Results of SVM

Algorithms	BRCA (Gene-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.877778	0.005856	0.757895	0.044383	0.685714	0.040156	0.812973	0.027349
PCA_DNA Methylation	0.876389	0.004392	0.747368	0.033287	0.676190	0.030117	0.806486	0.020512
PCA (Gene-DNA Methylation)	0.881944	0.021960	0.752632	0.049931	0.685714	0.060234	0.811892	0.037605
CCA	0.905714	0.042402	0.852632	0.195045	0.785714	0.162262	0.867194	0.113472
RCCA	0.926831	0.039083	0.868421	0.177618	0.814286	0.131756	0.885453	0.094030
SRCCA_TT	0.927994	0.030404	0.731579	0.127601	0.704762	0.104810	0.812500	0.076282
SRCCA_WL	0.933602	0.040726	0.878947	0.119118	0.833333	0.112799	0.901693	0.071398
SRCCA_WR	0.926905	0.044189	0.910526	0.124178	0.852381	0.108704	0.914100	0.069811
SRCCA_MI	0.935928	0.039731	0.905263	0.098621	0.857143	0.092555	0.917624	0.057518
SRCCA_RH	0.903709	0.009573	0.931579	0.096252	0.847619	0.073771	0.914658	0.049526
CuRSaR	0.913723	0.047024	0.936842	0.164202	0.866667	0.159995	0.919487	0.114662
FaRoC	0.977416	0.029206	0.921053	0.056849	0.909524	0.069006	0.947890	0.040159

Algorithms	BRCA (Gene-Protein)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.877778	0.005856	0.757895	0.044383	0.685714	0.040156	0.812973	0.027349
PCA_Protein	0.881944	0.021960	0.752632	0.049931	0.685714	0.060234	0.811892	0.037605
PCA (Gene-Protein)	0.881250	0.019764	0.742105	0.016644	0.676190	0.030117	0.805714	0.018070
CCA	0.919279	0.053594	0.642105	0.085228	0.623810	0.082326	0.752934	0.063423
RCCA	0.919572	0.029265	0.800000	0.213142	0.752381	0.164651	0.840054	0.119284
SRCCA_TT	0.967784	0.043600	0.921053	0.108857	0.900000	0.106361	0.940524	0.070368
SRCCA_WL	0.921805	0.033161	0.973684	0.037216	0.900000	0.035136	0.946245	0.019592
SRCCA_WR	0.927729	0.035592	0.936842	0.073601	0.876190	0.075125	0.930903	0.044582
SRCCA_MI	0.929734	0.041872	0.963158	0.078654	0.900000	0.085331	0.944658	0.050170
SRCCA_RH	0.918686	0.035395	0.942105	0.076270	0.871429	0.074620	0.928746	0.044525
CuRSaR	0.945084	0.034880	0.968421	0.036800	0.919048	0.039203	0.955836	0.021775
FaRoC	0.979181	0.035781	0.936842	0.054358	0.923810	0.060234	0.956551	0.034373

Results of SVM

Algorithms	BRCA (Protein-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Protein	0.881944	0.021960	0.752632	0.049931	0.685714	0.060234	0.811892	0.037605
PCA_DNA Methylation	0.876389	0.004392	0.747368	0.033287	0.676190	0.030117	0.806486	0.020512
PCA (Protein-DNA Methylation)	0.880754	0.010222	0.784211	0.087544	0.709524	0.079206	0.827973	0.050651
CCA	0.886791	0.005142	0.826316	0.043330	0.747619	0.039203	0.855073	0.025380
RCCA	0.892339	0.003961	0.873684	0.036800	0.790476	0.033296	0.882635	0.020549
SRCCA_TT	0.917544	0.032236	0.978947	0.036800	0.900000	0.035136	0.946508	0.019626
SRCCA_WL	0.901201	0.029756	0.884211	0.158478	0.809524	0.140187	0.886568	0.097932
SRCCA_WR	0.937337	0.048603	0.894737	0.164576	0.852381	0.162573	0.908667	0.115023
SRCCA_MI	0.925496	0.033852	0.963158	0.055755	0.895238	0.054062	0.942839	0.031118
SRCCA_RH	0.954365	0.050652	0.957895	0.048365	0.919048	0.074620	0.955430	0.041606
CuRSaR	0.974211	0.043716	0.947368	0.042974	0.928571	0.064476	0.960002	0.035594
FaRoC	0.963392	0.025310	0.963158	0.035524	0.933333	0.046004	0.963008	0.025854

Algorithms	OV (Gene-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.827915	0.026844	0.809091	0.204055	0.700000	0.157158	0.808460	0.116881
PCA_DNA Methylation	0.834361	0.034354	0.754545	0.221048	0.666667	0.161265	0.777771	0.128819
PCA (Gene-DNA Methylation)	0.830768	0.024537	0.739394	0.235681	0.653846	0.170619	0.765392	0.139100
CCA	0.769192	0.014937	0.609091	0.054302	0.515385	0.045948	0.679139	0.038996
RCCA	0.839146	0.039550	0.748485	0.224983	0.666667	0.163960	0.775962	0.130273
SRCCA_TT	0.838741	0.016204	0.930303	0.166621	0.792308	0.125876	0.875529	0.100376
SRCCA_WL	0.871139	0.046603	0.890909	0.225051	0.787179	0.146076	0.860160	0.131228
SRCCA_WR	0.850693	0.029233	0.924242	0.131119	0.797436	0.091617	0.880995	0.068573
SRCCA_MI	0.846314	0.030094	0.921212	0.159839	0.794872	0.131857	0.877046	0.095462
SRCCA_RH	0.846154	0.018131	0.933333	0.141270	0.800000	0.100259	0.882486	0.073810
CuRSaR	0.856280	0.015560	0.990909	0.028748	0.851282	0.026482	0.918437	0.015511
FaRoC	0.867137	0.021890	0.984849	0.015971	0.858975	0.027695	0.922080	0.014731

Results of SVM

Algorithms	OV (Gene-Protein)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.827915	0.026844	0.809091	0.204055	0.700000	0.157158	0.808460	0.116881
PCA_Protein	0.814437	0.037761	0.796970	0.219473	0.682051	0.178139	0.795386	0.132979
PCA (Gene-Protein)	0.823379	0.027464	0.781818	0.192079	0.676923	0.149120	0.793207	0.109827
CCA	0.863685	0.024480	0.787879	0.051505	0.715385	0.050492	0.823437	0.035102
RCCA	0.845282	0.023439	0.915152	0.072559	0.787179	0.068429	0.877994	0.044900
SRCCA_TT	0.865548	0.023348	0.933333	0.023903	0.820513	0.034188	0.897980	0.019315
SRCCA_WL	0.873063	0.038923	0.927273	0.015648	0.823077	0.045948	0.899035	0.024790
SRCCA_WR	0.852720	0.025981	0.942424	0.046178	0.812821	0.041959	0.894672	0.024966
SRCCA_MI	0.859386	0.026780	0.960606	0.037929	0.833333	0.047202	0.906890	0.026870
SRCCA_RH	0.845344	0.001707	0.993939	0.012777	0.841026	0.010811	0.913615	0.006433
CuRSaR	0.858234	0.019601	0.987879	0.015648	0.851282	0.026482	0.918377	0.014219
FaRoC	0.895928	0.064257	1.000000	0.000000	0.897436	0.066205	0.944030	0.035326

Algorithms	OV (Protein-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Protein	0.814437	0.037761	0.796970	0.219473	0.682051	0.178139	0.795386	0.132979
PCA_DNA Methylation	0.834361	0.034354	0.754545	0.221048	0.666667	0.161265	0.777771	0.128819
PCA (Protein-DNA Methylation)	0.832650	0.054048	0.651515	0.061025	0.594872	0.079996	0.730561	0.057004
CCA	0.842116	0.039270	0.787879	0.037795	0.694872	0.054661	0.813724	0.033526
RCCA	0.839619	0.013422	0.906061	0.063000	0.774359	0.052409	0.870792	0.034335
SRCCA_TT	0.846332	0.010679	0.951515	0.053830	0.812821	0.041959	0.895236	0.026597
SRCCA_WL	0.873655	0.036368	0.933333	0.042376	0.828205	0.051353	0.901851	0.029458
SRCCA_WR	0.877291	0.035949	0.927273	0.049895	0.828205	0.061693	0.901083	0.036584
SRCCA_MI	0.850110	0.010175	0.978788	0.032102	0.835897	0.024772	0.909669	0.015160
SRCCA_RH	0.851284	0.015873	0.969697	0.037795	0.830769	0.032434	0.906279	0.019433
CuRSaR	0.869575	0.052907	0.984848	0.032731	0.858974	0.054393	0.922515	0.029699
FaRoC	0.890846	0.057759	0.963636	0.051107	0.866667	0.075291	0.924716	0.043313

Results of SVM

Algorithms	BRCA (Gene-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	2.75E-06	1.15E-04	2.48E-05	2.89E-05	2.06E-03	3.68E-03	2.45E-03	2.49E-03
PCA_DNA Methylation	6.52E-07	4.27E-06	1.02E-06	8.46E-07	2.24E-03	2.39E-03	2.43E-03	2.49E-03
PCA (Gene-DNA Methylation)	2.49E-06	5.37E-05	1.60E-05	1.50E-05	2.24E-03	3.66E-03	2.47E-03	2.49E-03
CCA	5.27E-05	1.27E-01	1.12E-02	1.61E-02	3.58E-03	1.30E-01	1.24E-02	2.96E-02
RCCA	6.86E-03	1.64E-01	1.84E-02	2.46E-02	1.35E-02	2.00E-01	1.22E-02	2.96E-02
SRCCA_TT	1.99E-03	1.87E-04	1.51E-05	3.96E-05	3.84E-03	3.79E-03	2.45E-03	2.53E-03
SRCCA_WL	1.90E-02	2.11E-01	8.58E-02	8.85E-02	1.91E-02	2.17E-01	6.13E-02	6.93E-02
SRCCA_WR	8.93E-03	4.24E-01	1.37E-01	1.49E-01	1.39E-02	4.29E-01	1.47E-01	2.54E-01
SRCCA_MI	1.99E-02	3.49E-01	1.14E-01	1.24E-01	2.48E-02	3.61E-01	1.31E-01	1.07E-01
SRCCA_RH	9.54E-06	6.12E-01	5.13E-02	7.63E-02	2.49E-03	6.07E-01	3.24E-02	1.20E-01
CuRSaR	4.54E-03	6.16E-01	2.25E-01	2.36E-01	1.02E-02	9.07E-01	2.76E-01	4.76E-01

Algorithms	BRCA (Gene-Protein)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	3.23E-06	1.81E-05	1.09E-06	1.31E-06	2.24E-03	3.45E-03	2.36E-03	2.50E-03
PCA_DNA Methylation	6.16E-05	3.16E-05	1.85E-05	1.61E-05	2.50E-03	3.61E-03	3.61E-03	3.71E-03
PCA (Gene-DNA Methylation)	7.99E-06	1.66E-06	7.22E-07	4.77E-07	2.06E-03	2.39E-03	2.40E-03	2.47E-03
CCA	6.53E-03	2.44E-06	1.15E-06	2.69E-06	8.58E-03	2.49E-03	2.46E-03	2.53E-03
RCCA	6.97E-03	5.13E-02	6.50E-03	8.09E-03	3.54E-02	6.88E-02	8.65E-03	1.83E-02
SRCCA_TT	2.11E-01	3.14E-01	2.52E-01	2.45E-01	2.33E-01	4.58E-01	3.89E-01	4.17E-01
SRCCA_WL	6.95E-04	9.45E-01	1.99E-01	2.58E-01	5.26E-03	9.29E-01	1.53E-01	4.39E-01
SRCCA_WR	1.71E-03	5.00E-01	6.39E-02	7.82E-02	8.58E-03	5.00E-01	6.27E-02	1.30E-01
SRCCA_MI	1.14E-03	8.10E-01	1.90E-01	2.32E-01	5.66E-03	8.47E-01	1.54E-01	2.21E-01
SRCCA_RH	4.35E-04	5.66E-01	6.86E-02	8.87E-02	3.74E-03	6.34E-01	4.77E-02	1.20E-01
CuRSaR	1.38E-02	9.03E-01	4.30E-01	4.81E-01	3.10E-02	9.17E-01	4.32E-01	5.56E-01

Results of SVM

Algorithms	BRCA (Protein-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	2.95E-05	1.48E-07	7.22E-07	6.33E-07	2.34E-03	2.20E-03	2.36E-03	2.38E-03
PCA_DNA Methylation	1.36E-06	1.89E-07	1.40E-07	1.28E-07	2.40E-03	2.25E-03	2.40E-03	2.45E-03
PCA (Gene-DNA Methylation)	3.57E-06	4.60E-04	7.05E-05	8.21E-05	2.45E-03	4.27E-03	3.35E-03	3.35E-03
CCA	2.02E-06	1.58E-05	1.40E-06	1.89E-06	2.47E-03	2.45E-03	2.05E-03	2.47E-03
RCCA	1.90E-06	5.38E-05	5.07E-07	6.53E-07	2.47E-03	2.39E-03	2.39E-03	2.49E-03
SRCCA_TT	5.38E-03	8.61E-01	1.24E-02	1.90E-02	1.75E-02	8.72E-01	2.06E-02	8.29E-02
SRCCA_WL	4.06E-04	8.66E-02	1.38E-02	2.11E-02	2.46E-03	1.55E-01	8.98E-03	1.40E-02
SRCCA_WR	8.93E-03	1.18E-01	6.54E-02	7.98E-02	2.29E-02	8.35E-02	3.98E-02	5.79E-02
SRCCA_MI	1.99E-02	5.00E-01	2.64E-02	2.91E-02	2.93E-02	6.31E-01	5.30E-02	4.61E-02
SRCCA_RH	2.77E-01	3.63E-01	2.17E-01	2.31E-01	4.72E-01	2.90E-01	3.40E-01	4.72E-01
CuRSaR	7.34E-01	1.39E-01	4.11E-01	3.98E-01	8.01E-01	1.70E-01	4.15E-01	3.60E-01

Algorithms	OV (Gene-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	5.04E-03	9.60E-03	5.66E-03	6.56E-03	1.76E-02	2.29E-02	8.51E-03	8.58E-03
PCA_DNA Methylation	1.07E-03	4.64E-03	1.62E-03	2.72E-03	3.46E-03	1.77E-02	3.79E-03	3.46E-03
PCA (Gene-DNA Methylation)	4.60E-04	3.61E-03	1.74E-03	2.73E-03	5.81E-03	1.36E-02	5.81E-03	5.81E-03
CCA	8.12E-07	4.37E-10	2.23E-09	5.19E-09	2.50E-03	2.23E-03	2.46E-03	2.50E-03
RCCA	2.73E-02	4.03E-03	1.36E-03	2.16E-03	2.52E-02	1.39E-02	3.82E-03	3.82E-03
SRCCA_TT	2.91E-03	1.74E-01	7.16E-02	9.42E-02	1.03E-02	5.70E-01	1.75E-02	6.88E-02
SRCCA_WL	6.20E-01	1.11E-01	8.02E-02	8.80E-02	3.12E-01	3.40E-01	6.54E-02	1.46E-01
SRCCA_WR	1.29E-01	9.09E-02	3.01E-02	4.27E-02	6.92E-02	1.11E-01	6.19E-03	1.41E-02
SRCCA_MI	6.64E-03	1.31E-01	6.83E-02	7.84E-02	1.39E-02	4.57E-01	2.20E-02	8.78E-02
SRCCA_RH	3.28E-02	1.28E-01	3.68E-02	5.02E-02	2.47E-02	3.40E-01	8.31E-03	2.47E-02
CuRSaR	4.59E-02	7.46E-01	1.72E-01	2.14E-01	4.65E-02	7.60E-01	9.78E-02	2.88E-01

Results of SVM

Algorithms	OV (Gene-Protein)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	2.96E-03	8.00E-03	2.47E-03	3.31E-03	8.57E-03	2.06E-02	8.88E-03	8.88E-03
PCA_DNA Methylation	2.14E-03	8.44E-03	2.23E-03	3.01E-03	8.88E-03	2.16E-02	8.78E-03	8.88E-03
PCA (Gene-DNA Methylation)	1.35E-03	2.91E-03	6.85E-04	1.02E-03	5.66E-03	1.36E-02	5.76E-03	5.81E-03
CCA	5.54E-02	1.91E-07	6.00E-06	2.80E-06	8.44E-02	2.45E-03	2.47E-03	2.53E-03
RCCA	3.58E-02	2.47E-03	8.20E-03	7.96E-03	8.64E-02	3.48E-03	8.78E-03	3.82E-03
SRCCA_TT	4.14E-02	5.04E-06	5.27E-04	2.81E-04	1.66E-01	2.24E-03	3.30E-03	2.46E-03
SRCCA_WL	1.67E-01	6.73E-08	9.48E-03	5.52E-03	2.87E-01	1.93E-03	1.24E-02	6.20E-03
SRCCA_WR	1.92E-02	1.70E-03	2.51E-03	2.13E-03	1.77E-02	7.88E-03	5.61E-03	5.81E-03
SRCCA_MI	6.11E-02	4.73E-03	2.52E-02	2.13E-02	1.06E-01	1.28E-02	3.38E-02	1.89E-02
SRCCA_RH	1.65E-02	8.39E-02	9.53E-03	8.87E-03	1.16E-02	-	1.16E-02	1.16E-02
CuRSaR	4.02E-02	1.84E-02	3.38E-02	3.14E-02	3.70E-02	-	3.70E-02	3.70E-02

Algorithms	OV (Protein-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	5.09E-04	1.98E-02	2.04E-03	3.39E-03	2.53E-03	3.13E-02	6.26E-03	6.26E-03
PCA_DNA Methylation	2.87E-03	6.83E-03	1.12E-03	1.91E-03	3.84E-03	1.37E-02	5.40E-03	5.43E-03
PCA (Gene-DNA Methylation)	1.44E-02	2.91E-07	1.01E-05	5.50E-06	1.04E-02	2.47E-03	2.52E-03	2.53E-03
CCA	3.20E-02	3.50E-06	6.14E-05	2.46E-05	1.83E-02	2.47E-03	2.50E-03	2.52E-03
RCCA	1.68E-02	8.94E-03	5.00E-03	4.99E-03	6.26E-03	1.66E-02	2.45E-03	2.53E-03
SRCCA_TT	2.92E-02	2.73E-01	4.68E-02	5.42E-02	1.79E-02	2.85E-01	3.06E-02	4.65E-02
SRCCA_WL	1.72E-01	2.09E-02	4.06E-02	3.43E-02	1.31E-01	2.20E-02	6.15E-02	2.50E-02
SRCCA_WR	2.56E-01	5.19E-02	8.45E-02	7.54E-02	2.87E-01	6.14E-02	4.22E-02	3.71E-02
SRCCA_MI	3.28E-02	7.74E-01	1.17E-01	1.53E-01	3.30E-02	7.74E-01	1.30E-01	1.57E-01
SRCCA_RH	4.64E-02	6.15E-01	1.15E-01	1.39E-01	4.29E-02	6.11E-01	1.30E-01	1.57E-01
CuRSaR	2.02E-01	8.18E-01	3.94E-01	4.46E-01	1.07E-01	8.31E-01	4.16E-01	4.29E-01

Results of NNA

Algorithms	BRCA (Gene-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.938250	0.040060	0.863158	0.096730	0.823810	0.089932	0.896375	0.058214
PCA_DNA Methylation	0.894772	0.017382	0.852632	0.104677	0.776190	0.089932	0.870441	0.057333
PCA (Gene-DNA Methylation)	0.945359	0.043561	0.842105	0.099243	0.809524	0.074451	0.886223	0.052737
CCA	0.913022	0.027196	0.826316	0.119118	0.771429	0.104810	0.863473	0.069560
RCCA	0.905897	0.023157	0.915789	0.096730	0.838095	0.087518	0.908659	0.056315
SRCCA_TT	0.940347	0.045083	0.942105	0.057921	0.890476	0.045175	0.939279	0.025870
SRCCA_WL	0.955213	0.049195	0.942105	0.063012	0.904762	0.063492	0.946637	0.036823
SRCCA_WR	0.959102	0.047093	0.947368	0.055479	0.914286	0.070273	0.952153	0.039604
SRCCA_MI	0.955054	0.049582	0.942105	0.067720	0.904762	0.067344	0.946541	0.038690
SRCCA_RH	0.955054	0.049582	0.931579	0.055755	0.895238	0.049181	0.941298	0.028184
CuRSaR	0.964131	0.041689	0.952632	0.046084	0.923810	0.060234	0.957577	0.033554
FaRoC	0.965689	0.046114	0.968421	0.044383	0.938095	0.055214	0.965933	0.030285

Algorithms	BRCA (Gene-Protein)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.938250	0.040060	0.863158	0.096730	0.823810	0.089932	0.896375	0.058214
PCA_Protein	0.963889	0.052050	0.826316	0.136007	0.814286	0.137373	0.884599	0.088070
PCA (Gene-Protein)	0.942938	0.044126	0.800000	0.104677	0.771429	0.073771	0.860676	0.050960
CCA	0.921983	0.051228	0.889474	0.147723	0.833333	0.144174	0.900350	0.098939
RCCA	0.908496	0.020259	0.936842	0.048365	0.857143	0.044896	0.921820	0.026317
SRCCA_TT	0.949607	0.046766	0.942105	0.046084	0.900000	0.052405	0.944596	0.028962
SRCCA_WL	0.934637	0.041295	0.947368	0.055479	0.890476	0.055214	0.939590	0.031173
SRCCA_WR	0.949871	0.046759	0.947368	0.049622	0.904762	0.054986	0.947295	0.030468
SRCCA_MI	0.930659	0.050217	0.884211	0.139912	0.838095	0.144086	0.902830	0.098908
SRCCA_RH	0.941060	0.046204	0.889474	0.057921	0.847619	0.062693	0.913084	0.036770
CuRSaR	0.953868	0.044090	0.947368	0.042974	0.909524	0.061271	0.949889	0.033858
FaRoC	0.946379	0.048430	0.978947	0.036800	0.928572	0.056120	0.961504	0.030513

Results of NNA

Algorithms	BRCA (Protein-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Protein	0.963889	0.052050	0.826316	0.136007	0.814286	0.137373	0.884599	0.088070
PCA_DNA Methylation	0.894772	0.017382	0.852632	0.104677	0.776190	0.089932	0.870441	0.057333
PCA (Protein-DNA Methylation)	0.923563	0.045158	0.863158	0.090142	0.809524	0.080937	0.889551	0.050057
CCA	0.915691	0.051077	0.873684	0.126996	0.814286	0.131756	0.890804	0.087358
RCCA	0.912848	0.033891	0.926316	0.061778	0.852381	0.061271	0.918390	0.036003
SRCCA_TT	0.963392	0.034585	0.936842	0.033287	0.909524	0.041695	0.949333	0.023103
SRCCA_WL	0.947014	0.049708	0.894737	0.085947	0.857143	0.080937	0.917510	0.050039
SRCCA_WR	0.953759	0.050850	0.942105	0.052338	0.904762	0.074451	0.947041	0.041888
SRCCA_MI	0.954281	0.043523	0.947368	0.060774	0.909524	0.065253	0.949424	0.037189
SRCCA_RH	0.960426	0.051164	0.957895	0.041516	0.923810	0.060234	0.958118	0.032887
CuRSaR	1.000000	0.000000	0.942105	0.046084	0.947619	0.041695	0.969657	0.024964
FaRoC	0.970476	0.041303	0.978947	0.027179	0.952381	0.044896	0.974071	0.024038

Algorithms	OV (Gene-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.873864	0.053359	0.830303	0.106133	0.753846	0.101274	0.848403	0.066739
PCA_DNA Methylation	0.855501	0.033055	0.872727	0.090120	0.766667	0.072976	0.861755	0.048232
PCA (Gene-DNA Methylation)	0.874883	0.057215	0.836364	0.081060	0.758974	0.089805	0.853425	0.056873
CCA	0.838061	0.029317	0.836364	0.065773	0.725641	0.071560	0.836694	0.046084
RCCA	0.868761	0.049927	0.884848	0.145539	0.782051	0.083086	0.867081	0.068967
SRCCA_TT	0.862890	0.048874	0.915152	0.147627	0.797436	0.082380	0.878312	0.069763
SRCCA_WL	0.886128	0.067037	0.866667	0.081060	0.789744	0.091097	0.873979	0.056436
SRCCA_WR	0.870522	0.048985	0.848485	0.083295	0.761538	0.056759	0.856286	0.037255
SRCCA_MI	0.876863	0.071816	0.857576	0.112525	0.774359	0.105928	0.863125	0.070625
SRCCA_RH	0.863776	0.049436	0.887879	0.171450	0.779487	0.104119	0.863725	0.086168
CuRSaR	0.882135	0.066959	0.942424	0.061359	0.838462	0.055457	0.908272	0.031468
FaRoC	0.919293	0.063603	0.921212	0.098141	0.864103	0.113421	0.918337	0.071858

Results of NNA

Algorithms	OV (Gene-Protein)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Gene	0.873864	0.053359	0.830303	0.106133	0.753846	0.101274	0.848403	0.066739
PCA_Protein	0.886371	0.066781	0.857576	0.092632	0.782051	0.085683	0.868051	0.055290
PCA (Gene-Protein)	0.823379	0.027464	0.781818	0.192079	0.676923	0.149120	0.793207	0.109827
CCA	0.832563	0.014647	0.845455	0.059673	0.725641	0.049910	0.838164	0.035418
RCCA	0.845044	0.020093	0.945455	0.077981	0.807692	0.067570	0.891351	0.043883
SRCCA_TT	0.902323	0.065308	0.918182	0.051604	0.841026	0.049543	0.907589	0.027493
SRCCA_WL	0.899835	0.067725	0.878788	0.045173	0.810256	0.065316	0.887372	0.037076
SRCCA_WR	0.879662	0.061522	0.887879	0.068583	0.797436	0.059768	0.880799	0.035917
SRCCA_MI	0.899659	0.066575	0.900000	0.042974	0.825641	0.058968	0.897886	0.032762
SRCCA_RH	0.896882	0.069414	0.906061	0.048337	0.828205	0.074560	0.899827	0.042739
CuRSaR	0.927681	0.061135	0.903030	0.051108	0.853846	0.049910	0.912948	0.028749
FaRoC	0.908817	0.071956	0.954546	0.049997	0.876923	0.092687	0.929980	0.052384

Algorithms	OV (Protein-DNA Methylation)							
	precision		recall		accuracy		f1_score	
	mean	sd	mean	sd	mean	sd	mean	sd
PCA_Protein	0.886371	0.066781	0.857576	0.092632	0.782051	0.085683	0.868051	0.055290
PCA_DNA Methylation	0.855501	0.033055	0.872727	0.090120	0.766667	0.072976	0.861755	0.048232
PCA (Protein-DNA Methylation)	0.859270	0.037204	0.760606	0.074843	0.692308	0.075485	0.805719	0.051850
CCA	0.849344	0.019372	0.887879	0.063964	0.771795	0.053308	0.867218	0.035212
RCCA	0.863304	0.025163	0.881818	0.101464	0.782051	0.083086	0.870083	0.056013
SRCCA_TT	0.889912	0.065336	0.833333	0.290041	0.758974	0.216292	0.813962	0.269150
SRCCA_WL	0.901830	0.060449	0.878788	0.028570	0.812821	0.051353	0.888822	0.028168
SRCCA_WR	0.895873	0.060786	0.893939	0.049997	0.817949	0.051919	0.892835	0.030058
SRCCA_MI	0.868630	0.050678	0.909091	0.071425	0.805128	0.076638	0.886913	0.047569
SRCCA_RH	0.871382	0.052647	0.818182	0.288189	0.730769	0.204504	0.796963	0.262885
CuRSaR	0.909901	0.069114	0.881818	0.073467	0.820513	0.065092	0.892284	0.040470
FaRoC	0.936944	0.056813	0.884849	0.135368	0.848718	0.113034	0.903826	0.077453

Results of NNA

Algorithms	BRCA (Gene-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	8.86E-02	9.38E-03	1.05E-02	1.10E-02	8.82E-02	8.37E-03	1.32E-02	8.65E-03
PCA_DNA Methylation	5.25E-04	4.49E-03	1.54E-04	2.18E-04	3.82E-03	8.37E-03	3.71E-03	3.84E-03
PCA (Gene-DNA Methylation)	1.41E-01	4.31E-03	3.82E-03	4.65E-03	8.78E-02	5.61E-03	5.76E-03	3.84E-03
CCA	4.84E-03	1.05E-03	1.91E-04	2.82E-04	1.04E-02	5.66E-03	3.76E-03	3.84E-03
RCCA	3.87E-03	3.69E-02	1.98E-03	3.23E-03	6.23E-03	2.39E-02	3.63E-03	3.44E-03
SRCCA_TT	1.28E-01	1.22E-01	1.89E-03	1.68E-03	1.02E-01	1.23E-01	7.88E-03	5.43E-03
SRCCA_WL	2.95E-01	1.37E-01	8.63E-02	8.78E-02	2.30E-01	7.04E-02	1.32E-01	7.50E-02
SRCCA_WR	3.70E-01	8.39E-02	1.49E-01	1.36E-01	3.43E-01	7.87E-02	2.08E-01	1.24E-01
SRCCA_MI	2.97E-01	1.06E-01	5.54E-02	4.97E-02	2.94E-01	9.87E-02	5.12E-02	5.79E-02
SRCCA_RH	2.97E-01	3.31E-02	2.71E-02	2.34E-02	2.94E-01	3.42E-02	2.79E-02	2.48E-02
CuRSaR	4.53E-01	1.72E-01	2.17E-01	2.06E-01	3.77E-01	1.59E-01	3.04E-01	1.55E-01

Algorithms	BRCA (Gene-Protein)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	3.48E-01	2.00E-03	3.37E-03	3.50E-03	2.42E-01	3.71E-03	5.81E-03	3.84E-03
PCA_DNA Methylation	9.11E-01	2.94E-03	1.05E-02	9.13E-03	9.43E-01	6.31E-03	2.48E-02	1.04E-02
PCA (Gene-DNA Methylation)	4.47E-01	1.54E-04	1.14E-04	8.92E-05	5.00E-01	3.71E-03	3.71E-03	3.84E-03
CCA	1.21E-01	3.74E-02	4.10E-02	4.79E-02	1.13E-01	3.39E-02	2.32E-02	2.32E-02
RCCA	4.13E-02	5.35E-03	5.94E-03	5.44E-03	3.06E-02	1.16E-02	1.34E-02	8.88E-03
SRCCA_TT	7.75E-01	2.23E-02	2.55E-02	2.40E-02	5.00E-01	3.51E-02	2.37E-02	3.77E-02
SRCCA_WL	1.90E-01	4.06E-02	4.34E-02	4.15E-02	1.37E-01	3.28E-02	6.95E-02	2.32E-02
SRCCA_WR	7.39E-01	4.06E-02	8.86E-02	7.95E-02	5.00E-01	5.54E-02	6.07E-02	5.38E-02
SRCCA_MI	2.14E-01	2.55E-02	4.41E-02	5.10E-02	1.99E-01	1.34E-02	1.40E-02	8.65E-03
SRCCA_RH	3.81E-01	3.75E-03	5.81E-03	5.16E-03	2.00E-01	6.19E-03	1.22E-02	1.09E-02
CuRSaR	8.57E-01	5.57E-02	1.55E-01	1.40E-01	6.57E-01	4.40E-02	1.28E-01	1.47E-01

Results of NNA

Algorithms	BRCA (Protein-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	3.37E-01	3.23E-03	4.17E-03	4.27E-03	4.46E-01	8.88E-03	1.34E-02	8.98E-03
PCA_DNA Methylation	3.94E-04	3.38E-03	6.28E-05	1.04E-04	4.65E-03	8.44E-03	2.49E-03	2.53E-03
PCA (Gene-DNA Methylation)	3.75E-03	3.91E-03	1.71E-04	2.46E-04	5.81E-03	1.08E-02	2.45E-03	2.52E-03
CCA	5.70E-03	2.22E-02	8.55E-03	1.21E-02	1.04E-02	1.74E-02	4.56E-03	5.39E-03
RCCA	1.13E-03	1.89E-03	9.71E-05	1.19E-04	3.71E-03	7.59E-03	2.45E-03	2.50E-03
SRCCA_TT	2.31E-01	1.56E-03	5.00E-03	4.15E-03	8.59E-02	7.88E-03	6.92E-03	5.40E-03
SRCCA_WL	7.89E-02	1.84E-02	5.75E-03	6.62E-03	8.65E-02	1.73E-02	6.23E-03	7.53E-03
SRCCA_WR	1.18E-01	3.31E-02	1.60E-02	1.65E-02	6.90E-02	5.07E-02	1.30E-02	8.88E-03
SRCCA_MI	1.39E-01	1.09E-01	2.71E-02	2.78E-02	8.59E-02	1.44E-01	2.41E-02	4.26E-02
SRCCA_RH	2.73E-01	5.19E-02	1.19E-02	9.57E-03	2.49E-01	9.72E-02	2.06E-02	8.88E-03
CuRSaR	9.75E-01	3.31E-02	3.99E-01	3.38E-01	9.67E-01	3.97E-02	4.32E-01	2.41E-01

Algorithms	OV (Gene-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	7.50E-02	2.38E-02	2.37E-02	2.43E-02	5.71E-02	2.48E-02	3.30E-02	2.34E-02
PCA_DNA Methylation	7.70E-03	1.81E-01	3.80E-02	5.35E-02	1.09E-02	1.57E-01	3.71E-02	4.63E-02
PCA (Gene-DNA Methylation)	6.97E-02	1.47E-02	1.51E-02	1.54E-02	4.63E-02	1.63E-02	1.42E-02	1.09E-02
CCA	4.34E-03	3.04E-02	8.82E-03	1.24E-02	1.42E-02	2.62E-02	1.83E-02	1.83E-02
RCCA	5.76E-02	2.30E-01	4.98E-02	6.50E-02	4.29E-02	2.87E-01	5.49E-02	6.93E-02
SRCCA_TT	3.31E-02	4.48E-01	5.37E-02	8.74E-02	3.30E-02	6.24E-01	8.58E-02	8.64E-02
SRCCA_WL	2.07E-01	1.10E-01	1.05E-01	1.11E-01	1.66E-01	1.02E-01	6.91E-02	8.44E-02
SRCCA_WR	6.49E-02	3.58E-02	9.89E-03	1.18E-02	6.97E-02	3.77E-02	2.33E-02	2.34E-02
SRCCA_MI	9.29E-02	6.02E-02	4.16E-02	4.60E-02	6.93E-02	6.11E-02	5.46E-02	5.49E-02
SRCCA_RH	3.65E-02	2.96E-01	3.55E-02	5.85E-02	2.96E-02	5.67E-01	4.59E-02	4.62E-02
CuRSaR	1.70E-01	8.18E-01	2.64E-01	3.35E-01	1.20E-01	7.69E-01	1.91E-01	1.66E-01

Results of NNA

Algorithms	OV (Gene-Protein)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	1.33E-01	6.51E-03	7.57E-03	5.55E-03	1.11E-01	1.40E-02	8.66E-03	6.26E-03
PCA_DNA Methylation	2.46E-01	1.12E-02	2.30E-02	1.70E-02	2.88E-01	1.21E-02	2.89E-02	1.91E-02
PCA (Gene-DNA Methylation)	1.89E-01	6.06E-03	1.82E-02	1.39E-02	1.87E-01	1.03E-02	2.49E-02	2.53E-02
CCA	3.44E-03	3.12E-04	1.73E-04	1.35E-04	2.52E-03	2.45E-03	2.46E-03	2.52E-03
RCCA	1.80E-02	3.43E-01	3.61E-02	4.14E-02	2.96E-02	4.66E-01	4.05E-02	5.70E-02
SRCCA_TT	4.25E-01	6.67E-02	1.39E-01	1.10E-01	3.39E-01	8.62E-02	1.79E-01	1.01E-01
SRCCA_WL	3.94E-01	4.93E-04	3.92E-02	2.35E-02	3.84E-01	2.39E-03	6.91E-02	5.71E-02
SRCCA_WR	1.37E-01	1.21E-02	1.18E-02	9.40E-03	8.07E-02	1.39E-02	1.74E-02	1.04E-02
SRCCA_MI	3.92E-01	8.16E-03	6.91E-02	4.71E-02	3.37E-01	1.21E-02	6.92E-02	3.32E-02
SRCCA_RH	3.54E-01	8.06E-03	6.78E-02	4.82E-02	2.88E-01	1.33E-02	8.58E-02	4.29E-02
CuRSaR	7.02E-01	2.43E-02	2.72E-01	2.13E-01	7.43E-01	3.06E-02	2.70E-01	2.22E-01

Algorithms	OV (Protein-DNA Methylation)							
	Paired t-test (P-value)				Wilcoxon signed-rank test (P-value)			
	precision	recall	accuracy	f1_score	precision	recall	accuracy	f1_score
PCA_Gene	3.79E-02	2.36E-01	3.76E-02	6.64E-02	4.55E-02	2.20E-01	3.44E-02	6.17E-02
PCA_DNA Methylation	1.89E-03	4.17E-01	5.35E-02	1.05E-01	6.26E-03	3.60E-01	6.96E-02	1.01E-01
PCA (Gene-DNA Methylation)	1.56E-03	4.10E-03	3.78E-04	5.91E-04	6.23E-03	1.03E-02	3.44E-03	3.44E-03
CCA	2.23E-04	5.28E-01	2.55E-02	7.45E-02	3.46E-03	4.53E-01	2.94E-02	6.97E-02
RCCA	2.32E-03	4.78E-01	5.37E-02	1.16E-01	6.26E-03	4.19E-01	4.10E-02	6.97E-02
SRCCA_TT	4.00E-02	2.90E-01	1.20E-01	1.53E-01	3.32E-02	3.12E-01	1.54E-01	2.22E-01
SRCCA_WL	7.96E-02	4.43E-01	1.72E-01	2.75E-01	6.93E-02	4.39E-01	1.66E-01	2.54E-01
SRCCA_WR	4.47E-02	5.71E-01	2.32E-01	3.49E-01	5.49E-02	3.99E-01	2.96E-01	3.61E-01
SRCCA_MI	9.75E-03	7.08E-01	1.33E-01	2.50E-01	1.42E-02	6.37E-01	1.00E-01	2.54E-01
SRCCA_RH	5.25E-03	2.38E-01	6.29E-02	1.11E-01	7.58E-03	2.42E-01	6.91E-02	1.21E-01
CuRSaR	1.21E-01	4.75E-01	2.35E-01	3.29E-01	1.30E-01	3.41E-01	2.20E-01	1.66E-01