whole-body imaging of small animals. However, as the detector size is limited this results in an increasing overlap of the single projections (multiplexing) leading to a deterioration of the system matrix, and thus, causing new problems in tomographical image reconstruction. To study this further, researchers at the ZEL research center in Jülich and the Department of Nuclear Medicine at the University of Marburg analyzed the distribution of Radio Pharmaceuticals and the effect of multiplexing on image quality, in animal models. To visualize structures in the model organism, for instance, tumors or the bone metabolism, a substance (Tc99m-molecules) was injected. Subsequently, a commercial gamma camera (Siemens E.CAM) was equipped with a dedicated 7-hole and 10-hole collimator and images (for example, Fig A and B) were acquired. An iterative maximum likelihood algorithm (MLEM) can be used to reconstruct an image from the multi-pinhole projections (Fig. C and D). The MLEM algorithm produces reconstructions with excellent imaging properties, when about 60 projections with statistically sufficient information are acquired. However, the reconstruction quality decreases as the number of projections decrease and the multiplexing as well as the overlap increases.



Aim: Ultimately, the reconstruction algorithm estimates the concentrations for each structure (tumor, bone, organ, etc.) in the model organism. Therefore, this project aims to utilize modern machine learning technologies, to directly estimate the radio pharmaceutical concentrations, without the intermediate step of MLEM reconstruction. Deep Neural networks (DNN) have been shown to be extremely efficient in categorizing multi-label image data. Therefore, we will apply DNNs to the raw multiplex data, to estimate the Tc99m concentration for all structures in the animal model. Finally, we will analyze whether the same estimation quality can be achieved using smaller number of projections and decrease the stress for the animals.

If you have any questions or are interested in the project, please contact us:

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