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Deep Residual Inception Encoded-Decoder Neural Network for amyloid PET harmonization

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Abstract

Background: Amyloid PET is an *in vivo* technology to visualize and quantify beta-amyloid deposition in the brain. However, the use of multiple amyloid tracers with varied characteristics compounded by processing variabilities poses significant challenges to interpret or combine results from cross-center studies, and to define common positivity threshold. In this research, we developed an encoder-decoder based deep model as a harmonization strategy to render imputed amyloid PET images of one amyloid tracer to the images of another.

Method: 91 PiB-florbetapir (FBP) image pairs from the Open Access Series of Imaging Studies (OASIS) were processed using established pipelines to extract regional standard uptake value ratios (SUVRs), mean cortical SUVRs (mcSUVRs), and SUVR images. Residual Inception Encoder-Decoder Neural Network (RIED-Net) was implemented to learn the nonlinear mappings from the image pairs in 2D using encoding-decoding architecture in conjunction with residual inception blocks and generating imputed images. A 10-fold cross-validation was implemented on axial, coronal and sagittal views separately to generate imputed PiB SUVR imaging from FBP data. The average imputed PiB image from all three views was used for performance evaluation. Correlation was evaluated between the imputed vs. real PiB SUVR image voxel-wise, and between the virtual PiB mcSUVR derived from imputed PiB vs. the real PiB mcSUVR. The trained RIED-Net model was also applied to an independent dataset with 46 subjects from www.gaain.org/centiloid-project, and the same metric was used to assess performance.

Result: The imputed PiB SUVR images were visually more similar to real PiB SUVR images than FBP. Voxel-wise correlation improved from 0.89 between PiB and FBP to 0.95 between the synthetic and real PiB SUVR image ($p<0.0001$) in the cross-validation. The agreement of mcSUVR improved from $r=0.91$ to $r=0.96$ ($p<0.0001$) in

the cross-validation dataset and from r=0.92 to r=0.96 (p<0.001) in the independent dataset.

Conclusion: We proposed a novel encoder-decoder based deep model for synthetic imaging. The model discovered the voxel-wise nonlinear associations between the input images and the output images which significantly improved agreements of amyloid burden measurements from different tracers. The result was further confirmed in an independent dataset demonstrating the generalizability.

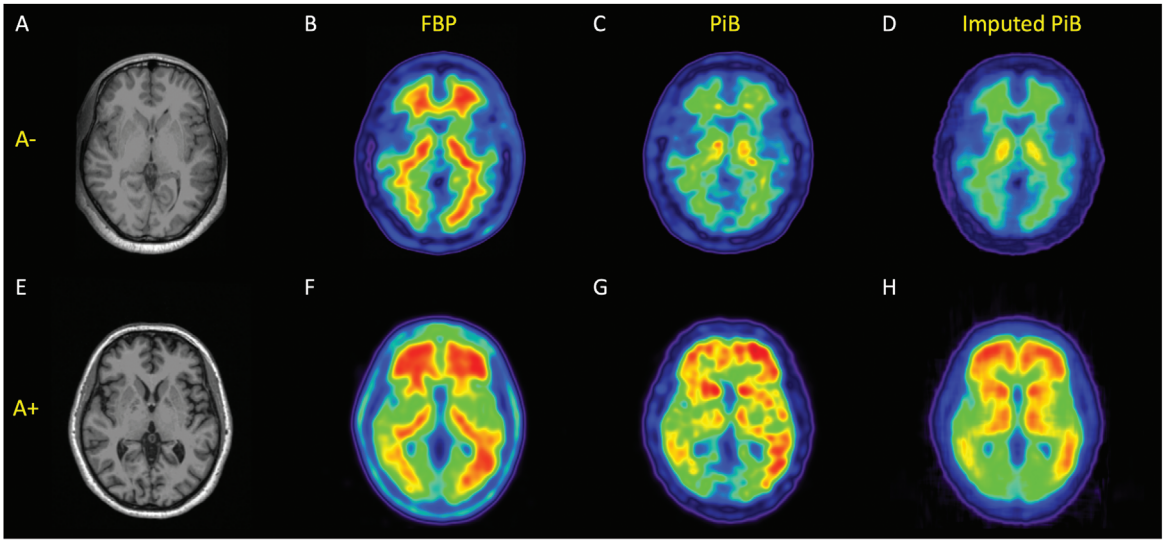

Figure 1. Example images for an amyloid negative participant (A-D) and an amyloid positive participant (E-H) from the independent testing dataset. T1-weighted image (A,E), florbetapir (B, F), PiB (C, G), and imputed PiB from florbetapir (D, H). The difference between florbetapir and PiB images can easily be observed including the substantially higher white matter uptake in florbetapir than PiB. The imputed PiB images from florbetapir demonstrated substantially improved similarity with true PiB data.

FIGURE 1

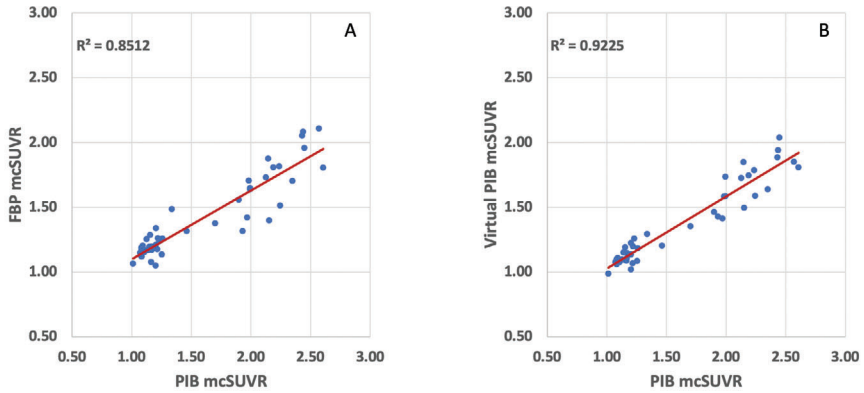

Figure 2. Comparison between FBP and PiB mean cortical SUVR (mcSUVR) measurements in the independent test dataset (A), and between virtual PiB mcSUVR estimated from the RIED-Net model using FBP data and actual PiB mcSUVR in the same set (B). Significantly improved correlation was observed with the application of the RIED-Net model (p<0.001).

FIGURE 2