

Supplementary Material

Table 1: Accuracy Measures and associated SNPs and Genes

Models	Training AUC	Testing AUC	SNPs	Genes
Whole-brain	0.88	0.72	149 SNPs at 5×10^{-6}	APOE
Logistic Regression	0.78	0.59	GWAS Not Performed	
SVM	0.79	0.61	GWAS Not Performed	
ResNet50 AlexNet VGG16	0.84-0.87	0.69-0.72	GWAS Not Performed	
Augmentation with respect to whole-brain	0.85	0.75	3 SNPs at 5×10^{-8} <i>rs2075650, rs11580593</i> <i>rs823955</i> 38 SNPs at 5×10^{-6}	APOE
AD vs CN	0.96	0.90	2 SNPs at 5×10^{-8} 53 SNPs at 5×10^{-6}	ADCY8, ADK, APOE
Multibranch CNN (27 Models)	0.86	0.76	8 SNPs at 5×10^{-8} 87 SNPs at 5×10^{-6} <i>rs1397645, rs10490381</i>	NDNF
Whole-image GM	0.82	0.70	No Significant genes were found	
Whole-image WM	0.88	0.68	No Significant genes were found	
Whole-image CSF	0.87	0.54	No Significant genes were found	
Multibranch GM	0.84	0.74	35 SNPs at 5×10^{-6} <i>rs173754, rs9257694</i>	APOE, OR14J1
Multibranch WM	0.82	0.70	35 SNPs at 5×10^{-6}	No Significant genes were found
Multibranch CSF	0.77	0.66	21 SNPs at 5×10^{-6}	No Significant genes were found

Relevant Plots

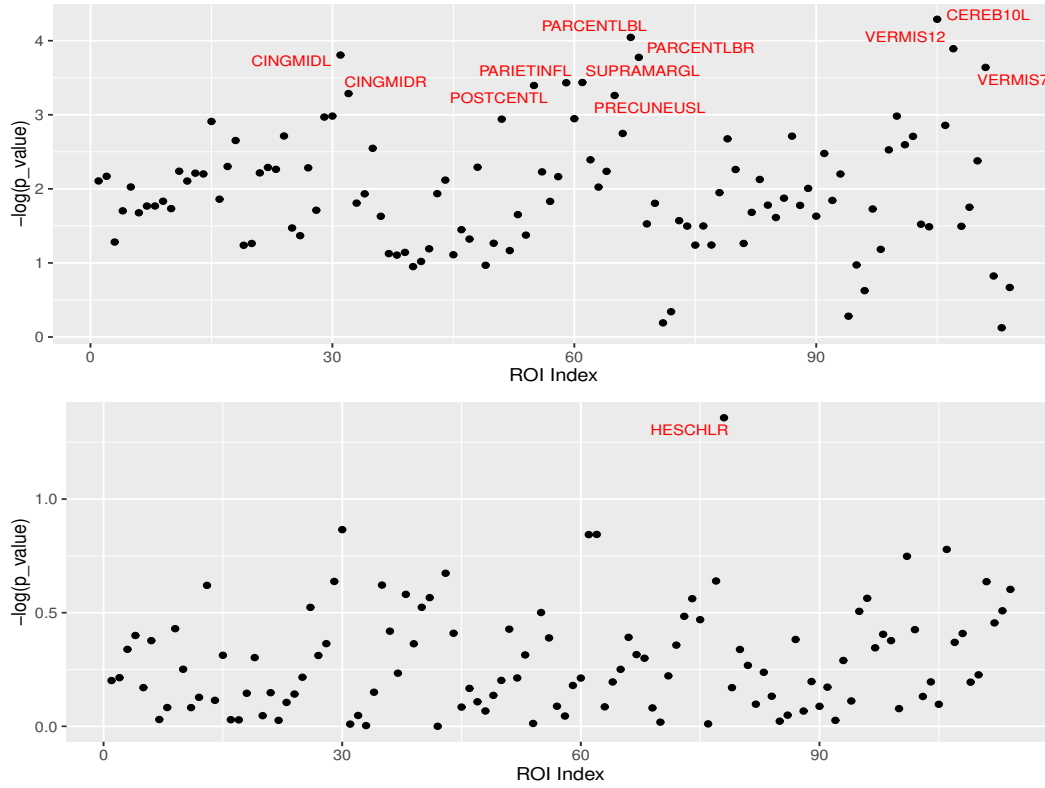


Figure 1: Not all the PCs are easy to interpret. The upper panel shows the plot of ROIs against the $-\log(p_value)$ for PC1 and it is hard to pin-point one specific part of the ROIs. Similarly, in the lower panel we have HESCHL (transverse temporal gyri, right hemisphere) but the corresponding PC8 doesn't play a significant part in the identification of the important SNPs.

Q-Q plots with Genomic Inflation factors

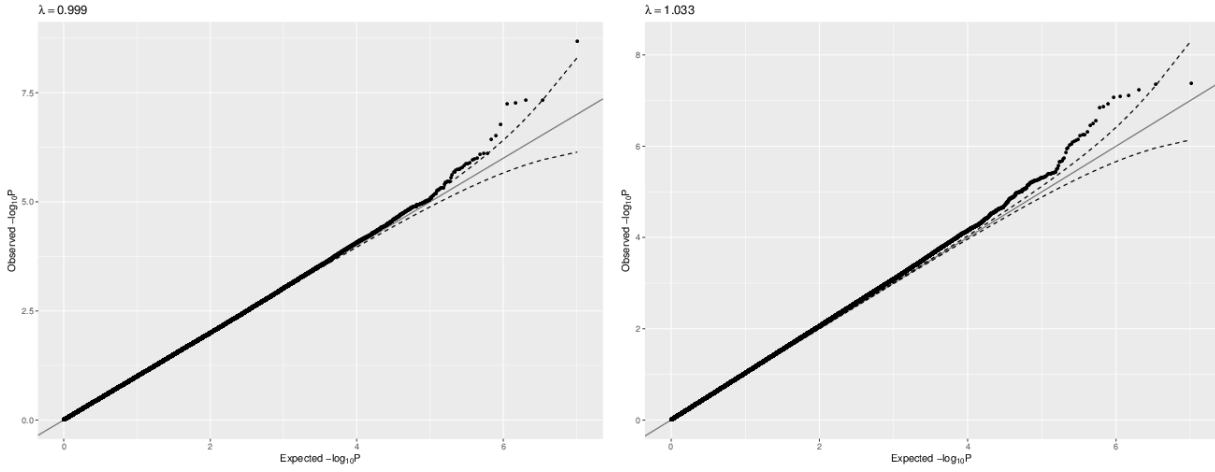


Figure 2: Left: Whole-brain structure with augmentation ,Right: Binary classification of AD vs CN. The X-axis corresponds to expected $-\log(p\text{-value})$ and the Y-axis corresponds to observed $-\log(p\text{-value})$.

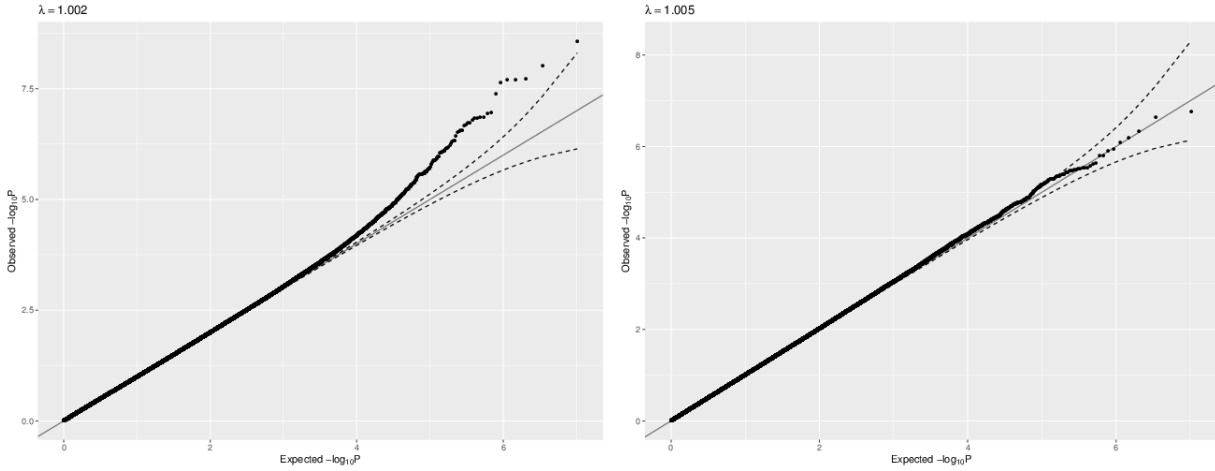


Figure 3: Left: Multi-branch model for the whole-brain structure, Right: Multi-branch model on GM images. The X-axis corresponds to expected $-\log(p\text{-value})$ and the Y-axis corresponds to observed $-\log(p\text{-value})$.

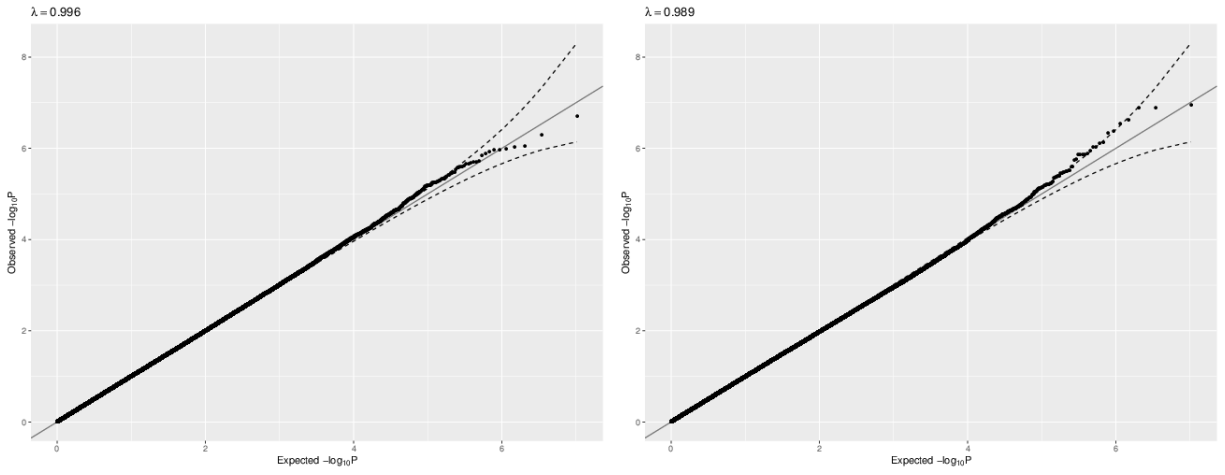


Figure 4: Left: multi-branch model on WM images, Right: Multi-branch model on CSF images. The X-axis corresponds to expected $-\log(\text{p-value})$ and the Y-axis corresponds to observed $-\log(\text{p-value})$.

The Genomic inflation factor (lambda value) obtained from the QQ plot indicated ranged between 0.989 and 1.033 for all models shown in Figures 2-4.