Supplementary Results of the Two Phase Cooperative Learning for Supervised Dimensionality Reduction

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A   Model architecture per dataset

Let $C_{i,j,k,l}$ along with $CT_{i,j,k,l}$ denote a convolutional 2D and a transpose convolutional 2D layer respectively, utilizing i filters, a $j \times j$ kernel, $k \times k$ stride and l padding. Let $Dr\left(p\right)$ denote a dropout layer with a probability of an element to be zeroed equal to p, and B representing a batch normalization layer. Assume, that $ReLU$ and $Sigmoid$ reflect the ReLU and Sigmoid activation functions, respectively. Suppose, that $CB_{r,i,j,k,l}$ corresponds to $C_{i,j,k,l} - B - ReLU$ repeated r times. Additionally, let $D\left(i\right)$ denote a dense layer composed out of i neurons and a linear activation function. Assume, that F denotes a flattening layer and R reflecting a reshape layer to 3D. Finally, suppose, that K corresponds to the dimensionality of the latent representations. The model architecture of the Two Phase Supervised Encoder for each employed dataset is presented thoroughly in Table 1.

Table 1: The structure of the Two Phase Supervised Encoder for each dataset.

MNIST and Fashion MNIST

Encoder
$C_{256,3,2,1} - B - Dr\,(0.3) - ReLU - C_{128,3,2,1} - B - Dr\,(0.3) - ReLU - F - D\,(K)$
Decoder
$D\,(6272) - ReLU - R - CT_{128,3,2,1} - B - ReLU - CT_{256,3,2,1} - B - ReLU - CT_{1,3,1,1} - Sigmoid$
Separator
$D\,(64) - Dr\,(0.5) - ReLU - D\,(10)$

SVHN

Encoder
$C_{256,3,2,1} - B - Dr\,(0.3) - ReLU - C_{128,3,2,1} - B - Dr\,(0.3) - ReLU - F - D\,(K)$
Decoder
$D\,(8192) - ReLU - R - CT_{128,3,2,1} - B - ReLU - CT_{256,3,2,1} - B - ReLU - CT_{3,3,1,1} - Sigmoid$
Separator
$D\,(64) - Dr\,(0.5) - ReLU - D\,(10)$

Brain Tumor Image dataset

Encoder
$CB_{2,64,3,1,1} - C_{64,3,2,1} - B - Dr\,(0.3) - ReLU - CB_{2,64,3,1,1} - C_{64,3,2,1} - B - Dr\,(0.3) - ReLU - CB_{2,128,3,1,1} - C_{128,3,2,1} - B - Dr\,(0.3) - ReLU - CB_{2,128,3,1,1} - C_{128,3,2,1} - B - Dr\,(0.3) - ReLU - F - D\,(K)$
Decoder
$D\,(8192) - ReLU - R - CB_{2,128,3,1,1} - CT_{128,3,2,1} - B - ReLU - CB_{2,128,3,1,1} - CT_{128,3,2,1} - B - ReLU - CB_{2,64,3,1,1} - CT_{64,3,2,1} - B - ReLU - CB_{2,64,3,1,1} - CT_{64,3,2,1} - B - ReLU - CT_{1,3,1,1} - Sigmoid$
Separator
$D\,(128) - Dr\,(0.5) - ReLU - D\,(3)$

SARS-COV-2 CT-Scan dataset

Encoder
$CB_{2,64,3,1,1} - C_{64,3,2,1} - B - Dr\,(0.3) - ReLU - CB_{2,64,3,1,1} - C_{64,3,2,1} - B - Dr\,(0.3) - ReLU - CB_{2,128,3,1,1} - C_{128,3,2,1} - B - Dr\,(0.3) - ReLU - CB_{2,128,3,1,1} - C_{128,3,2,1} - B - Dr\,(0.3) - ReLU - F - D\,(K)$
Decoder
$D\,(8192) - ReLU - R - CB_{2,128,3,1,1} - CT_{128,3,2,1} - B - ReLU - CB_{2,128,3,1,1} - CT_{128,3,2,1} - B - ReLU - CB_{2,64,3,1,1} - CT_{64,3,2,1} - B - ReLU - CB_{2,64,3,1,1} - CT_{64,3,2,1} - B - ReLU - CT_{1,3,1,1} - Sigmoid$
Separator
$D\,(128) - Dr\,(0.5) - ReLU - D\,(2)$

B Supplementary Results

Table 2: Comparison of the mean testing accuracy (%) between the proposed methodology with normal and reverse order of optimization phases for the employed datasets among 10 executions.

	MNIST	Fashion MNIST	SVHN
Proposed method			
TP-SE + Sep. ($K = 10$)	99.01	92.36	88.30
TP-SE + Sep. ($K = 18$)	99.09	92.44	88.60
TP-SE + k-NN ($K = 18$)	99.18	92.50	88.27
TP-SE + SVM ($K = 18$)	99.15	92.41	88.70
TP-SE + GNB ($K = 10$)	98.71	91.64	85.60
Proposed method - Reverse Order			
TP-SE + Sep. ($K = 10$)	99.01	92.31	88.22
TP-SE + Sep. ($K = 18$)	99.06	92.39	88.76
TP-SE + k-NN ($K = 10$)	99.05	92.34	87.70
TP-SE + k-NN ($K = 18$)	99.13	92.57	88.41
TP-SE + SVM ($K = 10$)	99.06	92.33	88.41
TP-SE + SVM ($K = 18$)	99.12	92.41	88.79
TP-SE + GNB ($K = 10$)	98.69	91.65	85.82
TP-SE + GNB ($K = 18$)	98.72	91.69	85.56

	Brain Tumor dataset	SARS-COV-2 CT-Scans dataset
Proposed method		
TP-SE + Sep. ($K = 18$)	94.94	97.22
TP-SE + k-NN ($K = 18$)	94.93	97.24
TP-SE + SVM ($K = 18$)	94.93	96.70
TP-SE + GNB ($K = 10$)	93.82	95.73
TP-SE + GNB ($K = 18$)	94.06	95.59
Proposed method - Reverse Order		
TP-SE + Sep. ($K = 10$)	94.32	96.96
TP-SE + Sep. ($K = 18$)	94.86	97.44
TP-SE + k-NN ($K = 18$)	95.29	97.44
TP-SE + SVM ($K = 10$)	94.44	96.68
TP-SE + SVM ($K = 18$)	94.94	96.96
TP-SE + GNB ($K = 10$)	93.74	96.26
TP-SE + GNB ($K = 18$)	93.98	96.26