Fig. 1: Forward and reverse training process.

Table 1: Description of the multi-omics datasets. CN: Cognitively Normal, MCI: Mild Cognitive Impairment, AD: Alzheimer's Disease.

Dataset	# Features before preprocessing	# Node features	# Samples (Groups)	# Edges
TCGA-BRCA	mRNA: 20,531 DNA methylation: 20,106 miRNA expression: 503	mRNA: 1,000 DNA methylation: 1,000 miRNA expression: 503	Basal-like: 131 HER2-enriched: 46 Luminal A: 436 Luminal B: 147 Normal-like: 115	mRNA: 2,629 DNA methylation: 2,629 miRNA expression: 2,631
TCGA-GBM	mRNA: 12,044 miRNA expression: 536	mRNA: 1,230 miRNA expression: 534	Proneural: 164 Neural: 97 Mesenchymal: 138 Classical: 120	mRNA: 1,559 miRNA expression: 1,559
ROSMAP	mRNA: 55,889 DNA methylation: 23,788 miRNA expression: 309	mRNA: 200 DNA methylation: 200 miRNA expression: 200	CN: 169 AD: 182	mRNA: 1,055 DNA methylation: 1,055 miRNA expression: 1,055
ADNI	SNPs: 2,126,516 Lipidomics: 781 Bileomics: 24	SNPs: 156 Lipidomics: 637 Bileomics: 24	CN: 214 MCI: 210 AD: 178	SNPs: 1,808 Lipidomics: 1,808 Bileomics: 1,808
PRAD	mRNA : 6037 SNV: 4422 miRNA expression:409	mRNA :1500 SNV: 2000 miRNA expression: 100	Recurrence: 100 Non-Recurrence: 150	mRNA :752 SNV: 870 miRNA expression: 752
BRCA	mRNA : 6038 SNV: 6569 miRNA expression: 437	mRNA :1000 SNV: 1000 miRNA expression: 100	Recurrence: 82 Non-Recurrence: 129	mRNA :635 SNV: 701 miRNA expression: 635
BLCA	mRNA : 6025 SNV: 6819 miRNA expression: 479	mRNA : 1000 SNV: 1000 miRNA expression: 100	Recurrence: 143 Non-Recurrence: 259	mRNA : 1208 SNV: 1222 miRNA expression:1208
LIHC	mRNA : 5823 SNV: 5797 miRNA expression: 469	mRNA : 1000 SNV: 1000 miRNA expression: 200	Recurrence: 171 Non-Recurrence: 183	mRNA : 1064 SNV: 1136 miRNA expression: 1064
TARGET-AML	mRNA: 6404 miRNA expression: 434	mRNA:2000 miRNA expression:100	Recurrence: 120 Non-Recurrence: 101	mRNA:665 miRNA expression:665
TARGET-WT	mRNA: 6758 miRNA expression: 441	mRNA: 2000 miRNA expression: 200	Recurrence: 88 Non-Recurrence: 24	mRNA: 338 miRNA expression: 338