Supplementary Material: A Multi-Surrogate Assisted Salp Swarm Feature Selection Algorithm with Multi-Population Adaptive Generation Strategy for Classification

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Table 1: The average classification balanced accuracy of MSA-MPSSA with different a in high-dimensional datasets

Dataset	a=0.1	a=0.2	a=0.3	a=0.4	a=0.5
Yale	0.7103	0.7126	**0.7169**	0.7156	0.7132
warpPIE10P	0.9721	0.9688	**0.9774**	0.9739	0.9755
lymphoma2	0.9677	0.9718	0.9721	**0.9742**	0.9734
Breast3	**0.7583**	0.7529	0.7539	0.7549	0.7463
Nci	0.8621	**0.8649**	0.8602	0.8587	0.8576
Leukemia1	1	1	**1**	1	1
9_Tumors	0.6853	0.6821	0.6809	0.6878	**0.6893**
Lung_Cancer	0.9779	0.9803	**0.9825**	0.9816	0.9819

a is set to 0.3.

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Table 2: The average classification balanced accuracy of MSA-MPSSA at different b

Dataset	b=0.1	b=0.2	b=0.3	b=0.4	b=0.5
HeartEW	0.8846	**0.8873**	0.8853	0.8793	0.8768
SpectEW	0.8428	0.8410	**0.8469**	0.8472	0.8323
Horse	0.8377	0.8449	**0.8453**	0.8416	0.8386
flags	0.6286	**0.6360**	0.6267	0.6332	0.6245
BreastEW	0.9628	0.9649	0.9653	0.9686	**0.9721**
ionosphere	0.9387	**0.9400**	0.9361	0.9350	0.9372
Sonar	0.9084	0.9107	**0.9203**	0.9152	0.8976
PenglungEW	**0.9552**	0.9545	0.9534	0.9428	0.9481
Yale	0.7096	0.7169	0.7132	**0.7192**	0.7149
warpPIE10P	0.9630	**0.9774**	0.9686	0.9753	0.9764
lymphoma2	**0.9731**	0.9721	0.9659	0.9662	0.9703
Breast3	0.7496	0.7539	0.7548	0.7563	**0.7574**
Nci	0.8532	**0.8602**	0.8571	0.8567	0.8493
Leukemia1	0.9998	**1.0000**	**1.0000**	0.9994	**1.0000**
9_Tumors	0.6823	0.6809	**0.6854**	0.6848	0.6789
Lung_Cancer	0.9804	**0.9825**	0.9786	0.9742	0.9685

b is set to 0.2.