**Table 15**. Parameter settings

|  |  |  |
| --- | --- | --- |
| Optimizers | Parameters | Value |
| BGSA |  | 20 |
|  |  |
| BPSO | Min inertia weight | 0.4 |
| Min inertia weight | 0.9 |
|  | 0.2 |
| BBA | Frequency minimum | 0 |
| Frequency maximum | 2 |
| Loudness , Pulse rate | 0.5 |

**Table 16**. Comparison of BSSMA with other GS optimizers in terms of the average number of the selected genes

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | BSMA | bMFO | bGWO | BGSA | BPSO | bALO | BBA | BSSA | BCSSA |
| **Colon** | std | **18.6971** | 1.7280 | 0.0800 | 1.0284 | 3.1119 | 2.5131 | 2.0399 | 1.6543 | 16.0228 | 2.8519 |
| avg | **9.7468** | 557.389 | 490.5909 | 771.0912 | 1597.348 | 5306.767 | 5425.851 | 5380.783 | 4544.048 | 4237.062 |
| **Brain\_Tumor2** | std | **30.5335** | 32.8339 | 2.2357 | 5.4100 | 6.5012 | 1.3080 | 4.3883 | 8.9284 | 35.8369 | 5.8424 |
| avg | **45.5145** | 596.8526 | 494.8818 | 937.699 | 2230.157 | 5958.206 | 6075.36 | 5934.06 | 5049.068 | 4717.464 |
| **Tumors\_14** | std | 652.9486 | **226.5187** | 550.0394 | 31.1929 | 102.6942 | 32.0528 | 54.5956 | 20.4403 | 421.3056 | 22.8581 |
| avg | 1058.9364 | **699.9769** | 2285.862 | 2112.173 | 7132.804 | 7356.197 | 7269.983 | 6124.133 | 6328.426 | 5364.214 |
| **Leukemia2** | std | 0.3621 | **2.8851** | 2.2526 | 4.8227 | 2.9777 | 1.4747 | 3.9347 | 10.6488 | 78.0710 | 8.3205 |
| avg | 867.637 | **692.7334** | 1203.093 | 1905.684 | 6723.298 | 6869.336 | 6842.604 | 5753.221 | 5442.631 | 5026.698 |
| **SRBCT** | std | 0.4184 | **0.7901** | 0.6509 | 1.1760 | 1.8208 | 3.2014 | 1.1369 | 2.4780 | 20.6810 | 0.9067 |
| avg | 823.487 | **662.5315** | 1152.605 | 1598.439 | 5530.752 | 5641.873 | 5622.097 | 4725.758 | 4497.568 | 4127.895 |
| **Tumors\_11** | std | 41.0554 | **82.1695** | 155.3916 | 30.6875 | 40.9245 | 27.4678 | 21.2096 | 20.9159 | 270.3483 | 23.8720 |
| avg | 651.8107 | **650.1224** | 1047.25 | 1802.561 | 6404.623 | 6600.226 | 6562.808 | 5545.595 | 5378.316 | 4838.545 |
| **Brain\_Tumor1** | std | 3.8504 | **20.3921** | 2.6162 | 4.6864 | 9.1538 | 7.1780 | 5.5327 | 8.1517 | 56.2075 | 5.9156 |
| avg | 577.6526 | **549.0633** | 763.4597 | 1538.971 | 5489.7 | 5652.609 | 5616.599 | 4756.354 | 4300.654 | 4158.099 |
| **Prostate\_Tumor** | std | 1.5399 | **39.9257** | 2.8517 | 11.6574 | 9.8269 | 4.6263 | 5.3587 | 14.9613 | 93.7022 | 2.6206 |
| avg | 556.5519 | **508.2601** | 743.9253 | 1679.022 | 6073.68 | 6252.562 | 6208.533 | 5274.165 | 4758.56 | 4587.182 |
| **Tumors\_9** | std | 17.1990 | **16.6737** | 35.9762 | 4.2458 | 9.1376 | 5.9844 | 5.2551 | 6.0519 | 27.0442 | 3.5315 |
| avg | 620.7084 | **582.8409** | 876.1708 | 1594.846 | 5669.508 | 5817.75 | 5777.13 | 4907.087 | 4617.2 | 4273.203 |
| ARV | | 1.7 | **1.5444** | 2.8444 | 3.9111 | 7.3444 | 9.6333 | 9.2444 | 7.2111 | 6.3444 | 5.2222 |
| Rank | | 2 | **1** | 3 | 4 | 8 | 10 | 9 | 7 | 6 | 5 |

**Table 17**. Comparison of BSSMA with other GS optimizers in terms of average error rate

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | BSMA | bMFO | bGWO | BGSA | BPSO | bALO | BBA | BSSA | BCSSA |
| **Colon** | std | **0.000E+00** | 3.066E-03 | 0.000E+00 | 2.670E-02 | 4.851E-02 | 3.212E-02 | 4.244E-02 | 6.726E-02 | 3.416E-02 | 4.244E-02 |
| avg | **0.00000** | 0.08068 | 0.11258 | 0.16716 | 0.13441 | 0.16489 | 0.16894 | 0.14915 | 0.28756 | 0.21522 |
| **Brain\_Tumor2** | std | **1.275E-03** | 2.824E-03 | 0.000E+00 | 6.674E-03 | 1.942E-02 | 1.711E-02 | 1.666E-02 | 1.852E-02 | 1.078E-02 | 1.344E-02 |
| avg | **0.00040** | 0.08044 | 0.11258 | 0.16083 | 0.14050 | 0.15840 | 0.15700 | 0.13990 | 0.28026 | 0.22131 |
| **Tumors\_14** | std | 3.230E-02 | 6.083E-02 | 7.208E-02 | **6.811E-02** | 5.244E-02 | 5.572E-02 | 4.472E-02 | 4.387E-02 | 6.059E-02 | 1.103E-01 |
| avg | 0.20572 | 0.29207 | 0.23134 | **0.20367** | 0.32150 | 0.32250 | 0.29980 | 0.39359 | 0.35793 | 0.31294 |
| **Leukemia2** | std | **2.926E-17** | 0.000E+00 | 0.000E+00 | 2.926E-17 | 2.926E-17 | 2.926E-17 | 2.926E-17 | 3.234E-02 | 1.882E-02 | 0.000E+00 |
| avg | **0.14048** | 0.19268 | 0.28034 | 0.17033 | 0.23976 | 0.21316 | 0.17070 | 0.36112 | 0.31552 | 0.35340 |
| **SRBCT** | std | **2.926E-17** | 0.000E+00 | 5.851E-17 | 2.926E-17 | 0.000E+00 | 4.877E-03 | 2.926E-17 | 1.896E-02 | 5.851E-17 | 0.000E+00 |
| avg | **0.13374** | 0.18394 | 0.26723 | 0.16196 | 0.22865 | 0.20471 | 0.16309 | 0.34040 | 0.29508 | 0.33679 |
| **Tumors\_11** | std | **5.349E-03** | 1.817E-02 | 1.340E-02 | 1.648E-02 | 3.652E-02 | 5.430E-02 | 3.427E-02 | 4.097E-02 | 3.812E-02 | 2.836E-02 |
| avg | **0.08167** | 0.12988 | 0.17023 | 0.10724 | 0.17254 | 0.18083 | 0.11432 | 0.30498 | 0.22894 | 0.24335 |
| **Brain\_Tumor1** | std | **1.219E-02** | 2.026E-02 | 1.642E-02 | 3.929E-02 | 3.671E-02 | 2.282E-02 | 3.923E-02 | 1.337E-02 | 2.330E-02 | 3.685E-02 |
| avg | **0.08533** | 0.12749 | 0.16690 | 0.13668 | 0.21544 | 0.19454 | 0.14162 | 0.34737 | 0.26394 | 0.25719 |
| **Prostate\_Tumor** | std | **1.463E-17** | 0.000E+00 | 0.000E+00 | 9.183E-03 | 3.799E-02 | 6.982E-02 | 1.463E-17 | 6.175E-02 | 6.160E-02 | 0.000E+00 |
| avg | **0.07955** | 0.11258 | 0.15872 | 0.10730 | 0.16229 | 0.18192 | 0.09753 | 0.33821 | 0.22431 | 0.21492 |
| **Tumors\_9** | std | **1.093E-02** | 9.925E-03 | 1.233E-02 | 1.149E-02 | 1.063E-02 | 2.002E-02 | 1.195E-02 | 1.681E-02 | 1.658E-02 | 1.440E-02 |
| avg | **0.09416** | 0.15190 | 0.17131 | 0.12617 | 0.17618 | 0.19177 | 0.14331 | 0.35903 | 0.24393 | 0.26983 |
| ARV | | **1.1667** | 3.5889 | 5.2889 | 3.5333 | 5.9778 | 5.9889 | 3.8889 | 8.6556 | 8.4556 | 8.4556 |
| Rank | | **1** | 3 | 5 | 2 | 6 | 7 | 4 | 10 | 8 | 8 |

**Table 18**. Comparison of BSSMA with other GS optimizers in terms of average fitness

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | BSMA | bMFO | bGWO | BGSA | BPSO | bALO | BBA | BSSA | BCSSA |
| **Colon** | std | **4.674E-04** | 2.939E-03 | 2.001E-06 | 2.536E-02 | 4.605E-02 | 3.053E-02 | 4.032E-02 | 3.961E-02 | 3.254E-02 | 4.029E-02 |
| avg | **0.00024** | 0.07859 | 0.10866 | 0.16203 | 0.13677 | 0.17992 | 0.18416 | 0.13702 | 0.25600 | 0.22283 |
| **Brain\_Tumor2** | std | **1.308E-03** | 2.695E-03 | 1.078E-05 | 6.347E-03 | 1.843E-02 | 1.625E-02 | 1.583E-02 | 1.631E-02 | 1.022E-02 | 1.277E-02 |
| avg | **0.00088** | 0.07852 | 0.10868 | 0.15635 | 0.14312 | 0.17402 | 0.17314 | 0.12779 | 0.24955 | 0.22875 |
| **Tumors\_14** | std | **3.156E-02** | 5.734E-02 | 6.786E-02 | 6.465E-02 | 4.961E-02 | 5.294E-02 | 4.236E-02 | 4.861E-02 | 5.639E-02 | 1.047E-01 |
| avg | **0.19896** | 0.27980 | 0.22739 | 0.20052 | 0.32919 | 0.33088 | 0.30903 | 0.34061 | 0.36112 | 0.31516 |
| **Leukemia2** | std | **1.613E-06** | 1.285E-05 | 1.003E-05 | 2.148E-05 | 1.326E-05 | 6.569E-06 | 1.753E-05 | 3.011E-02 | 1.800E-02 | 3.706E-05 |
| avg | **0.13635** | 0.18536 | 0.27034 | 0.16848 | 0.25149 | 0.22678 | 0.18634 | 0.32213 | 0.31890 | 0.35350 |
| **SRBCT** | std | **9.064E-06** | 1.712E-05 | 1.410E-05 | 2.548E-05 | 3.945E-05 | 4.696E-03 | 2.463E-05 | 1.168E-03 | 4.480E-04 | 1.964E-05 |
| avg | **0.12982** | 0.17701 | 0.25775 | 0.16006 | 0.24000 | 0.21832 | 0.17858 | 0.29452 | 0.29858 | 0.33746 |
| **Tumors\_11** | std | **5.181E-03** | 1.726E-02 | 1.291E-02 | 1.565E-02 | 3.477E-02 | 5.162E-02 | 3.260E-02 | 3.291E-02 | 3.596E-02 | 2.695E-02 |
| avg | **0.07986** | 0.12572 | 0.16544 | 0.10846 | 0.18739 | 0.19602 | 0.13269 | 0.25455 | 0.23723 | 0.24894 |
| **Brain\_Tumor1** | std | **1.158E-02** | 1.926E-02 | 1.559E-02 | 3.730E-02 | 3.484E-02 | 2.162E-02 | 3.726E-02 | 1.139E-02 | 2.218E-02 | 3.500E-02 |
| avg | **0.08309** | 0.12324 | 0.16121 | 0.13619 | 0.22781 | 0.20886 | 0.15841 | 0.29249 | 0.26875 | 0.26207 |
| **Prostate\_Tumor** | std | **7.327E-06** | 1.900E-04 | 1.357E-05 | 8.723E-03 | 3.611E-02 | 6.632E-02 | 2.550E-05 | 2.506E-02 | 5.843E-02 | 1.247E-05 |
| avg | **0.07747** | 0.10874 | 0.15330 | 0.10832 | 0.17753 | 0.19693 | 0.11657 | 0.24637 | 0.23125 | 0.22187 |
| **Tumors\_9** | std | **1.033E-02** | 9.455E-03 | 1.164E-02 | 1.088E-02 | 1.010E-02 | 1.899E-02 | 1.134E-02 | 1.455E-02 | 1.566E-02 | 1.367E-02 |
| avg | **0.09191** | 0.14682 | 0.16642 | 0.12641 | 0.19082 | 0.20633 | 0.16009 | 0.29452 | 0.25113 | 0.27410 |
| ARV | | **1.1111** | 3.0889 | 4.8556 | 3.0889 | 6.1444 | 6.4222 | 4.8889 | 7.9778 | 8.7333 | 8.6889 |
| Rank | | **1** | 2 | 4 | 3 | 6 | 7 | 5 | 8 | 10 | 9 |

**Table 19**. Comparison of BSSMA with other GS optimizers in terms of average computational time

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | BSMA | bMFO | bGWO | BGSA | BPSO | bALO | BBA | BSSA | BCSSA |
| **Colon** | std | **0.2420** | 0.0263 | 0.0175 | 0.0367 | 0.0312 | 0.0177 | 0.0131 | 0.0331 | 0.0617 | 0.0250 |
| avg | **10.1259** | 95.7496 | 42.5338 | 38.7992 | 110.2704 | 90.3138 | 79.0814 | 81.8076 | 73.9614 | 76.1687 |
| **Brain\_Tumor2** | std | **0.3126** | 0.1126 | 0.0364 | 0.1201 | 0.0639 | 0.0255 | 0.0391 | 0.0549 | 0.0301 | 0.0209 |
| avg | **29.8885** | 99.1031 | 43.2925 | 48.9751 | 113.3905 | 91.8475 | 80.5264 | 83.5294 | 75.4451 | 77.4102 |
| **Tumors\_14** | std | 16.4265 | **1.2738** | 6.0355 | 1.0548 | 1.7824 | 1.1489 | 3.0445 | 2.8057 | 0.9866 | 1.1525 |
| avg | 164.2648 | **67.1009** | 74.5598 | 168.9557 | 162.0657 | 146.7049 | 145.0222 | 140.8298 | 142.8944 | 103.034 |
| **Leukemia2** | std | 0.1007 | 0.0751 | **0.0650** | 0.1812 | 0.0712 | 0.0545 | 0.1007 | 0.0493 | 0.0808 | 0.0840 |
| avg | 138.3282 | 58.701 | **53.1983** | 148.8339 | 132.9177 | 117.2682 | 119.5258 | 110.113 | 112.9523 | 80.5242 |
| **SRBCT** | std | 0.0373 | 0.0340 | **0.0259** | 0.0276 | 0.0254 | 0.0212 | 0.0181 | 0.0173 | 0.0142 | 0.0225 |
| avg | 126.5336 | 51.5193 | **49.6869** | 127.6778 | 121.5234 | 108.8397 | 111.0251 | 102.3774 | 105.1409 | 74.9948 |
| **Tumors\_11** | std | 1.0989 | 0.5541 | **0.8405** | 0.3843 | 0.3028 | 0.2192 | 0.5826 | 0.2618 | 0.5612 | 0.2583 |
| avg | 111.5587 | 52.1004 | **42.2527** | 135.188 | 106.393 | 92.5343 | 95.0452 | 86.1841 | 87.9906 | 63.6687 |
| **Brain\_Tumor1** | std | 0.0877 | 0.0649 | **0.0650** | 0.1199 | 0.0707 | 0.0495 | 0.0491 | 0.0408 | 0.1501 | 0.0422 |
| avg | 98.9109 | 44.9758 | **36.72** | 116.6679 | 93.2634 | 81.3578 | 84.0248 | 75.8471 | 78.0679 | 56.3569 |
| **Prostate\_Tumor** | std | 0.2892 | 0.5070 | **0.1933** | 0.3130 | 0.0799 | 0.0537 | 0.1582 | 0.0890 | 0.3559 | 0.0895 |
| avg | 102.2164 | 48.0188 | **37.2137** | 126.1273 | 96.1694 | 82.78 | 85.625 | 77.201 | 79.4563 | 57.1478 |
| **Tumors\_9** | std | 0.0559 | 0.0391 | **0.0337** | 0.0756 | 0.0336 | 0.0326 | 0.0290 | 0.0460 | 0.0459 | 0.0259 |
| avg | 99.1614 | 45.3749 | **36.653** | 118.6053 | 92.9993 | 80.4889 | 83.2676 | 75.1215 | 77.6358 | 55.4992 |
| ARV | | 7.2 | 3.4556 | **1.4333** | 8.3 | 8.5 | 6.5111 | 6.6667 | 4.7111 | 4.7778 | 3.4444 |
| Rank | | 8 | 3 | **1** | 9 | 10 | 6 | 7 | 4 | 5 | 2 |



Fig. 14 Boxplots of comparative results in terms of number of the selected genes on all datasets



Fig. 15 Boxplots of comparative results in terms of the classification error rate on all datasets



Fig. 16 Boxplots of comparative results in terms of fitness on all datasets

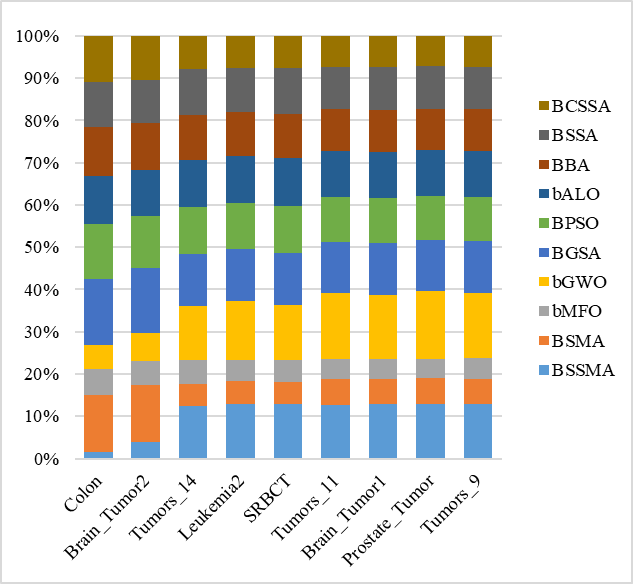


Fig. 17 Proportion of computational time expended by each GS optimizer

Fig. 18 Bonferroni-Dunn test for comparing BSSMA with other competitors in terms of the average number of selected genes

Fig. 19 Bonferroni-Dunn test for comparing BSSMA with other competitors in terms of average error rate

Fig. 20 Bonferroni-Dunn test for comparing BSSMA with other competitors in terms of average fitness

Fig. 21 Bonferroni-Dunn test for comparing BSSMA with other competitors in terms of computational time