Demystifying T1-MRI to FDG^{18}-PET Image Translation via Representational Similarity (Appendices)

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1 The canonical components of the layer activation maps

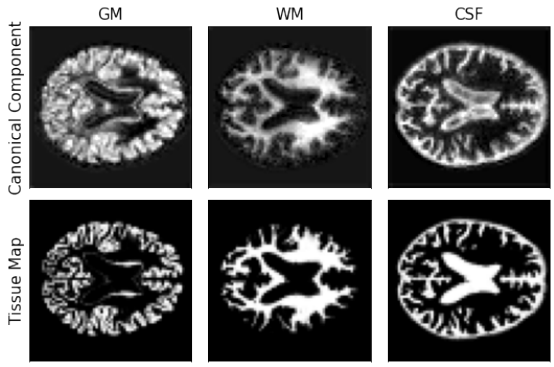

Figure S1: Visualization of the canonical components of activation maps from layer *actv3* of translation model, identified by computing CCA between layer activation maps against the GM, WM, and CSF maps.

2 Qualitative comparison between different translation models

	Input	MAE	SSIM	PSNR	#param
U-Net	MRI	0.027	0.911	26.55	13M
	Tissue	0.028	0.909	26.45	13M
ESIT	Tissue	0.028	0.895	26.16	0.6M

Table S1: Comparison between different translation models in terms of the quality of results (i.e., the PET images). We have the U-Net translation models taking different inputs (i.e., T1-MR images or the brain tissue maps), as well as our proposed Explainable and Simplified Image Translation (ESIT) model.

3 Visualization of the canonical components of the activation maps from the decoding layer

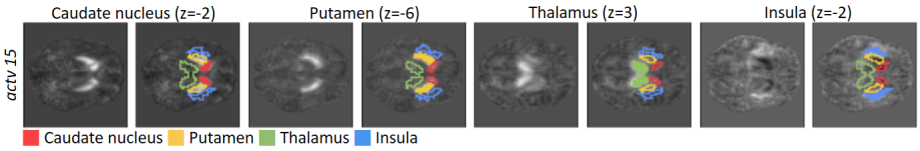

Figure S2: Visualization of the canonical components of two decoding layers, learnt using CCA to maximize the correlation between the activation maps and respectively the four brain region templates (indicated by colorized mask). The spatial dimension of the activation maps obtained from decoding layers *actv15* is 64×64. Adjacent brain regions are highlighted by dotted lines to illustrate that the translation model tends to jointly represent caudate nucleus, putamen and thalamus. The z value represents the z-coordinate in the standard MNI space.

4 Extraction of Regional Gray Matter Volume Information from Brain Tissue Maps

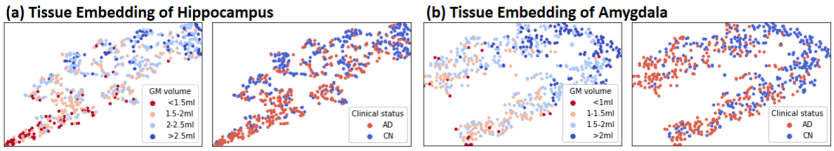

Figure S3: Visualization of the tissue embedding of (a) the hippocampus and (b) amygdala using t-SNE, obtained from 100 cognitively normal (CN) and 100 Alzheimer's disease (AD) subjects, colorized by gray matter (GM) volume (left) and clinical status (right).